



Great Smoky Mountains National Park Science Colloquium

Thursday, March 6, 2025 — 9 am to 3 pm — virtual via Zoom

Co-hosted by Great Smoky Mountains National Park & Discover Life in America

Free & open to the public. • Register to tune in: shorturl.at/BShLX

Presenters: no need to register. • More information: dliia.org/colloquium-2025



Schedule

- 9:00** **Welcome and introductions**
Superintendent's Office (GSMNP) & Will Kuhn (Discover Life in America)
- 9:10** **Hurricane Helene and the wash-out of I-40: Observations from the Duke GSM Rain Gauge Network**
Douglas K Miller (UNC, Asheville)
- 9:30** **Relative impacts of projected climate and land-use change on biodiversity in the Appalachian Highlands**
Sam Jantz (UTK, NIMBioS), Narayani Barve, Paul Armsworth, Xingli Giam & Mona Papes
- 9:50** **Using machine learning to correct long-lead precipitation forecasts and advance flash-flooding forecasts**
Mochi Liao (Univ Illinois Urbana-Champaign), Ana Barros
- 10:10** 15-minute break
- 10:25** **Ramping it up: Assessing genetic diversity of the *Allium tricoccum* Aiton complex in GSMNP using Next-Gen sequencing**
Lauren Gray (Appalachian State) & Matt C Estep
- 10:45** **Estimated effects of imidacloprid use on the aquatic and terrestrial abundance of stream-breeding plethodontid salamanders**
John C Maerz (UGA), Cassandra Waldrop, Jade A Samples, Danielle R Bradke, Hadley Copeland, Cheyana Bassham, James A Martin, Jeffrey Hepinstall-Cymerman, Anthony F Lagalante & Elizabeth McCarty
- 11:05** **Connecting people to parks, science and the Dragonfly Mercury Project: Findings from GSMNP**
Colleen Flanagan Pritz (NPS), C Eagles-Smith, SJ Nelson, J Willacker, C Emery, K Ko, A Miller-Rushing
- 11:25** **Pollen Evidence of Cherokee Horticulture in Cades Cove, GSMNP**
Anna G LaFollette & Sally P Horn (UTK)
- 11:45** 55-minute lunch break
- 12:40** **Fates and movements of relocated conflict American black bears (*Ursus americanus*) from GSMNP to Cherokee National Forest**
Kristin J Botzet (UTK), Joseph D Clark, Ryan H Williamson & William H Stiver
- 1:00** **Assessing avian species change in response to hemlock decline: A 25-year follow-up in GSMNP**
Allison Melrose (UNC-Asheville), Nicole Mooradian, Andrew Laughlin & Lazarus Pomara
- 1:20** **Untangling the impacts of kleptoparasitism on bee health and bee-behavior**
Erika Dalliance (UTK) & Laura Russo
- 1:40** 15-minute break
- 1:55** **Patterns of nematode abundance in GSMNP as assessed by molecular methods**
Seán O'Connell (Western Carolina Univ), Ivan Emrich, Kayla Stovall & Ammon Hottensmith
- 2:15** **NEON in the Smokies: Overview of the National Ecological Observatory Network GSMNP field site**
Margaret Cumberland (NEON-Battelle)
- 2:35** **Developing a roadmap for the restoration of mussel fauna of Abrams Creek**
Caleb Moses (UTK), Augustin Engman, Gerry Dinkins, Matt Kulp & Luke Etchison
- 2:55** **Conclusions and farewell**

Presenting author in bold; see abstracts for full author information.

Abstracts

Abstracts are sorted by last name of the presenting author (in bold).

