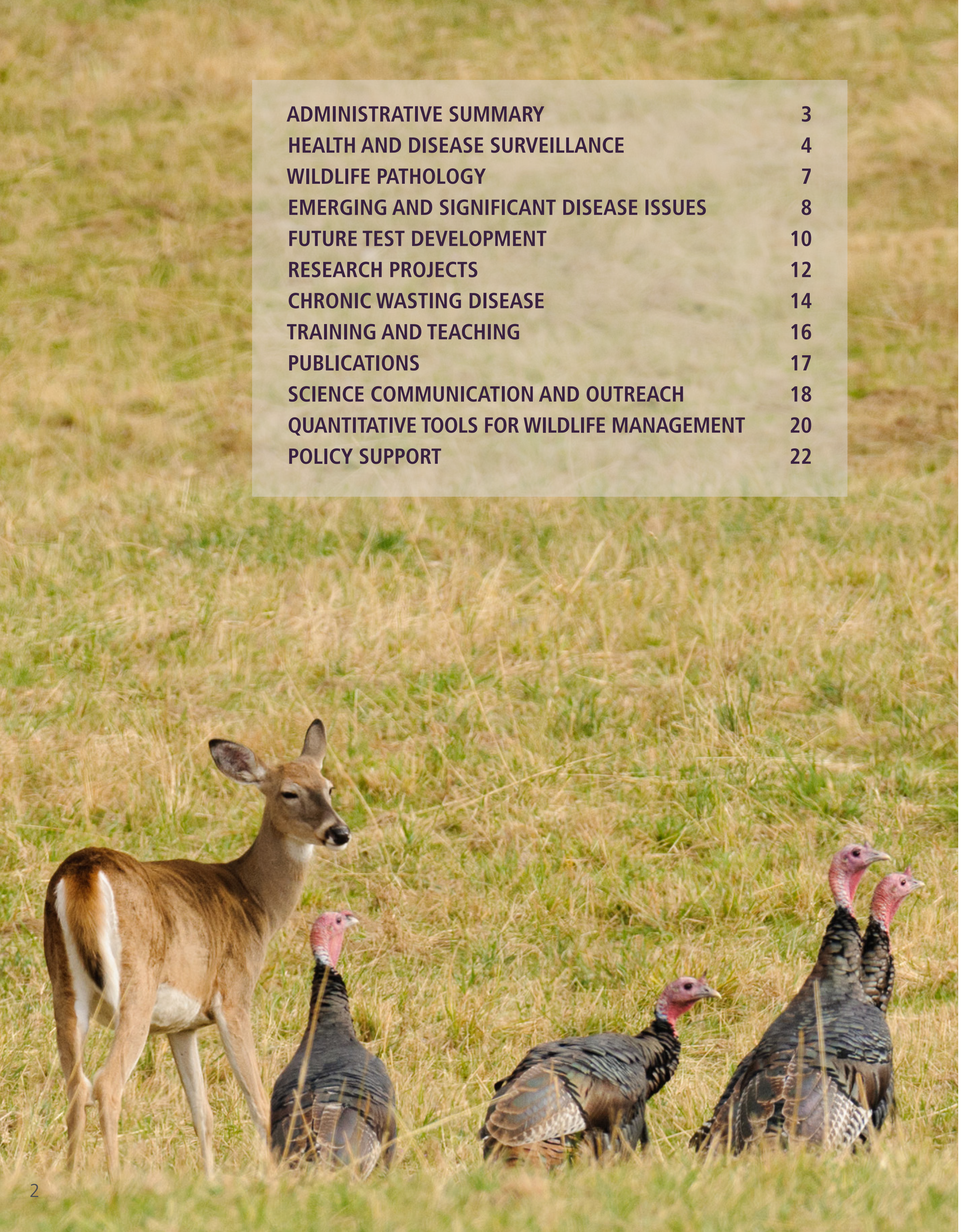
New York State Wildlife Health Program

10 Year Summary Report 2011-2021

Promoting the health and sustainability of wildlife populations through integration of wildlife ecology and veterinary medicine



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ADMINISTRATIVE SUMMARY

The New York State Wildlife Health Program (WHP) was the concept envisioned by Patrick Martin, long time head of the Department of Environmental Conservation (DEC) Special Licenses Unit and our first program leader. He saw a need for the agency to have additional support to prevent, detect, and manage wildlife disease outbreaks after witnessing the introduction of white-nose syndrome, chronic wasting disease and West Nile virus in New York. As a hub of international travel, New York is a high-risk location for the emergence of wildlife disease, including those that can impact humans. The Wildlife Health Unit in Delmar had existed for decades, but was struggling to keep up with increased demands.

This new program was a unique partnership between the veterinary college and a state agency. We started with a five-year strategic plan developed by a working group of DEC administrators, regional wildlife managers, wildlife health biologists, and Cornell veterinarians and a disease ecologist. The basis was the One Health principle that wildlife, human, and domestic animal health are intertwined. A product of six months of discussion in spring of 2011, the program focus areas were defined as Surveillance, Training, Research, Policy, and Communications.

The first few years of the official program were spent building a strong statewide surveillance network, training staff in personnel safety, and identifying critical needs for research and policy support. We have improved our case management system from paper stored in filing cabinets to a robust data management system with thousands of cases available in a system searchable by species, diagnosis and location. Archived samples from hundreds of animals are catalogued and stored in our "biobank" to facilitate research projects and genetic analysis. In 2012, we started visiting regions every other year to host wildlife health workshops, get to know the staff, and provide critical training to ensure their safety in handling diseased wildlife.

In the second five-year strategic plan, we worked with our newly formed DEC Wildlife Health Team to identify needs in improving communications and use of data analysis to inform management decisions. Biologists can access safety training videos and lectures, disease fact sheets, and population modeling tools on our program website. There are new policy documents for humane euthanasia, chemical immobilization, and disease outbreak response, as well as a streamlined chronic wasting disease surveillance system. The program has collaborative research projects with numerous other universities, agencies, and disease labs, which have produced new diagnostic tests, assessed population impacts at a regional scale, and identified new and emerging diseases. Our website, listservs, social media, and networks of professional relationships allow us to routinely communicate with other state and federal agencies to coordinate disease surveillance and response. We continue to strive to share wildlife disease information with key stakeholders and the public as well.

We've come a long way in 10 years. What does the future hold? We are on our third strategic plan that identifies areas we need to strengthen. We are looking forward to getting back out to conduct regional wildlife health workshops in 2022. We have more test development and models in development to make the most of the animals DEC staff works so hard to get to the labs. COVID-19 has opened many eyes to the importance of wildlife health, and New York is positioned to provide tools and strategies to improve the overall level of wildlife health nationally.

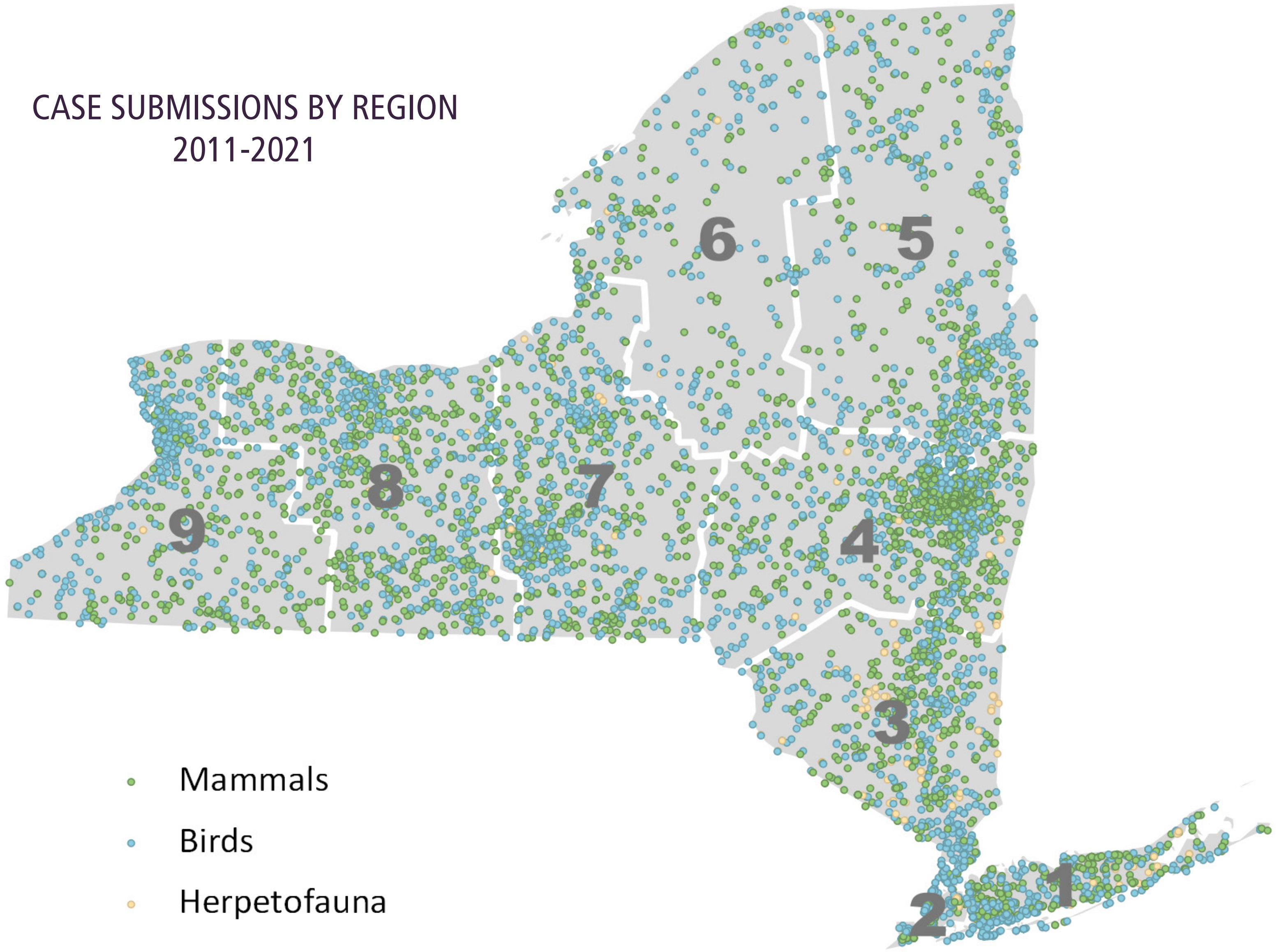
HEALTH AND DISEASE SURVEILLANCE

The WHP investigates wildlife mortality events across New York State to monitor the health of wildlife populations. These investigations are critical for detecting novel diseases and identifying significant patterns that may be associated with emerging diseases.

