SCWDS BRIEFS

A Quarterly Newsletter from the

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Asian Longhorned Tick Confirmed in Georgia and Update on SCWDS Surveillance Efforts

In September 2021, SCWDS received ticks that were removed from a cow in Pickens County, Georgia, because the veterinarian noted a very high tick burden and reported it to the Georgia Department of Agriculture (GDA) who initiated an investigation. These ticks were confirmed to be *H. longicornis* (Asian longhorned tick, ALHT). This represents the most southern detection of this tick in the United States and the first report for Georgia. SCWDS is working with the GDA, Georgia Department of Natural Resources, and other partners to better understand the geographic distribution of this exotic tick in Georgia.

Tick drags at the index cattle farm detected very high numbers of larval and nymphal ALHT with greater numbers being detected in parts of the pasture near forested areas (Figure 1).

Figure 1. The underside of leaf from a plant in the field at the index site showing numerous nymphal *Haemaphysalis longicornis*.

A single adult female ALHT was also detected during manual inspection of plants. Finding primarily larval and nymphal stages in the fall is similar to observations from ALHT phenology studies in VA and NY. SCWDS trapped wildlife at the index farm, and to date, the rodents sampled (13 cotton rats, 3 house mice, and a *Peromyscus* sp.) have been negative for ticks, but ALHT was found on the 11 opossums sampled. A single *Dermacentor variabilis* and two larval *Amblyomma americanum* were found on a single opossum each. In addition, one of the owner's domestic cats was infested with a single ALHT nymph. Environmental surveillance at some neighboring properties also resulted in the finding of multiple *H. longicornis* nymphs and larvae; however, environmental sampling at other greenspace locations near the index farm were negative. Surveillance will continue until the tick enters diapause for the winter.

Since ALHT was first found in the United States in New Jersey in 2017, SCWDS has been actively involved in research and surveillance. SCWDS, in collaboration with partner agencies and member states, has played a significant role in adding new state, county, and host records to the rapidly growing body of knowledge on *H. longicornis* in the United States. This has been done largely through a passive tick surveillance program working with state and federal wildlife agencies and wildlife rehabilitation centers distributed throughout parts of the eastern and southeastern United States. Since beginning this surveillance, 2,380 samples from 73 species have been submitted from 22 states. To date, *H. longicornis* has been detected from 10 different states (DE, KY, MD, NC, NJ, TN, PA, VA, WV, and GA) (Figure 2). The vertebrate host range was extensive and included 13 mammalian hosts (black bear, coyote, domestic cat, domestic dog, eastern cottontail, elk, gray fox,

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raccoon, red fox, white-tailed deer, woodchuck, Virginia opossum, and cow) and 4 avian species (brown booby, barred owl, great-horned owl, and red-tailed hawk). In addition to providing key data about *H. longicornis*, this collaborative tick surveillance program provides valuable information regarding the host associations and distributions of other tick species native to the United States and relevant to wildlife, domestic animal, and human health.

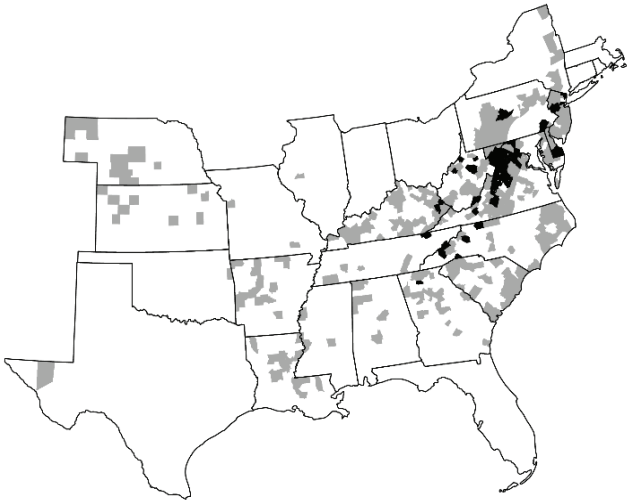

Figure 2. Passive surveillance efforts by SCWDS and partners from 2017-2021. Sampled counties with detection of *Haemaphysalis longicornis* are shown in black, grey counties are sampled but negative.