Fates and movements of relocated conflict American black bears (*Ursus americanus*) from Great Smoky Mountains National Park to Cherokee National Forest

Kristin J Botzet¹ (kbotzet@vols.utk.edu), Joseph D Clark², Ryan H Williamson³ & William H Stiver³

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Great Smoky Mountains National Park (GRSM) in Tennessee and North Carolina, USA, has a high-density American black bear population (*Ursus americanus*) and frequent human-bear conflicts. Previous research at GRSM based on VHF telemetry and tag returns found that the fates of relocated conflict bears were largely unknown, thereby leaving many questions about the efficacy of relocation as a mitigation tool unanswered. We fitted 50 conflict bears relocated from GRSM with GPS-radio collars and released them in the Cherokee National Forest, Tennessee. Some of these bears were released in the Pigeon River Gorge (PRG), where we also collared 37 resident non-conflict bears for comparison. We used those GPS location data to evaluate survival, recurrence of conflict activity, homing rate, and settling rate for relocated and resident bears, as appropriate. Known-fate models indicated that the mean annual survival probability for relocated bears was 0.102 (95 % CI = 0.000–0.356) when we censored lost signals. Survival of relocated bears was much lower than non-relocated conflict bears in GRSM (0.869, 95% CI = 0.863–0.875) and non-conflict resident bears in the PRG (0.836, 95% CI = 0.659–1.000). Harvest was the greatest mortality risk for both relocated (0.482, 95% CI = 0.326–0.638) and resident bears (0.136, 95% CI = 0.000–0.280), and relocated bears were at greater risk of harvest than residents ($\beta = 2.407$, 85% CI = 0.948–3.866). The annual probability of relocated bears returning to their original capture location decreased with distance relocated ($\beta = -0.025$, 85% CI = -0.046–-0.004) and averaged 0.615 (95% CI = 0.341–0.889) for adults and 0.111 (95% CI = 0.000–0.318) for subadults. The annual probability of recurrent conflict, defined as a report to agency officials by landowners, for relocated bears was 0.445 (95% CI = 0.225–0.666). Recurrent conflict increased with the level of food conditioning ($\beta = 0.274$, 85% CI = 0.036–0.511), as determined by stable isotope analysis, and decreased with distance from the release-site to the nearest urban area ($\beta = -0.0921$, 85% CI = -0.1842–0.0002). Our results suggest that public education is paramount to avoid human-bear conflicts before they begin, as relocation and other ‘bear-centered’ options may have only limited success.

NEON in the Smokies: Overview of the National Ecological Observatory Network GSMNP field site

Margaret Cumberland (mcumberland@battelleecology.org)

National Ecological Observatory Network (NEON) Program, Domain 7 – Appalachians & Cumberland Plateau, Oak Ridge, TN

The National Ecological Observatory Network (NEON) provides open ecological data from 81 field sites across the United States, including one site at Great Smoky Mountains National Park (GSMNP). NEON data cover a wide range of subject areas within ecology, including organismal observations, biogeochemistry, remote sensing, and micrometeorology. Many datasets already span a decade of data collection. In addition to open data, NEON also provides many resources that support land managers, researchers, and educators; including sampling protocols, data skills training, and classroom-ready lesson plans. This talk will provide a brief introduction to resources for access and working with a variety of NEON data for your research. It will also highlight case studies of researchers using NEON data from the GSMNP field site, as well as other field sites, to show how NEON science can be integral to protecting and preserving natural communities.

Untangling the impacts of kleptoparasitism on bee health and bee-havior

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Aggregating ground-nesting bees are essential and often understudied pollinators that may be increasingly threatened by anthropogenic change. In this study, we investigated whether parasite load could be an indicator of the health of ground-nesting bee aggregations. Nest parasites (kleptoparasites) often wait at nest aggregations for female hosts to provision their young with pollen before laying their own, faster hatching eggs, on the pollen provision. Kleptoparasites kill the host bee larvae and may also decrease the overall fitness of the aggregation through behavioral changes. To better understand how these kleptoparasites affect the health of ground-nesting bees, we explored how kleptoparasite density impacts chimney bee (*Anthophora abupta*) behaviors and several indicators of overall aggregation health. We conducted a field study to obtain foundational data such as host behavior, parasite and host density, host body size, pollen quality, and pollen abundance. Our study found evidence that kleptoparasite abundance at the aggregation correlates with bee body size and behavior frequency, which allows us to explore how host-parasite interactions influence bee health. Understanding the intricacies of bee health and the impact of nest parasites is paramount for effective conservation pathways.