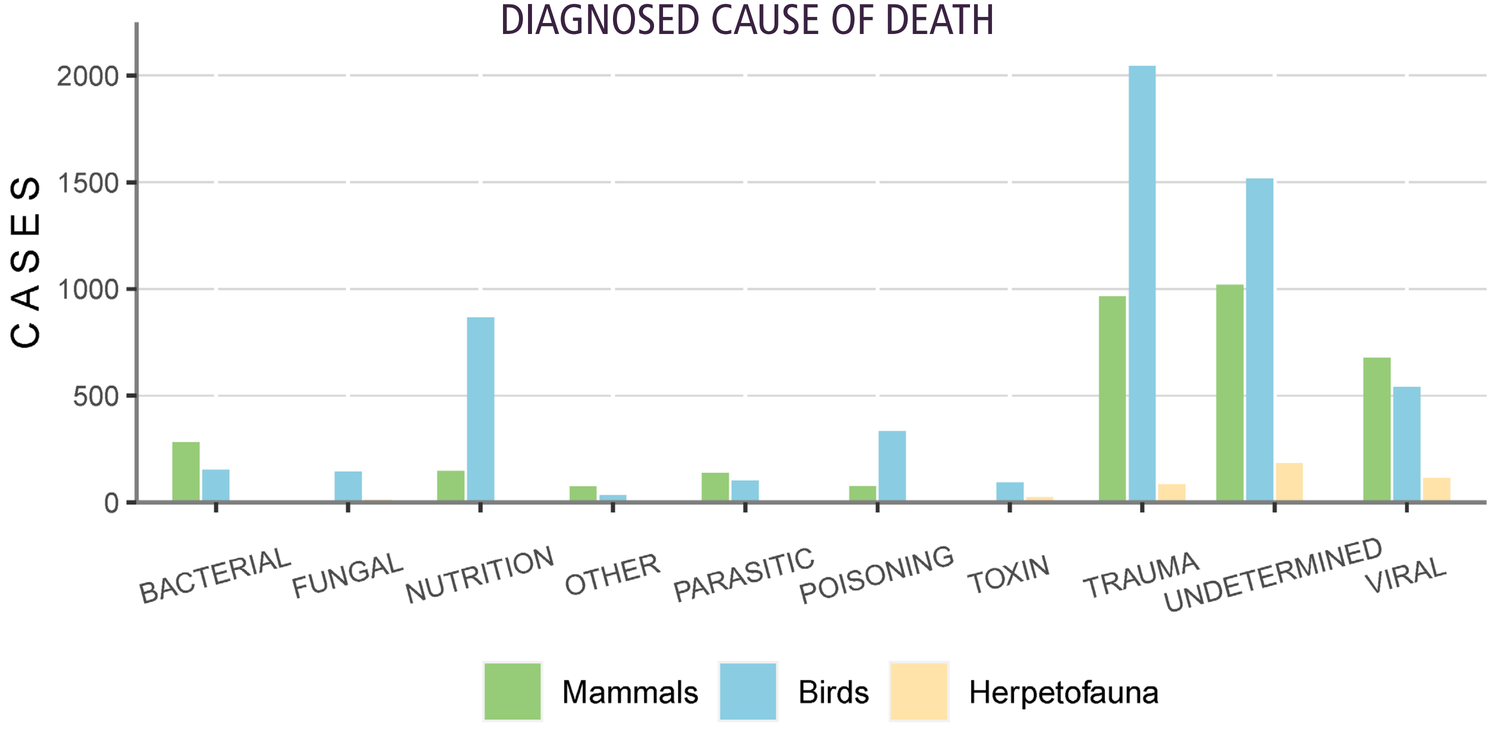
After a wildlife mortality event is identified (usually through public reporting), DEC staff conduct a site visit, gather information, and collect specimens. The specimens are sent to the Wildlife Health Unit in Delmar, NY, the Animal Health Diagnostic Center in Ithaca, NY, and the Cornell Duck Lab on Long Island for necropsy and diagnostic testing.

Between 2011 and 2021, the WHP examined 12,915 specimens representing 267 species. This includes 173 species of birds, 37 species of reptiles and amphibians, and 57 species of mammals. Full necropsies are performed on approximately 70% of specimens submitted. Between 2019 and 2021, an average of 800 necropsies were performed each year. In addition, the Wildlife Health Unit has conducted 297 forensic examinations to assist law enforcement. We now average 51 forensic examinations per year.

CASE SUBMISSIONS BY REGION
2011-2021



DIAGNOSED CAUSE OF DEATH



DIAGNOSIS SUMMARY

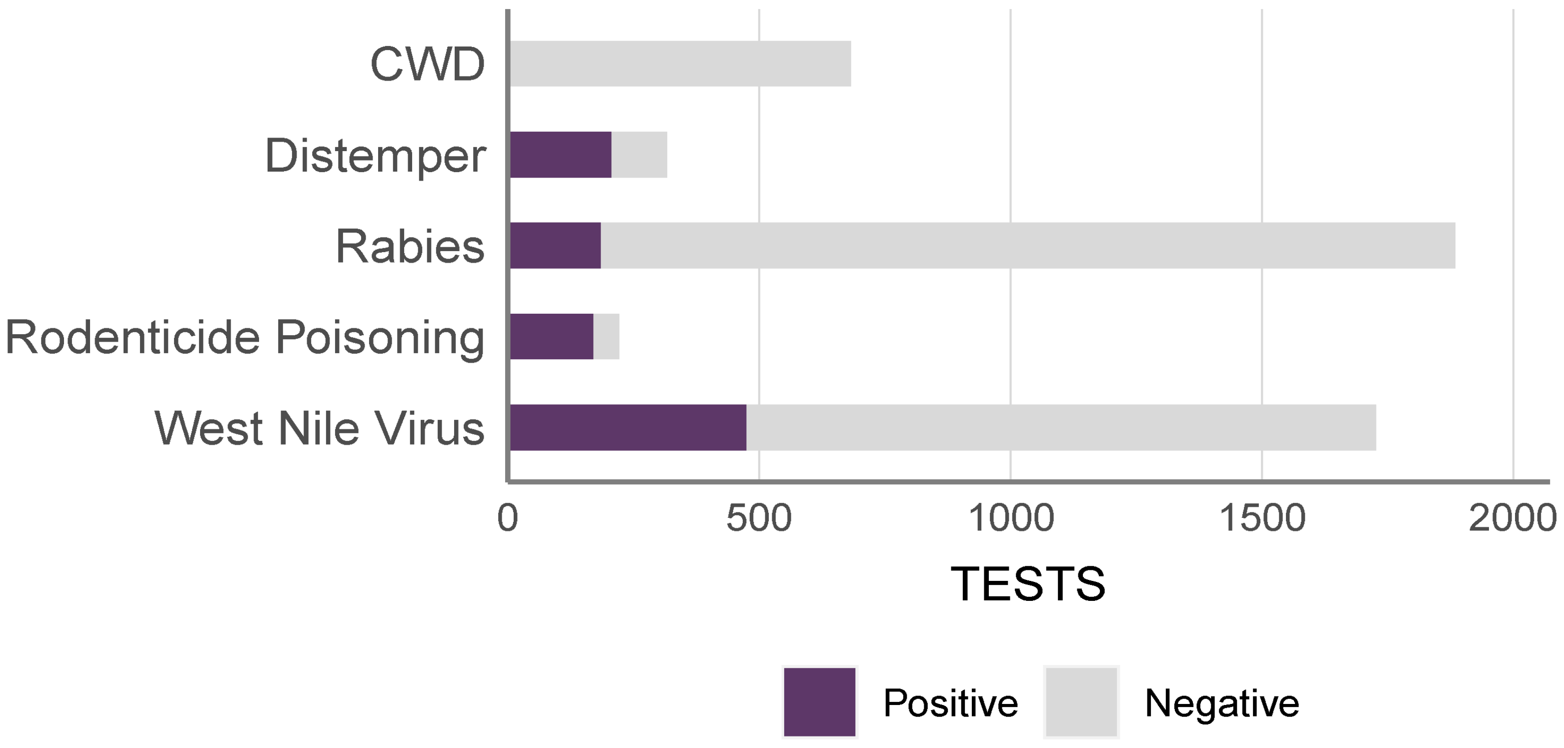
The most frequent primary cause of death for animals examined by the WHP is physical trauma, affecting 32% of the animals examined. Common types of physical trauma include vehicle strikes, weather events, and predator attacks. It is sometimes difficult in mortality investigations to determine cause of death if the specimen is in poor condition or if there isn't enough additional information about the event.

