

GREAT SMOKY MOUNTAINS NATIONAL PARK SCIENCE COLLOQUIUM

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

THURSDAY, MARCH 2, 2023 — 9 AM TO 4 PM — VIRTUAL VIA ZOOM

SCHEDULE

- 9:00 WELCOME AND INTRODUCTIONS**
Superintendent's Office (GSMNP) & Will Kuhn (Discover Life in America)
- 9:10 Estimated effects of wildfire on Smoky Mountain Salamanders**
William E Peterman (Ohio State Univ), Andrew J. Wilk, John A. Crawford, Ethan J. Kessler, Joseph R. Milanovich
- 9:30 Impacts of hog disturbance on high-elevation terrestrial plethodontid assemblages in GSMNP**
Alexander T Funk (Eastern Kentucky Univ), Stephen C Richter
- 9:50 Estimating the effects of hemlock imidacloprid treatment on terrestrial salamander abundance**
John C. Maerz (Univ Georgia), Jade Samples, Danielle R. Bradke, James A. Martin, Cheyana Bassham, Vanessa K. Terrell, Cassandra Waldrop, Elizabeth McCarty
- 10:10 15-MINUTE BREAK**
- 10:25 Native brook trout reintroductions: Do a source's population genetics influence reintroduction success?**
Rebecca Smith (UTK), Dave Kazyak, Matt Kulp, Barb Lubinski, Ben Fitzpatrick
- 10:45 Great Smoky Mtns and LeConte Creek NEON Update: How we've been progressing and what the future holds**
Margaret Cumberland (NEON, Oak Ridge)
- 11:05 The African American Experiences in the Smokies: The Black Mingus Family**
Antoine Fletcher (GSMNP)
- 11:25 LUNCH BREAK**
- 12:25 A seedling survival guide to the spruce-fir forests of GSMNP: How to succeed in a forest plagued by invasion, disturbance, and competition**
Tori Hongo (Purdue Univ), Michael Jenkins
- 12:45 Physics-guided AI framework to predict and correct radar QPE errors**
Mochi Liao (Duke Univ), Anna Barros
- 1:05 Bryophyte communities change over a 12-year period along an elevational gradient in GSMNP**
Eric Shershen (UTK), Sarah Stehn, Jessica Budke
- 1:25 15-MINUTE BREAK**
- 1:40 Diversity in the duff - what does DNA metabarcoding reveal about leaf-litter arthropods in the Smokies?**
Michael S. Caterino (Clemson Univ Arthropod Collection), Ernesto Recuero, Frank E. Etzler, Patricia L. Wooden, Adam Haberski
- 2:00 Microbial communities as indicators of ecosystem function and sustainability**
Elin Swank (Western Carolina Univ), Seán O'Connell
- 2:20 Forty years of avifaunal change in GSMNP**
Graham Montgomery (Univ California, Los Angeles), David Wilcove, Morgan Tingley
- 2:40 CONCLUSIONS AND FAREWELL**

* Presenting author bolded, full author information below. UTK = University of Tennessee, Knoxville. GSMNP = Great Smoky Mountains National Park.

HOW TO PARTICIPATE

Colloquium information:

Audience registration:

Speaker registration:

<https://dlia.org/event/colloquium-2023/>

<https://bit.ly/3lkB0jh>

No need. You'll receive a link via email.



2023 SCIENCE COLLOQUIUM ABSTRACTS

(by last name of bolded presenting author)

Diversity in the duff - what does DNA metabarcoding reveal about leaf-litter arthropods in the Smokies?

Michael S Caterino (*mcateri@clemsun.edu*), Ernesto Recuero, Frank E Etzler, Patricia L Wooden, and Adam Haberski

Clemson University Arthropod Collection, Dept. of Plant & Environmental Sciences, Clemson, SC

The highest elevations of the southern Appalachians host a distinct type of forest, and with that comes a distinctive arthropod fauna. The arthropod species living in the leaf litter of the forest floor are particularly diverse, with numerous high elevation endemics. Yet, most of the litter fauna has received little taxonomic attention. We have intensively sampled and thoroughly DNA barcoded these arthropod communities, and have found that each peak tends to host a highly distinctive community, with a third or more of the species endemic to a site. Comparing communities from four peaks in the Smokies to other high elevation sites in the southern Appalachians reveals more than half of the litter arthropod species to be found nowhere else.