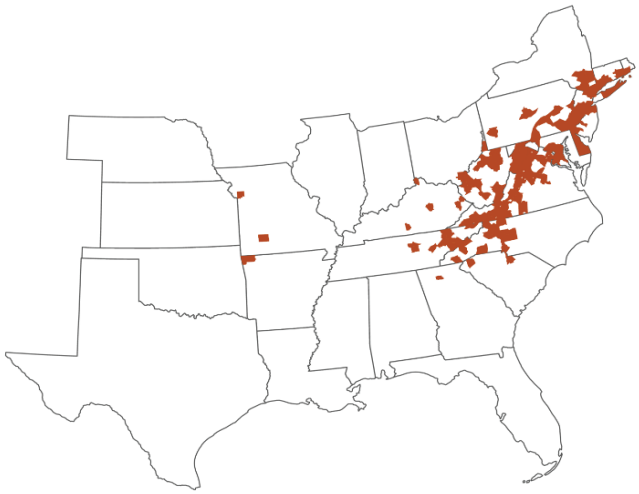

Figure 3. Known county-level distribution of *Haemaphysalis longicornis* in the United States based on SCWDS surveillance combined with published reports and other efforts reported to the USDA.

Finally, since the last SCWDS BRIEFS update, ALHT has been reported from another new state, Missouri (Greene County from the environment and Clay County from a horse). ALHT is now found in 17 states (Figure 3). SCWDS maintains a regularly-updated website (https://scwds.shinyapps.io/haemaphysalis/) that is accessible to the public, which highlights basic information about *H. longicornis*, SCWDS' tick surveillance program, hosts from which *H. longicornis* has been recorded, and a map with known *H. longicornis* collections. Surveillance is ongoing and will be maintained moving forward, so please continue to submit ticks and encourage your staff to collect ticks as well. To participate in our regional study, please request tick collection kits by contacting Alec Thompson (alec.thompson@uga.edu), Seth White (sacwhite@uga.edu), or Dr. Michael Yabsley (myabsley@uga.edu). (Prepared by Michael Yabsley and Alec Thompson)

RHDV2 Update

In the January 2021 issue of the *SCWDS BRIEFS*, we provided an update on the ongoing outbreak of rabbit hemorrhagic disease (RHD) virus 2 (RHDV2) in the U.S. and Mexico. At that time, RHDV2 had recently (December 2020) been confirmed in domestic rabbits in Lake County, Florida, making Florida the 9th and most eastern state with confirmed RHDV2 since March 2020. Unfortunately, the virus continues to be confirmed in new locations. Over the past 10 months, RHDV2 has been detected in wild lagomorphs and/or domestic/feral rabbits in seven additional states, including midwestern and western states (Idaho, Minnesota, Montana, Oregon, and South Dakota) and the Southeast (Georgia and Mississippi). Further, additional domestic rabbit cases occurred in Florida (St. Johns County) during October 2021. Genetic sequencing of RHDV2 from domestic rabbits in Florida (December 2020) and Georgia (June/July 2021) performed by the United States Department of Agriculture (USDA) suggest the viruses are connected to the RHD outbreak in the western U.S. and do not likely represent new introductions. The specific mechanisms of virus spread across the country remain unclear. Overall, since the initial recognition of the RHD outbreak in March 2020, RHDV2 has been confirmed in wild lagomorphs and/or domestic (or feral) rabbits in 16 states (Figure 1).

In the western and southwestern U.S. (including western Texas), outbreaks have frequently involved both domestic rabbits and wild lagomorphs. However, in states with confirmed RHDV2 in the eastern U.S. (Florida, Georgia,

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Minnesota, and Mississippi), only domestic rabbits are known to be involved. Whether this contrasting pattern of known RHDV2 epidemiology between the western and eastern U.S. is a surveillance artifact, or reflects variation in disease ecology (e.g., host susceptibility, climatic variation, habitat variation) remains unclear. However, the cases in the eastern U.S. that are distant from the core endemic-stable area in the western U.S. highlight the risk of unintentional movement of virus across the landscape.

As with any emerging pathogen in a new landscape, there is much to learn about the interactions between the hosts, pathogen, and environment over time. Continued vigilance for wild lagomorph mortality events and sustained surveillance and monitoring will be important moving forward. Wildlife agencies in the Southeast are largely relying upon passive surveillance approaches, leaning on the public and others to promptly report wild rabbit mortalities. Since May 2020, SCWDS has received 74 wild lagomorph carcasses or tissues from 13 states, and all have tested negative for RHDV2.

