



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

Volume 37

July 2021

Number 2

Update on Mange Research and Diagnostics

SCWDS continues to be involved in collaborative research to understand the epidemiology of mange in wildlife. For several years we have worked with partners to understand the emerging problem of mange in black bears (*Ursus americanus*). In the past decade, the spread of sarcoptic mange has been documented in the mid-Atlantic and Northeastern states and several studies on this spread as well as appropriate diagnostic methods, other disease issues associated with mange, and persistence of mites off the host have been [published](#) (see [July 2019 BRIEFS](#)). This emergence and expansion of mange as well as continued diagnoses in other wildlife species and regions highlight the need for increased surveillance and accurate diagnostic testing.

Through our diagnostic service, SCWDS receives tissues/carcasses from many mange suspects each year. These submissions not only contribute to our research, but they also provide valuable data on ecology of these parasites and the disease in various wildlife species. Specifically, these samples can provide data on new hosts or new or expanded geographic locations of cases. This BRIEFS article provides two such examples.

In January 2021, the first case of sarcoptic mange in an American black bear in Georgia was confirmed. The adult, male bear was found in an emaciated condition with mange-like lesions in Gordon County (Figure 1). This case is unusual because Virginia and West Virginia are the closest states that have a notable amount of confirmed cases. Also, in March 2019, a yearling, male black bear from Massachusetts with patchy hair loss and crusting over the entire body was presented to Tufts University for care. This bear was ultimately diagnosed with chorioptic mange which is the first report of *Chorioptes* and clinical disease in black bears. Analysis of genetic sequence from the ITS-2 region confirmed the mites were most closely related to a *Chorioptes* sp. collected from a panda in China and were distinct from bovid and cervid *Chorioptes* spp. As mange is increasingly recognized as an important disease in black bears, this case emphasizes the importance of performing appropriate skin scrapes and mite identification in animals with hyperkeratotic skin lesions because of the clinical similarities of sarcoptic, ursicortic, chorioptic, and

to a lesser extent, demodectic mange. Confirming the disease as well as the causative agent in these cases is important as these mite species have different health implications for humans, bears, as well as other wild and domestic animals. This last case was recently published in the *Journal of Wildlife Diseases* (<https://doi.org/10.7589/JWD-D-20-00143>).



Figure 1. Black bear from Georgia with sarcoptic mange (Photo taken by Brian Avery).



Figure 2. Marsh rabbit from Florida with sarcoptic mange. Note crusting and hair loss on front limbs.

In addition to these new data on mange in black bears, SCWDS has recently received two interesting mange cases from rabbits in Florida. In December 2020 an adult,

Continued...

male eastern cottontail (*Sylvilagus floridanus*) was found in Lee County. This rabbit was diagnosed with notoedric mange caused by *Notoedres centrifera*. The detection of *N. centrifera* is interesting as it is primarily a pathogen of squirrels, but little is known about the ecology of this mite genus. Importantly, at least five sick or dead rabbits had been seen in the same neighborhood since May 2020, and this was one of several reports of lethargic rabbits with crusty skin disease in Florida; the other animals were not available for diagnostic evaluation. In April 2021, a male, adult marsh rabbit (*Sylvilagus palustris*) from Pinellas County (Figure 2) was submitted for diagnostic evaluation. This rabbit was diagnosed with sarcoptic mange. Similar to the *Chorioptes* in bears, this case highlights the need to determine the causative agent of mange as the epidemiology of these different mite species may vary.

In addition to increasing our knowledge of host and geographic range, these samples are also used for an ongoing study investigating population genetics of *Sarcoptes scabiei* mites in the U.S. to better understand mite lineage-host-geographic interactions. As part of this research, SCWDS is requesting that our partners submit any skin samples from wildlife that have lesions consistent with mange. These lesions could include crusty skin or those animals with large amounts of hair loss. A sample collection protocol can be provided upon written request to Ryan Grunert (grunertryan@uga.edu) or Michael Yabsley (myabsley@uga.edu). (Prepared by Ryan Grunert and Michael Yabsley).

Outbreak of Conjunctivitis in Passerines in the Eastern US

In May of 2021, nestling and juvenile birds of numerous passerine species presented with eyelid lesions that included swelling (conjunctivitis), discharge and/or crusts. Some birds also had signs of neurologic disease (weakness, lack of coordination, twitching, head tilt) and later died or were euthanized. Early in the outbreak, most of the affected birds were in Virginia, Maryland, and Washington, D.C. Soon after, additional states, including West Virginia, Kentucky, Tennessee, Florida, Pennsylvania as well as north to New Jersey and west to Ohio and Indiana received reports of suspect or confirmed cases. Missouri, Georgia, and Kansas have also been vigilant to report any potentially associated passerine mortalities. SCWDS has worked closely with our member state wildlife agencies (including Virginia Department of Wildlife Resources, West Virginia Division of Natural Resources, Kentucky Department of Fish and Wildlife Resources, Tennessee Wildlife Resources Agency, and the Florida Fish and Wildlife Conservation Commission, Missouri Department of Conservation, and Georgia Department of Natural Resources), the National Wildlife Health Center (USGS) and University of Pennsylvania Wildlife Futures Program to strategize on collection and submission of affected birds, as well as to share and compare diagnostic information.

