

PENNSYLVANIA CHAPTER OF THE WILDLIFE SOCIETY

2017 Annual Conference & Workshop



*Wildlife Management in the 21st Century –
Dealing with Complex Conservation Challenges*

March 31 - April 1, 2017
Raystown Lake Resort Conference Center
Entriken, PA

Abstracts

Paper Presentations

(Listed alphabetically by last name of presenter--italicized)

Relationship of Invasive Berry Producing Plants on Bird Communities and an Assessment of Observer Bias on Avian Transect Studies

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Zachary S. Adams, (717) 926-3926, adamszs15@juniata.edu; undergraduate student presentation

In continuation with the 2014 and 2015 studies, I compared avian feeding guild structure between two wetlands with differing abundances of invasive berry producing plants in Huntingdon County, PA in the fall of 2016. Few to no invasive berry producing plants were found at one wetland (Old Crow wetlands; Huntingdon, PA), while high numbers of invasive berry producing plants such as Autumn Olive (*Eleaegnas umbellatum*) were found at the second wetland (Fouse's Crossing; Marklesburg, PA). In the 2014 and 2015 study, two transects at each of the two wetlands were surveyed for birds six times in the fall, by one observer. In 2016 both locations were surveyed for birds under the same parameters, but with the addition of adding a second observer. Both observers recorded birds along both transects sequentially. Vegetation was sampled at both locations multiple times throughout the fall and abundance, richness, and berry abundance of all berry producing plants was recorded. Avian average abundance, density, and conservation scores were calculated at each site. We compared the first and second observations at each transect per day to evaluate observer differences and the impact of disturbance. Both the 2015 and 2016 studies did not differ between the wetlands in average abundance, density, and richness in bird communities (Bird Density $p=0.32$, Fall 2016) but overall differed dramatically from the 2014 study. Short term datasets are often inadequate to address some research questions. Observer bias, particularly related to low detectability bird species and disturbance, could have possible impacts on study results.

Comparison of cytology and histopathology for diagnosis of avian pox in wild turkeys

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Justin Brown, (814) 863-8370, judbrow@pa.gov; professional oral presentation

Avian poxvirus is a common cause of proliferative skin lesions in wild turkeys (*Meleagris gallopavo*); however, other etiologies may produce grossly indistinguishable lesions (e.g. neoplasia, bacterial infections). Histopathology and polymerase chain reaction (PCR) are common diagnostic approaches for avian pox. While these methods are sufficient in most cases,

both have limitations (e.g. antemortem testing, lack of preservative or laboratory support). Cytology is a rapid approach that may be useful when histopathology or PCR are not feasible. The objective of this study was to evaluate cytology relative to histopathology and PCR for avian pox diagnosis in wild turkeys. Thirty-seven wild turkeys with proliferative skin lesions were included in this study; 19 of these birds also had lesions in gastrointestinal tract. Samples were collected from skin and gastrointestinal tract lesions for cytology, histopathology, and PCR. There were no significant differences between cytology and histopathology for skin ($p = 0.2482$) or gastrointestinal tract ($p = 1$) lesions. Relative to histopathology, cytology had a sensitivity of 90% and a specificity of 100% for skin lesions and a sensitivity of 75% and a specificity of 0% (all 19 samples were due to avian pox) for gastrointestinal tract lesions. There were no significant differences between PCR and histopathology ($p = 0.6171$) or cytology ($p = 0.2482$) for skin lesions. Relative to PCR, cytology had a sensitivity of 89.3% and a specificity of 100%. These results suggest cytology may serve as a useful tool for diagnosing avian pox in wild turkeys.

Soil Chemistry and its Effect on the Occupancy of Understory Plant Species

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Danielle R. Begley-Miller, (937) 733-8981, dfb5098@psu.edu; graduate student presentation

The Pennsylvania Department of Conservation and Natural Resources (DCNR) faces many challenges while managing 2.2 million acres of public land in Pennsylvania. Past land use, deer herbivory, and fire history are just some of the many factors that interact to influence forest plant community composition. Additionally, it is well documented that soil acidification changes forest soil conditions, but the specifics of how soil chemistry influences occurrence of many understory plant species is not well understood. To investigate this relationship, we used single-species occupancy models to compare baseline forest inventory data to site-specific soil chemistry (pH, extractable nutrients, effective cation exchange capacity, and toxic metal saturation) for several species. Data were collected at 24 sites on the Rothrock and Bald Eagle state forests in central Pennsylvania. Probability of detection (p) for all species (mountain laurel (*Kalmia latifolia*), huckleberry (*Gaylussacia* spp.), blueberry (*Vaccinium* spp.), red maple (*Acer rubrum*), red oak (*Quercus rubra*), and black birch (*Betula lenta*)) was constant and high ($\square \rightarrow 0.70$). Lower pH (2.5-3.5) and higher elevation (550m-685m) were predictors of increased occupancy (y) for mountain laurel and huckleberry. Higher basal area of overstory trees (0.2-0.4 m²/plot) and increased understory plant species richness (8-15 species/plot) was related to greater probability of occupancy of both red oak and red maple. Black birch and blueberry had constant probability of occupancy ($y = 0.10$ and $y = 0.76$, respectively) regardless of soil chemistry. These results highlight how plant responses to soil chemistry are species specific and complicate inferences about plant species distribution and abundance in relation to deer herbivory.

Draft reference genome sequence of the bobcat and comparative analysis of genome wide patterns in polymorphism

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The bobcat (*Lynx rufus*) is a successful generalist predator with a broad range across North America. As a generalist, it inhabits a diverse array of habitats with their prey use depending on the ecosystem they inhabit. The objective of this project is to examine bobcats from diverse ecosystems and to identify loci contributing to adaptation. Previously, bobcat reads produced through double digest restriction-site associated DNA sequencing (ddRADSeq) were mapped to a domestic cat reference genome to infer putative chromosomal regions under selection. While all felids are closely related at the genomic level, this introduced bias when generating single nucleotide polymorphism (SNP) data from the ddRADseq sequencing. To address this issue, a New Mexico bobcat was sequenced on the NextSeq500 generating 584,153,154 reads after quality trimming. This was combined with an additional 2,067,170 reads previously generated via ddRADSeq to produce an average read-depth of 20.8. The recent domestic cat genome update presented the perfect opportunity to create a comprehensive bobcat genome sequence based on the structure of the domestic cat genome. A total of 400,155,644 reads were mapped, covering 97% of the domestic cat reference. Currently, we are identifying and exploring differences between the domestic cat and bobcat. This bobcat genome is an important tool for mapping functional loci, understanding species history, and comparing adaptations between bobcat populations.

