

SCWDS BRIEFS

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

Phone (706) 542-1741

FAX (706) 542-5865

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Working Together: The 40th Anniversary of the National Hemorrhagic Disease Survey

In the last issue of the SCWDS BRIEFS, hemorrhagic disease (HD) report data from Indiana, Ohio, Kentucky, and West Virginia were highlighted to demonstrate how these long-term data can help detect and map the northern expansion of HD over time. In addition to providing a means to detect temporal changes in HD patterns, this long-term data set provides a window to better understand spatial patterns and risks within areas where HD has historically occurred. In part two of this four-part series, we will explore HD patterns in another area – the Great Plains, where HD is commonly reported and large-scale outbreaks occasionally occur. These states were included in the survey in 1982, and thanks to their continued support, this data set now spans 38 years.

Part 2: Hemorrhagic Disease in the eastern Great Plains states

The distributions of epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV) include most of the eastern Great Plains states from Texas to North Dakota. However, as in other areas in the United States, reports of HD are highly variable across this region. This variation includes areas of recurring epidemic HD, as well as areas where disease seldom occurs. To visualize the distribution of reported HD in this region, we mapped the number of years HD mortality was reported in individual counties in Oklahoma, Kansas, Nebraska, South Dakota, and North Dakota from 1982 to 2019. To minimize effects of under- or over-reporting at individual county levels, county data were averaged with total annual reports from all adjoining counties (Figure 1). As shown, the prevailing patterns are very consistent across state lines, and HD reporting varies greatly in a north-to-south direction as is observed in most of the United States. On the southern edge, the

limited HD reports probably relate to enzootic stability; on the northern edge, the low frequency of reports is likely driven by limited EHDV and BTV transmission due to either the absence of vectors or environmental conditions that reduce vector numbers or their ability to transmit these viruses. Within these states, east-west gradients in HD reporting also are evident. The factors that drive this within-state variation are not well understood and possibly relate to habitat gradients and complex vector/host/environmental interactions that are unique to each individual state.

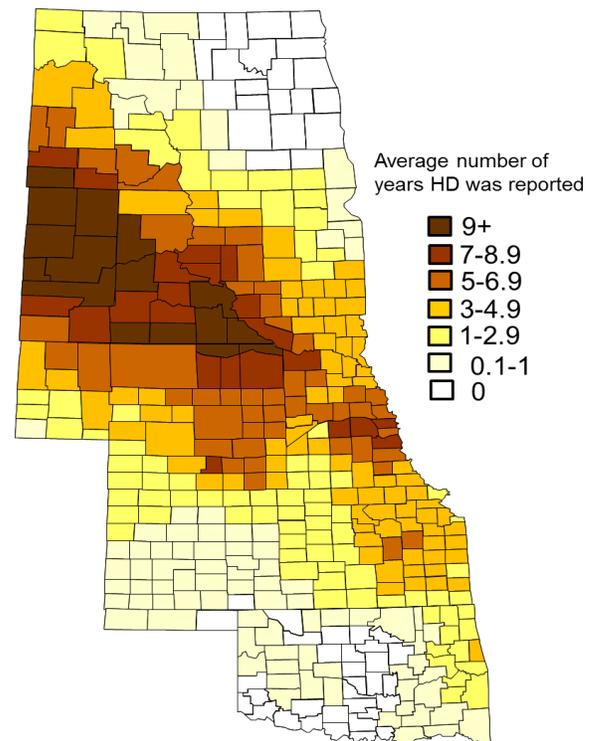


Figure 1. Reported hemorrhagic disease 1982-2020.

The few reports from Oklahoma primarily indicate HD in the northeastern corner of the state. The number of years HD was reported in any individual Oklahoma county over the 38-year period was low (0 to 5 years per county), and over this period HD was reported in

Continued...

only 15 of Oklahoma’s 77 counties (19%). In years when HD was reported, few counties appear to be affected. This pattern is consistent with that of Texas, where HD is also rarely reported despite a high level of infection. In a previous study of HD in Texas done in collaboration with Texas Parks and Wildlife Department, we reported a very high antibody prevalence to EHDV and BTV, as well as extensive serotype diversity. This pattern is consistent with enzootic stability, where infection rates and resulting antibody prevalence are very high but disease incidence is low.

