

GREAT SMOKY MOUNTAINS NATIONAL PARK SCIENCE COLLOQUIUM

Co-hosted by Great Smoky Mountains National Park and Discover Life in America
THURSDAY, MARCH 4, 2021 – 9:00 AM TO 3:30 PM – VIRTUAL VIA ZOOM

2021 SCIENCE COLLOQUIUM SCHEDULE

- 9:00 WELCOME AND INTRODUCTIONS**
Superintendent's Office (GSMNP) & Todd Witcher (Discover Life in America)
- 9:10 Assessing the role of habitat and phylogeny in shaping the amphibian skin microbiome**
Ben Holt (Dept Ecology & Evolutionary Biology, UTK)
- 9:30 Predicting distributions of cryptic species across a landscape with a complex history**
Andrew Wilk (Ohio State University)
- 9:50 Benthic macroinvertebrate and biofilm response to antimycin during brook trout restoration**
Keith Gibbs (Western Carolina University)
- 10:10 20-MINUTE BREAK**
- 10:30 Can the ion transport characteristics of different aquatic insect species provide clues about their sensitivities to changing salinity regimes?**
Jamie Cochran (Dept Biological Sciences, North Carolina State University) & David Buchwalter
- 10:50 Assessing the integrated ecohydrological changes in GSMNP surrounding the 2016 fire season**
Tiffany M Wei (Dept Civil & Environ Engineering, Duke University), Mochi Liao, Paul E Super & Ana P Barros
- 11:10 Bouncing back from burn: Long-term monitoring of GSMNP soil microbial stability from the Chimney Tops 2 fire**
Kendall Beals (Dept Ecology & Evolutionary Biology, UTK), Joe Bailey & Jen Schweitzer
- 11:30 LUNCH BREAK**
- 12:30 What trajectories of the Smokies' synchronous fireflies reveal about their behavior**
Julie Hayes (University of Colorado, Boulder; University of New Mexico), **Raphael Sarfati** (University of Colorado Boulder) & Orit Peleg
- 12:50 NEON in the Smokies**
Sarah Szito (National Ecological Observatory Network Program, Battelle) & Marie Faust
- 1:10 Developing genetic tools to safeguard harvested species in GSMNP**
Matt Estep (Appalachian State University) & Jennifer Rhode Ward
- 1:30 An examination of introgression in the *Trillium erectum* species complex using microsatellite analysis**
Austin Brenek (Dept Biology, Western Carolina University)
- 1:50 20-MINUTE BREAK**
- 2:10 2019 assessment of cumulative pesticide and pharmaceutical risk in GSMNP streams**
Paul M Bradley (South Atlantic Water Science Center, USGS) & Matt Kulp
- 2:30 Winter torpor and arousal activity of four cave-hibernating bat species in Tennessee**
Reilly T Jackson, Emma V Willcox (Dept Forestry, Wildlife & Fisheries, UTK), Riley F Bernard & John M Zobel
- 2:50 Spatially explicit estimates of abundance of black bears in and adjacent to GSMNP**
Joseph D Clark (Southern Appalachian Research Branch, USGS) & Jacob Humm
- 3:10 CONCLUSIONS AND FAREWELL**

* Presenting author in bold; see abstracts for full author information. UTK = University of Tennessee, Knoxville. GSMNP = Great Smoky Mountains National Park.

HOW TO VIEW

Information: <https://dlia.org/event/science-colloquium-2021/>

Register here to view the colloquium on Zoom: https://us02web.zoom.us/webinar/register/WN_ibU_JRA_RyaJoBKfp1g7aA

Speakers do not need to register but will be contacted directly and registered through a separate process.

2021 SCIENCE COLLOQUIUM ABSTRACTS

(by last name of bolded presenting author)

Bouncing back from burn: Long-term monitoring of Great Smoky Mountains National Park soil microbial stability from the Chimney Tops 2 fire

Kendall Beals (kbeals2@vols.utk.edu)¹, Joe Bailey¹, Jen Schweitzer¹
¹Dept Ecology & Evolutionary Biology, University of Tennessee, Knoxville

Very little research has examined how soil microbial communities recover from wildfire disturbance over time. Some of our previous work has found that the Chimney Tops 2 wildfire that burned parts of the GSMNP in late 2016 greatly reduced soil bacterial and fungal diversity and altered soil abiotic properties. To understand the relative amount of the soil microbiome that is vulnerable and tolerant to wildfire and to predict recovery time of soil microbial communities to wildfire, we collected soil from multiple undisturbed and severely burned sites within GSMNP annually for 4 years post-fire and conducted amplicon metagenomic sequencing. We identified sensitive, opportunistic, and resistant microbial response strategies to wildfire. We then assessed if the proportion of each response strategy change within soil microbial communities changed with time since wildfire.