Using Maximum Entropy Modeling to Approximate the Distribution and Habitat Associations of the Northern Long-eared Bat

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Predictions of species occurrence using statistical modeling techniques have practical and diverse applications in ecology, evolution, and conservation biology. The geographic distribution of northern long-eared bats (*Myotis septentrionalis*) found in the Monongahela National Forest of West Virginia was analyzed, using maximum entropy modeling and mist-netting data from 1997 through 2012. The software program MAXENT is being used with increasing frequency and relies on a maximum entropy modeling technique to create an environmental niche model that predicts the probability of presence of a species over a geographic area. 3,877 capture records (80%) were used to train the model and 969 (20%) were used to test the model ($AUC_{test} = 0.771$). The model had a high degree of discrimination, with both high and low probability of presence being found throughout the forest (Fraction Predicted Area = 0.844; $P < 0.0001$). Forest type

accounted for over half of the probability of importance (50.5) with land cover diversity index (22.3), and hydrologic features (10.5) also contributing to the model. The results of this study allow for insight into the distribution and foraging habitat preferences of the northern long-eared bat and indicate that maximum entropy modeling is a robust tool allowing for predicting where species occur.

Regional Wildlife Action Plan Opportunities: Integrating Species, Habitats, and Threats to Identify Actions

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The first revision of State Wildlife Action Plans (SWAPs) marks a decade of implementation, learning and updates since the original 2005 SWAPS. These comprehensive strategic planning documents have served State Fish and Wildlife Agencies and their partners by guiding the conservation of priority species of greatest conservation need and their key habitats over the last decade. In 2015, the Northeast Association of Fish and Wildlife Agencies, and their Northeast Fish and Wildlife Diversity Technical Committee undertook a project to synthesize all 14 State Wildlife Action Plans from Northeast Region States and explore shared species of greatest conservation need, key habitats, priority threats, and regional conservation actions. What do the northeast SWAPS tell us collectively are the key priorities that will guide collaborative conservation for the next decade? Experts from every state were engaged to evaluate all 2958 Species of Greatest Conservation Need (SGCN) to determine the Regional Species of Greatest Conservation Need. Data from all 14 State Wildlife Action Plans were incorporated in an access database so that threats to these Regional SGCN could be analyzed. These top threats to the most imperiled species in our region are now being organized to determine conservation actions that will best be undertaken collaboratively throughout the region.

Linking multiple data sources to inform inference on spotted salamander population abundance

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Despite being relatively well studied, there are still large knowledge gaps regarding wetland-breeding amphibian species, such as the spotted salamander (*Ambystoma maculatum*). We analyze data from an extensive mark-recapture study of adult spotted salamanders in 12 wetlands within an isolated vernal pool network in central Pennsylvania. Visual encounter surveys were conducted at 34 additional wetlands following the breeding season to count egg masses and monitor larval growth and development at each wetland (n = 46). We recorded 2252 captures of 1461 unique adult individuals in the spring of 2015. Using these mark-recapture data, we validated the use of egg mass counts as an index of population size. Estimated abundance was

highly correlated with the maximum number of egg masses counted at each wetland ($r = 0.88$; ~ 2 egg masses per adult female). We then used generalized linear models to relate both average egg mass counts to wetland site characteristics and heterospecific interactions with other wetland-breeding amphibian species. We found that wetland hydroperiod (i.e., length of inundation) (-0.723 ± 0.577), area (0.002 ± 0.001), and average pond temperature (1.351 ± 0.207) were important site attributes contributing to variation in egg mass counts and, therefore, population abundance. Heterospecific interactions also appear to be important in determining spotted salamander abundance. We show how an integrated data approach allowed us to validate our index and understand drivers of population abundance. We will further discuss the development of an integrated population model that combines egg mass counts and mark-recapture data into a single estimator.

White-tailed deer fawn survival in North America

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Tess M. Gingery, (801) 910-6968, tjg5474@psu.edu; graduate student presentation

A meta-analysis of white-tailed deer (*Odocoileus virginianus*) fawn survival identifies the effect of various sources of mortality at a broader scale than is possible when evaluating a single study. We present a meta-analysis of fawn survival from 9 populations in 8 states across North America. We used published data on fawn survival rates that reported a survival rate for fawns that lived to 3-6 months, sample sizes, landscape descriptions, and cause-specific mortality. We analyzed survival estimates between 3 to 6 months simultaneously because most mortality occurred before this time frame. We modeled the relationship of fawn survival to agricultural land cover and to deer density. We classified cause-specific mortality as human caused, natural (excluding predation), and predation. We classified the proportion of these causes in agriculturally dominated, forested, and mixed landscapes. Survival from 3-6 months was 51.3% in contiguous forest landscapes (no agriculture), and for every 10% increase in agricultural land area fawn survival increased 3.4% (SE = 0.07). We detected no relationship between fawn survival and deer density. Habitats with mixed forest and agricultural landscapes had greater proportions of human-caused mortalities, and less mortality due to predators, than either forested or agriculturally dominated landscapes. The proportion of natural deaths did not differ among mixed, forested, and agricultural landscapes even though overall mortality rates differed. Fawn survival studies that focus on factors affecting fawn susceptibility to mortality, and report habitat composition and predator population information, will enhance the ability of meta-analyses to detect patterns not evident from individual population studies.

Osprey Recovery in Pennsylvania: A Conservation Success Story

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The Osprey (*Pandion haliaetus*), a migratory piscivorous raptor, was extirpated in Pennsylvania as a breeding species by mid-twentieth century. Never a common or widespread nester in the state, it declined due to persecution, water pollution, pesticides, and nesting habitat loss. Environmental and wildlife regulations removed these limiting factors, allowing recovery from extirpation. In a series of hacking projects with many partners, over 300 osprey fledglings were released between 1980 and 2007 including the Poconos, Tioga Lakes, Lake Arthur, Raystown Lake, and Glendale Lake. Dr. Larry Ryman, East Stroudsburg University (ESU), and then-student Charles “Hoagy” Schaadt initiated this recovery. Osprey gradually recovered from state Endangered to Threatened status, eventually to a population of 115 nests found in 2010 PGC survey. Assisted by Dr. Terry Master (ESU), PGC formally adopted a management plan in 2015 with goal of a stable or increasing population of minimum of 50 pairs including at least 10 nests in 4 HUC6 watersheds, ensuring broad distribution. In 2016, the PGC found 148 nests with over 10 nests in 6 HUC6 watersheds. Most osprey nests are now on human-made structures (> 90%) and near impoundments (> 50%), not attributes usually associated with a listed species but rather one well-adapted to the current human-affected landscape. It has met the recovery objectives of the management plan for upgrading / delisting to Protected status. The future of this popular species looks bright as long as environmental and wildlife regulations protect it and the high quality aquatic habitats it represents.