Although an official case definition has not yet been developed, knowledge of any apparent clinical disease, as well as observations of other affected birds in the region are important background information. Postmortem examination has involved testing for a variety of potential avian pathogens (e.g., *Salmonella* spp., West Nile virus, paramyxoviruses), including those that may cause eye or eyelid disease (e.g., herpesvirus, poxvirus, *Chlamydia* sp., and *Mycoplasma* spp.). No infectious agent has been consistently detected among the birds examined at SCWDS, although *Mycoplasma* has been detected in a subset of birds. *Mycoplasma* species can cause conjunctival swelling in a variety of species, but it should be noted that this bacteria likely infects many birds with no ill effects, so its role as a primary or opportunistic pathogen in the development of this disease is not yet clear. Toxicologic and other diagnostic testing are ongoing as we continue to work collaboratively on this outbreak investigation.



Figure 1. Juvenile common grackle with conjunctivitis and crusty discharge.



Figure 2. Juvenile American robin with conjunctivitis and bulging ocular tissue.

Variable severity of eyelid inflammation (Figure 1) has been observed both grossly and microscopically in these cases. The inflammation is not always grossly evident. Some birds also have trauma (including hemorrhage

around the eyes and bulging eyes; Figure 2), as well as secondary bacterial infections of the eyelids and other apparent concurrent infections affecting internal organs, likely due to impaired vision and incomplete immune system development, respectively. The latter is suspected due to the young age of the affected birds, most of which have been blue jays, European starlings, common grackles, and American robins. Other passerine species, as well as raptors, are being carefully evaluated for any similar lesions.

Field reports suggest that the outbreak is waning but state wildlife agencies throughout the eastern U.S. remain vigilant. Levels of concern among biologists, veterinarians, as well as the public are elevated, which has contributed to both our knowledge of the scope of this outbreak and led to submitted cases. Additional epidemiologic and diagnostic data are needed to further our understanding of this outbreak, in conjunction with insights into avian biology and behavior. As for all wildlife disease outbreaks, environmental and ecological factors, as well as host and etiologic (e.g., infectious agent, toxin, etc.) factors must be carefully and collectively considered, with recognition that multiple factors likely are contributing. Thus far, there have been no confirmed reports of associated disease in poultry, other domestic livestock, pet birds, or humans but standard precautions should be taken to avoid disease spread among these groups. To make a long story short – the cause and potential underlying factors driving this event remain unclear and may only come to light through additional research. Updates can be found at: <https://www.usgs.gov/centers/nwhc/news>. (Prepared by Nicole Nemeth)

Evidence of SARS-CoV-2 in Wild White-tailed Deer

The susceptibility of white-tailed deer to SARS-CoV-2 infection has been previously demonstrated through experimental infections conducted by the USDA Agricultural Research Service. In this work, deer-to-deer transmission of this virus also was documented. More recently, USDA Wildlife Services reported the detection of SARS-CoV-2 antibodies in deer sampled during 2021 in Illinois, Michigan, Pennsylvania, and New York. These four states were the only states included in the study. To validate these serologic findings, test results were confirmed by parallel testing at the National Veterinary Services Laboratories using virus neutralization tests. In addition, pre-COVID-19 pandemic deer sera also were tested, and antibodies were not detected in these samples. Sample sizes were relatively small within the individual counties included in this work (range 1-54) but of the 32 counties sampled, SARS-CoV-2 antibodies were detected in 17 (53%). In addition, in some of these counties, antibody prevalence was 100%.

At present, these results should not be overinterpreted; additional work is needed to fully understand their significance and address questions generated by these

findings. To date, a confirmed SARS-CoV-2 infection, as determined by RT-PCR or virus isolation, has not been detected in free-ranging white-tailed deer, but few have been tested. Although the high SARS-CoV-2 antibody prevalence estimates reported in this study suggest widespread infection within the areas sampled, they do not provide a means to determine actual infection rates. The means by which deer were exposed or infected also are unknown and need to be identified. This may be extremely difficult, with possibilities ranging from direct contact between deer and humans such as would occur in a rehabilitation setting, or via remote contact through SARS-CoV-2 contaminated feed/bait or contaminated environments. At this time, we cannot eliminate any possibility. The SARS-CoV-2 antibody status of white-tailed deer populations outside of these 32 sampled counties also is unknown, and it is important to keep in mind that deer in many of the counties tested in the USDA study were antibody negative. This was especially true in the Illinois sample, in which antibodies were detected in 7% of deer representing only 4 of 12 sampled counties. We cannot predict where this is going. It is possible that these infections are dependent on a high level of infection in humans and will not persist in deer if we gain control of this virus in our own population. It also is possible that deer will represent a new mammalian reservoir for this virus; the implications, should this event occur, are not clear.