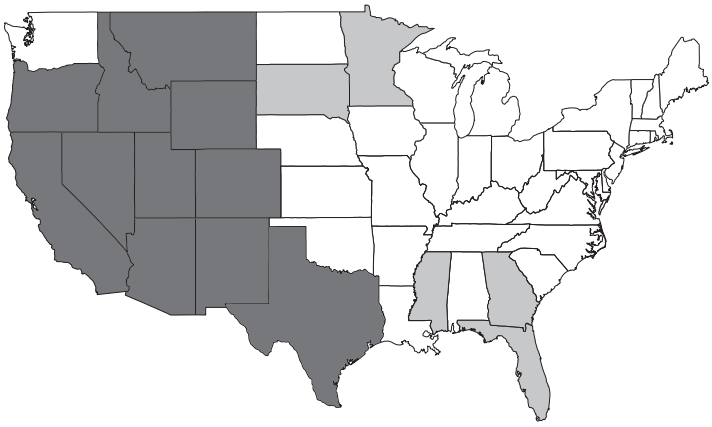

Figure 1. State-level RHDV2 confirmations since March 2020. Dark grey: RHDV2 has been confirmed in domestic rabbits and wild lagomorphs. Light grey: RHDV2 has been confirmed only in domestic rabbits.

Disease prevention and management in domestic animals often centers on the availability and effectiveness of vaccines. Previously, the only RHDV2 vaccines available were not produced in the U.S. and required importation from Europe. However, this recently changed. In October 2021, an inactivated (killed) vaccine (https://medgenelabs.com/rhdv2/) produced by Medgene Labs (Brookings, SD) was granted Emergency Use Authorization by the USDA Center for Veterinary Biologics. This vaccine is now available for distribution to over 40 states and is being used in domestic rabbits. Studies performed by Medgene Labs and reported on at the 125th Annual Meeting of the United States Animal Health Association suggest the 2-dose vaccine is effective at preventing severe and fatal disease associated with RHDV2 infection in domestic rabbits. However, the unpublished research findings suggest that vaccinated rabbits were still able to become infected after challenged with RHDV2. It remains unclear whether vaccinated rabbits that later become infected with RHDV2 are able to shed virus and transmit the infection to either domestic or wild rabbits. Therefore, it is important that domestic rabbit vaccination not replace infection control and biosecurity measures to mitigate the potential spread of RHDV2, but rather supplement those measures. We encourage wildlife agencies to continue to work with their agricultural agency counterparts to promote good preventive practices. (Prepared by Mark Ruder)

Lack of Herd Immunity After Increasing HD Outbreaks in West Virginia

Beginning in the early 2000s, both localized and large-scale hemorrhagic disease (HD) outbreaks in white-tailed deer began to occur with increasing frequency and intensity in parts of the midwestern, mid-Atlantic, and northeastern United States. Certainly, the 2021 HD season was a great example of this and we will highlight diagnostic and surveillance findings in the next issue of the SCWDS BRIEFS. While the majority of outbreaks in this region have been associated with EHDV-2, a variety of other viruses (EHDV-1, & -6; BTV-1, -3, -10, -11, -13, -17) have also been detected. The underlying factors involved in this changing pattern of HD in the region remain unclear, although climate change is suspected to be playing a role. Climate change affects many short- and long-term weather patterns and influences variables that have potential to alter vector seasonality, competence, abundance, and distribution.

Herd immunity plays a significant role when trying to make sense of patterns of infection and disease with HD of deer. In regions of the U.S. with endemic circulation of EHDV and BTV, high herd immunity (evidenced by high prevalence of

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EHDV/BTV antibodies in the deer population) helps protect against severe and fatal disease resulting in minimal to mild HD outbreaks. However, in the northeastern, midwestern, and mid-Atlantic states, HD activity has been historically infrequent and herd immunity is not thought to play a significant role in mitigating deer mortality during outbreaks in these regions. With the increasing frequency of outbreaks and viral circulation in the region during the last two decades, there is need to investigate if levels of herd immunity are increasing in response. If herd immunity in the northeastern and midwestern regions is increasing, deer herds would likely experience reduced mortality and less severe disease when outbreaks occur. To explore this question, we examined long-term statewide EHDV/BTV serological data from 724 deer in West Virginia in conjunction with annual HD survey records collected by SCWDS from 1981 to 2020. Serum samples were sourced from healthy deer, predominantly adult does, collected annually by agency personnel in August and September during deer herd health checks, as well as several EHDV/BTV serosurveillance projects.