The frequency of HD reports increases in Kansas, but a marked east-west variation is evident, with most reports being associated with the eastern part of the state. For individual counties over the 38-year period, HD was reported from 0 to 8 years per county in 75 of the state’s 105 counties (71%). From 1982 to 2010, outbreaks in Kansas were restricted to <15% of the state’s counties. In 2012, however, a large-scale outbreak included reports from >40% of counties. Previous work in Kansas suggests that two patterns exist over the state. In western Kansas, as in Texas and Oklahoma, conditions consistent with enzootic stability are present. In the eastern part of the state, where HD is almost annually reported, historic serologic data suggest that a moderate level of herd immunity exists.

Nebraska and South Dakota are at the center of the higher-risk HD area, but as with Kansas, a marked east-west variation in reported HD is evident. For individual Nebraska counties, HD has been reported 0 to 12 of the total 38 years. In South Dakota, county reports range from 0 to 16 of the total 38 years. In both states, HD is widely distributed with reports from 89 of 93 (96%) and 65 of 66 (98%) counties in Nebraska and South Dakota, respectively. There also have been recent large-scale outbreaks reported in both states, including 2012 in Nebraska and 2012 and 2016 in South Dakota. In both states, east-west variation in frequency is apparent with most reports associated with the western portion of these states.

While large historic outbreaks of HD have been reported in North Dakota, disease appears to be limited geographically to the southwest portion of the state. Statewide annual reports of HD for individual counties range from 0 to 10 years and the disease has been reported from 19 of 53 counties (36%). North Dakota represents the reported northern range of *Culicoides sonorensis*; therefore, the limited distribution of HD is likely driven by the presence or

absence of this or other potential *Culicoides* vectors. Whether HD will expand its range in a northern or even eastern direction within the state is currently unknown, but data suggest that the distribution has been relatively stable during the last 38 years.

To support the HD survey, virus testing is used to confirm HD as the cause of reported mortality. Diagnostic data can also provide a unique window to HD patterns that is not shown by HD reports alone. This additional perspective is particularly evident when looking at virus isolation data from Kansas, shown in Figure 2.

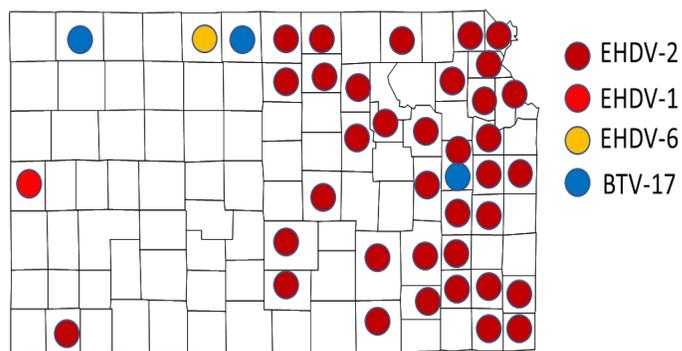


Figure 2.

As expected, most viruses were isolated from deer distributed in the eastern part of the state, where HD is most often reported. Unexpectedly, there appears to be some interesting variation in EHDV and BTV serotype diversity. EHDV-2 predominates in eastern Kansas, as it does in most of the eastern United States. In western Kansas, we have only isolated EHDV or BTV on five occasions, but with high serotype diversity, including EHDV-1, EHDV-2, EHDV-6, and BTV-17. This potential variation in serotype diversity needs further confirmation but may be related to broader ecological conditions affecting *Culicoides* and host species diversity.

Improving our understanding of the epidemiology of HD in the Great Plain states deserves our attention, and what better way to achieve this than assigning this task to a talented graduate student. Ms. Emma Kring, currently a biologist with the Nebraska Game and Parks Commission, will be moving to Athens this fall to begin her Master’s research project with SCWDS and the UGA Deer Lab (Warnell School of Forestry and Natural Resources) to better understand these patterns of HD that we have observed in the Great Plains. Look to hear from Emma in the coming years on her findings! (Prepared by David Stallknecht, Natalie Stilwell, and Mark Ruder).