Connecting people to parks, science and the Dragonfly Mercury Project: Findings from GSMNP

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The Dragonfly Mercury Project (DMP) is one of the most recognized citizen science initiatives within the National Park Service, providing a decade-long, nationwide assessment of mercury (Hg) risk using dragonfly larvae as bioindicators. Mercury, a global pollutant responsible for 80% of fish consumption advisories in the U.S., poses risks to both human and wildlife health, including park visitors. Great Smoky Mountains National Park (GRSM) was among the first parks to join the DMP, which now spans over 800 water bodies across 49 states and 180 protected areas. Eleven years of data collection from 10 GRSM sites reveal that most samples fall within moderate to high impairment categories, indicating that top predator fish may exceed human consumption thresholds and wildlife may be at risk from elevated Hg levels. These findings enhance our understanding of Hg dynamics in GRSM, including its presence in fish and litterfall, and inform strategies for mitigating its impact. Additionally, long-term dragonfly Hg data contribute to assessing the effectiveness of Hg emission reductions. Public participation in DMP sampling at GRSM strengthens connections between people and parks while advancing citizen science at multiple levels. The program's success informs broader efforts to develop nationwide citizen science initiatives within the federal government.

Ramping it up: Assessing genetic diversity of the *Allium tricoccum* Aiton complex in GSMNP using Next-Gen sequencing

Lauren Gray (grayla1@appstate.edu) & Matt C Estep

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Our world today faces an unprecedented loss of biodiversity, and understanding the extent to which species lose genetic diversity is imperative for conservation efforts. Reduced genetic diversity causes species to be less resilient to stochastic change and more susceptible to extirpation and possibly extinction. This is especially problematic for species that have small population sizes or have modes of reproduction that do not facilitate gene flow. *Allium tricoccum* complex is a highly sought-after edible plant that is culturally significant to Native Americans, specifically the Eastern Band of Cherokee. However, due to its strong onion flavor and aroma, foraging for, and commercially harvesting this plant has become increasingly popular, leading to concern that some populations may be eradicated due to irresponsible harvesting. This study uses SNP genetic markers obtained via the Next-Generation sequencing technique, MIG-seq to assess the genetic diversity of *A. tricoccum* populations throughout Great Smoky Mountains National Park with the hopes of empowering sustainable, indigenous harvest. Populations throughout the park show low levels of genetic diversity and high levels of inbreeding, as to be expected in predominantly clonal plant populations. Analyses have revealed genetic structure and two distinct genetic clusters within the park, providing molecular evidence for the potential presence of the sister taxa, *Allium burdickii*. The data generated in this study will play a crucial role in the long-term monitoring of the *A. tricoccum* complex, as well as highlight genetic methods for obtaining population-level information that can be used in future studies analyzing seemingly abundant clonal plant populations.

Pollen evidence of Cherokee horticulture in Cades Cove, Great Smoky Mountains National Park, USA

Anna G LaFollette & Sally P Horn (shorn@utk.edu)

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We present records of vegetation and fire history from three wetlands along Forge Creek Road in the southwestern portion of Cades Cove: Pumphouse Marsh 2 in the Pumphouse Marsh wetland complex, and nearby sites we call Additional Wetland 1 and 2. Pollen grains and microscopic charcoal fragments preserved in these wetland sediments offer evidence of changes in plant communities and fire occurrence during the late Holocene, some linked to human activity. The Pumphouse Marsh 2 record, in particular, offers evidence of Indigenous forest clearance and agricultural disturbance predating Euro-American settlement in Cades Cove. Here distinct changes in the pollen record paired with the presence of maize (corn) pollen before the period of Euro-American settlement indicate that Indigenous inhabitants cleared forests and established agriculture near the marsh. All records show increased sediment accumulation after ca. 1800 CE, during the period of Euro-American settlement in Cades Cove, while Pumphouse Marsh 2 and Additional Wetland 1 also show increases in fire activity and pine abundance during this interval.