Overall, we observed no evidence herd immunity is increasing as a result of more frequent HD outbreaks in West Virginia. We compared reported HD and prevalence of antibodies against EHDV and BTV between two time periods: 1981-2000 and 2001-2020. From 1981-2000, HD was reported during just 5 years (average of one county/year), compared with 19 years of reported HD (average 8.7 counties/year) from 2001-2020. Despite these dramatic differences in both the number of years and number of counties with reported HD during the two time periods, prevalence of EHDV and/or BTV antibodies (a proxy for herd immunity) was quite low across the state during both time periods: 5.7% from 1981-2000 vs 2.7% from 2001-2020.

To further characterize changes in EHDV and/or BTV antibody prevalence in association with reported HD in West Virginia, we examined the same serological data immediately before and after outbreak years from 1981-2020. Antibody prevalence leading up to outbreak years was expectedly low (e.g., <6%) and peaked, as expected, in the year immediately following an outbreak, though never exceeding 14% as a maximum estimate. Within 3 years of an outbreak, seroprevalence had returned to 0%. In summary, while it appears some animals do survive EHDV and/or BTV infection in West Virginia, the proportion is relatively low and there is no evidence any lasting, protective level of herd immunity is reached following an outbreak.

As the majority of deer represented in our serological data were adults, they represent animals with the greatest chance of prior exposure. While only 17 of West Virginia's 55 counties are represented in the serological data, these counties represent a reasonable geographic sampling distribution statewide with multiple counties sampled in each of WV's defined ecoregions. While there is typically a five-year rotational cycle for herd health collections in each WV county represented, sample sizes are small, and collections generally occur at the same location with each visit, so it is possible we missed detecting seropositive animals following a localized outbreak. However, in the case of a highly-localized outbreak it is reasonable to conclude no significant herd-level immunity to HD would result.

While we acknowledge the limitations in interpreting these results, it appears unlikely the increase in reported HD in West Virginia has led to any meaningful increase in herd immunity as of 2021. Localized and large-scale HD outbreaks in WV will likely continue to be characterized by sporadic, severe disease with high mortality. As serum antibodies were not detected in any sampled deer on the third year following outbreaks of HD, it appears any level of herd immunity- even low levels- that may arise following an outbreak is fleeting given current epidemiological patterns. Further complicating the picture is the increasing circulation of exotic viruses and serotypes, including EHDV-6, BTV-1, and BTV-3, in the region.

While more outbreak follow-up serology will be needed over time to fully evaluate the impact of changing patterns of HD upon the establishment of deer herd immunity in the northeast and mid-Atlantic regions, our case study in West Virginia suggests no such immunity currently exists. (Prepared by Ethan Barton and Mark Ruder)

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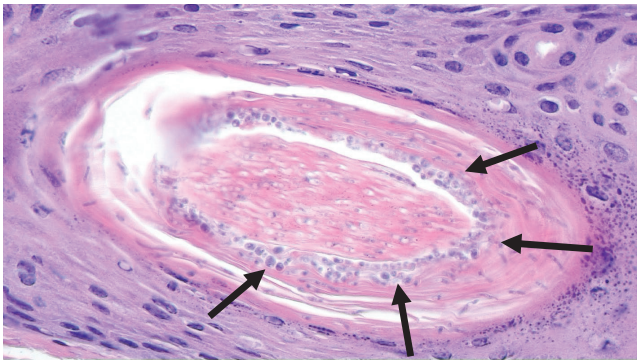
Dermatophytosis in a Mule Deer

During December 2020, an adult male mule deer (*Odocoileus hemionus*) in southcentral Nebraska was observed with notable fur loss and worsening nutritional condition over the previous two weeks. The buck was dispatched and a biologist with Nebraska Game and Parks Commission shipped the deer's head to SCWDS for examination and diagnostic testing. Necropsy revealed marked, patchy to widespread areas of fur loss (alopecia) in the skin over the head, with multifocal, variably sized, raised nodules in the skin.

Microscopic examination of the skin lesions revealed numerous dilated hair follicles that had various fungal elements (i.e., arthrospores and rare hyphae; Figure 1) within and surrounding degenerated hair shafts, with associated skin ulceration and inflammation. Occasional protozoan cysts (most likely *Sarcocystis* sp.), were noted within the underlying muscle and are considered an incidental finding.