12,915 animals examined
297 forensic examinations

7,564 birds **173** species
4,701 mammals **57** species
567 herpetofauna **37** species

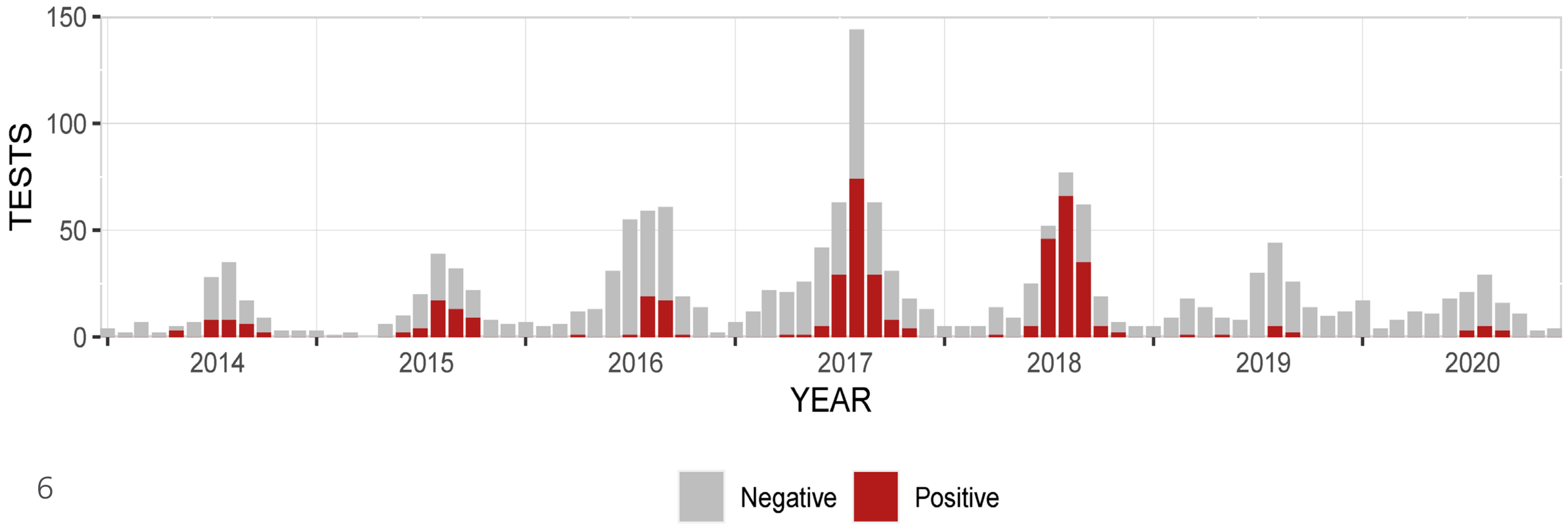
TARGETED DISEASE SURVEILLANCE

The WHP routinely tests all mammal specimens for rabies and all white-tailed deer and other cervids for chronic wasting disease (CWD).



WEST NILE VIRUS SURVEILLANCE 2014-2020

Long term monitoring of wildlife diseases can be useful for describing trends and identifying deviations from those trends, which can lead to important insights, such as environmental or anthropogenic factors that may affect disease prevalence. The WHP monitors a number of wildlife diseases of concern, including West Nile virus (WNV). As shown in the figure, WNV exhibits a strong seasonal pattern, peaking in the warmest months of the year. Between 2014 and 2020, the WHP tested 1,670 birds from across New York State.



WILDLIFE PATHOLOGY

NECROPSY SERVICE

The core function of the WHP is to conduct disease surveillance to identify pathogens of concern and monitor trends. This is accomplished by three laboratories working in concert: the Wildlife Health Unit (WHU) in Delmar, the Animal Health Diagnostic Center (AHDC) in Ithaca, and the Cornell Duck Lab on Long Island. Gross necropsies are performed at all three facilities and board-certified pathologists at the AHDC and Duck Lab examine the histopathology (tissue) slides. The positioning of these three labs makes it easier for DEC staff to get specimens in for examination.

The necropsy services see a wide diversity of species. Mammals and birds comprise most cases, with smaller numbers of reptiles and amphibians. We have examined 18 orders of birds and 11 families of mammals. Our diagnostic results show fluctuations in diseases throughout the state. Submissions of birds increase during years of high West Nile virus prevalence, outbreaks of reovirus infections in crows, and *Salmonella* outbreaks in finches. Diseases in white-tailed deer drive variation in mammal cases, with peak numbers occurring during Epizootic Hemorrhagic Disease outbreaks.

DISEASE AND DATA

High caseload and case diversity along with long-term diagnostic tracking allow us to establish a baseline prevalence of disease in wildlife in New York State. For instance, we are able to recognize novel conditions or increases in endemic disease prevalence each year, prepare to respond to these changes, and educate the public and DEC about the natural patterns of wildlife disease. The strength of baseline data is best exemplified by our recent publication reporting the use of our detailed necropsy records to identify the most common causes of death in white-tailed deer.

Similar data is available for other commonly encountered species, such as raptors which succumb to West Nile virus or whose numbers increase during Snowy owl irruptive years. Other species have more seasonal or irregular patterns of disease. We have also been able to pinpoint and track parvovirus and distemper virus outbreaks in raccoons and increase our surveillance for Rabbit Hemorrhagic Disease, a lethal disease in wild and domestic rabbits.

We regularly detect novel diseases of interest, including those that have zoonotic potential (i.e. transmissible from animals to humans) and pathogens that may be of concern to domestic species. We work closely with NYS Departments of Health, Agriculture and Markets, and NYC Mental Health and Hygiene to communicate our findings.

5,681 **necropsies performed**

EMERGING AND SIGNIFICANT DISEASE ISSUES

THEN AND NOW

Over the past 10 years, WHP has seen outbreaks of diseases with impacts on various wildlife species. WHP monitors these outbreaks to protect wildlife species and minimize potential human health consequences. Some of these investigations have resulted in development of diagnostic tests, creation of online tracking and mapping tools, publication of peer-reviewed journal articles, and implementation of in-depth investigations.

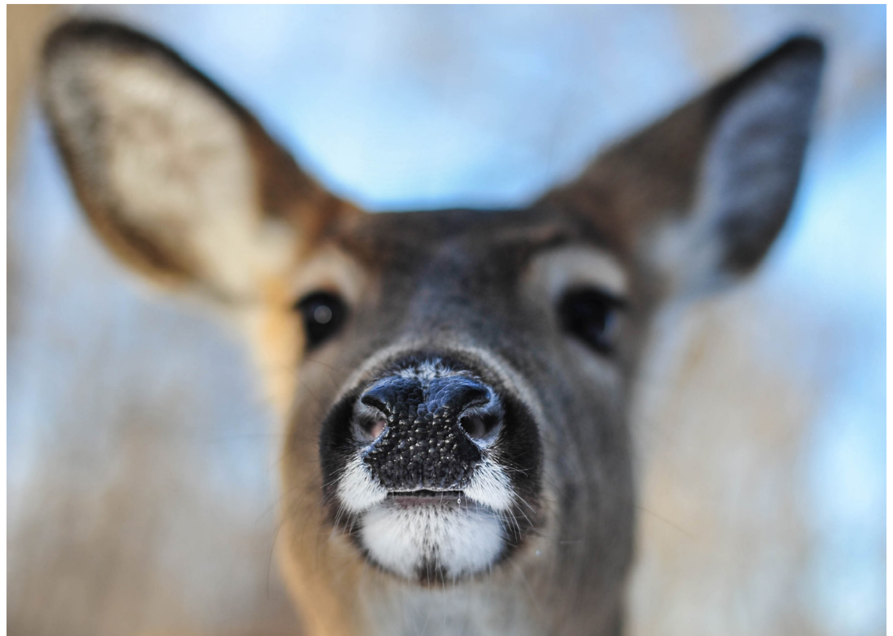
The 2015 outbreak of highly pathogenic avian influenza (HPAI) was the largest in the United States, resulting in over 40 million poultry being euthanized in the Midwest. Only a few cases were found in wild birds. We increased surveillance in New York but did not detect any positives.

Since late November 2021, numerous outbreaks of HPAI have been detected again in the US and Canada in both wild and domestic birds. This HPAI strain likely came from Europe where it has been circulating since 2020-2021. The first case of HPAI in New York was confirmed in February 2022 in a sanderling from Suffolk County. Cases are continuing in backyard poultry, rehabilitation facilities, shooting preserve/game bird breeder facilities, zoos, and free-ranging wild birds around the state. Species of wild birds affected include snow geese, Canada geese, ducks, bald eagles, and great horned owls. Unlike in 2015, this virus is substantially impacting wild birds and may become endemic.

The importance and relevance of emerging diseases to both human and wildlife health was reinforced in 2020 with the emergence of SARS-CoV-2, the virus causing COVID-19. As the pandemic took hold, the virus was transmitted through close contact from infected humans to animals, including domestic pets (dogs, cats and ferrets), zoo animals (tigers, lions, puma, snow leopards, and gorillas), and farmed mink.

Laboratory trials done by the National Wildlife Health Center indicated big brown bats are resistant to infection, but there is still concern that other North American bat species might be susceptible. Additional research has shown that large numbers of white-tailed deer have been infected and that they transmit it to other deer. There is concern about possible transmission back to humans.

Work in New York found 18% of deer samples collected here had antibodies to SARS-CoV-2. Field samples were collected opportunistically, so may not accurately reflect overall exposure rates in free-ranging deer. It is not known how free-ranging deer were exposed to the virus, but it is speculated that it could have been through people, the environment, other deer, or another animal species. CWHL and partners are contributing to a collaborative study assessing the prevalence of SARS-CoV-2 infection in New York white-tailed deer and the relationship between infection rates in humans and deer.