The bats of Michaux State Forest: Spatial and temporal use of public lands as revealed using mobile acoustic transects

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Mobile acoustic transect surveys have been used for several years to determine the species of bats using corridors through forests. These surveys have provided a tool with which biologists can determine where, along corridors, bats are present and, to an extent, what portions of a corridor may provide the necessary elements providing foraging and travel habitat. The present study took it a step further by duplicating, on a monthly basis, an established mobile transect through the Michaux State Forest, a large tract of forest owned and maintained by the PA Department of Conservation and Natural Resource’s Bureau of Forestry. As per protocols set up by the PA Game Commission, a thirty-mile transect was established and driven 4 times from April to October, 2016. Bats were recorded via a roof-mounted AR-125 (Bio Acoustic Technology) as well as a single night with an IFR-IV unit and analyzed using SonoBat 4.0.7™. Over 13,000 files were recorded with almost 500 (2.9%) of these determined to be bat call files. This presentation will present the results of the surveys and how these results could be used by forest resource managers to determine what areas of the forest may be important to bats as well as when bats occur along portions of the corridor. It is anticipated that management practices can be developed to focus on conserving habitats along the corridor that appear to support bats as well as

developing tools to both predict where other such habitat occurs and how to enhance the management of those habitats.

The effects of forest stand type and prescribed fire frequency on bat activity at Fort Indiantown Gap, PA

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As White-nose Syndrome (WNS) and other threats cause declines in North American bat species, a better understanding is needed of how land management practices influence bat activity and habitat use. Our objective was to assess impacts of habitat type and management on bat activity within forested habitats at Fort Indiantown Gap, a military training facility in south-central Pennsylvania. We used Pettersson D500x acoustic detectors to passively record bat passes within unburned forests of 4 stand types: 1) oak (*Quercus* spp.); 2) tulip poplar (*Liriodendron tulipifera*); 3) softwoods; and 4) miscellaneous hardwoods. We further delineated oak stands into 3 treatments of prescribed fire: 1) burned 1-2 times; 2) burned 3-5 times; and 3) burned ≥ 6 times since 2004, resulting in 7 treatments. We hypothesized that bat activity would be higher in oak stands, particularly those that had been frequently burned. Bat passes were recorded at 186 sites from 19 May-13 September 2016 and when possible, identified to species using SonoBat 4.0.7 software. Big brown (*Eptesicus fuscus*) and eastern red bats (*Lasiurus borealis*) comprised 97% of identified passes. Northern long-eared myotis (*Myotis septentrionalis*) and tri-colored bats (*Perimyotis subflavus*) were recorded at 6 and 5 sites, respectively. Preliminary results, from analyses incorporating only the main effect of treatment but without covariates, indicate no significant effect of forest stand type or prescribed fire frequency on total and species-specific activity levels. These data will be used to develop multivariate models, incorporating additional covariates that may further explain variation in bat activity onsite.

Evaluating the risk of chronic wasting disease infection in Mid-Atlantic cervid populations

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Chronic wasting disease (CWD) is a fatal neurological disorder that affects cervids and has become a significant concern for wildlife professionals given the cultural, economic, and ecological importance of the species it impacts. A key management priority is to prevent the geographic spread of the disease in areas of recent infection, such as the Mid-Atlantic region. Understanding patterns of disease susceptibility and population connectivity can provide insights into future epidemiology and infection intensity, and may aid in the development of targeted

disease mitigation strategies. In this study, we (1) measured patterns of population connectivity for the primary vector (white-tailed deer) in order to determine potential transmission dynamics; and (2) determined the distribution and frequency of the most susceptible prion gene variants in order to assess potential infection risk. Tissue samples were collected from an area encompassing 25,000 km² in Maryland, Pennsylvania, and Virginia. Population connectivity was assessed using microsatellite genotypes collected from 945 white-tailed deer. Prion gene sequences were collected from 159 white-tailed deer and 256 elk in order to determine perceived CWD susceptibility. Both species exhibited substantial spatial heterogeneity in prion genotype frequencies, indicating differential CWD susceptibility, even within the study region. Population genetic analyses indicated widespread gene flow ($F_{ST} < 1.0$) and an isolation-by-distance pattern of population structure, although landscape boundaries (e.g. rivers, ridges) seem to impede fine-scale movements. Migration was inferred between areas with known CWD incidence and counties with no known CWD cases in free-ranging populations; however, no known CWD positive individuals were detected among migrants.

Population genetics of a reintroduced population of bobcats and its relevance for felid management

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Habitat fragmentation and genetic isolation of populations is of concern for wildlife managers. Management of isolated populations is particularly important for carnivores, which are keystone species and may require management interventions such as translocation to maintain genetic diversity. This talk will discuss a case study of a reintroduced population of bobcats (*Lynx rufus*) on Cumberland Island National Seashore (CUIS), GA, and implications for the use of translocation as a management tool for re-establishing felid populations. In 1989-1990, 32 bobcats were reintroduced to CUIS. At the time, the population was predicted to stabilize at 12-13 individuals after 10 years. In 2012, we collected scat samples from the current population on CUIS. We used both molecular methods and spatially explicit capture-recapture population estimation to estimate current abundance at ~14 individuals. Although genetic diversity remained relatively high, there were indications that the CUIS bobcats have experienced a genetic bottleneck. Furthermore, coyotes (*Canis latrans*) established a breeding population on CUIS and may adversely affect bobcats through interspecific competition. Ongoing work is examining relatedness of coyotes on CUIS to estimate their current status and immigration history. Opportunities for natural immigration of bobcats to CUIS are limited, and we are therefore also comparing genetic diversity of the isolated CUIS bobcats to a naturally-maintained population on Kiawah Island, SC. Understanding the demographic and genetic stochasticity of these insular bobcat populations has important implications for conservation management decisions for endangered felids.

Quantifying threats that impact federally listed threatened and endangered species

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This project involves the review of Federal Register documents for threatened and endangered (T&E) species from 1975-2016. Working in collaboration with student researchers from the College of William and Mary, our goal is to quantify and compare the last 40+ years of documented threats that impact T&E species. We will be reviewing all Federal Register listing documents outlining the justification for why species have become federally listed as threatened or endangered. Upon completion, we will identify the top human impacts causing T&E species to become listed and quantify how these threats have changed over time. Preliminary results suggest that not only are alien species and habitat degradation still major threats causing species to become listed, but that climate change has since emerged as another major threat in the last 20 years, impacting 32% of listed species. In addition, we will compare the threats affecting federally listed species in the continental United States in comparison to species located in just Region 5 of the U.S., which includes Pennsylvania.