Great Smoky Mountains and LeConte Creek NEON Update: How we've been progressing and what the future holds

Margaret Cumberland (*mcumberland@battelleecology.org*)

National Ecological Observatory Network (NEON) Program, Domain 7, Appalachian Mountains and 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 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. The GSMNP datasets currently span from 2015-2022 and will continue expanding until 2036. This talk will cover the many and varied types of data being collected, as well as a few interesting glimpses of what they can tell us. It will also review the many resources beyond data NEON provides to support land managers, researchers, and educators. This includes sampling protocols, data skills training, and classroom-ready lesson plans.

The African American Experiences in the Smokies: The Black Mingus Family

Antoine Fletcher (*antoine_fletcher@nps.gov*)

Appalachian Highlands Science Learning Center, GSMNP

While the story of the Mingus Mill and the white settler Mingus family is well known in the Smokies, many people do not know the stories of the Black Minguses. Because Mingus is such a well-known name in the park, it is important that we acknowledge and be aware of those who have been previously left out of the story telling of the Mingus legacy. In doing so, a brighter light is shed on the social and racial climate in the late 19th century Smokies, as well as what life was like for African Americans in this area at the time.

Impacts of hog disturbance on high-elevation terrestrial plethodontid assemblages in Great Smoky Mountains National Park

Alexander T Funk (*alexander_funk5@mymail.eku.edu*), and Stephen C Richter

Dept. of Biological Sciences and Division of Natural Areas, Eastern Kentucky University

The foraging behavior of invasive feral hogs (i.e., rooting) negatively impacts forest ecosystems in the southeastern United States through effects on understory plant, small mammal, and macroinvertebrate assemblages. No comprehensive investigation has yet assessed the potential impacts of rooting on terrestrial plethodontid salamanders, which are particularly concerning at high elevations that support numerous endemic species. We investigated the impacts of rooting on plethodontid abundance, species diversity, and age class distribution at high elevations in Great Smoky Mountains National Park via seasonal nighttime visual encounter surveys in plots either rooted or unrooted during 2021. One survey was conducted per plot in early spring, mid-summer, and late fall 2022. We assessed seasonal and cumulative direct effects of recent and legacy rooting, habitat features, and environmental conditions on assemblage characteristics with AICc model selection and averaging. We then investigated indirect effects of rooting using significance tests of relationships between rooting metrics and habitat features with significant impacts on assemblage characteristics. Plethodontid abundance, species diversity, and age class distributions were directly and indirectly associated with rooting history and intensity, and the strength and direction of effects differed among seasons. Effects of both recent and legacy rooting were detected, although effects of recent rooting were more prevalent. Our results suggest that periodic rooting by feral hogs dynamically impacts high-elevation plethodontid assemblages and highlight the importance of utilizing both seasonal and cumulative analyses when investigating the impacts of a seasonally-active invasive species.

A seedling survival guide to the spruce-fir forests of Great Smoky Mountains National Park: How to succeed in a forest plagued by invasion, disturbance, and competition

Tori Hongo (hongo@purdue.edu), and Michael Jenkins

Dept. of Forestry & Natural Resources, Purdue University

The decimation of the southern Appalachian endemic Fraser fir (*Abies fraseri* (Pursh) Poir.) was caused by the widespread infestation of mature trees by the non-native insect balsam woolly adelgid (*Adelges piceae* [Ratzeburg]) in the 1950s. The disappearance of fir from the overstory of high-elevation (> 5,100 ft) spruce-fir (*Picea rubens-Abies fraseri*) forests was a major disturbance. Newly formed canopy gaps provide resources for seedlings and surviving trees, which compete for growing space and sunlight. We sampled woody vegetation in 36 plots from the long-term spruce-fir monitoring network distributed across five summits in Great Smoky Mountains National Park: Mount Sterling, Mount Collins, Mount Le Conte, Mount Guyot, and Clingmans Dome. Here, we evaluate seedling regeneration dynamics across mountain peaks by species composition, density, and ground-layer substrate preference. Patterns of post-adelgid forest succession provide an essential indicator of both recovery from past die-off and resilience in the face of future stressors.