Figures 1. Histologic section showing the surface of the skin with a central cross-section of a hair shaft infiltrated by many arthrospores (pale, round, purple structures). Arrows point to the arthrospores.

The observed gross and microscopic skin lesions are characteristic of dermatophytosis (also known as "ringworm"), which is caused by fungal organisms known as dermatophytes that invade keratinized tissues (e.g., skin, hair, nails). Dermatophytosis commonly occurs in numerous domestic species (e.g., dogs, cats, cattle, horses, goats), with the vast majority of cases caused by *Microsporum* and *Trichophyton* spp. Transmission typically is via direct contact with fungal contaminated hair or scales on infected animals, fomites, or from contaminated environments. The susceptibility to dermatophyte infection is increased in young or immunocompromised animals, animals in hot and humid environments, and those living in overcrowded or dirty surroundings with inadequate nutrition. Clinical signs and gross lesions are variable and depend on the interaction between the fungus and the host immune system. Lesions can be found anywhere on the body but often are seen on the head, ears, legs, feet, or tail. In animals with normal immune systems, this disease is considered self-limiting and typically resolves over a period of weeks to months.

There are few cases of dermatophytosis currently published in wildlife species, including mule deer, white-tailed deer, red foxes, Florida panthers, North American porcupines, wild boars in Italy, swamp wallabies in Wales, and European hedgehogs. Currently, there are only two published case reports of dermatophytosis in mule deer, both of which were in Canada (Alberta and Saskatchewan). Gross lesions in these two cases varied in severity and localization but most frequently involved the face and legs with similar microscopic findings to our current case. In 2011, a survey of approximately 60 hunter-harvested white-tailed deer from Virginia, USA, found no overt dermatophyte cases. While documented cases of dermatophytosis in free-ranging mammals are rare, the gross and microscopic lesions often are similar across species.

Dermatophytosis generally is not considered a significant threat to wildlife populations. Further, dermatophytes are common inhabitants of the soil, and unapparent carrier animals are common among domestic species. Therefore, infected wildlife species typically do not pose an additional risk of infection for domestic animals. However, humans are susceptible to dermatophytosis, and gloves should be worn when handling potentially contaminated objects and hands should be washed with warm, soapy water after exposure. SCWDS would like to thank the Nebraska Game and Parks Commission for submission of this case, which reveals a classic disease in an uncommonly affected species. (Prepared by Hailee Butler, Michigan State University, Melanie Kunkel, and Nicole Nemeth)

Changing SCWDS Faces

The SCWDS family tree, with branches all over the world, continues to change and grow. Over

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the last year, we have had several new students and staff join SCWDS.

Mr. Ethan Barton is the Wildlife Health Specialist for West Virginia Division of Natural Resources (WVDNR) and joined SCWDS (January 2021) to begin his PhD. Originally from Pennsylvania, Ethan received his BS and MS from Pennsylvania State University in Wildlife Science in 2011 and 2014, respectively. Ethan has worked for WVDNR since 2016. In this unique position, Ethan remains a full-time employee with WVDNR and part-time PhD student at SCWDS. He began his curriculum virtually in January 2021, and has been in Athens full-time during the Fall 2021 semester focusing on completing his coursework. His PhD research at SCWDS will focus on multiple aspects of CWD ecology and management.

Ms. Katy Callaghan joined the SCWDS Research and Diagnostic Service as Necropsy Technician in July 2021, immediately after completing her Master of Natural Resources (MNR) at UGA's Warnell School of Forestry and Natural Resources. During her MNR program she worked with SCWDS and USDA partners to investigate the prevalence and distribution of *Trichinella* and *Toxoplasma gondii* in feral pigs. Katy has a wealth of experience, including pursuing certification as an Associate Wildlife Biologist and having interned with both the USDA Natural Resources Conservation Service in Nebraska and USDA APHIS Wildlife Services in Georgia.

Dr. Sarah 'Mighty' Coker has returned to SCWDS. Previously Sarah completed a MS degree at SCWDS through the Warnell School of Forestry and Natural Resources during which time she worked on blood parasites of ibis and related birds. Sarah then went to New Zealand where she earned a PhD studying parasites of kiwi. We were excited when Sarah recently returned to SCWDS where she is assisting with many aspects of the Guinea worm project including development and validation of novel molecular diagnostic tools and field work in Ethiopia.