Relative impacts of projected climate and land-use change on biodiversity in the Appalachian Highlands

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The temperate forests of the Appalachian Highlands in the eastern United States are a biodiversity hotspot facing threats from climate change and habitat loss due to land-use changes. We investigated the potential individual and combined impacts of these threats on over 300 forest dependent, vertebrate species of conservation concern. We utilized climate and land-use change projections from the Shared Socioeconomic Pathways (SSPs) from the most recent the IPCC Assessment Report to quantify the change in amount and distribution of habitats in the mid-21st century. Potential impacts due to climate change were quantified for each species by fitting an ecological niche model under current climate conditions and projected onto future climates from each SSP scenario. Coarse resolution land-use data for each SSP was downscaled to match the resolution of the climate projections and only areas projected to be forested were assumed to be suitable habitat. Our models predict land-use change will have a much more marked impact on the distribution and amount of suitable habitat area for these species than will climate change by 2050.

Using machine learning to correct long-lead precipitation forecasts and advance flash-flooding forecasts

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The accuracy of Numerical Weather Prediction (NWP) rainfall forecasts has improved generally during the last two decades due to improved models and data assimilation techniques. However, orographic rainfall in mountainous regions remains a challenge due to unresolved small-scale physics and improper parameterizations. Liao et al. (2025) presented a new methodology to improve NWP rainfall, specifically High-Resolution Rapid Refresh (HRRR) rainfall forecasts, by using a Random Forest Classifier (RFC) algorithm to map HRRR rainfall to ground-based radar rainfall. The RFC method is applied to over 200 extreme precipitation events covering the entire period of the HRRR version 4 precipitation records, using a traditional machine learning split method (training-validation-test). The accuracy of HRRR forecasts shows: a) a strong lead time dependency, with 12-30 hours showing the best agreements against radar rainfall estimations, and b) strong geographic organization according to weather regimes and regional hydrology with strong differences between the Southern Appalachians and the Central and Northern Appalachians conditional on regional weather. Overall, the RFC results show significant improvement in HRRR overestimation cases, effectively reducing false alarm cases. The improvement by the RFC is also significant in terms of hydrological performance, dramatically improving forecast skill metrics for lead times up to 36 hours in the Central and Northern region. HRRR severe underestimation cases are mostly hurricane and tropical depression events, which will be addressed separately. This approach provides a pathway to characterizing and modeling NWP rainfall uncertainty at high resolution (~250m) conditional on lead time, precipitation, geographic regimes in complex terrain.

Estimated effects of imidacloprid use on the aquatic and terrestrial abundance of stream-breeding plethodontid salamanders

John C Maerz (jcmaerz@uga.edu), Cassandra Waldrop, Jade A Samples, Danielle R Bradke, Hadley Copeland, Cheyana Bassham, James A Martin, Jeffrey Hepinstall-Cymerman, Anthony F Lagalante & Elizabeth McCarty