COVID-19 Pandemic

Impact on SCWDS Activities

Amid one of the most severe global public health crises humanity has ever experienced, few individuals or organizations on the planet have escaped direct or indirect impacts of the COVID-19 pandemic. SCWDS is no exception. Since mid-March 2020, the University of Georgia adopted numerous important disease mitigation strategies to protect public health that impact SCWDS research, service, and instructional activities. Non-essential travel has been temporarily suspended, and field and laboratory research activities have been greatly decreased. SCWDS staff and faculty, alongside all other UGA employees, are primarily working from home and all UGA students will continue with distance learning through the summer semester. The SCWDS Diagnostic Services Section continues to operate under some new practices to limit human interaction. Without our full complement of personnel on hand, minor reporting delays can be expected but we are willing and able to continue assisting member agencies with wildlife mortality investigations. Similar to most organizations, SCWDS students, staff, and faculty have adapted to this new temporary normal, so please contact us if you need assistance.

The Role of Wildlife in the Coronavirus Pandemic

In recent months, the rapid spread of a novel coronavirus classified as severe acute respiratory syndrome (SARS)-CoV-2 has resulted in a pandemic. Based on current knowledge, this virus originated from a wildlife source, although the wildlife species involved (bat, pangolin, or other) remain unclear. Unfortunately, this is not the first time an animal coronavirus has caused severe human disease. We've seen this twice in the past two decades with SARS- and Middle East respiratory syndrome (MERS)-coronaviruses, which also caused fatal respiratory disease in affected humans. With the 2003 SARS-CoV outbreak, the virus first passed from a primary reservoir (bat) to an intermediate host (civet cat) before affecting humans. Likewise, the 2012 MERS-CoV was acquired through human contact with camels. In both of those cases, the coronaviruses caused no symptoms in their natural hosts.

Coronavirus infections are common in mammals and birds, including dogs, cats, cattle, poultry, and some wildlife species. While most coronaviruses are

species-specific and cause mild to no disease, SARS-CoV-2 has been an exception. In late 2019, an early cluster of human COVID-19 cases was linked to a wildlife market in Wuhan, China, where two-thirds of the affected individuals had either worked or visited. Like many markets throughout China, the main area of the Wuhan market offered seafood; however, the market's exotic animal section offered a staggering variety of wildlife. Such markets are poorly regulated, with animals housed and butchered in crowded and unsanitary conditions. This unnatural human-animal interface enables and perhaps facilitates levels of cross-species pathogen transmission and virus adaptation that would not occur in nature.

Whether the wildlife market in question was the initial site of animal-to-human transmission of SARS-CoV-2 remains unknown, as evidence suggests the virus rapidly spread and was already circulating throughout Asia once the outbreak associated with this market hit the news. The virus was detected in 5% of samples taken from the market's animals in weeks following the outbreak which, in combination with epidemiologic data from human cases, suggests a potential link between the site and viral spread. The market was quickly closed, and China banned the sale and consumption of wild animals until the coronavirus pandemic resolves. Many are pushing to make the ban permanent, although certain loopholes still allow the trade of wildlife that are farmed or intended for traditional medicine or research. Until stronger protection practices are enforced to prevent poaching and illegal handling and trafficking, scenarios involving zoonotic transmission of novel pathogens will continue.

As the world begins to deal with the economic, psychological, and sociological consequences of the global SARS-CoV-2 outbreak, we must explore ways to minimize the opportunity for cross-species transmission of pathogens in the future. Emerging pathogens are an ongoing threat to global public health, with roughly 70% of diseases originating from animal hosts (for example, HIV/AIDS, Ebola, Nipah virus, and influenza). Privatization and overexploitation of wildlife, urbanization, and subsequent wildlife habitat destruction are considered important drivers of novel human-animal interfaces. Until we confront these broader issues and prioritize the health of wild animals and their ecosystems, devastating public health and economic events like the current pandemic are likely to recur.

SARS-CoV-2 in North American Wildlife?