Ms. Morgan Friedman is a first-year PhD student in UGA's College of Veterinary Medicine and has been at SCWDS since August 2020. She has a bachelor's in Ecology and Evolutionary Biology from the University of Colorado-Boulder and has worked previously as a veterinary technician in California. She joined SCWDS through UGA's Post-Baccalaureate Research Education Program (PREP), where she focused on identifying African ticks, before continuing into her graduate program. Morgan's PhD research focuses on ticks and tick-borne diseases in the Southeastern United States.

Dr. Chloe Goodwin just finished her anatomic pathology residency at UGA (including successful completion of the board certification examination!) and joined SCWDS as a full-time PhD student in August 2021. She received her DVM from Texas A&M University (2018). Chloe managed to initiate her PhD research during the residency, which focuses on various aspects of lymphoproliferative disease virus in wild turkeys, such as better understanding disease development and virus distribution in the host, virus transmission routes, and developing additional diagnostic tools. Chloe also serves SCWDS member agencies as a wildlife disease diagnostician.

Dr. Ellen Haynes joined SCWDS as a Post-doctoral Research Associate in June 2021. She received her DVM from Cornell University (2013) and her PhD in Ecology, Evolution, and Conservation Biology from the University of Illinois (May 2021). Her PhD research focused on the epidemiology, pathology, and treatment of ophidiomycosis, a fungal disease impacting snakes worldwide. More broadly, her research interests include wildlife health and infectious diseases of free-ranging wildlife. At SCWDS, Dr. Haynes is involved in numerous projects with Guinea worm and other parasites of native wildlife species, in addition to continuing her work with ophidiomycosis.

Ms. Corinna Hazelrig joined SCWDS in August 2021 to begin her PhD in the Comparative Biomedical Sciences program at the College of Veterinary Medicine. She graduated from UGA with her Bachelor of Science in Forest Resources in May 2021. Her previous research projects focused on surveillance of *Batrachochytrium dendrobatidis* in amphibian species and coinfections of vector-borne diseases in shelter dogs in the eastern United States. Corinna's PhD research will focus on comparative susceptibility to ophidiomycosis

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between semi-aquatic and terrestrial North American snakes and the evaluation of risk factors such as coinfections.

Ms. Avery Korns joined SCWDS in August 2020 and is working on a MS degree through the Warnell School of Forestry and Natural Resources. She has a BS with a double major of Animal Science and Animal Ecology from Iowa State University. Avery's MS research focuses on the potential role of wildlife as hosts for human Guinea worm in Chad. Specifically, Avery is investigating the use of habitat by wildlife surrounding villages with varying prevalence of Guinea worm in dogs.

Ms. Patty Torres is a new PhD Integrative Conservation student in the Warnell School of Forestry and Natural Resources. Patty has a BS in Wildlife Management from Humboldt State University. After graduation, she worked with the Wiyot tribe as a Natural Resources Technician and a Project Manager of the North Coast Health Improvement and Information Network during which time she gained a diversity of field experience, was heavily involved in outreach, and oversaw numerous natural resource projects. Her PhD research will focus on ticks and tick-borne pathogens.

Typically, when we have new arrivals at SCWDS that also means we have some departures as people move on to pursue their careers. After joining SCWDS as a Post-doctoral Research Associate in June 2019, Dr. Brian Dugovich left SCWDS in October 2020 and is now a Disease Ecologist with the United States Geological Survey's Northern Rocky Mountain Science Center. Dr. Natalie Stilwell joined SCWDS in September 2019, as a Post-doctoral Research Associate. She finished her post-doc in August 2021, and accepted a faculty position as Clinical Assistant Professor in the Department of Pathobiology and Population Medicine at Mississippi State University's College of Veterinary Medicine. Mr. Michael Tanner joined SCWDS as a research technician in October 2019 and played a critical role in the virology lab until his departure in January 2021. After five years of serving SCWDS member agencies as our necropsy technician, Ms. Michelle Willis left SCWDS in July 2021 to pursue new adventures as an educator. We miss Brian, Natalie, Michael, and Michelle and wish them nothing but the best in their new adventures.

As SCWDS is a research unit at a land grant university, training the next generation of wildlife health professionals is an important part of what SCWDS does 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, and public health communities. We look forward to watching their continued growth and expect great things. We also are very excited to welcome our new arrivals and look forward to sharing their successes at SCWDS. (Prepared by SCWDS Faculty)

SCWDS BRIEFS

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