With outdoor activity at record peaks and deer hunting season approaching, we should all take these events seriously and do our part not to make matters worse. As previously stated, we do not know how this virus entered these deer populations, but we do know that humans are the current reservoir and all of us (vaccinated and unvaccinated) are a potential source of infection to other species.

Of all recreational groups, hunters will have direct close contact with deer that they harvest. Although we do not know if there is a need for concern related to deer-to-human transmission of SARS-CoV-2, the following information and suggestions may help hunters navigate this unknown.

- There is evidence that *wild* WTD have been or are infected with SARS-CoV-2.
- This evidence is based on antibodies. Deer naturally infected and shedding SARS-CoV-2 have not been detected to date.
- Current information on SARS-CoV-2 antibodies in WTD is extremely limited, and the current status of most WTD populations in the United States is unknown.
- Based on experimental data, SARS-CoV-2 infected deer have a high viral load that should be considered as a potential source for human infection; however, there currently are no documented cases of humans becoming infected from WTD.
- At present there is no known risk of SARS-CoV-2 exposure associated with cleaning deer or eating

cooked venison. However, when handling a WTD carcass, individuals are in contact with an animal of unknown SARS-CoV-2 infection status.

- The risk, if any, of SARS-CoV-2 infection from handling an infected harvested deer can be reduced by following the same guidelines recommended to reduce human-to-human transmission (hand washing, gloves, and masks). Likewise, the risk of severe or fatal COVID-19 can be greatly reduced through personal vaccination.
- If vaccination is not a possibility such as in the case of the immunocompromised, having assistance with carcass handling could be considered.

See additional sources for further information on food safety recommendations from the CDC (<https://www.cdc.gov/coronavirus/2019-ncov/daily-life-coping/food-and-COVID-19.html>), as well as recommendations on lowering risk of SARS-CoV-2 transmission between people and wildlife (<https://www.cdc.gov/healthypets/covid-19/wildlife.html>).

For further information related to SARS-CoV-2 infection and antibodies in white-tailed deer see:

Palmer et al. Susceptibility of white-tailed deer (*Odocoileus virginianus*) to Sars-CoV-2. https://journals.asm.org/doi/full/10.1128/JVI.00083-21?rfr_dat=cr_pub++0pubmed&url_ver=Z39.88-2003&rfr_id=ori%3Arid%3Acrossref.org.

Chandler et al. SARS-CoV-2 exposure in wild white-tailed deer (*Odocoileus virginianus*) <https://www.biorxiv.org/content/10.1101/2021.07.29.454326v1.full.pdf>.

(Prepared by Dave Stallknecht)

Experimental SARS-CoV-2 Infection in Raccoons and Striped Skunks

As SARS-CoV-2 continues to circulate in humans around the globe, there is increasing evidence that animals can be infected and that these infections are in most cases associated with spillover from people. Although humans are the reservoir for SARS-CoV-2, it is important to minimize exposure of animal populations to mitigate the risk of human-to-animal transmission (i.e., reverse zoonosis). Several species belonging to Musteloidea (e.g., mink (*Mustela vison/Neovison vison*) and domestic ferrets (*Mustela putorius furo*) have previously been shown to be susceptible to SARS-CoV-2. While the majority of documented incidences of reverse zoonosis within the United States have occurred in companion animals (e.g., cats and dogs), certain susceptible wildlife and production species (e.g., mustelids, felids, non-human primates) in captive settings (i.e., production fur farms, zoological institutions) are at increased risk.

In a recent SCWDS study two Musteloidea, striped skunks (*Mephitis mephitis*) and raccoons (*Procyon lotor*), were evaluated for SARS-CoV-2 susceptibility. These two

species were chosen because they are opportunistic, omnivorous generalists and are often associated with habitats with high human populations. Both species adapt well to peridomestic habitats, resulting in frequent interactions with domestic animals, humans, and their waste, providing opportunity for potential exposure to SARS-CoV-2. Further, orphaned and injured raccoons are commonly rehabilitated in some states, which puts those animals into close and unique contact with humans.