Over the past few months, many questions have surfaced regarding the potential risk of transmission of SARS-CoV-2 from humans to North American wildlife species (reverse zoonosis). Although experimental infections with SARS-CoV-2 have been reported for fruit bats and domestic ferrets and naturally acquired infections have occurred in tigers and lions in zoos, farmed mink, and domestic cats and dogs, there is no indication that this virus can be transmitted or maintained in a North American wildlife population. That said, transmission from humans to wildlife during routine handling or contact cannot be discounted, and this represents our first line of defense in preventing a wildlife reservoir scenario. There are several options that can be considered at this time to prevent such transmission and these are consistent with current recommendations to prevent infections between humans. These include avoiding contact with wildlife species when ill, prioritizing the need for such contact and eliminating or delaying non-essential management or research associated with species of concern, and wearing basic personal protective equipment (e.g., gloves, face masks) when handling or in close contact with wildlife. At present reverse zoonosis concerns are centered on bats, mustelids, canids, and felids. Recommendations and guidance associated with these concerns in bats have been addressed by the Association of Fish and Wildlife Agencies (AFWA) Bat Working Group and Fish and Wildlife Health Committee (*Voluntary Interim Guidance for Bat-related Activities in Response to COVID-19*). The Centers for Disease Control and Prevention also has issued guidance on testing of animals (including wildlife) for SARS-CoV-2 (<https://www.cdc.gov/coronavirus/2019-ncov/php/animal-testing.html>). Additional guidance may follow as we learn more about this virus in nature. (Prepared by Natalie Stilwell, Mark Ruder, and Dave Stallknecht).

Avian Influenza A Viruses – A Southeastern Shorebird Connection

Ruddy turnstones (RUTU; *Arenaria interpres*) are long-distance, migrating shorebirds and a recognized natural host for avian influenza A viruses (AIV). During their spring migration from overwintering sites in the southeastern US and South America to breeding sites in the Arctic, these shorebirds rely on stopover locations that have an abundance of high-quality food items. Horseshoe crab eggs are an important part of this diet and provide much of the fuel

necessary for RUTU to continue their northward journey; this migration is intricately timed with the seasonal spawning of horseshoe crabs every spring. One such location is Delaware Bay, a prime spring migratory stopover site for thousands of RUTU and other shorebirds every May. Collaborative research at Delaware Bay involving St. Jude Children's Research Hospital, the New Jersey Department of Environmental Protection (NJDEP), Wildlife Restoration Partnerships (WRP), and SCWDS has revealed long-term trends in AIV prevalence and subtype diversity. However, despite being considered a "hot-spot" for AIV, the seasonal sources of viruses into this system are not well understood; historically, surveillance for AIV in shorebirds has been lacking in other areas used during and prior to migration.

To fill this knowledge gap and with support from National Institutes of Health, SCWDS has increased AIV surveillance efforts in shorebirds to include areas outside of the Delaware Bay hot spot and during times of year outside of the annual spring migration. Through the collection of shorebird fecal samples during the winter and pre-migration periods (December-April from 2010 to the present) we have consistently demonstrated AIV infections in RUTU from Florida, Georgia, and South Carolina and thus far have isolated 40 shorebird-origin AIV. Additionally, >85 AIV have been isolated from RUTU utilizing these southeastern coastlines during the month of May, which represents the peak period of spring migration; this work has been done in collaboration with the Georgia Department of Natural Resources (DNR) and South Carolina DNR. Full genome analyses and subtype comparisons have demonstrated the flow of AIV and AIV gene segments from the Southeast to Delaware Bay, where these viruses and genes become assimilated into the larger and more genetically diverse pool of AIV. However, not all AIV or AIV genes detected in the Southeast are detected at Delaware Bay.

Given that subtypic and genetic linkages continue to be identified, our interest in understanding the connectivity between shorebirds utilizing migratory stopover habitats of the southeastern US and Delaware Bay has been further informed by RUTU that were outfitted with geolocators on wintering areas in Brazil. This work was done in collaboration with WRP and the NJDEP. Data from these geolocators indicated that not all RUTU use Delaware Bay as a stopover site and that habitat selection can change among years. To better

understand shorter-term movement of RUTU and AIV and to determine what proportion of RUTU are using both southeastern sites and Delaware Bay as stopover areas, in May 2018 and 2019, with help of SCDNR and USFWS, we outfitted more than 90 RUTUs with nanotags. Data recovery from these small battery-operated tracking devices relies on an extensive network of Motus towers. In both years, these tracking data indicated that >70% of RUTU bypassed Delaware Bay and instead headed north/northwest towards breeding grounds after stopping at southeastern locations.