The effects of roads on bird species occupancy in Pennsylvania's core forested landscape

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Roadways are a prominent feature on the landscape and a major factor in determining the impact of human development on wildlife populations. This is especially true in areas characterized by low development, such as north-central PA where roads act as the major source of land modification and fragmentation. Roads act to affect wildlife through multiple mechanisms including fragmentation, alteration of habitat structure, and traffic disturbance. Our goal was to determine whether and how bird communities differ between roadside and off road surveys and identify which road-characteristics have the greatest effect on forest bird communities. During the 2015 and 2016 breeding seasons we conducted point counts at 1088 locations within public lands in Northcentral Pennsylvania. We analyzed data using multi-species occupancy models, allowing us to determine how average road effects differed among different species-groups. Our results show that canopy width opening has a negative effect for forest interior species with a mean estimated effect size (logistic regression coefficients for the effect of increasing canopy width on occupancy) of -0.028 (95% Credible Interval (CI) -0.054 – -0.002) while positive for edge/early successional species (0.075, CI 0.032 – 0.118). Forest edge understory cover also has a negative impact on forest interior species (-0.131, CI -0.245 – -0.017) while positive for edge/early successional and canopy gap specialists (0.297, CI 0.092 – 0.505; 0.408, CI 0.085 – 0.717 respectively). We will discuss the implications this has on the interpretation of results from large

scale surveys utilizing roadside counts, as well as minimizing road impacts on forest bird communities in Pennsylvania's core forested landscape.

The North American Model of Wildlife Conservation: Through the Eyes of the North American River Otter

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Tom Serfass, (301) 687-4171, tserfass@frostburg.edu, professional oral presentation

Over the last decade the “North American Model of Wildlife Conservation” (NAM) has been widely portrayed as both a historical account of how wildlife were conserved in North America in the past and a prescriptive model for how wildlife should be conserved in the future. NAM is comprised of 7 primary elements, each depicted in a manner that supports and justifies recreational hunting and trapping as the “cornerstone” of wildlife conservation in North America. I am both intrigued and concerned that a hunter/trapper-centric focused approach has been put forth (marketed) as the primary dictum defining wildlife conservation. The basic precepts of NAM largely have been embraced within the wildlife profession in the United States (US), despite the general absence of meaningful scrutiny to assess the appropriateness of a hunter-centric approach for addressing the entirety of wildlife conservation issues in North America and beyond. I critically review NAM and its 7 elements in the context of conserving the North American river otter (*Lontra canadensis*) in the US, with particular focus on 3 of NAM's core elements: 1) wildlife as a public trust resource; 2) science as the basis for implementing conservation practices; and 3) elimination of markets for wildlife. Important to my discussion is a review of what I consider inappropriate application of science to further specific management goals/agendas pertaining to the river otter. I argue that wildlife conservation is hindered and the “public trust” compromised when science and marketing are inappropriately integrated to achieve predetermined management outcomes.

Herpetofaunal Abundance and Diversity within small Tropical Cloud Forests embedded in a Human-Dominated Matrix: the Role of Sustainable Agriculture Practices in Central American Conservation

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Victoria L. Strange, (610) 613-0188, v.l.strange@iup.edu; graduate student presentation.

Private conservation lands play an important role in maintaining biodiversity across human-modified landscapes in Central America. However, there is limited understanding as to the effects of different land-use practices on amphibians and reptiles remaining within smaller privately-owned forests. We surveyed the herpetofaunal composition as related to environmental conditions within an Integrated Open Canopy (IOC) coffee plantation in the agriculturally-dominated landscape of north-central Nicaragua. Surveys completed between May-June 2016 assessed diversity and relative abundance along 48 transects spread over 4 land-cover types: interior forest, IOC coffee fields, forest-IOC coffee edge, and forest-pasture edge. We also measured vegetation

structure along each transect to identify species associations with environmental conditions. During our surveys, we observed 289 amphibians belonging to 10 species, along with 93 reptiles from 7 species. Two dominant species of frogs (*Pristimantis ridens* and *Diasporus diastema*) comprised 70.6% of total amphibians detected, while 4 species of *Norops* lizards comprised 78.5% of total reptiles. Amphibian diversity and overall abundance were greatest within interior forest and forest-IOC coffee edge, and comparatively lower in forest-pasture edge and IOC coffee transects ($P < 0.001$). Reptile diversity was lower within IOC coffee compared to forest interior and both edge habitats, with overall abundance similar to amphibian trends ($P = 0.0123$). We will examine how these trends relate to environmental measurements. Our results should help inform local land management, and future conservation plans to connect private forest reserves to larger conservation areas in the region.

Changes in bird community composition following eastern hemlock decline

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Matthew J. Toenies, (320)-360-5589, mkt5213@psu.edu; graduate student presentation

Forest die-offs have occurred repeatedly across North America over the last century, but research has devoted relatively little attention to avian community-wide responses to these declines. The current decline of hemlock forests due to the hemlock woolly adelgid (*Adelges tsugae*) provides a useful model of the effects of a forest die-off on both forest type specialists and other guilds, given the unique communities associated with hemlock forests. This study examined (1) how bird community composition has changed over a fifteen-year period of hemlock decline and (2) whether changes were correlated with degree of hemlock decline. We conducted variable-radius point counts at 80 sites across 11 hemlock stands and 11 hardwood stands at Delaware Water Gap National Recreation Area in northeastern Pennsylvania and northwestern New Jersey, and compared results to previous surveys conducted in the same stands in 2000, which coincided with early stages of adelgid infestation. Results of occupancy models show that hemlock-associated species declined (mean effect -1.2), and that occupancy of this group was related to the combined effect of hemlock health and hemlock abundance. All other species groups showed positive responses to hemlock decline, with the greatest effects occurring in species associated with the shrub-layer (mean effect 1.35), woodland edge (mean effect 1.13), and early successional habitat (mean effect 1.12). Our results indicate that degradation of hemlock stands has led to shifts in bird community composition. Continued die-offs may result in similar changes to bird communities within hemlock forests and other forest types.