Physics-guided AI framework to predict and correct radar QPE errors

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A Physics-guided Artificial Intelligence (PAI) framework consisting of a weather regime classifier and a suite of precipitation error prediction models applied to Radar Quantitative Precipitation Estimates (QPE) using machine learning is presented. The weather regime classifier is based on Empirical Orthogonal Function (EOF) analysis of Residual Errors from standard products and from the previous application of hydrologic Inverse Rainfall Correction (IRC, Liao and Barros, RSE, 2022) to storms producing large floods in headwater basins. The precipitation error model is a Multilayer Perceptron (MLP) that predicts the space-time evolution of precipitation errors during a storm event conditional on season, antecedent hydrometeorological conditions, that is initial conditions, and local and basin-scale precipitation characteristics. The PAI framework is demonstrated for warm and cold season precipitation in the Great Smoky National Park in Southern Appalachian Mountains (SAM) for 50 largest flood-producing storms during 2008-2018, achieving large improvements on Nash-Sutcliffe Efficiency (NSE) across most events with an average improvement of 0.75 for warm season events, and 0.42 for cold season events. Corrected QPEs demonstrate excellent skill against high elevation gauge locations. The probability distribution function (PDF) of the predicted precipitation errors varies significantly with season, and the spatial distribution of errors for the same precipitation regime varies from basin to basin depending on landform.

Estimating the effects of hemlock imidacloprid treatment on terrestrial salamander abundance

John C. Maerz (jcmaerz@uga.edu), Jade Samples, Danielle R Bradke, James A Martin, Cheyana Bassham, Vanessa K Terrell, Cassandra Waldrop, and Elizabeth McCarty

Warnell School of Forestry and Natural Resources, University of Georgia, Athens

Forest management such as the use of pesticides requires managers must consider both the benefits and the risks of the pesticide. For example, managers need to know whether pesticide residues occur in system in sufficient quantities to negatively affect non-target organisms so they can judge the trade-off between management goals and non-target consequences. Hemlock woolly adelgid (HWA) has decimated hemlock populations in the southern Appalachians. Imidacloprid, a neonicotinoid insecticide, is currently used to suppress HWA populations and conserve hemlock trees and the habitats they create. Recent concern has developed about possible non-target impacts of hemlock imidacloprid treatments on salamander populations. Eastern North America, particularly the Southern Appalachian Mountains, are a global hotspot for salamander diversity. Robust information is needed on the magnitude and extent of any potential impacts of imidacloprid application on salamander populations to inform decisions on imidacloprid applications for hemlock conservation in sensitive areas. We conducted repeated depletion samples among 15 replicate plots at each of 25 sites across north Georgia, western NC, and eastern Tennessee including 10 sites within Great Smoky Mountains National Park. We used a hierarchical model to account for differential salamander availability and detection as well as climatic effects on abundance to estimate the effects of imidacloprid application on terrestrial salamander abundance. We found no measurable effect of imidacloprid application on terrestrial salamander abundance. Variation in salamander abundance was primarily affected by climate, most notably mean annual precipitation or daily vapor pressure deficit. Our results suggest that imidacloprid application for the conservation of Eastern hemlock does not negatively impact terrestrial salamander abundance.