DIAGNOSTICS FOR EMERGING DISEASES

To effectively detect and track wildlife disease outbreaks, diagnostic tests are needed to confirm the presence of specific pathogens. WHP's close connection with Cornell's AHDC allows development of new tests specific for wildlife diseases, including Chytridiomycosis, caused by the fungus *Batrachochytrium dendrobatidis* (Bd). This is an emerging disease that has caused the decline or complete extinction of over 200 species of frogs and other amphibians and has been detected in most US states. A new strain of chytrid fungus, *Batrachochytrium salamandrivorans* (Bsal), is threatening salamander species globally. While the fungus has not been detected in the US, efforts are underway to survey wild populations. And in the past 10 years, wildlife agencies in the Northeast and Midwest detected increasing numbers cases of snake fungal disease (SFD) caused by *Ophidiomyces ophiodiicola*. In New York, multiple snake species, including timber rattlesnakes and Eastern Massasauga, are susceptible. In response to these threats, we now have tests for Bd, Bsal, and SFD.

TRACKING EMERGING DISEASES

Epizootic Hemorrhagic Disease (EHD) is endemic in the southern US and is becoming more common in the northern parts of the US. In some states, large outbreaks have affected thousands of deer. Once infected with the virus that causes EHD, deer usually die within 36 hours. Deer in New York have little immunity to this virus. We now have a molecular diagnostic test for EHD.

Outbreaks of EHD in New York are becoming more frequent and severe. In response to the most recent outbreak in 2021 in which there were over 2,000 reports of deer mortalities, CWHL developed an online reporting tool to assist DEC in collection of reports of dead and dying deer made by the general public. The reports fed into a map which DEC biologists used to determine their sample collection efforts for diagnostic testing. In this way, the outbreak was tracked and documented in an efficient and timely manner allowing DEC to determine the impacts on the deer population. The Southeastern Cooperative Wildlife Disease Study (SCWDS) at the University of Georgia compiles and maps trends in EHD. They identified two strains in NY in 2021: EHDV-2 and EHDV-6 which can infect cattle.

Research of emerging wildlife diseases is an important component of the WHP. In response to the emergence of EHD in New York, a CWHL graduate student has begun to investigate the disease in New York deer. Knowledge resulting from this type of study can help wildlife managers develop strategies to combat new diseases and predict impacts to wildlife populations.

By conducting routine surveillance and in-depth research and data analysis, the WHP is able to identify trends in wildlife disease occurrence and detect new pathogens. In this way, the program works to fulfill its goal of safeguarding the long-term health of the wildlife populations of New York.

FUTURE TEST DEVELOPMENT

WILDLIFE DIAGNOSTIC TEST DEVELOPMENT

With mounting global biodiversity losses and continued expansion of human-wildlife contact, the need for effective tools to monitor wildlife and their pathogens is ever-growing. Unfortunately, there are myriad challenges to the development and application of these tools ranging from practical constraints on obtaining appropriate control samples for tool development to incomplete knowledge of the life history of at-risk species. Through effective collaborations with diverse stakeholders, the WHP has developed valuable novel tools for many wildlife health issues. These tools include tests for wildlife pathogens including Epizootic Hemmorhagic Disease (EHD), *Batrachochytrium dendrobatidis* (Bd), *Batrachochytrium salamandrivorans* (Bsal), *Ophidiomyces ophiodiicola* (SFD), *Cytauxzoon felis*, Pigeon circovirus, Lymphoproliferative Disease Virus (LPDV) and more, which are now available at the AHDC molecular laboratory, as well as a suite of cutting-edge molecular biology tools including environmental DNA (eDNA) monitoring and Real-Time Quaking-Induced Conversion (RT-QuIC).

RT-QuIC

Prion diseases like chronic wasting disease (CWD) can be challenging to monitor, because prions are not detectable with typical test methods used for bacteria and viruses. Currently, the “gold standard” tests for CWD can only be done on tissues collected postmortem. These tests are both time- and labor-intensive and can miss low-grade infections. To improve testing capabilities for CWD, the CWHL has built capacity for a new test for prions, Real-Time Quaking Induced Conversion (RT-QuIC).

RT-QuIC testing uses the ability of CWD prions to convert normal proteins to misfolded prions. The test combines the deer sample with the normal protein and a dye that sticks to the prions and fluoresces. If there are CWD prions in the sample, they will convert the normal proteins, increasing the quantity and making it easier to detect. We measure the resulting fluorescence to determine if a sample contains CWD prions.

Importantly, RT-QuIC has potential to be faster and more sensitive than the current “gold standard” tests. By improving test sensitivity, we may be able to use RT-QuIC to find CWD prions from tissue samples collected from live deer or even non-invasive samples like urine and feces. This can help us find infections faster, so that we can prevent the spread of CWD through deer populations.

eDNA

Since 2015, the WHP has partnered with the DEC herpetofauna health team to develop and deploy novel, non-invasive methods for monitoring threatened species and their pathogens. These methods capture and characterize the trace genetic material that an animal has left behind in their environment, or environmental DNA (eDNA). We can capture and concentrate eDNA in bulk environmental samples to provide targeted information about the occupancy status of a specific host, identify the presence of pathogens, or catalog the biodiversity of a site.

Since its inception, the eDNA program at WHP has established a dedicated eDNA processing laboratory, trained DEC biologists in eDNA sample collection methods, created molecular tests for detection of five species of conservation concern, and pioneered new methods for pathogen eDNA surveillance. Currently, development of eDNA surveillance tools for three additional species is in progress.

LEAD TOXICOSIS IN BALD EAGLES: POPULATION-LEVEL IMPACTS

In 2018, the CWHL received funding from the Morris Animal Foundation to hire a quantitative modeler to lead the *Lead Toxicosis in Bald Eagle* research project.

This collaboration included over 60 regional professionals representing the fields of pathology, veterinary medicine, ecology, ornithology, wildlife management, mathematics, and statistics. We worked as a regional team to gather and analyze over 1,200 records from necropsies on eagles collected from a 7-state area (CT, MA, ME, NJ, NH, NY, and VT) between 1990-2018. Our findings, published in the *Journal of Wildlife Management*, demonstrated lead toxicosis depressed the long-term growth rate of the wild eagle population in the region by 4.2-6.4% over the past 30 years.

The research garnered significant media attention, with coverage appearing in 300 news outlets across the US and globe. More recently, the eagle team has submitted two additional manuscripts for peer review, one specifically for New York State and another that expands the use of the mathematical method to managers in other areas of the country and world.

The published paper, *Environmental Lead Reduces the Resilience of Bald Eagle Populations*, and quantitative tools developed for the analysis are free and openly available on the CWHL tools page entitled Population Dynamics of Bald Eagles in the Northeast US.

IMPROVING EASTERN HELLBENDER SURVIVAL

After years of documenting poor survival in captively reared and released hellbender salamanders, DEC biologists teamed with the WHP in 2014 to systematically monitor hellbenders for post-release health and survival. The field trial showed that all the released animals became rapidly infected with *Batrachochytrium dendrobatidis* (Bd) fungus; 19 of 21 died within 6-8 weeks of release.

In 2015-16, the WHP experimentally tested a Bd vaccine on a colony of 70 hellbenders in our laboratory. During the experimental vaccination and infections, we banked samples to measure infection severity, identify hellbender immune responses, and monitor the symbiotic communities of hellbender skin microbes which play a role in Bd infections. We found that hellbenders mounted an immune response to oral vaccination, but that neither their natural immunity, skin bacteria or vaccination protected them from disease. These findings can help inform prioritization of future management and conservation actions.

ENVIRONMENTAL DNA

Recently, collection and analysis of trace genetic material in environmental samples, or environmental DNA (eDNA), has emerged as a powerful toolkit for biodiversity monitoring. Currently, the majority of eDNA monitoring tools focus on detection of large-bodied aquatic animals. The WHP has advanced the leading edge of eDNA applications by developing and testing eDNA approaches for the study of pathogens and small-bodied, terrestrial animals.

In collaboration with Cornell Dept. of Natural Resources and the Environment and SUNY ESF, we developed eDNA tools for monitoring ranavirus, a globally-distributed virus that has caused die-offs of amphibians, reptiles, and fish. By analyzing tadpoles and matched water samples in a group of experimental ponds, we documented relationships between viral presence in hosts and their environment. We found that ranavirus levels in water samples were not exclusively a result of infections in tadpoles, suggesting this tool may aid in broader environmental monitoring of the virus.

With support from the DEC herpetofauna team, the WHP began developing methods to monitor the four-toed salamander, a terrestrial salamander categorized as a species of greatest conservation need in New York. We collaborated with biologists to collect eDNA samples from pools with known historic presence of four-toed salamanders and pools with known contemporary presence of the species on adjacent uplands. We found that four-toed salamanders are still present at sites of known historic occupancy, but that presence of adults in nearby uplands cannot be detected with eDNA collection. Additionally, we found widespread presence of the viral pathogen ranavirus in pools that four-toed salamanders may occupy, suggesting that conservation efforts for this species may need to consider threats from the virus.

CHRONIC WASTING DISEASE

NEW YORK LEADING THE WAY

New York has the distinction of being the only state to have eliminated chronic wasting disease (CWD) in free-ranging wild deer following a detection and takes its commitment to CWD prevention seriously. In 2005, CWD was detected in Oneida county in captive white-tailed deer in two facilities. Two wild deer were identified nearby. An intensive management effort followed, including maintaining a disease containment area for five years. Every hunting season, regional staff collect deer heads and samples from meat processors and taxidermists. Some regions pull samples themselves, but the majority are taken by staff at the WHU Lab. Testing is conducted at the AHDC. None of the 60,176 deer tested up to January 2022 have been positive. We are currently working with US Dept. of Agriculture and other states' testing labs to bring RT-QuIC as an approved test to have increased sensitivity and faster turn-around time.