These telemetry data, taken together with the known abundance of available springtime food resources in the Southeast (horseshoe crab eggs, Coquina clams), support the important role that parts of the GA and SC coastline play in the survival and migration of many shorebirds. Better understanding the connectivity that exists between migratory, ecologically vulnerable RUTU populations and the pathogens they can transmit, like AIV, will continue to be important in the long-term maintenance of healthy and robust shorebird populations across the Americas, as well as their fragile habitats. (Prepared by Deb Carter and Becky Poulson).

SARS-CoV-2 and Ticks?

No, there is no evidence that SARS-Coronavirus (CoV)-2 is transmitted by arthropod vectors, despite the rumors. However, there is concern that an unintended consequence of the coronavirus infectious disease (COVID)-19 pandemic is a decreased focus on non-COVID-19 related health issues, including vector-borne diseases. Currently, due to the increasing numbers of COVID-19 cases, many local governments have issued stay-at-home orders to mitigate the spread of the virus. These orders generally do not mandate that individuals stay confined within their household; rather, they urge the practice of social distancing and discourage large gatherings and nonessential travel to public places such as restaurants. Most of these orders allow individuals to continue physical activities outdoors so long as they maintain social distancing.

With a greatly increased number of Americans no longer working from their offices or workplaces, or attending educational institutions during the day, many individuals are potentially spending more time outdoors than they normally would. Unfortunately, ticks do not social distance, and if you are spending your time in tick habitat, there may be increased

opportunities to come into contact with ticks. This is especially true for individuals who may not normally spend time outdoors but are now doing so because of cabin fever; these people may not be as 'tick aware' and may not take appropriate precautions.

The unfortunate timing of these stay-at-home orders coincides with the seasonal emergence of many tick species relevant to human and animal health. Already, there have been multiple reports from various news outlets throughout the U.S. indicating an increase in the number of people who are reporting finding ticks. To understand the potential effects of changes in social behavior resulting from the COVID-19 stay-at-home order on tick-borne disease dynamics over the coming year, researchers at the SCWDS, Hollins University, Duke University, Clemson University, East Stroudsburg University and the University of Rhode Island have come together to develop a survey.

This short, online and anonymous survey (~10-15 minutes or less) will help us understand how behavior is changing in response to COVID-19, how "tick aware" people are, and how this translates to tick exposure. We invite everyone, not just those who typically spend time outdoors, to participate in this study by completing the survey at <https://ugaticks.weebly.com> or by scanning the QR code below. Please share this within your personal and professional circles and on social media. And, don't forget about the ticks! (Prepared by Alec Thompson and Michael Yabsley).



Rabbit Hemorrhagic Disease Virus 2 Reported in Wild Lagomorphs

In the January 2019 issue of the SCWDS BRIEFS, we highlighted an outbreak of a reportable foreign animal pathogen, rabbit hemorrhagic disease (RHD) virus 2 (RHDV2), in domestic rabbits (*Oryctolagus cuniculus*) in Ohio. Disconcertingly in the spring of 2020, multiple fatal RHDV2 outbreaks were

confirmed in wild lagomorphs for the first time in North America. In New Mexico, outbreaks in black-tailed jackrabbits (*Lepus californicus*, Eddy County) and desert cottontails (*Sylvilagus audubonii*, Dona Ana County) were reported by the New Mexico Department of Game and Fish. In Arizona, RHDV2 was then confirmed by the Arizona Game and Fish Department in black-tailed jackrabbits (Cochise, Greenlee, and Graham counties) and desert cottontails (Cochise County). In Costilla County, Colorado, an outbreak in cottontails (*Sylvilagus* sp.) was reported by Colorado Parks and Wildlife. Finally, in Texas, RHDV2 was confirmed in black-tailed jackrabbits (Lubbock County) and desert cottontails (Hudspeth County) by Texas Parks and Wildlife Department. The extent of these current outbreaks remains unclear, and there have been concomitant outbreaks in domestic rabbits in New Mexico, Arizona, and Texas. Confirmatory testing for these cases was performed at the USDA-APHIS National Veterinary Services Laboratories Foreign Animal Disease Diagnostic Laboratory with either ELISA and/or RT-PCR.