Managing Ruffed Grouse Populations in the Age Of West Nile Virus: The Case For Adaptive Management

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Lisa M. Williams, (814) 422-8243, liswilliam@pa.gov, professional oral presentation

Since its arrival to North America in 1999, West Nile virus (WNV) has had unprecedented adverse effects on the health of native birds across numerous taxa. In Pennsylvania, WNV was first documented statewide in 2002, soon after which precipitous population declines were observed in Pennsylvania ruffed grouse (*Bonasa umbellus*). Statewide, grouse populations have not since recovered. Susceptibility of ruffed grouse to ongoing cycles of high-WNV prevalence has important implications for managing this important game bird. The ongoing influence of WNV can be seen in statewide population indices such as hunter flush rates and summer sighting survey (brood) data. Recent analysis indicates that WNV and availability of young forest on the landscape act together to influence local grouse colonization, persistence and extinction. Population demographics data collected via a Parts Collection Survey (2013-present) show dramatic changes have occurred since the population demographics of the 1980s when the current grouse season framework was established. In response to these changes, the Pennsylvania Game Commission has restricted the grouse hunting season length for 2017-18 and is working to develop an adaptive management framework to guide ruffed grouse management.

Modeling Potential Habitat for Pheasant Population Restoration in Pennsylvania

Lacey T. Williamson, Pennsylvania Cooperative Fish and Wildlife Research Unit, 436 Forest Resources Building, The Pennsylvania State University, University Park, PA 16802; Scott R. Klinger, Pennsylvania Game Commission, 2001 Elmerton Avenue, Harrisburg, PA 17110; Duane R. Diefenbach, and W. David Walter, U.S. Geological Survey, Pennsylvania Cooperative Fish and Wildlife Research Unit, 403 Forest Resources Building, The Pennsylvania State University, University Park, PA 16802

Lacey T. Williamson, (540) 931-4450, lkw5184@psu.edu; graduate student presentation

Ring-necked pheasants (*Phasianus colchicus*) are a non-native species that reached peak numbers in Pennsylvania in the 1970's, but have since declined most likely due to a lack a suitable habitat. We investigated the habitat needs of pheasants to restore population sizes and reach a population goal of 10 hen pheasants/mi² as set by the Pennsylvania Game Commission. For our objectives, we estimated the population densities of wild pheasants in Pennsylvania and explored if habitat type has an effect on the densities. Crowing counts, crowing frequency, observer's ability to detect pheasants, and sex ratio were used to calculate population estimates of hen pheasants at the study areas. Only one study area approached the hen density goal, with all other study area densities below 5 hens/mi². A random selection of points used for crowing counts were mapped to obtain microhabitat data within a 0.35 mi radius, which yielded 113 mapped points in 2013 and 178 mapped points in 2014. The microhabitat data and estimated densities have been included in a model to isolate the habitat characteristics that had the most influence on pheasant populations. With the model, efforts for habitat restoration can be directed to features that will have the most likely success of increasing the pheasant population.

A quantitative survey of bird SGCN in boreal peatlands throughout Pennsylvania

David Yeany II, Mary Ann Furedi, Pennsylvania Natural Heritage Program, Western Pennsylvania Conservancy, 800 Waterfront Drive, Pittsburgh, PA 15222; and Douglas A. Gross, Pennsylvania Game Commission, 106 Winters Road, Orangeville, PA 17859

David Yeany II, (412) 586-2313, dyeany@paconserve.org; professional presentation

Some of Pennsylvania's rarest breeding birds, including state Endangered yellow-bellied flycatcher (*Empidonax flaviventris*) and blackpoll warbler (*Setophaga striata*), have long been documented in high elevation boreal wetlands. These wetlands include a variety of bogs, fens, and other communities characterized by plant species more commonly found north of Pennsylvania and soils consisting of slowly decomposing organic material. Because these ecosystems are more associated with northern latitudes, higher elevations, and represent refugia for boreal species, they have high ecological value and may be sensitive to climate change. We used GIS to identify more than 1,300 potential peatlands across the commonwealth. We identified a suite of co-occurring avian SGCN in these peatlands and designed the first large-scale systematic and quantitative survey within these difficult-to-access habitats for a multi-year study with three planned field seasons (2016-2018). We conducted point count surveys and rapid vegetation assessments at 195 off-road point locations across 30 peatland sites during May-July 2016. We sampled dominant peatland community types at each site and detected 29 SGCN bird species and 20 out of 22 peatland bird target species. Boreal SGCN found with regular frequency included Canada warbler (*Cardellina canadensis*; 50%), northern waterthrush (*Parkesia noveboracensis*; 27%), white-throated sparrow (*Zonotrichia albicollis*; 25%) and Nashville warbler (*Leiothlypis ruficapilla*; 17%). We also demonstrated promising results for detecting very rare species like olive-sided flycatcher (*Contopus cooperi*) and those above. When completed, our study will describe breeding bird assemblages in Pennsylvania peatland communities and quantify densities for many conservation priority species, aiding in management efforts.

Abstracts

Posters

(listed alphabetically by last name of presenter--italicized)

The RoarPlex – A Novel Tetranucleotide Microsatellite and Sex-ID Panel for Accurate Individual Identification of Felids and Sharing of Genetic Data across Institutions

Colton L. Ames and Jan E. Janecka, Ph.D., Duquesne University Forensic Science and Law Program and the Department of Biological Sciences, 600 Forbes Avenue, Pittsburgh, PA 15218

Colton Ames, (814) 771-8522, amesc1@duq.edu; Undergraduate student poster

The bobcat (*Lynx rufus*) is an elusive species located in regions of Pennsylvania and other parts of the Northeast. Due to their cryptic nature, research based on direct observations required for effective management is problematic and can be supplemented by noninvasive surveys and genetic analysis. A multiplex containing 8 tetranucleotide microsatellites and a sex-determining region Y marker was developed for population abundance and distribution studies on larger geographic scale and to aid investigation of poaching incidences. To date, most bobcat genetic studies relied on dinucleotide repeats that are difficult to score and difficult to combine across different data sets. Tetranucleotide repeats reduce the errors caused by slippage and “+A” stutter, making for unambiguous allele interpretation. An allelic ladder is in development to ensure consistent allele designation across laboratories, with validation according to SWGDAM and ISFG recommendations. Sixteen markers have been screened in felids. Using M13 labeling, 15 amplified microsatellites were fluorescently tagged and genotyped. Resulting peaks were noticeably more distinct and allele calling was simplified. An informative multiplex for bobcats will be constructed through data analysis, primer redesign, and compatibility determination. The tetranucleotide panel will provide more information, including sex, in one multiplex. The ability to utilize one reaction reduces the cost, error, and time required to perform the assay. The capability to share data across institutions will drastically increase the impact of population studies. The panel will simultaneously improve research methods and assist with transboundary initiatives.