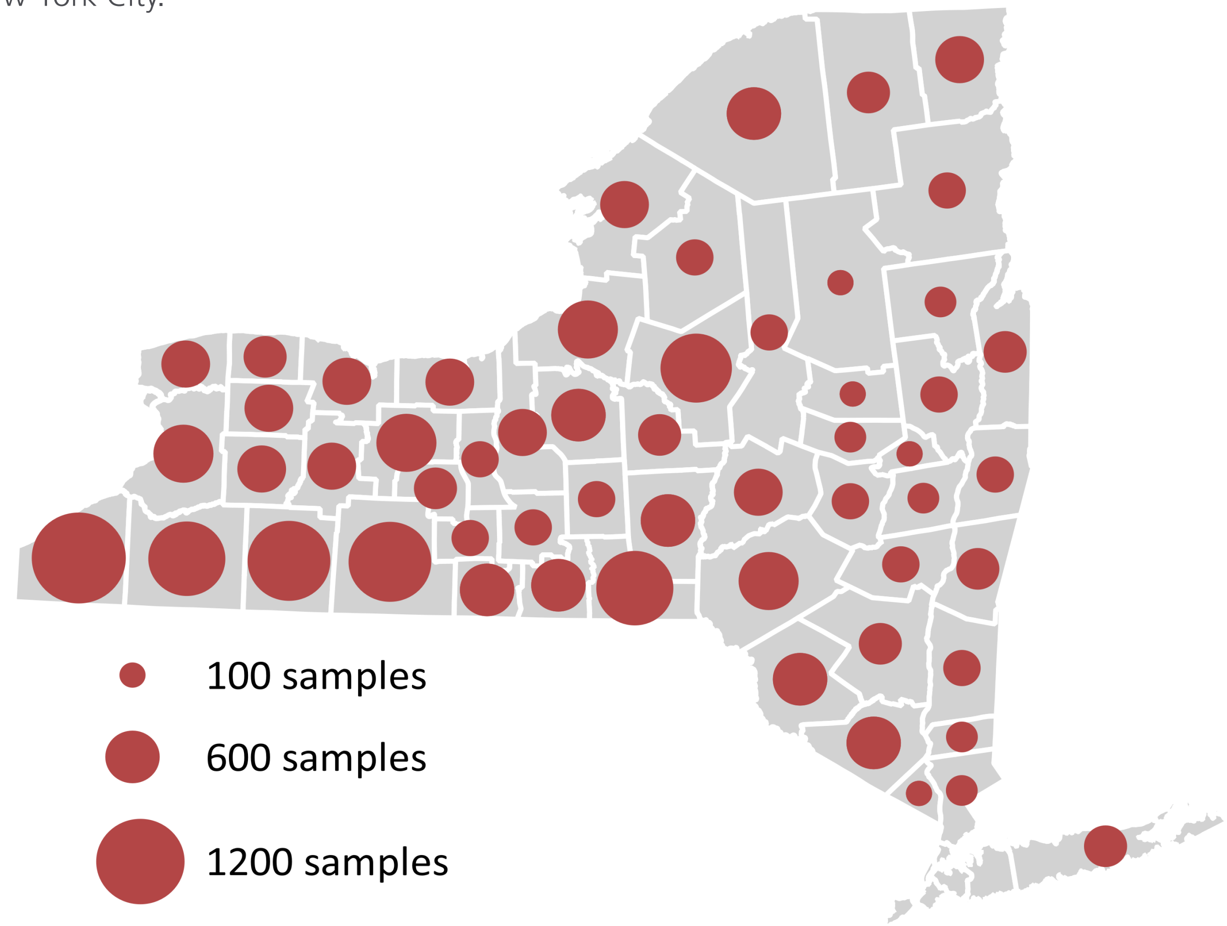
Other states across the country have not been so lucky; CWD has spread to 30 states as of April 2022. New York remains vigilant under the continuing threat of CWD and has taken a series of actions to prevent the disease from entering the state. An Interagency CWD Working Group, including DEC, Dept. of Agriculture and Markets (DAM), and Cornell wildlife health specialists, formed in 2011 to perform risk assessments and devise a risk-weighted surveillance plan to detect the earliest intrusion of CWD into the state. Biologists across the state have implemented a "county-quota system" and other states have adopted NYS's surveillance program.

We have an outstanding Taxidermy Partnership Program to have them collect high-value samples directly. The Working Group also penned a multi-agency response plan for wild or captive cases. Finally, the most unique product to come out of the Working Group was a Risk Minimization Plan to take actions identified in the risk assessment to lower the likelihood of CWD introduction and spread. For example, the DEC and DAM took regulatory actions to ban importation of live cervids and whole carcasses from all states.

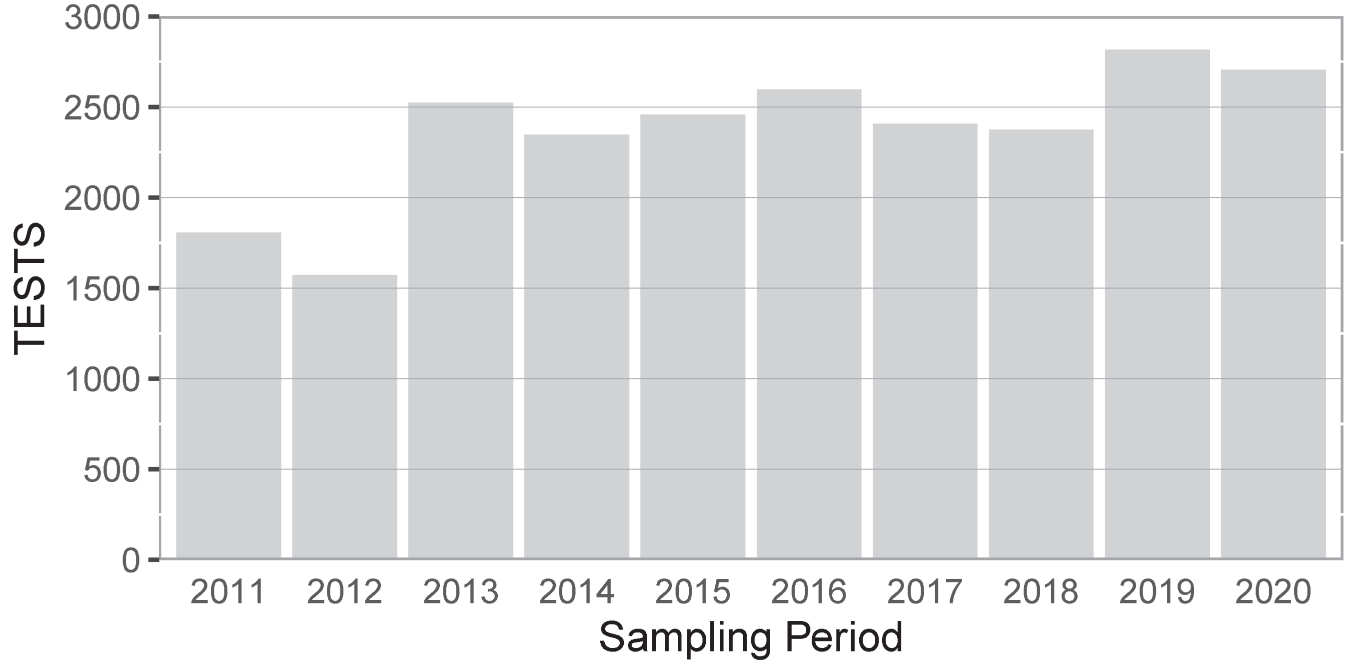
The activities and conditions of other states impact the risk of CWD introduction into New York. Therefore, it was imperative to raise the profile of surveillance activities across the region. We started the Surveillance Optimization Project (SOP4CWD) to provide maps, models, and data management tools to states free-of-charge. We have developed four state-specific and two region-wide applications to visualize sampling information, determine areas at higher risk for disease outbreaks, identify habitats that are more likely to have infected deer, and optimize cost-effectiveness of surveillance while improving disease detection efficiency. In the next year, we will begin using the CWD Warehouse, specially developed software that will have all the utility of a data management system with modeling and visualization capabilities.

One of the key components of the Risk Minimization Plan was stakeholder education. We have created numerous educational documents, provided content for the DEC Hunting Guidebook, and given public presentations. In addition, we have partnered with the Cornell Center for Conservation Social Science on surveys of hunters to determine their knowledge and attitudes toward CWD. We are focusing on hunters in the southern tier of New York who might be more likely to travel into Pennsylvania, a CWD-positive state. We also are completing a marketing campaign to identify different media and messages that resonate with the hunting public.

During the 10-year time period from July 2011 through June 2021, 23,603 samples were collected and tested for CWD. Since the DEC adopted a risk-weighted approach, the number of samples collected annually has remained close to or above 2,500. The surveillance effort is truly statewide, as samples are collected in every county in the state, excluding only the five counties corresponding to the boroughs of New York City.



23,603
white-tailed deer CWD tested 2011-2020



TRAINING AND TEACHING

WORKSHOPS, VIDEOS AND MORE

Keeping biologists and technicians current in an ever-changing world of wildlife health and disease is no easy task. In the last decade, we've given dozens of training workshops, presentations and webinars on wildlife health. We've covered personnel safety, outbreak response, chemical immobilization, risk communication and sponsored hands-on workshops and wet labs. But the world of wildlife health and disease stops for no one. We add to our list of topics continuously, working to keep everyone in wildlife health safe while moving the health field forward.