RHDV2 is a highly contagious virus (family *Caliciviridae*, genus *Lagovirus*) that infects multiple lagomorph species and emerged in France in 2010 in European rabbits (*Oryctolagus cuniculus*). Since then, RHDV2 has been documented throughout much of Europe, multiple African countries, Australia, New Zealand, Israel, Canada, and the United States. In wild lagomorph populations in Europe, RHDV2 partially escapes immunity from classic RHDV and has largely replaced the older virus. In Spain, an estimated 60% decrease in European rabbit populations due to RHDV2 was followed by declines in endangered Iberian lynx (*Lynx pardinus*) and Spanish imperial eagle (*Aquila adalberti*) recruitment. In Australia, RHDV2 has suppressed the abundance of the invasive European rabbit by 60%. Transmission primarily occurs by direct contact with infected urine, feces, and/or respiratory secretions; indirect contact with a contaminated environment (e.g., food, water, bedding) can also occur. However, the virus is environmentally stable for multiple months depending on the local conditions. It also can survive on fomites and insects, and may remain infectious after digestion in predators (i.e., in feces). RHDV2 infection in susceptible lagomorphs results in an acute febrile disease that affects all age classes (classical RHDV/RHDV1 is subclinical in young rabbits) and often leads to sudden death. Reports of outbreaks in wild populations have included many carcasses conspicuously found in the open. Clinical

signs can include fever, lethargy, anorexia, vocalization, wasting, diarrhea, difficulty breathing, ocular bleeding, and neurological signs. RHDV2 is not infectious to humans or non-rabbit pets. The RHDV2 vaccine used in domesticated rabbits is not currently available in the United States.

Domestic rabbits can escape and establish feral colonies that increase the risk of RHDV2 spillover to wild species. RHDV2 was first detected in domestic rabbits in North America in Quebec, Canada in 2016. A different strain of RHDV2 was detected in multiple locations on Vancouver Island, Canada in 2018. Since the 2018 outbreak in Ohio, RHDV2 has been detected in domestic rabbits in multiple locations in North America: British Columbia, Washington, New York, New Mexico, Arizona, and Texas. In April of 2020 in Chihuahua, Mexico, an RHD outbreak occurred in backyard rabbits, but the serotype was unknown.

Continued surveillance will be necessary to understand RHDV2 distribution in ecosystems of the southwestern US, as the disease is unlikely to be contained in wild populations. Removed from domestic rabbit biosecurity measures, RHDV2 is expected to spread (or has spread) among wild rabbits due to its contagiousness and environmental persistence. Cottontail subspecies are widespread throughout the eastern US and may be susceptible to RHDV2. Dead wild rabbits reported by the public should be promptly investigated by wildlife agencies and postmortem examinations should be performed. Close collaboration with state and federal agricultural agencies will be important to the response, and educating hunters, rabbit enthusiasts, and the general public on this significant wildlife threat will be crucial to prevent its spread in wild and domestic lagomorph populations. These outbreaks in wild lagomorphs substantially expand the distribution and host range of RHDV2 with potential for additional affected species, and possible declines in wild rabbit populations have unknown consequences for ecosystem health. (Prepared by Brian Dugovich and Mark Ruder).

Fungal Pneumonia in a White-tailed Deer

In November of 2019, while field dressing a white-tailed deer, a hunter in Knox County, Nebraska, noticed an unusual nodular pattern throughout the lungs of the deer. No other abnormalities were noted in the other parts of the carcass. The hunter had concerns about an infection and provided a lung

sample to a Nebraska Game and Parks Commission (NGPC) biologist at a local check station. Upon examination, the biologist was concerned about the possibility of bovine tuberculosis and submitted the lung sample to the SCWDS Diagnostic Service. Gross examination revealed hundreds of up to 0.5 cm diameter, firm, white to tan, round, raised nodules scattered throughout the lung sample with a few small hemorrhages (Figures 1 and 2).