Forty years of avifaunal change in Great Smoky Mountains National Park

Graham Montgomery (montgomery.graham@gmail.com), David Wilcove, and Morgan Tingley

Dept. of Ecology & Evolutionary Biology, University of California, Los Angeles

In an era of global change, ecological monitoring is crucial for informing conservation and management. Avifauna (birds) can be particularly good candidates for monitoring and indicators of change due to their abundance, diversity, & detectability. Indeed, in some cases, such as at Great Smoky Mountains National Park, bird communities have even been well-surveyed in the past, which provides an opportunity to perform resurveys and document change. Based on a series of "snapshot" surveys, we document changes in avian communities and species abundance, richness, and biomass. Some species have declined markedly, but others have increased, with habitat change likely being responsible for many of these patterns. We then compare local trends to continent-wide trends in order to elucidate other potential drivers and ways in which Great Smoky Mountains National Park may act as a refugium for some species in the face of global change.

Estimated effects of wildfire on Smoky Mountain Salamanders

William E Peterman (peterman.73@osu.edu), Andrew J Wilk, John A Crawford, Ethan J Kessler, and Joseph R Milanovich

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Fire is an important natural disturbance that can promote biodiversity by creating a diverse landscape and regulating wildlife populations. However, due to historical fire suppression and climate change, wildfires are becoming more frequent and severe. Once such wildfire was the Chimney Tops 2 wildfire in 2016 that burned more than 6,000 ha of Great Smoky Mountains National Park and the surrounding landscape. As the self-proclaimed 'Salamander Capital of the World, understanding the effects of wildfire generally, and this fire specifically, are important for the future management of the park's unique salamander diversity. In this study we examine five species of plethodontid salamander in Great Smoky Mountains National Park that were affected by the Chimney Tops 2 wildfire. We surveyed 100 transect within and adjacent to the burned area and examined the effect that burn severity had on abundance and size distribution of each species. We found that salamander abundances were meaningfully reduced within the burn boundary, regardless of severity, but increased severity exacerbated the magnitude of reduction. Additionally, we found evidence that distance from the burn boundary was negatively related to abundance for 3 species, suggesting dispersal limitations that may shape future recovery. Finally, salamanders in burned areas were disproportionately larger in size compared to salamanders in unburned areas. Taken together, we found complex and varied responses of salamanders to the Chimney Tops 2 fire.

Bryophyte communities change over a 12-year period along an elevational gradient in Great Smoky Mountains National Park

Eric Shershen (eshershe@vols.utk.edu)¹, Sarah Stehr², and Jessica Budke¹

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There are a number of concurrent disturbances impacting the spruce-fir zone in the Great Smoky Mountains National Park (GSMNP), including that of invasive pests (e.g., the Balsam Woolly Adelgid (BWA) (*Adelges piceae*)) that reduce canopy cover and ecosystem-level changes due to climate change (e.g., fluctuations in annual temperatures, stochasticity and intensity of precipitation events). These disturbances raise the question as to how understory conditions have changed over time. Bryophytes are major biodiversity contributors to the understory community of this high elevation ecosystem. This study examined if bryophyte communities have changed over time and if the observed changes were driven by environmental factors such as elevation, slope, slope aspect, and change in gap fraction as well as how bryophyte functional groups differ. I visited plots established in 2008 from a master's thesis conducted by researcher Sarah Stehn. These plots varied in elevation and the dominant tree species present. I mirrored her study by positioning three, 20-meter transect lines across the plot and measured the coverage of every bryophyte species in each plot. This provided a direct comparison examining how bryophyte communities have changed over time. Collected specimens were identified using microscopy and deposited in the University of Tennessee Knoxville Herbarium (TENN). Species richness and coverage from 2008 and 2020 were analyzed using paired t-tests with Holm-Bonferroni corrections. Pairwise dissimilarity across various orders of q were also analyzed to determine if any changes in species richness were due to species turnover. I found that bryophyte species richness significantly declined across the plots, independent of elevation, and that bryophyte coverage has remained stable except at the highest elevations that are dominated by fir trees. However, when examining percent coverage on a species-by-species basis, some species significantly declined in percent cover whereas others have remained stable. None of the species significantly increased in percent cover. My results suggest that bryophytes are not responding as I initially predicted wherein higher elevations would have an increased bryophyte richness and cover, suggesting that there may be other factors impacting the bryophyte communities of the GSMNP.