Surveillance for lymphoproliferative disease virus in wild upland game birds in Pennsylvania

Justin Brown, Lisa Williams, and Mary-Jo Casalena, Pennsylvania Game Commission, 2001 Elmerton Avenue, Harrisburg, PA 17110; and Christopher Cleveland and Michael Yabsley, Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA 30602

Justin Brown, (814) 863-8370, judbrow@pa.gov; poster presentation

Lymphoproliferative disease virus (LPDV) is a retrovirus recently identified in wild turkeys (*Meleagris gallopavo*) in the Eastern United States. Historically, LPDV has been a rare cause of lymphoid tumors in domestic turkeys in the Middle East and Europe. However, in 2012, LPDV was identified in a wild turkey from Arkansas with systemic lymphoid tumors. This was the first

identification of LPDV in wild turkeys and in North America. Subsequent surveillance showed LPDV infection was widespread and common in wild turkeys throughout the Eastern US, but the occurrence of tumors was rare. Currently, there is little information on LPDV host range, but experimental data indicates chickens and turkeys are susceptible to infection and domestic ducks and geese are resistant. To provide insights into the host range of LPDV, bone marrow samples were collected from wild turkeys, ring-necked pheasants (*Phasianus colchicus*), and ruffed grouse (*Bonasa umbellus*) from Pennsylvania during 2012-2016. None of the birds included in this surveillance had evidence of tumors. Samples were tested for LPDV proviral DNA using polymerase chain reaction (PCR). Consistent with previous surveillance results in surrounding Northeastern states, LPDV infection in wild turkeys was common (51/64 positive). In contrast, LPDV was not detected in any ruffed grouse (n=77) or ring-necked pheasant (n=13) samples. These results indicate LPDV infection in ruffed grouse and ring-necked pheasants is significantly less common than in wild turkeys and suggest that the natural LPDV host range is relatively restricted.

Quantitative food webs associated with recently metamorphosed Fowler's Toads (*Anaxyrus fowleri*) in four habitat types

Rachael Berry, Taylor M. Braunagel, and Kurt J. Regester, Department of Biology, Clarion University, Clarion, PA 16214

Rachael G. Berry, (724) 591-0743, R.G.Berry@eagle.clarion.edu; undergraduate student poster

Fowler's Toad (Bufonidae: *Anaxyrus fowleri*) is a broadly distributed, generalist amphibian in eastern North America. Although recently metamorphosed individuals are a numerically dominant component of many habitat types, particularly during seasonal emergences, few studies have examined the diets of toadlets or assessed their importance in terrestrial food webs. In this study, we quantified the diets of toadlets inhabiting four habitat types (riparian, pond-edge, wetland-edge, and beach) and constructed quantitative food webs using estimates of energy flow. During June and July of 2016, we collected and preserved toadlets (n=78) from six sites distributed throughout northwestern Pennsylvania and then dissected stomachs in the lab. We identified all prey items to taxonomic order, and then photographed and measured each prey item for total length (n ~ 1000) using a microscope and digital image processing software. Our results will include statistical comparisons of toadlet diet across habitat types, including analyses of the abundance and occurrence of each prey type. Published allometric relationships will be used to estimate energy content of individual prey items based on body size measurements. These data will provide the basis for constructing a quantitative food web associated with recently metamorphosed Fowler's Toads and prey taxa for each habitat type. Our findings will provide novel insights into the ecological roles of toads in the terrestrial habitats adjacent to freshwater breeding sites. Conclusions from our study will be valuable for elucidating the multiple roles of amphibians in freshwater and terrestrial systems and assessing their importance relative to other taxonomic groups.

Testing the effectiveness of small mammal identifiable markers in the field

Tyler S. Bridgehouse, Grace Nussbaum, and Aaron Haines, Millersville University of Pennsylvania, 198 Creek Dr, Millersville, PA 17551

Tyler Bridgehouse, (717) 808-3320, tsbridge@millersville.edu, undergraduate student poster.

Mark-recapture is used in wildlife research to provide estimates of population density, survival, recruitment and movement to help guide management decisions. For small mammal research, ear-tagging has been successfully used to mark individuals, however ear-tags can inhibit grooming and promote infection. The use of Passive Integrated Transponder (PIT) tags have also been used to mark small mammals, but PIT tags are prone to falling out of the body and causing infection. Hair dyes are favored for short term mark-recapture studies because they are relatively low cost, can be applied easily and are less stressful and damaging to marked individuals. Our objective was to test the effectiveness of Clairol hair-dye and The Muromachi Kikai hair-dye marker on *Peromyscus leucopus* and *Blarina brevicauda*. Our study was conducted within Millersville University and consisted of two transect lines, each with ten Sherman traps checked three times a week over three months. We captured 33 individuals and marked each of them once with both hair-dyes. These individuals were then monitored based on recapture events (n=116). All captured individuals were photo recorded to validate the effectiveness of the hair-dye marks. Results showed that the Muromachi Kikai hair-dye marker outlasted the Clairol hair-dye and can be used to distinguish most individuals after 7 weeks in the field. We concluded that the Muromachi Kikai hair-dye marker could be used in short-term (<3 months) studies of small mammals.

Variation in Arthropod Communities Associated with Native and Nonnative Vegetation at the Baker-Henry Peace Chapel and Nature Preserve in Central Pennsylvania

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Max Ferlauto, (703) 407-4847, ferlamh15@juniata.edu: undergraduate student poster

We investigated the difference in arthropod communities associated with introduced and native vegetation in an open, early successional habitat found Central Pennsylvania. Using a beat sheet, arthropods were collected from two native (*Quercus alba*, *Juglans nigra*) and two nonnative plant species (*Elaeagnus umbellata*, *Lonicera japonica*) that comprised the dominant woody vegetation at the site. We identified arthropods to family and differentiated them by species. Then we calculated species richness and abundance. We analyzed our data for significance using a nested ANOVA test. Native vegetation hosted an average of 20 arthropods and 12 species while nonnative vegetation hosted an average of 13 arthropods and 10 species. We found that, while native vegetation hosted a greater abundance and species richness of herbivorous arthropods, it did not have a significant effect on predatory arthropods. We believe this is because predatory arthropods are less directly dependent on the vegetation for nutrition. Addressing the relationships between vegetation nativity and arthropod communities may aid our broader understanding of the role that nonnative vegetation plays in affecting higher trophic levels.