Figure 1. Nodules visible on the surface of the lung.

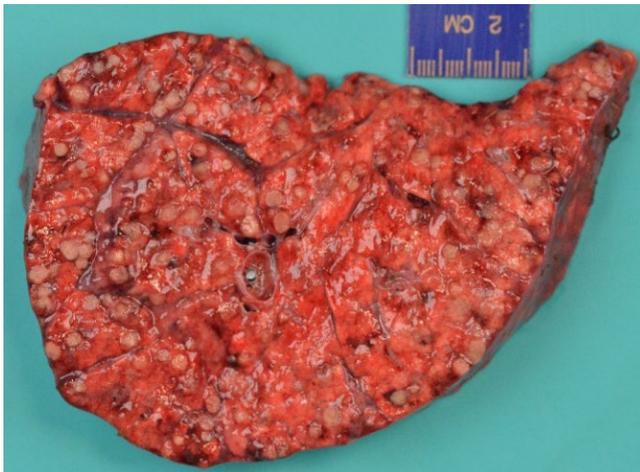


Figure 2. Cut surface of the lung, revealing nodules throughout the tissue.

Immediately upon receipt, a tissue sample was submitted for *Mycobacterium* species testing (culture and polymerase chain reaction). In addition, a lung sample was formalin-fixed for both routine histopathology and acid-fast staining aimed at the detection of *Mycobacterium* species. Fortunately, no mycobacteria were detected. Histology revealed that the nodules consisted of fungal granulomas characterized by countless fungi centered around necrotic (i.e., dead) lung tissue. This pattern of fungal infection differs from that of “green lung” disease, which has been increasingly diagnosed in white-

tailed deer submitted to SCWDS. Deer with green lung disease often have a large, focal, green abscess in the lung that is likely caused by a fungal or fungal-like organism. The fungus in the lung of the present white-tailed deer was identified as *Fusarium* species.

Published reports of *Fusarium* species infections in wildlife are scarce, and along with those described in domestic animals (e.g., horses), these infections are most often attributed to ingestion of moldy corn. In such cases of “moldy corn toxicosis,” a mold or fungus, such as *Fusarium* species, produces a variety of toxins (i.e., mycotoxins) facilitated by certain environmental conditions. Such was the case in a white-tailed deer in North Carolina with severe brain damage (i.e., leukoencephalomalacia); this is also how the disease manifests in horses.

However, in the present white-tailed deer, the pneumonia was attributed to the presence of the fungus itself. *Fusarium* infections are most commonly reported in humans, including reports of superficial, locally invasive, and widespread, multi-organ infections. Multiple routes of entry into the body are possible, and while infection is most common in immune-compromised or –suppressed individuals, detection in immunocompetent patients also can occur. Examination of the entire deer carcass would provide a more accurate assessment of possible route(s) of fungal entry in the present case; although the high number and wide distribution of the fungi in the lungs suggest direct (inhaled) entry into the lungs or spread to the lungs via the blood (hematogenous).

Fusarium infection is unlikely to have significant population-level impacts on white-tailed deer or other wildlife species. However, due to the lack of currently available information and the wide variety of infectious agents that can cause pneumonia in deer, it is important to be vigilant for pulmonary lesions in deer and to be cautious about the potential risks to humans in handling diseased deer and other wildlife. Further, changing climatic conditions may either facilitate or deter fungal proliferation in the environment, thus affecting risk levels to wildlife, domestic animals, and humans. This case adds to the knowledge of potential causes of pneumonia in deer and underscores the need to better understand the effects of fungal pathogens in wildlife. SCWDS would like to thank the Nebraska deer hunter as well as Lucas Negus and the NGPC for the submission of this fascinating case. Laboratory tests were performed at the Athens Veterinary Diagnostic Laboratory. (Prepared by Alisia Weyna and Nicole Nemeth).

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Southeastern Cooperative Wildlife Disease Study
College of Veterinary Medicine
The University of Georgia
Athens, Georgia 30602-4393

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