2019 assessment of cumulative pesticide and pharmaceutical risk in Great Smoky Mountains National Park streams

Paul M Bradley (pbradley@usgs.gov)¹, Matt Kulp²

¹South Atlantic Water Science Center, USGS, Columbia, SC; ²Resource Management and Science, Great Smoky Mountains National Park, Natl Park Service

Recent assessment of designed-bioactive contaminants (pesticides and pharmaceuticals) in protected-streams within the urbanized NPS Southeast Region indicated the importance of fluvial inflows from external sources as drivers of aquatic contaminant-mixture exposures. Great Smoky Mountains National Park (GRSM) also lies within the Southeast Region, but straddles a high-elevation hydrologic divide, a hydrogeologic setting that limits fluvial-inflows of contaminants. We utilized the same analytical toolbox employed in the previous Southeast Region study to 1) provide a reconnaissance of pesticide and pharmaceutical contaminants in surface-waters across GRSM, 2) further test the hypothesized importance of fluvial inflows as drivers of protected-stream contaminant-mixture exposures and 3) inform the relative importance of potential additional mechanisms of contaminant transport to GRSM.

An examination of introgression in the *Trillium erectum* species complex using microsatellite analysis

Austin Brenek (awbrenek1@catamount.wcu.edu)¹

¹Dept Biology, Western Carolina University, Cullowhee, NC

There are seven named taxa of the *Trillium erectum* L. species complex that are native to North America, many of which are experiencing secondary contact and hybridizing due to a lack of reproductive isolating mechanism. This project will focus on *T. erectum* var. *album*, a white flowered taxa, *T. erectum* var. *erectum*, a red flowered taxa, and *T. rugelii*, a white flowered taxa, each of which occurs in the southern Appalachian Mountains and are found in populations that overlap in geographic range and flowering phenology. Using three microsatellite loci developed for a related trillium species, this study examines hybridization and genetic structure of several populations of the *T. erectum* species complex, located in three counties in the western region of North Carolina, to determine if different taxa growing in mixed populations are interbreeding, and if so, quantify the amount of admixture and examine what factors, taxon identity, geographic range or flower color, are most influencing hybridization. Allele frequency analyses of microsatellite loci were used to compare the populations. We performed Principal Components Analysis comparing using pairwise comparisons of both fixation index and Nei's Genetic distance calculations for each geographic population. Structure analysis was used to identify populations and quantify admixture based on allele frequency and assumptions of gene flow using Bayesian statistical methods. Results from population genetics and Structure analyses suggest that allele sharing occurs primarily based on taxon identity and geographic proximity, but flower color may also play a role in influencing gene flow.

Spatially explicit estimates of abundance of black bears in and adjacent to Great Smoky Mountains National Park

Joseph D Clark (jclark1@utk.edu)¹, Jacob Humm²

¹Southern Appalachian Research Branch, Northern Rocky Mountain Science Center, USGS; ²Dept Forestry, Wildlife & Fisheries, University of Tennessee, Knoxville

American black bears (*Ursus americanus*) are an iconic wildlife species in the southern Appalachian highlands. Wildlife managers need reliable population data for assessing the effects of management actions for this high-profile species, but most estimation methods are suitable only across small spatial extents. Our goal was to use DNA extracted from hair collected at barbed-wire enclosures coupled with cluster sampling methods. We established 888 barbed wire hair sampling sites arranged in 174 clusters of 2–9 traps/cluster in the southern Appalachian highlands in Georgia, North Carolina, South Carolina, and Tennessee, including Great Smoky Mountains National Park. We collected 9,137 bear hair samples from those sites over 6 weeks of sampling in 2017 and 2018, of which 2,273 were successfully genotyped to 462 individual females. Densities ranged up to 0.410 female bears/km² and regional abundance was 5,949.8 (SE = 536.7) female bears. The mean density within Great Smoky Mountains National Park was 0.349 female bears/km² (SE = 0.055, 95% CI = 0.257–0.474). Our estimate of female bear abundance in the 2,103-km² park was 733.9 (SE = 115.3, 95% CI = 540.4–996.7). The total abundance estimate, including males and cubs based on a simulated stable age distribution for an unharvested population in the Park, was 1,909.2 bears. Our large study area (66,678 km²) enabled costs to be shared by several state wildlife agencies and illustrates the value of inter-jurisdictional collaboration. This methodology could be adapted for scat, hair, or camera sampling for estimating population parameters for other species managed across large spatial extents.

Can the ion transport characteristics of different aquatic insect species provide clues about their sensitivities to changing salinity regimes?