Raccoons and skunks were intranasally inoculated with either a high dose (4 raccoons, 4 skunks) or low dose (4 raccoons, 4 skunks) of SAR-CoV-2. Approximately 48 hours after direct inoculation, an additional subset of naïve animals (4 raccoons, 4 skunks) were commingled with the inoculated animals to evaluate potential for animal-to-animal virus transmission. All directly inoculated animals and contact control animals were sampled at regular intervals and real-time reverse transcriptase PCR (rRT-PCR) and virus isolation were used to assess the quantity, duration, and route of viral shedding. Serum was evaluated for development of an antibody response to SARS-CoV-2. Lastly, animals were necropsied at staggered intervals to evaluate for lesions attributable to SAR-CoV-2 at various time points post-inoculation.

No animals experienced clinical disease during this study. Low quantities of SARS-CoV-2 were isolated from nasal swabs in two of four directly inoculated skunks up to 5 days post-inoculation. No virus was detected from inoculated raccoons. All inoculated skunks and raccoons developed antibodies to SARS-CoV-2. However, there was no evidence (e.g., virus isolation, rRT-PCR, serology) of virus transmission to direct contact control animals that were commingled with inoculated animals. No gross lesions attributable to SARS-CoV-2 were observed but occasional, chronic, mild (deemed representative of recovery) pneumonia was observed in 5 of 8 inoculated skunks. The findings of this study demonstrated that while striped skunks and raccoons are susceptible to SARS-CoV-2 infection, efficient animal-to-animal transmission required for establishment in wild populations would be unlikely.

Out of an abundance of caution, care should be taken to avoid transmission of SARS-CoV-2 to skunks and raccoons and other wildlife in captive (e.g., wildlife rehabilitation, exhibition) and field research and management settings. Appropriate use of personal protective equipment (PPE), such as gloves and masks, should be used when interacting with either free-ranging or captive North American wildlife, as discussed in the Fish and Wildlife Health Committee of the Association of Fish and Wildlife Agencies' "COVID-19 and North American Species of Mustelidae, Felidae, and Canidae" and the Zoo and Aquarium All Hazards Preparedness, Response, and Recovery (ZAHP) Fusion Center's "Considerations for the Management of Non-Domestic Species in Human Care During COVID-19" (links provided below). Vaccination of humans in contact with these animals also will reduce the risk of human-to-animal transmission.

Besides the potential transmission of SARS-CoV-2 to these species, skunks and raccoons are also reservoirs of pathogens that have substantial impacts on other wildlife and humans (e.g., rabies virus, canine distemper virus, protoparvovirus, *Baylisascaris* spp., etc.) and should be handled and housed with caution.

AFWA guidance:

https://www.fishwildlife.org/application/files/2415/9230/2533/AFWA_Statement_on_COVID-19_and_Mustelids_Felids_and_Canids_June_9_2020.pdf

ZAHP guidance:

<https://zahp.aza.org/covid-19-animal-care/>

(Prepared by Raquel Francisco, Sonia M. Hernandez, and Nicole Nemeth)

Recent SCWDS Publications Available

Below are some recent publications authored or co-authored by SCWDS staff. Many of these can be accessed online from the web pages of the various journals. If you do not have access to this service and would like to have a copy of any of these papers, let us know. Many can be sent to you electronically with minimum effort; others will be mailed to you. For your convenience, please indicate requested publications, fill out the form on page 7, and check the appropriate box to receive either an electronic copy or a hard copy and return it to us: SCWDS, College of Veterinary Medicine, University of Georgia, Athens, GA 30602 or email at brewton@uga.edu.