Native brook trout reintroductions: Do a source's population genetics influence reintroduction success?

Rebecca Smith (rsmit267@vols.utk.edu)¹, Dave Kazyak², Matt Kulp³, Barb Lubinski², and Ben Fitzpatrick¹

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Wildlife reintroductions are a conservation tool to re-establish native species to their historical ranges. However, identifying appropriate source populations for reintroductions can be a challenge because introduced genotypes may not be well suited for the target environment. In practice, reintroductions are rarely preceded by detailed genetic evaluation. A threatened species in Southern Appalachia is the Southern Appalachian Brook Trout (*Salvelinus fontinalis*), which has been extirpated from its historical range due to anthropogenic impacts and competition with non-native species. In the Great Smoky Mountain National Park (GRSM), brook trout are the only native salmonid but have been isolated in remote headwater systems since the early 1900s, exchanging little to no genetic information between populations. State and federal agencies have been strategizing to restore the genetically unique Southern Appalachian Brook Trout to their native range and reintroduction efforts are ongoing in GRSM. Currently there are over 30 miles of reintroduced brook trout habitat in the National Park, which encompasses 13 different streams. To prevent depleting source populations managers use multiple native brook trout populations as sources in one reintroduced habitat. Previous studies used parentage analyses and inferred multiple source populations do not readily admix as a consequence of being too genetically differentiated. This suggested nonrandom admixture raises concerns about assortative mating or outbreeding depression. My research addresses admixture concerns using ancestry analyses to assess genetic composition of the reestablished populations in GRSM. Future research will use High-Throughput sequencing to assess ancestry and set up strategic experiments in empty trout streams to test the best mixture of source populations. My research aim is to contribute and guide management's selection of source populations in a single reintroduction site.

Microbial communities as indicators of ecosystem function and sustainability

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Microbial and plant community interactions within soil have been linked to differences in nutrient cycling and availability (Powell et al., 2015; Levy-Booth et al., 2014). These effects may help us understand what role soil microbiomes play in shaping plant life and ecosystem function (Phillips et al., 2013; Isobe et al., 2011; Hacquard and Schadt, 2015). To establish causal relationships there is a need for data quantity and quality regarding soil microbial communities and their spatial distribution in ecosystems (Mushinski et al., 2017). Microbial community analysis was conducted to address the need for microbial data and to describe the utility of this type of data. Mineral soil samples from within the mycorrhizosphere of Northern Red Oak were taken from the Cataloochee and Purchase Knob All Taxa Biodiversity Inventory (ATBI) sites (n = 12 replicates from each site). These samples were pooled by subsite location (upslope, side slope, downslope) around an oak tree (n = 3 from each ATBI site) and sent to Azenta, Inc. (South Plainfield, NJ) for DNA extraction and next generation sequencing of both bacterial 16S rRNA and fungal internal transcribed spacer (ITS) rRNA regions. Twenty-six phyla of bacteria were recovered from the samples, with Acidobacteria and Proteobacteria co-dominating in all six samples and key genera included *Bradyrhizobium*, containing symbiotic nitrogen fixers, and *Rhodoplanes*, a group normally known for photosynthesis. Seven phyla of fungi were also discovered with Ascomycota and Basidiomycota co-dominating most samples except for two where Mucoromycota was found in greater numbers. From these phyla approximately 15 abundant genera containing mostly saprophytic and ectomycorrhizal species, but also known plant and animal pathogens were found. Principal components analysis (PCA) of the distributions of sequences showed a clear difference between the Cataloochee and Purchase Knob sites with greater variability in community composition at Cataloochee for both bacteria and fungi. Ongoing analyses include linking microbial taxa, communities, and emergent properties to plants, including oaks, their communities, and ecosystem functions. Prevalent taxa of plant-associated bacteria and fungi have been identified along with others key to nitrogen cycling. This suggests that relationships between bacteria, fungi, and plants play a role in biogeochemical cycling and that these pathways may become clearer with more study.