Examining the Influence of Rodent Abundance on the Nest success of the Golden-winged Warbler (*Vermivora chrysoptera*) in Managed Habitats of Central Pennsylvania

Theresa H. L. Illo, Sydney J. Tomechko, Lauren M. Prasko, Cameron J. Fiss, Jeffery L. Larkin, Joseph E. Duchamp. Department of Biology, Indiana University of Pennsylvania, Indiana, PA 15705

Theresa H. L. Illo, (717) 572-7167, BHMT@iup.edu, undergraduate student poster

Rodents are considered a significant predation threat to nesting birds in a variety of habitats. We examined the presence and abundance of small mammals in and around the nesting sites of Golden-winged Warblers (*Vermivora chrysoptera*) in 3 managed habitat areas in Central Pennsylvania. Small mammals were captured using Sherman traps arranged in small 3x3 grids centered on nest locations located earlier in the summer. These nests had been monitored for success or failure during the most recent breeding season. While we did find differences in mammal abundance when comparing the 3 management areas, we found no relationship between the observed abundance and the failure of a nest location ($F_{2,20}=4.54$, $P=0.237$). Our study was intended as a pilot study on these relationships. Based on our results, we recommend modifying the approach to assessing small mammal abundance and incorporating a wider suite of potential threats before attempting a more intensive study on the mechanisms driving nest success and failure for the Golden-winged Warbler. We also discuss habitat associations found to be related to small mammal abundance in these managed areas.

Feeding ecology of the Eastern Red-backed Salamander (*Plethodon cinereus*) in forest patches dominated by fern

Dylan M. McGlone, Chelsey L. Slater, and Kurt J. Regester, Department of Biology and Geosciences, Clarion University, Clarion, PA 16214

Dylan McGlone, (717) 676-7692, d.m.mcglone@eagle.clarion.edu, undergraduate student poster

In many Pennsylvania forests, the dominance of ferns in extensive areas is associated with high densities of White-tailed Deer and changes in forest structure. Although the Red-backed Salamander (*Plethodon cinereus*) is an abundant predator in the leaf litter and plays an important role in the forest food web, no previous studies have examined effects of fern on salamander feeding ecology. We conducted a field experiment to compare salamander feeding in dense fern patches and in adjacent areas dominated by leaf litter. We captured adult salamanders ($n = 17$) at a different location, held them in the lab to clear gut contents (48 hrs), and then randomly placed each in a “foraging bucket” located within dense fern or within adjacent leaf litter for 24 hours. In addition, we opportunistically collected adult salamanders ($n = 20$) actively foraging in areas dominated by fern and in adjacent areas of leaf litter. Individual prey items were removed from the stomachs of all individuals retrieved from the field, identified to taxonomic order, and then photographed and measured for total length using a microscope and digital image processing software. Our results will include statistical comparisons of diet composition and feeding rates, along with quantitative food webs associated with salamanders foraging in fern or leaf litter. Findings from our study will be valuable for clarifying the roles of amphibians in forest food webs and assessing the various impacts of changes in forest structure.

The regal fritillary butterfly (*Speyeria idalia*) reintroduction

Erika N. McKinney and Virginia Tilden, Temple University at Fort Indiantown Gap National Guard Training Center Annville, PA 17003; Tim Becker, Zoo America, Hershey Park, 201 Park Avenue, Hershey, PA 17033; Joseph Hovis and Mark Swartz, The Pennsylvania Department of Military and Veterans Affairs, Fort Indiantown Gap National Guard Training Center, Annville PA 17003

Erika N. McKinney, (717) 861-2949, c-emckinne@pa.gov; professional poster presentation

The regal fritillary butterfly (*Speyeria idalia*), was once a common butterfly species in much of the mid-western and northeastern United States. Over the last several decades, an extreme decline in numbers occurred, primarily due to the loss of native, open grassy habitats. The most significant decline took place in the East; where one known population still exists at Fort Indiantown Gap National Guard Training Center (FIG-NGTC). FIG-NGTC provides some of the largest expanses of remaining native grassland habitat in the East. In an effort to conserve the rare butterfly, FIG along with multiple partnerships such as ZooAmerica and the Pennsylvania Game Commission (PGC), developed a reintroduction plan aimed towards helping the recovery of this species. At ZooAmerica, regals are reared from individuals collected at FIG, and released at sites on state game lands. PGC is managing these sites to enhance native grassland vegetation, including the plants required to support the regal. The goal of the reintroduction plan is to establish sustaining viable populations of regal outside of FIG. This will likely take years of releasing individuals and adaptive habitat management.

Barriers to managing for climate change: a case study

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David Muñoz, (919) 602-1516, djm516@psu.edu; graduate student poster

Climate change is already impacting wildlife populations from shifts in disease dynamics to shifts in phenology. Unlike other management issues where a solution may exist on a site or landscape level, managing the greenhouse gases that cause climate change is not a solution for wildlife managers. Managers must instead focus on minimizing the impacts of climate change, but for most species it is unclear what those impacts may be and how populations might respond. Here we present preliminary findings in how a common woodland amphibian, the red-backed salamander (*Plethodon cinereus*), is impacted by weather conditions. We use three years of mark-recapture data on two different PA populations and five years of data on a Maryland population to look at how individual growth rates may be impacted by climate change. Our findings show that warmer summers reduce the growth rates of salamanders by 75%. Reduced growth rates mean it will either take longer for salamanders to reach reproductive maturity or that fecundity will decrease given reproduction at smaller sizes. This threatens population persistence under climate change. These findings are part of a distributed research network that aims to understand how

these responses vary across the species' range. By understanding impacts and variation in responses to impacts, we can begin to create effective climate adaptation management options.

Spatial, Morphometric, and Reproductive Characteristics of Gray Squirrels (*Sciurus Carolinensis*) Harvested in Central Pennsylvania

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Kyle P. Santerian, (814) 641-3436, ramakrishnan@juniata.edu; Undergraduate Poster

Previous studies have recorded special variations in various characteristics of gray squirrels. The goal of our study is to attempt to identify such potential variations in a gray squirrel populations in Central Pennsylvania. We collected data from squirrels brought to the Shamokin Mountain Squirrel hunt in January 2017. A total of 350 squirrels were harvested by 150 hunters from 17 different townships during the one-day tournament. Using ArcGIS we mapped the distribution of all registered participants and the distribution of successful harvest locations. We then collected morphometric measurements and photographs of a randomly selected subset of 120 squirrels from this harvest. The morphometric measurements and photographs can be used to look at geographic variability and overall health of squirrels. We also collected testes, ovaries and uteri from this subsample. To identify the reproductive condition and health of mature squirrels, we plan to calculate the gonadosomatic index and conduct a histological analysis of the testes and ovaries, and look at potential geospatial variability. Public hunting tournaments represent a unique opportunity for researchers to collect biological data, and can be a valuable opportunity for undergraduate students to gain hands-on experience.