- ____ Allen, S.E., C.M. Jardine, K. Hooper-McGrevy, A. Ambagala, A.M. Bosco-Lauth, M.R. Kunkel, D.G. Mead, L. Nituch, M.G. Ruder, and N.M. Nemeth. 2020. Serological evidence of arthropod-borne virus infections in wild and captive ruminants in Ontario, Canada. *The American Journal of Tropical Medicine and Hygiene* 103(5): 2100-2107. doi: 10.4269/ajtmh.20-0539.
- ____ Ayala, A., S. Hernandez, L. Haas, S. Fink, and M. Yabsley. 2020. Risky business in Georgia's wild birds: Contact rates with backyard chickens may influence pathogen transmission in passerines. *Epidemiology and Infection* 148.
- ____ Ayala, A.J., M.J. Yabsley, and S.M. Hernandez. 2020. A review of pathogen transmission at the backyard chicken-wild bird interface. *Frontier Veterinary Science* 7: 539925; doi: 10.3389/fvets.2020.539925.
- ____ Bloodgood, J.M. Kiupel, J. Melotti, and K. Straka. 2021. Chronic wasting disease diagnostic discrepancies: The importance of testing both medial retropharyngeal lymph nodes. *Journal of Wildlife Diseases* 57(1) 194-198. doi: 10.7589/JWD-D-20-00007.
- ____ Box, E.K., C.A. Cleveland, K.B. Garrett, R.K. Grunert, K. Hutchins, A.A. Majewska, A.T. Thompson, S.T. Wyckoff, C. Ehlers, and M.J. Yabsley. 2021. Copepod consumption by amphibians and fish with implications for transmission of *Dracunculus* species. *International Journal of Parasitology Parasites and Wildlife* 15: 231-237. doi: 10.1016/j.ippaw.2021.06.001.
- ____ Box, E.K., M.J. Yabsley, K.B. Garrett, A.T. Thompson, S.T. Wyckoff, and C.A. Cleveland. 2021. Susceptibility of anurans, lizards, and fish to infection with *Dracunculus* species larvae and implications for their roles as paratenic hosts. *Science Reports* 11(1): 11802. doi: 10.1038/s41598-021-91122-5.
- ____ Carmen, J., D. Stallknecht, C. Leyson, R. Berghaus, B. Jordan, M. Patin-Jackwood, G. Hitchener, and M. Franca. 2020. Recombinant hemagglutinin glycoproteins provide insight into binding to host cells by H5 influenza viruses in wild and domestic birds. *Virology* 550: 8-20.
- ____ Carter, D.L., P. Link, G. Tan, D.E. Stallknecht, and R.L. Poulson. 2021. Influenza A viruses in whistling ducks (Subfamily Dendrocygninae). *Viruses* 13(2): 192. doi: 10.3390/v13020192.
- ____ Casey, C.L., S.L. Rathbun, D.E. Stallknecht, and M.G. Ruder. 2021. Spatial analysis of the 2017 outbreak of hemorrhagic disease and physiographic region in the eastern United States. *Viruses* 13(4): 550. doi: 10.3390/v13040550.
- ____ Cleveland, C.A., M.L. Eberhard, K.B. Garrett, A.T. Thompson, L. Swanepoel, E.A. Miller, O.L. Stephens, and M.J. Yabsley. 2020. *Dracunculus* species in Meso-mammals from Georgia, United States, and implications for the Guinea Worm Eradication Program in Chad, Africa. *Journal of Parasitology* 106(5): 616-622.
- ____ Cleveland, C.A., L. Swanepoel, J.D. Brown, M.J. Casale, L. Williams, and M.J. Yabsley. 2020. Surveillance for *Borrelia* spp. in upland game birds from Pennsylvania, USA. *Ticks and Tick-borne Diseases* 7(3): 82. doi: 10.3390/vetsci7030082.
- ____ Conrad, J., J. Norman, A. Rodriguez, P.M. Dennis, R. Arguedas, C. Jimenez, J.G. Hope, M.J. Yabsley, and S.M. Hernandez. 2021. Demographic and pathogens of domestic, free-roaming pets and the implications for wild carnivores and human health in the San Luis Region of Costa Rica. *Veterinary Science* 8(4): 65. doi: 10.3390/vetsci8040065.
- ____ Criado, M.F., K.A. Moresco, D.E. Stallknecht, and D.E. Swayne. 2021. Low-pathogenicity influenza viruses replicate differently in laughing gulls and mallards. *Influenza and Other Respiratory Viruses* doi: 10.1111/irv.12878. PMID: 34109758.
- ____ Davy, C.M., L. Shirose, D. Campbell, R. Dillon, C. McKenzie, N. Nemeth, T. Braithwaite, H. Cai, T. Degazio, T. Dobbie, S. Egan, H. Fotherby, J.D. Litzgus, P. Manorome, S. Marks, J.E. Paterson, L. Sigler, D. Slavic, E. Slavik, J. Urquhart, and C. Jardine. 2021. Revisiting Ophidiomycosis (Snake Fungal Disease) after a decade of targeted research. *Frontiers in Veterinary Science* 8: 665805. doi: 10.3389/fvets.2021.665805.