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When considering the use of pesticides, forest managers need to make decisions about potential trade-off among management objectives such as conserving target species while limiting non-target effects. Imidacloprid is a neonicotinoid insecticide used to suppress Hemlock woolly adelgid (HWA) and conserve Eastern and Carolina hemlock populations and the habitats they create. In 2024, we reported on our research showing that climate but not the use of imidacloprid was a substantial driver of fully-terrestrial salamander (*Plethodon* spp.) abundance. We now report on estimated effects on the aquatic (larval) and terrestrial abundance of stream-breeding plethodontid salamanders. We used repeated transect surveys of 12 streams through imidacloprid-treated forests and 10 reference streams, and we used repeated depletion samples among 15 replicate terrestrial plots at each of 15 imidacloprid-treated and 9 untreated reference sites across north Georgia, western North Carolina, and eastern Tennessee. As with fully-terrestrial species, mean daily vapor pressure deficit from 2011-2020, a measure was negatively associated with terrestrial abundance of stream-breeding salamanders. However, unlike fully-terrestrial salamanders, we found a negative association between salamander abundance and imidacloprid dose that was comparable in size to the natural effect of climate on abundance. We did not find any measurable difference in larval salamander abundance between imidacloprid-treated and reference streams. Assuming our estimates of larval relative abundance are unbiased, our results suggest that imidacloprid might be modest having negative effects on some stream-breeding salamander species through exposure in the aquatic environment, but the effects are subacute and potentially realized through reduced terrestrial fitness of those salamanders after they metamorphose. Hemlocks are an iconic and ecologically important tree, and hemlock conservation has many merits independent of potential benefits to salamanders. None of the stream-breeding species we encountered are considered rare or threatened and all occur in areas with and without hemlocks. Therefore, the continued use of imidacloprid near streams may be warranted at those sites where the salamander species present are common and widely distributed. However, managers treating sites where there are rare or threatened stream-breeding salamander species present should weigh potential risks to those species until more is known about the effect of imidacloprid on those species.

Assessing avian species change in response to hemlock decline: A 25-year follow-up in Great Smoky Mountains National Park

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Eastern hemlocks are a foundation species, providing unique structure and microclimates that support forest biodiversity. However, since the spread of the invasive hemlock woolly adelgid (HWA) to the Southern Appalachians, eastern hemlocks have experienced widespread die-off. Studies in the northeastern US suggest that hemlock loss leads to the decline of regionally hemlock-associated bird species, such as the Black-throated Green Warbler and Acadian Flycatcher. To understand the effects of hemlock decline on birds in the Southern Appalachians where warmer winters may accelerate the spread of HWA, we compared bird survey data before and after HWA infestation. We repeated surveys from the late 1990s using 10-minute point counts across 200 sites during the breeding season. At each site, we calculated a hemlock decline value (i.e., loss of hemlock basal area) by counting all hemlocks within a 30-meter radius and categorizing them by size and health class. We then used both raw bird abundances and occupancy modeling to understand how bird dynamics were influenced by hemlock decline at each site. We documented 5,843 hemlocks at these sites, of which 57% were dead and only 1% showed no sign of defoliation, with the remaining 42% a mixture of minor to severe defoliation. The bird abundance analysis revealed significant bird declines related to hemlock loss in six species, Acadian Flycatcher, Dark-eyed Junco, Ovenbird, Veery, Blackburnian Warbler, and Black-throated Blue Warbler. Meanwhile, Brown Creeper, Eastern Towhee, and Swainson's Warbler increased in sites with greater hemlock loss.

Hurricane Helene and the wash-out of I-40: Observations from the Duke Great Smoky Mountains Rain Gauge Network

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As Hurricane Helene strengthened in the southern Gulf of Mexico, a predecessor rain event (PRE) was impacting eastern Tennessee and western North Carolina with significant rainfall, saturating the soil of the region on 25-26 September 2024. After making landfall in Florida on 27 September as a major hurricane, Helene tracked almost due north and caused major devastation in western North Carolina due to flooding and landslides, along with uprooted trees and the resulting power outages. Rainfall associated with the PRE and Helene will be examined using observations from the Duke GSMRGN, located in the Pigeon River Basin (Haywood County, NC) and near the I-40 washout. Although the PRE and Helene events covered a broad area over eastern Tennessee and western North Carolina, rainfall observations of the gauge network indicates significant spatial variability that is a combination of convective systems embedded within the larger storm and of topographic relief.