Observations and potential trophic implications of the exotic fruit fly, *Drosophila suzukii*, on the Allegheny National Forest ecosystem

Scott H. Stoleson and Robert Long, USDA Forest Service, Northern Research Station, 335 National Forge Road, Irvine, PA 16329; Richard M. Turcotte, Craig Larcenaire, and Terry M. Jenkins, USDA Forest Service, Northeastern Area State and Private Forestry, 180 Canfield Street, Morgantown, WV 26501

Scott H. Stoleson, (814) 563-1080, sstoleson@fs.fed.us; professional, poster presentation

The Spotted-winged Drosophila (SWD, *Drosophila suzukii*), a non-native pest of berry and stone fruit first recorded in North America in California in 2008, has spread rapidly across the continent since then. Unlike native fruit flies which oviposit on overripe or decaying fruit, SWD has a saw-like ovipositor that enables it to lay its eggs in unripe fruit, and thus prevent full ripening. Although the effect of SWD on commercial fruit production has been well-studied globally, its prevalence and impacts on native forest ecosystems remain virtually unknown. In 2016, we discovered an infestation of SWD in the Allegheny National Forest while sampling birds in two recent timber harvests dominated by wild blackberry (*Rubus allegheniensis*). As berries began to ripen, extremely large numbers of fruit flies appeared; within 2 weeks the entire *Rubus* crop across both sites failed. Concurrently, the capture rate of primarily frugivorous songbirds plummeted to less than 25% of our 10-yr August average. A separate study of black cherry

(*Prunus serotina*) seed viability revealed approximately 30% of fruit sampled were found to contain SWD maggots, and vinegar traps captured many thousands of SWD within 4 cherry stands. Considering the importance of both blackberry and black cherry fruits to birds, rodents, bear, fishers and other species, loss of these fruits to SWD are likely to have direct impacts on wildlife populations. Further, should infestation also affect the viability of seeds within the fruit, then SWD may also have indirect effects on wildlife through shifts in plant species composition.

Development of the *Field Isolation and Amplification of DNA Assay (FIA-DNA) kit: A Revolutionary Method for Species Identification of Unknown Samples*

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Nickolas Walker, (716) 445-0525, walkern1@duq.edu; undergraduate student poster

A major challenge in biodiversity conservation is the identification of unknown samples collected in the field. Most endangered species are elusive, therefore many monitoring programs rely on noninvasive sampling using scat or hair. One difficult hurdle is identifying unknown biological samples in the field due to the reliance on genetic analysis in a laboratory. This can cause delays in obtaining important information and is often infeasible for many on-the-ground conservation efforts with limited resources. We are working to develop a *Field Isolation and Amplification of DNA Assay (FIA-DNA) Kit* for genetic field identification of species for both International conservation and management of Pennsylvania wildlife without the need for PCR and agarose gel electrophoreses. Preliminary results tested efficacy on snow leopard (*Panthera uncia*), bobcat (*Lynx rufus*), and coyote (*Canis latrans*) samples for species-specific identification. Our method using loop-mediated isothermal amplification (LAMP) of DNA has exhibited 100% specificity for over 30 previously extracted Snow Leopard scats. Coupling it with a modified FTA extraction has yielded successful detection in over 40% of tested scat samples to date. This method can be completed in under one hour with minimal equipment, using UV fluorescence within the reaction tube to confirm the species identification. We are optimizing this method for field deployment of the FIA-DNA kit at the Powdermill Nature Reserve in Rector, PA. The FIA-DNA kit will be tested for precision in identifying a wide range of scat samples in the field, eliminating the time and cost of lengthy lab-based analyses.

Susceptibility of Ruffed Grouse (*Bonasa Umbellus*) To West Nile Virus in Pennsylvania

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Lisa M. Williams, (814) 422-8243, liswilliam@pa.gov; professional poster presentation

Since its arrival to North America in 1999, West Nile virus (WNV) has had unprecedented adverse effects on the health of native birds across numerous taxa. In Pennsylvania, WNV was first documented statewide in 2002, soon after which precipitous population declines were observed in Pennsylvania ruffed grouse (*Bonasa umbellus*). Statewide, grouse populations have

not since recovered. The present study assessed the potential impacts of WNV on Pennsylvania ruffed grouse populations through integrating laboratory- and field-derived data. Methods included both experimental infections of juvenile grouse and serology on field-collected blood samples. Grouse were susceptible to experimentally-induced WNV morbidity and mortality. Viremia was generally detectable for 4-6 days, and for up to 8 days in birds with clinical illness. Forty percent (4/10) of naïve inoculated grouse were euthanized on 7-8 days post-inoculation (DPI) due to severe clinical disease; lesions in these birds included severe myocarditis and minimal encephalitis. Subclinically-infected grouse that survived to the end of the trial at 14 DPI (6/10) had moderate myocardial lesions and more widespread brain lesions. These results suggest encephalitis is more likely a chronic manifestation of WNV in grouse, and that longer-term survival may have been compromised in some of these surviving birds. All inoculated grouse surviving to 14 DPI seroconverted based on virus neutralization assays performed on serum and Nobuto filter strips. No in-contact sham-inoculated controls had evidence of infection. Susceptibility of ruffed grouse to ongoing cycles of WNV prevalence has important implications for managing this important game bird.

Prevalence of West Nile Virus in Ruffed Grouse (*Bonasa Umbellus*) In Pennsylvania: Evidence of Population Impacts

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Since its arrival to North America in 1999, West Nile virus (WNV) has had unprecedented adverse effects on the health of native birds across numerous taxa. In Pennsylvania, WNV was first documented statewide in 2002, soon after which precipitous population declines were observed in Pennsylvania ruffed grouse (*Bonasa umbellus*). Statewide, grouse populations have not since recovered. To test the prevalence of WNV in wild grouse populations, the PA Game Commission undertook two years of hunter-harvested blood sampling. Nobuto filter strips collected from hunter-harvested Pennsylvania ruffed grouse during Year 1 (the 2015-2016 season) revealed a WNV seroprevalence of 14% (28/202). Seropositive birds were detected in every region of the state and 16 of 31 counties in which birds were sampled. Preliminary findings from Year 2 (2016-17 season) will be presented. Collectively, experimental challenge data and field-derived serologic data provide insight into the distribution and extent of WNV prevalence and the potential impacts of WNV on Pennsylvania ruffed grouse. Preliminary indications suggest that habitat can play a role in mitigating the population-level impacts of WNV in areas where high-quality grouse habitat is abundant on the landscape.