- ____ Durrant, C., E. Thiele, N. Holroyd, S.R. Doyle, G. Salle, A. Tracey, G. Sankaranarayanan, M. Lotkowska, H. Bennett, T. Huckvale, Z. Hance, A.I. Schulte-Hostedde, J. Foster, C.A. Cleveland, M.J. Yabsley, E. Ruiz-Tiben, M. Berriman, M.L. Eberhard, and J.A. Cotton. 2020. Population genomic evidence that human and animal infections in Africa came from the same populations of *Dracunculus medinensis*. *PLoS Neglected Tropical Diseases* 14(11): e0008623. doi: 10.1371/journal.pntd.0008623.
- ____ Egizi, A., L. Bulaga-Seraphin, E. Alt, W.I. Bajwa, J. Bernick, M. Bickerton, S.R. Campbell, N. Connally, K. Doi, R.C. Falco, D.N. Gaines, T.L. Greay, V.L. Harper, A.C.G. Heath, J. Jiang, T.A. Klein, L. Maestas, T.N. Mather, J.L. Occi, C.L. Oskam, J. Pendleton, M. Teator, A.T. Thompson, D.M. Tufts, R. Umemiya-Shirafuji, M.C. VanAcker, M.J. Yabsley, and D.M. Fonseca. 2020. First glimpse into the origin and spread of the Asian longhorned tick, *Haemaphysalis longicornis*, in the United States. *Zoonoses Public Health* 67(6): 637-650. doi: 10.1111/zph.12743.
- ____ Escobar, L.E., S. Carver, P.C. Cross, L. Rossi, E.S. Almberg, M.J. Yabsley, K.D. Niedringhaus, P. Van Wick, E. Dominguez-Villegas, F. Gakuya, Y. Xie, S. Angelone, C. Gortazar, and F. Astorga. 2021. Sarcoptic mange; an emerging panzootic in wildlife. *Transbound Emerging Diseases* doi: 10.1111/tbed.14082.
- ____ Fenton, H., S. McBurney, E.J. Elsmo, C.A. Cleveland, and M.J. Yabsley. 2021. Lesions associated with *Bartonella taylorii*-like bacterium infection in a free-ranging, young-of-the-year raccoon from Prince Edward Island, Canada. *Journal of Veterinary Diagnostic Investigation* 33(2): 362-365. doi: 10.1177/1040638720988515.
- ____ Gettings, J.R., S.C.W. Self, C.S. McMahan, D.A. Brown, S.K. Nordone, and M.J. Yabsley. 2020. Regional and local temporal trends of *Borrelia burgdorferi* and *Anaplasma* spp. seroprevalence in domestic dogs; contiguous United States 2013-2019. *Frontier Veterinary Science* 7: 561592. doi: 10.3389/fvets.2020.561592.
- ____ Gibson, D.J., N.M. Nemeth, H. Beaufreire, C. Varga, M.M. Garner, and L. Susta. 2021. Lymphoma in psittacine birds: A histological and immunohistochemical assessment. *Veterinary Pathology* 3009858211002180. doi: 10.1177/03009858211002180.
- ____ Guagliardo, S.A.J., E. Ruiz-Tiben, D.R. Hopkins, A.J. Weiss, P.T. Ouakou, H. Zirimwabagabo, K. Unterwegner, D. Tindall, V.A. Cama, H. Bishop, S.G.H. Sapp, and S.L. Roy. 2021. Surveillance of human guinea worm in Chad, 2010-2018. *American Journal of Tropical Medicine and Hygiene* doi: 10.4269/ajtmh.20-1525.
- ____ Guagliardo, S.A.J., R. Wiegand, S.L. Roy, C.A. Cleveland, H. Zirimwabagabo, E. Chop, P.T. Ouakou, E. Ruiz-Tiben, D. Hopkins, and A. Weiss. 2021. Correlates of variation in Guinea worm burden among infected domestic dogs. *American Journal of Tropical Medicine and Hygiene* 104(4): 1418-1424. doi: 10.4269/ajtmh.19-0924.
- ____ Hernandez, S.M., J.J. Maurer, M.J. Yabsley, V.E. Peters, A. Presotto, M. Murray, S. Curry, S. Sanchez, P. Gerner-Smidt, K. Hise, J. Huang, K. Johnson, T. Kawn, and E.K. Lipp. 2021. Free-living aquatic turtles as sentinels of *Salmonella* spp. for water bodies. *Frontiers in Veterinary Sciences* doi.org/10.3389/fvets/2021.674973.
- ____ Jerry, C., D. Stallknecht, C. Leyson, R. Berghaus, B. Jordan, M. Pantin-Jackwood, G. Hitchener, and M. Franca. 2020. Recombinant hemagglutinin glycoproteins provide insight into binding to host cells by H5 influenza viruses in wild and domestic birds. *Virology* 550: 8-20.
- ____ Kariithi, H.M., H.L. Ferreira, C.N. Welch, L.O. Ateya, A.A. Apopo, R. Zoller, J.D. Volkening, D. Williams-Coplin, D.J. Parris, T.L. Olivier, D. Goldenberg, Y.S. Binepal, S.M. Hernandez, C.L. Afonso, and D.L. Saurez. 2021. Surveillance and genetic characterization of virulent Newcastle Disease Virus Subgenotype V.3 in indigenous chickens from backyard poultry farms and live bird markets in Kenya. *Viruses* 13(1): E103. doi: 10.3390/v13010103.
- ____ Keel, M.K., S. Keeler, J. Brown, H. Fenton, B. Munk, R. Gerhold, N. Gottdenker, M. Ruder, E. Elsmo, and N. Nemeth. 2020. Granulomatous inflammation of the muzzle in white-tailed deer (*Odocoileus virginianus*) and mule deer (*Odocoileus hemionus*) associated with *Mannheimia granulomatis*. *Veterinary Pathology* 57(6): 838-844. doi: 10.1177/0300985820948825.
- ____ McKenzie, C.M., P.T. Oesterle, B. Stevens, L. Shirose, B.N. Lillie, C.M. Davy, C.M. Jardine, and N.M. Nemeth. 2020. Pathology associated with ophidiomycosis in wild snakes in Ontario, Canada. *Canadian Veterinary Journal* 61(9): 957-962.
- ____ McKenzie, C., P. Oesterle, B. Stevens, L. Shirose, G.F. Mastromonaco, B.N. Lillie, C.M. Davey, C.M. Jardine, and N.M. Nemeth. 2020. Ophidiomycosis in red cornsnakes (*Pantherophis guttatus*): Potential roles of brumation and temperature on pathogenesis and transmission. *Veterinary Pathology* 57(6): 825-837. doi: 1177/0300985820953423.
- ____ Nemeth, N.M., J. Root, A.E. Hartwig, R.A. Bowen, A.M. Bosco-Lauth. 2021. Powassan virus experimental infections in three wild mammal species. *American Journal of Tropical Medicine and Hygiene* 104(3): 1048-1054. doi: 10.4269/ajtmh.20-0105.
- ____ Nemeth, N.M., L.M. Williams, A.M. Bosco-Lauth, P.T. Oesterle, M. Helwig, R.A. Bowen, and J.D. Brown. 2021. West Nile virus infection in ruffed grouse (*Bonasa umbellus*) in Pennsylvania, USA: A multi-year comparison of statewide serosurveys and vector indices. *Journal of Wildlife Diseases* 57(1): 51-59. doi: 10.7589/JWD-D-19.00016.
- ____ Niedringhaus, K.D., J.D. Brown, M. Murray, B.C.M. Oliveira, and M.J. Yabsley. 2021. Chorioretinitis