Developing a roadmap for the restoration of mussel fauna of Abrams Creek

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Abrams Creek is a watershed nearly entirely contained in the boundaries of the Great Smoky Mountains National Park (GRSM). The Abrams Creek watershed supports a diverse array of fish, aquatic macroinvertebrates and mussels due to portions of its watershed being underlain by limestone. In 1957 a rotenone treatment was conducted to establish a trophy rainbow trout fishery, which extirpated 31 of the 63 species of fishes and other native aquatic fauna of Abrams Creek. Since the 1957 treatment some natural fish recolonization has occurred and has been aided by species reintroductions by the National Park Service and local partners, but this system has remained disconnected from the Little Tennessee river due to the Chilhowee impoundment. Freshwater mussels require a fish host to complete their life cycle, so the loss of native fishes undoubtedly negatively affected mussels in this system. Several extirpated fish species have been restored to this system, so the National Park Service is considering actions to restore other extirpated aquatic fauna. The goals of this project are to: 1) characterize the extant mussel assemblage of Abrams Creek, and 2) identify and test candidate species for reintroduction to Abrams Creek. We characterized the current mussel assemblage using timed search surveys at thirty randomly selected sites throughout Abrams Creek. Five mussel species were observed, and areas of high relative abundance were identified during these surveys. We are currently identifying species with high reintroduction potential by combining archaeological and historical survey data with an ongoing in-situ experiment that tests the viability of Abrams Creek as habitat for two species: Spike (*Eurynia dilatata*) and Slippershell (*Alasmidonta viridis*). The in-situ experiment is still ongoing despite some interference from vandalism, but growth has been observed in several test specimens. Identifying the potential environmental drivers of abundance hotspots observed in the timed search surveys is one of the next steps in the project- understanding species success and factors that influence their success area are critical to determining what species would be viable for reintroduction in Abrams Creek. Due to the protected nature of this watershed, Abrams Creek could be vital to the conservation of several endangered mussel species threatened by habitat loss across their range.

Patterns of nematode abundance in Great Smoky Mountains National Park as assessed by molecular methods

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Soil-dwelling nematodes are of importance to humans in ways such as being pest species in agricultural plants and as one of the most important model animals used in science (*Caenorhabditis elegans*). The ecological roles and diversity of nematodes have received recent attention due to their importance across trophic levels in soil, including acting as predators of microorganisms, herbivores, and detritivores. Limited work had been conducted on inventorying nematodes in Great Smoky Mountains National Park until the work in this study commenced in 2023. We report on the use of quantitative polymerase chain reaction (qPCR) methods used to survey 22 sites across a range of elevations, habitat types, and historical land uses. Twenty-six of 40 nematode taxa found are new records for GSMNP and spanned all known feeding patterns. The number of taxa ranged from 9 to 28 per site including two genera, *Mesocriconema* (herbivores) and *Labronema* (omnivores) found at all sites and five taxa observed in all but one location. Sites that yielded the most taxa included Abrams Creek/Rabbit Creek Trail and the Tremont, Twin Creeks, Cataloochee, and Purchase Knob ATBI Sites. Two ATBI sites, Goshen Prong and Indian Gap, displayed high abundances of nematodes, with single taxa accounting for an order or more of magnitude greater numbers than anywhere else (e.g., the fungivorous genus *Filenchus* and herbivorous genus *Heterodera* found at Goshen Prong and the omnivorous genera *Microdorylaimus* and *Eudorylaimus* from Indian Gap). Co-occurrence modeling of nematodes based on other DNA recovered from the soil samples yielded inferred relationships between the nematode taxa *Pseudacrobeles*, *Eucephalobus*, and *Pristionchus* to bacteria and *Dorylaimellus* to fungi as well as one fungal genus (*Mortierella*) to numerous nematodes. Ongoing lab work involves growing nematodes from soil and testing feeding preferences on bacterial and fungal species. This study expanded upon the known diversity of nematodes in GSMNP, documenting an average of 19 taxa per site. The activities of nematodes in soil are not well understood in situ and it is hoped that this work will open up avenues to better determine their roles in the soil ecosystems in the Park and beyond.