STUDENTS

The WHP plays an active role in training the next generation of wildlife health practitioners. Our program has connected trainees from high schoolers to post-doctoral scholars with expertise and resources to advance their skills in wildlife health practice. Over 80 students have come through our program to experience real-world applications in wildlife health sciences.

During training with the WHP, these early career trainees have gained diverse experience and expertise spanning field work, laboratory research, clinical practice, modelling, and communication. Our trainees are now strong contributors to the field of wildlife health, such as a state wildlife veterinarian, zoo veterinarians, researchers, a USDA importation inspector, and an ecologist at the USGS-National Wildlife Health Center.

Above: Kevin Hynes doing a necropsy demonstration during a regional wildlife health workshop.

Below: CWD sampling wet lab training with DEC and vet students at Cornell's Animal Health Diagnostic Center

PUBLICATIONS

Peer-reviewed research papers published in scientific journals are an opportunity to present data and conclusions for wildlife managers to use in making decisions on issues that impact wildlife populations.

MOST RECENT

Emergence of black bear mange in New York

Mange is a skin disease of mammals caused by an infection with microscopic mites—most commonly one species of mite called *Sarcoptes scabeii*. After wildlife biologists in Pennsylvania and New York noticed increasing numbers of black bears with mange, the WHP began tracking reports of affected bears to determine the distribution and progression of the disease across the state. A retrospective study using historic, opportunistic data from necropsy records and visual sighting reports collected from 2009 to 2018 was designed to determine whether geographic, seasonal, and demographic factors were associated with mange in this species in NYS. We confirmed black bear mange reports have increased in recent years. Necropsy data revealed an increase in bears submitted because of mange, mainly caused by *Sarcoptes scabiei*; of those animals, females were more likely to present with mange than males.

Cases of mange in the Northern zone were widely disseminated throughout the region, whereas cases in the Southern zone were concentrated in two areas along the Pennsylvania border. Seasonally, mange cases emerged with peaks occurring in late spring, fall, and late winter. The study concluded that a comprehensive statewide surveillance program would be useful to better understand the apparent increase in prevalence of mange and the potential population impacts to NYS black bears.

Additional research on the timing of transmission dynamics associated with females in winter dens may be helpful to wildlife managers to identify strategies to mitigate deleterious spread of the disease in black bears.

Rojas-Sereno, Z., R.C. Abbott, K. Hynes, E. Bunting, J. Hurst, S. Heerkens, B. Hanley, N. Hollingshead, P. Martin, K. Schuler. Occurrence of mange in black bears in New York, USA. Journal of Wildlife Diseases, in review.

Immune priming prior to pathogen exposure sheds light on the relationship between host, microbiome, and pathogen in disease

Dynamic interactions between host, pathogen, and host-associated microbiome dictate infection outcomes. Though these interactions determine disease development and severity, their inherent complexity challenges studies of the relationship between each component and disease. Pathogens including *Batrachochytrium dendrobatidis* (Bd) threaten global biodiversity, but efforts to protect at-risk species are hindered by limited understanding of amphibian host, Bd, and microbiome interactions.

We investigated these interactions with a vaccination and infection experiment of eastern hellbender salamanders (*Cryptobranchus alleganiensis alleganiensis*) challenged with Bd. We longitudinally quantified pathogen load, monitored skin microbiome, and characterized gene expression of host, pathogen, and microbiome using novel metatranscriptome methodology. Vaccination did not affect hellbender survival or pathogen burden; all infected hellbenders maintained high load infections during the experiment. Post-vaccination, orally but not topically vaccinated animals upregulated immune genes. In early infection, topically vaccinated animals upregulated immune genes; orally and sham vaccinated animals downregulated immune genes. In late infection, sham vaccinated animals had higher immune gene expression than vaccinated. Bd increased pathogenicity-associated gene expression in late infection; Bd load increased concurrently. The microbiome was altered by Bd, but there was no correlation between anti-Bd microbe abundance or richness and pathogen burden.

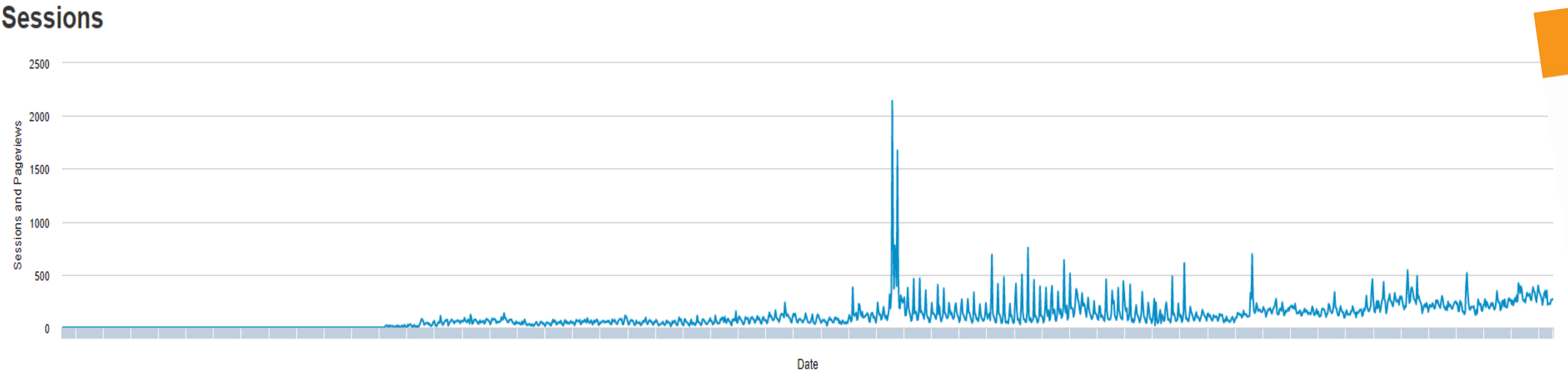
Our observations suggest that hellbenders initially generate a vigorous immune response to Bd, but it is ineffective at controlling symptoms and is subsequently modulated. Interactions with antifungal skin microbiota did not influence disease progression.

Kaganer, A. W., R. J. Ossiboff, N. I. Keith, K. L. Schuler, P. Comizzoli, M. P. Hare, R. C. Fleischer, B. Gratwicke, and E. M. Bunting. Immune priming prior to pathogen exposure sheds light on the relationship between host, microbiome, and pathogen in disease. Royal Society Open Science, submitted.

SCIENCE COMMUNICATION AND OUTREACH

GETTING THE WORD OUT

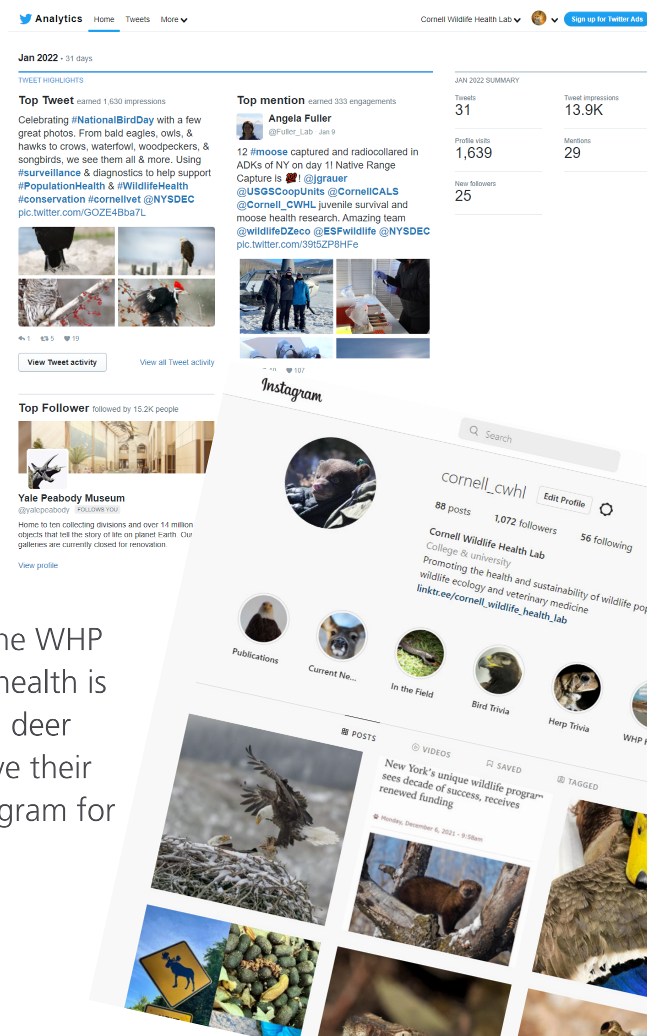
Communication about wildlife diseases is a key function of the WHP. Members of the public may have questions about a dead animal they find in their backyard or a sick bird at their feeder. Field biologists need to be informed about pathogens they may encounter in their daily tasks and how to protect themselves. Policy makers need reliable data to inform decisions on how to manage specific wildlife populations. The WHP uses different methods of communication to educate a variety of audiences about wildlife diseases and research results. Our website launched in July of 2016, and we have progressivly increased to over 200 website visitors every day.



Sessions	Users	Pageviews	Pages / Session	Avg. Session Duration	Bounce Rate	% New Sessions
178 431	0	292 098	1.64	01:29	69.14%	82.43%

SOCIAL MEDIA

Using platforms like Twitter and Instagram can support science outreach. One well-worded, well-timed message with a visually stimulating image can propel a wildlife health topic far and wide. We joined these platforms in 2018 and so far the use of these tools has proven successful. Both drive traffic to the Cornell Wildlife Health Lab website and increase the number and duration of visits on key pages like the Wildlife Disease Resource Library. Messages on wildlife health topics are reinforced and help keep the science moving forward.