in an American black bear (*Ursus americanus*) from Massachusetts, USA. *Journal of Wildlife Diseases* doi: 10.7589/JWD-D-20-00143.

Niedringhaus, K.D., N.M. Nemeth, S. Gibbs, J. Zimmerman, L. Shender, K. Slankard, H. Fenton, C. Bahnson, M.F. Dalton, E.J. Elsmo, R. Poppenga, B. Millsap, and M.G. Ruder. 2021. Anticoagulant rodenticide exposure and toxicosis in bald eagles (*Haliaeetus leucocephalus*) and golden eagles (*Aquila chrysaetos*) in the United States. *PLoS One* 16(4): e0246134. doi: 10.1371/journal.pone.0246134.

Niedringhaus, K.D., L.A. Shender, A. DiNuovo, L.J. Flewelling, G. Maboni, S. Sanchez, P.J. Deitschel, J. Fitzgerald, and N.M. Nemeth. 2021. Mortality in common (*Sterna hirundo*) and sandwich (*Thalasseus sandvicensis*) terns associated with Bisgaard taxon 40 infection on Marco Island, Florida, USA. *Journal of Comparative Pathology* 184(3): 12-18. doi: 10.1016/j.jcpa.2021.01.009.

Poulson, R., D. Carter, S. Beville, L. Niles, A. Dey, C. Minton, P. McKenzie, S. Krauss, R. Webby, R. Webster, and D.E. Stallknecht. 2021. Influenza A viruses in ruddy turnstones (*Arenaria interpres*); connecting wintering and migratory sites with an ecological hotspot at Delaware Bay. *Viruses* 12(11): 1205. doi: 10.3390/v12111205.

Priest, J.W., B.N.R. Ngandolo, M. Lechenne, C.A. Cleveland, M.J. Yabsley, A.J. Weiss, S.L. Roy, and V. Cama. 2021. Development of a multiplex bead assay for the detection of canine IgG₄ antibody responses to Guinea worm. *American Journal of Tropical Medicine and Hygiene* 104(1): 303-312. doi: 10.4269/ajtmh.20-0914.

Ramey, A.M., A.B. Reeves, J.Z. Drexler, J.T. Ackerman, S. De La Cruz, A.S. Lang, C. Leyson, P. Link, D.J. Prosser, G.J. Robertson, J. Wight, S. Youk, E. Spackman, M. Pantin-Jackwood, R.L. Poulson, and D.E. Stallknecht. 2020. Influenza A viruses remain infectious for more than seven months in northern wetlands of North America. *Proceedings of Biological Sciences* 287(1934): 20201680.