Jan 2022 · 31 days

TWEET HIGHLIGHTS

Top Tweet earned 1,630 impressions

Celebrating #NationalBirdDay with a few great photos. From bald eagles, owls, & hawks to crows, waterfowl, woodpeckers, & songbirds, we see them all & more. Using #surveillance & diagnostics to help support #PopulationHealth & #WildlifeHealth #conservation #cornellvet @NYSDEC pic.twitter.com/GOZE4Bba7L

1 5 19

Top mention earned 333 engagements

Angela Fuller @Fuller_Lab · Jan 9

12 #moose captured and radiocollared in ADKs of NY on day 1! Native Range Capture is 💯! @jgrauer @USGSCoopUnits @CornellCALS @Cornell_CWHL juvenile survival and moose health research. Amazing team @wildlifeDZeco @ESFwildlife @NYSDEC pic.twitter.com/39t5ZP8HFe

107

JAN 2022 SUMMARY

Tweets 31	Tweet impressions 13.9K
Profile visits 1,639	Mentions 29
New followers 25	

Top Follower followed by 15.2K people

Yale Peabody Museum @yalepeabody FOLLOWS YOU

Home to ten collecting divisions and over 14 million objects that tell the story of life on planet Earth. Our galleries are currently closed for renovation.

cornell_cwhl

88 posts 1,072 followers 56 following

Cornell Wildlife Health Lab

College & university

Promoting the health and sustainability of wildlife populations through integration of wildlife ecology and veterinary medicine

linktr.ee/cornell_wildlife_health_lab

New York's unique wildlife program sees decade of success, receives renewed funding

Monday, December 6, 2021 - 9:58am

Podcasts and Facebook Watch events on current health concerns help engage the public in wildlife health and give them an opportunity to hear and/or see the hands-on-science the WHP is doing for New York. Engaging hunters in wildlife population health is a high priority. With the threat of CWD's impact on white-tailed deer in New York, some conscientious hunters have requested to have their harvested deer tested for CWD. As a result, we now have a program for Hunter Harvest CWD Testing.

WILDLIFE DISEASE FACT SHEETS

The WHP has written and posted 44 disease fact sheets on the website for a range of wildlife diseases, with more on the way. The front of each fact sheet contains basic information on the pathogen, clinical signs, species affected, transmission modes, methods of diagnosis, treatment, and precautions and prevention. The back side contains more details about each of these areas.

With an average of 500-1,600 views per month on different fact sheets and over 70,000 total views during the year, these valuable tools continue to educate and inform the public, DEC biologists, technicians, and staff.

Rodenticide Toxicity

BASICS

Rodenticide toxicity can be caused by any of several types of rodent poisons that fall into two general categories, anticoagulants and non-anticoagulants. ANTICOAGULANT RODENTICIDES work by interfering with the activation of Vitamin K, a critical component in the production of blood clotting factors in the liver. NON-ANTICOAGULANT RODENTICIDES vary in their mechanism of action and include bromethalin, strychnine, cholecalciferol, and zinc phosphide.

Rodenticides are TOXIC to many species of birds and mammals including pets, farm animals, and wildlife species. The time between EXPOSURE AND DEVELOPMENT of clinical signs is dependent upon the specific chemical and amount consumed.

Ingestion of a significant amount of ANTICOAGULANT rodenticides results in interference with blood coagulation and spontaneous bleeding. Specific CLINICAL SIGNS can include widespread bruising, bleeding into body cavities, and blood in the urine or feces; if the bleeding is sudden and significant, then cardiovascular shock and death can result. Bleeding can occur INTERNALLY OR EXTERNALLY and can affect any part of the body.

NON-ANTICOAGULANT rodenticide toxici
are more variable and are dependent on th
dose. The CLINICAL SIGNS include rapid
muscle tremors, limb weakness, ataxia, ne
respiratory paralysis, anorexia, nausea, vo
and lethargy.

There are currently NO BLOOD TESTS F
anticoagulant rodenticide exposure.

Diagnosis of non-anticoagulant rodent
based on detection of the chemical in
SYSTEM OR TISSUES of the animal.

Vitamin K is used to treat anticoagul
intoxication and help restore normal
treatment for non-anticoagulant ro
typically only supportive care.

The NYS Wildlife Health Program | cwhl.ve
A partnership between NYS Dept. of Environm

Snake Fungal Disease

BASICS

The organism responsible is the fungus *Ophidiomyces ophiodiicola*, within the family Onygenacea. Snake Fungal Disease (SFD) was first definitively identified in a population of Timber Rattlesnakes residing in New Hampshire in 2006.

KNOWN AFFECTED species include milk snakes, black rat snakes, garter snakes, timber rattlesnakes, eastern massasauga, cotton mouth snakes, and black racer snakes.

he characteristic CLINICAL SIGN of SFD is
cial swelling. The disease can progress from
nasal cavity internally via the eyes, throat,
lungs causing eye infections and pneumonia.
ungus additionally SPREADS EXTERNALLY
the neck, body, and tail forming scattered
s (lumps) or ulcerations.

us can be shed into the environment
d animals and

Health Lab

Mange

BASICS

Mange is a skin disease that affects mammals caused by microscopic mites that burrow into skin.

There are different species ofmites that can cause the disease. SARCOPTIC MANGE can affect wild and domestic mammals and is often reported in wild canids such as red foxes, coyotes, gray wolves, and red wolves. NOTOEDRIC MANGE is generally host specific to squirrels and has been reported in the western gray squirrel, eastern gray squirrel, fox squirrel, and rarely in bobcats. DEMODECTIC MANGE, also called demodicosis, has been reported in many mammalian species including white-tailed deer, mule deer, elk, and black bears.

CLINICAL SIGNS vary by type but a common sign is hair loss.

SARCOPTIC MANGE signs often include hair thinning and hair loss and thickening and wrinkling of the skin. Scabs and foul-smelling crusts result from secondary infections with bacteria and yeast. NOTOEDRIC MANGE results in hair loss in affected squirrels that begins over the chest and shoulders and progresses to affect the entire body. DEMODECTIC MANGE signs include hair loss and dry, flakey, thickened skin. Disease is more severe in stressed animals with weakened immune systems or poor nutrition.

TRANSMISSION occurs when a host becomes infected by direct contact with an affected animal or by coming into a contaminated environment like burrows or nests where free-living mites can survive for several weeks in high humidity and low temperatures.

Mites can be IDENTIFIED by examining SKIN SCRAPINGS from affected animals under a microscope. Differences in appearance can help determine the type of mite.

Oral administration of Ivermectin can TREAT mange but is not typically used in free-ranging wildlife because of the need for repeat treatments several weeks apart.

The NYS Wildlife Health Program | cwhl.vet.cornell.edu
A partnership between NYS Dept. of Environmental Conservation and Cornell Wildlife Health Lab

QUANTITATIVE TOOLS FOR WILDLIFE MANAGEMENT

REINTRODUCTION SOFTWARE

Reintroduction is a practice used by wildlife agencies to replenish a local animal population to desired levels. Often the goal of restorative reintroduction is to produce a desired population level without the need for constant intervention. We developed a quantitative tool to aid managers in identifying how to use innate population dynamics of each species to enhance success of introductions. The software couples mathematics with a user-friendly interface making restoration planning easy for any species containing 2-stage, 3-stage, 4-stage, or 5-stage life histories, representing thousands upon thousands of possible applications.

The work is described in the article, "How can we augment the few that remian? Using stable population dynamics for an iteroparous species," published in *PeerJ*.

Hanley, B. J., Bunting, E. M., & Schuler, K. L. (2019). How can we augment the few that remain? Using stable population dynamics to aid reintroduction planning of an iteroparous species. PeerJ, 7, e6873. https://doi.org/10.7717/peerj.6873

THEORETICAL POPULATION MATRIX MODELING

Demographers use the concepts of eigenvalues to assess population viability of wildlife populations, but the jargon of eigenvalues and vectors makes these mathematics prohibitively opaque for most practitioners. We developed interactive software to demonstrate how vital rates of a wildlife species collapse into the growth rate that produces increasing or decreasing population trends. The software is described in the article, "Another look at the eigenvalues of a population matrix model," published in *PeerJ*. This work is our most visited tool, solidifying the significance (and importance) of science communication aimed at bridging the gap between mathematical theory and boots-on-the-ground application in wildlife management.

Hanley B, Connelly P, Dennis B. Another look at the eigenvalues of a population matrix model. PeerJ. 2019 Nov 11;7:e8018. doi: 10.7717/peerj.8018. PMID: 31737449; PMCID: PMC6855200.

MOOSE IN THE ADIRONDACKS

We used the life cycles of cow and bull moose in conjunction with a projection matrix to identify moose population dynamics in the presence and absence of liver fluke and brain worm in the Adirondacks of New York State between 2015-2019. Soon to be submitted for publication, this work aids in the study of how these diseases can hinder population dynamics of this iconic species.

CWD IN WHITE-TAILED DEER

The Surveillance Optimization Project for Chronic Wasting Disease (SOP4CWD) is a collaborative international effort to develop quantitative tools and software to aid state and provincial wildlife agencies responding to CWD. Initiated in 2019 and led jointly by the Cornell Wildlife Health Lab at Cornell University and the Boone and Crockett Quantitative Wildlife Center at Michigan State University, the project has produced custom web-based software applications to provide participating state (23) and provincial (1) wildlife agencies access to quantitative tools and information useful for regional CWD surveillance and response. In addition to nearly half of the state wildlife agencies in the US, the collaboration includes researchers representing Penn State, USGS, UT, and MSU, who are working to derive novel mathematical and statistical tools and online infrastructure to conduct "big data" science on shared wildlife health data.