Reeves, A.B., M.L. Killian, M.E. Tanner, B.J. Lagassé, A.M. Ramey, D.E. Stallknecht, and R.L. Poulson. 2021. Coding-complete genome sequence of Avian orthoavulavirus 16, isolated from Emperor goose (*Anser canagicus*) feces, Alaska, USA. *Microbiology Resource Announcements* 10(1): e01275-20. doi: 10.1128/MRA.01275-20.

Reeves, A.B., A.M. Ramey, R.L. Poulson, and D.E. Stallknecht. 2020. The genome sequence of an H6N5 influenza A virus strain isolated from a northern pintail (*Anas acuta*) sampled in Alaska, USA, shares high identity with that of a South Korean wild bird strain. *Microbiology Resource Announcements* 9(33): e00639-20.

Richards, R.L., C.A. Cleveland, R.J. Hall, R.T. Ouakou, A.W. Park, E. Ruiz-Tiben, A. Weiss, M.J. Yabsley, and V.A. Ezenwa. 2020. Identifying correlates of Guinea worm (*Dracunculus medinensis*)

infection in domestic dog populations. *PLoS Negl Trop Dis* 14(9): e0008620.

Rojas-Jimenez, J., J.A. Morales-Acuna, M. Arguello-Saenz, S.E. Acevedo-Gonzalez, M.J. Yabsley, and A. Urbina-Villalobos. 2021. Histopathological findings of infections caused by canine distemper virus, *Trypanosoma cruzi*, and other parasites in two free-ranging white-nosed coatis (*Nasua narica*) (Carnivora: Procyonidae) from Costa Rica. *Journal of Threatened Taxa* 13(1): 17521-17528.

Sapp, S.G.H., D.A. Elsemore, R. Hanna, and M.J. Yabsley. 2020. Experimental comparison of *Baylisascaris procyonis* definitive host competence between domestic dogs and raccoons (*Procyon lotor*). *Parasitology* 147(12): 1344-1351.

Stilwell, N.K., L.L. Clarke, E.W. Howerth, C. Kienzle Dean, A. Fojtik, L.P. Hollander, D. Carter, D.A. Osborn, G.J. D'Angelo, K.V. Miller, D.E. Stallknecht, and M.G. Ruder. 2021. The effect of maternal antibodies on clinical response to infection with epizootic hemorrhagic disease virus in white-tailed deer (*Odocoileus virginianus*) fawns. *Journal of Wildlife Diseases* 57(1): 189-193.

Teitelbaum, C.S., J. Hepinstall-Cymerman, A. Kidd-Weaver, S.M. Hernandez, S. Altizer, and R.J. Hall. 2020. Urban specialization reduces habitat connectivity by a highly mobile wading bird. *Movement Ecology* 8(1): 49. doi: 10.1186/s40462-020-00233-7.

Thompson, A.T., S.A. White, D. Shaw, K.B. Garrett, S.T. Wyckoff, E.E. Doub, M.G. Ruder, and M.J. Yabsley. 2021. A multi-seasonal study investigating the phenology, host and habitat associations, and pathogens of *Haemaphysalis longicornis* in Virginia, USA. *Ticks and Tick-borne Diseases* 12(5): 101773. doi: 10.1016/j.ttbdis.2021.101773.

Young, K.T., K.K. Lahmers, H.S. Sellers, D.E. Stallknecht, R.L. Poulson, J.T. Saliki, S.M. Tompkins, I. Padykula, C. Siepker, E.W. Howerth, M. Todd, and J.B. Stanton. 2021. Randomly primed, strand-switching, MinION-based sequencing for the detection and characterization of cultured RNA viruses. *Journal of Veterinary Diagnostic Investigation* 33(2): 202-215. doi: 10.1177/1040638720981019.

PLEASE SEND REPRINTS MARKED TO:

NAME _____

E-MAIL _____

ADDRESS _____

CITY _____

STATE _____ ZIP _____

ELECTRONIC COPY ☐

HARD COPY ☐

SCWDS BRIEFS

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

Nonprofit Organization
U.S. Postage
PAID
Athens, Georgia
Permit No. 11

RETURN SERVICE REQUESTED



Information presented in this newsletter is not intended for citation as scientific literature. Please contact the Southeastern Cooperative Wildlife Disease Study if citable information is needed.

Information on SCWDS and recent back issues of the *SCWDS BRIEFS* can be accessed on the internet at <https://vet.uga.edu/scwds>. If you prefer to read the BRIEFS online, just send an email to Jeanenne Brewton (brewton@uga.edu) or Michael Yabsley (myabsley@uga.edu) and you will be informed each quarter when the latest issue is available.