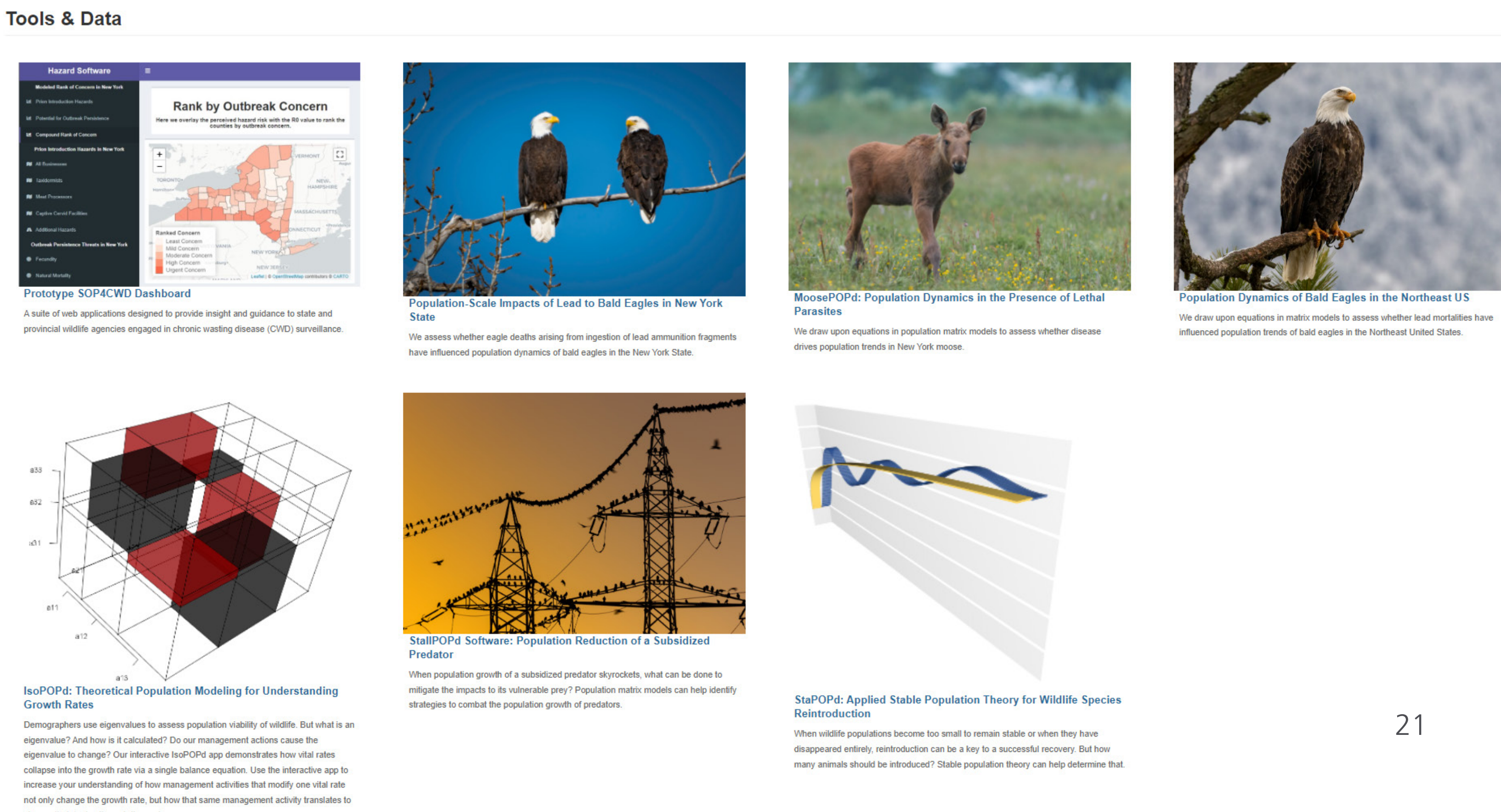
FURBEARERS (BOBCATS, FISHERS, MARTENS, MUSKRATS, AND OTTERS)

Since 2020, the CWHL has been working with the DEC and other regional partners in VT and ME to quantitatively analyze regional harvest data and population trends for bobcats, fishers, martens, muskrats, and otters. The development of these quantitative tools has proven that the mathematics used in both the eagle and moose studies can be pivoted to wildlife species with differing life histories to analyze time series data. With each additional species, we build evidence that historical trapping or harvest data may be analyzed using combinatorial optimization techniques drawn from computer and other quantitative sciences.

ACCESSING THE TOOLS

All free and openly available quantitative tools used for these analyses, including links to the open-access peer-reviewed articles, can be found on the CWHL tools page.

- Population Dynamics of Bald Eagles in the Northeast US
- StaPOPd: Applied Stable Population Theory for Wildlife Species Reintroduction
- StallPOPd Software: Population Reduction of a Subsidized Predator
- IsoPOPd: Theoretical Population Modeling for Understanding Growth Rates
- MoosePOPd: Population Dynamics in the Presence of Lethal Parasites
- Prototype SOP4CWD Dashboard



Tools & Data

Prototype SOP4CWD Dashboard

A suite of web applications designed to provide insight and guidance to state and provincial wildlife agencies engaged in chronic wasting disease (CWD) surveillance.

Population-Scale Impacts of Lead to Bald Eagles in New York State

We assess whether eagle deaths arising from ingestion of lead ammunition fragments have influenced population dynamics of bald eagles in the New York State.

MoosePOPd: Population Dynamics in the Presence of Lethal Parasites

We draw upon equations in population matrix models to assess whether disease drives population trends in New York moose.

Population Dynamics of Bald Eagles in the Northeast US

We draw upon equations in matrix models to assess whether lead mortalities have influenced population trends of bald eagles in the Northeast United States.

IsoPOPd: Theoretical Population Modeling for Understanding Growth Rates

Demographers use eigenvalues to assess population viability of wildlife. But what is an eigenvalue? And how is it calculated? Do our management actions cause the eigenvalue to change? Our interactive IsoPOPd app demonstrates how vital rates collapse into the growth rate via a single balance equation. Use the interactive app to increase your understanding of how management activities that modify one vital rate not only change the growth rate, but how that same management activity translates to

StallPOPd Software: Population Reduction of a Subsidized Predator

When population growth of a subsidized predator skyrockets, what can be done to mitigate the impacts to its vulnerable prey? Population matrix models can help identify strategies to combat the population growth of predators.

StaPOPd: Applied Stable Population Theory for Wildlife Species Reintroduction

When wildlife populations become too small to remain stable or when they have disappeared entirely, reintroduction can be a key to a successful recovery. But how many animals should be introduced? Stable population theory can help determine that.

POLICY SUPPORT

PROGRESS

One of the program focus areas was informing DEC's management and policies. In addition to reviewing research permits and management plans and attending team meetings to provide wildlife health consultation, we worked to acquire and analyze data to ensure evidence-based decision making.

TACKLING CWD

With CWD a looming threat to New York, policies were addressed in a comprehensive way by DEC and DAM. Through a comprehensive risk assessment, we identified that carcasses and live cervid movement presented the greatest threats for prion introduction. Both agencies subsequently banned movement of these animals, parts, and products. We also collaborated on an economic analysis of the value of the wild deer herd, estimating the annual worth at $1.5 billion. This information highlighted the need to enforce existing regulations and educate hunters and the public about threats related to CWD.

SPECIAL LICENSES

Each year, wildlife rehabilitators and other license holders provide summaries of their case load to the Special Licenses Unit. These paper summaries proved difficult to manage and summarize particularly when information is needed in a crisis. The program digitized and analyzed three years of rehabilitator data, which was over 20,000 animals handled per year. This caseload provides a wealth of potential surveillance information, such as changes in populations over time, novel disease outbreaks, or analysis of treatment options. The program is finalizing a web-based system to allow rehabilitators to standardize and upload their case information, providing both the rehabilitation community and the DEC with the ability to monitor wildlife health in real time. This system could also be expanded to other license holders when the need for tracing sources of disease outbreaks becomes critical.

WILDLIFE DISEASE FIELD RESPONSE

The Field Response for Wildlife Diseases guide was completed in October 2020 and is available to DEC online. This wildlife response plan identifies steps to take if wildlife morbidity or mortality is detected and a response is appropriate. It outlines the process for regional wildlife field staff to follow during wildlife disease investigation to ensure their safety and obtain the best quality wildlife specimens.

VETERINARY SUPPORT

Biologists often use anesthetic drugs to remove dangerous wildlife from dwellings, transfer injured wildlife from public areas, or tag or collar wildlife for monitoring. Drug protocols have changed markedly over the past decade as new drugs become available. Regulations concerning the storage, purchase, and field use of the drugs have also changed. The WHP worked with local and federal DEA agents, NY State Bureau of Narcotic Enforcement, AFWA, and DEC staff to standardize the use of anesthetic procedures across the agency, ensure compliance with federal and state laws, and petition for changes when needed.

The DEC now has a new all-inclusive guide to Chemical Immobilization with details on human safety, dosages, and animal monitoring. Each year, Safe Capture International provides training on chemical immobilization to ensure staff stays up to date on the latest processes and equipment. In addition, DEC staff and Division of Law Enforcement have been provided with a guide to humane euthanasia containing recommendations for safe handling of multiple species in a variety of situations.

Above right: Working with DEC biologists in the field with chemical immobilization techniques during bear den survey (2012).

Above left: CWD sampling lab at Cornell (2019).

Left: Cornell vet students still smiling after providing support in the DEC goose banding program (2013).

NEW YORK STATE OF OPPORTUNITY
Department of Environmental Conservation

Cornell University
College of Veterinary Medicine
Animal Health Diagnostic Center

WILDLIFE RESTORATION