Jamie Cochran (jkcochra@ncsu.edu)¹, David Buchwalter¹

¹Dept Biological Sciences, North Carolina State University, Raleigh

Aquatic insects play critical roles in freshwater ecosystems worldwide. Biomonitoring programs typically rely on these organisms to make inferences about water quality and ecological conditions. Salinity (the ionic composition of water) plays a fundamental role in determining where different species thrive. In the central Appalachians for example, mountaintop coal mining has increased the concentrations of several major ions and ecologists report associated biodiversity losses. Elsewhere, acid deposition and weathering have reduced the concentrations of calcium and raised concerns about the ability of certain taxa to thrive under more dilute conditions. Our laboratory is working on an NSF-funded project to understand how the way aquatic insects osmoregulate determines which waters are suitable for supporting them. We use radiotracers (²²Na, ⁴⁵Ca and ³⁵SO₄) to measure the rates of ionic uptake and efflux under different water chemistry scenarios. We are comparing how different species (including some collected in the Smokies) take up ions and assessing how their ability to retain them under dilute challenge varies. For example, at 4 mg/L Na, we observed that uptake rates were in ~22-fold higher in *Isonychia* sp. than in *Atherix* sp. When we challenge insects with deionized water for 9 hours, *Hydropsyche* sp. lost 45.03% of its total whole-body Na while *Acroneuria* sp. lost only 3.77%. While these studies are in early stages, clear physiological differences are emerging among species - which may help us understand how their physiologies determine where they can occur.

Developing genetic tools to safeguard harvested species in Great Smoky Mountains National Park

Matt Estep (estepmc@appstate.edu)¹, Jennifer Rhode Ward²

¹Appalachian State University, Boone, NC; ²University of North Carolina, Asheville

Many plant species are being driven towards rarity due to exploitation for food, medicine, or the nursery trade. Land managers in the Smoky Mountain National Park are particularly concerned about two plant species: cutleaf coneflower / Sochan (*Rudbeckia laciniata*), and ramps (*Allium tricoccum*). Both of these species are traditionally foraged for food and ceremonial use by the Eastern Band of Cherokee Indians, and parklands will soon open to limited collection by EBCI members. To ensure the health and vitality of these species, a combination of demographic and genetic data are being collected. These will be used to assess baseline genetic diversity and prioritize populations for conservation. To date, loci have been identified and developed into genetic markers to assess genetic diversity with the species. Developing novel molecular tools for monitoring imperiled plant species is one avenue towards safeguarding their futures, as these tools can be used to identify problematic reductions in genetic diversity over time.

Benthic macroinvertebrate and biofilm response to antimycin during brook trout restoration

W Keith Gibbs (wgibbs@email.wcu.edu)¹, **Aden J Blackburn**², **Justin n Murdock**²

¹Dept Geosciences & Natural Resources, Western Carolina University, Cullowhee, NC; ²Dept Biology, Tennessee Technological University, Cookeville

The piscicide antimycin has been used to effectively eradicate nuisance fish in small streams. In many cases, antimycin is the preferred piscicide because it is undetectable by fish, highly effective in coldwater systems, and breaks down rapidly in the environment. The objective of our study was to identify negative effects of antimycin, as well as its neutralizing agent, potassium permanganate, on benthic macroinvertebrates, periphyton, and water quality in a headwater system. Our study was conducted during a brook trout (*Salvelinus fontinalis*) restoration project in Great Smoky Mountains National Park in the fall of 2017. Nine sites within adjacent treated and untreated streams were sampled multiple times bracketing an antimycin treatment to remove nonnative rainbow trout (*Oncorhynchus mykiss*). At each site, macroinvertebrate composition, periphyton chlorophyll and ash-free dry mass, and water quality were collected. Results suggest minimal long-term negative effects on periphyton for both antimycin and potassium permanganate treatments. Although the treatment had significant effects on macroinvertebrate communities initially, negative effects were not long lasting. This reinforces the idea that antimycin can be used effectively to remove nonnative fish species in coldwater streams with minimal effects on native aquatic resources.

What trajectories of the Smokies' synchronous fireflies reveal about their behavior

Julie Hayes (julie.hayes@colorado.edu)^{1,2}, **Raphael Sarfati** (Raphael.Sarfati@colorado.edu)¹, **Orit Peleg**¹

¹University of Colorado, Boulder; ²University of New Mexico

The synchronous flashing of thousands of *Photinus carolinus* fireflies in Great Smoky Mountains National Park is a natural spectacle that elicits bewilderment, attracting hundreds of visitors to Elkmont every year in June. It also presents a fascinating scientific puzzle, challenging our understanding of insect collective behavior and social synchrony. In order to understand how fireflies communicate and synchronize, we used 360-degree cameras placed directly in the natural habitat and recorded flashing trajectories in 3D. These trajectories offer an unprecedented insight into how these fireflies behave collectively and self-organize as a group. In this presentation, we will discuss some of our latest findings based on trajectory analysis. For example, we will show that *P. carolinus* males behave differently in a swarm than they do individually; that flash patterns reveal social differentiation, with leaders and followers; and that flashing entrainment propagates across the swarm through a social network of visual connections.

Assessing the role of habitat and phylogeny in shaping the amphibian skin microbiome

Ben Holt (bholt20@vols.utk.edu)¹

²Dept Ecology & Evolutionary Biology, University of Tennessee, Knoxville

Over the past century, global amphibian declines, associated with chytrid fungi *Batrachochytrium dendrobatidis* and *Batrachochytrium salamandrivorans*, have designated amphibians as the most imperiled group of vertebrates in the world. However, the skin microbiome has been shown to mitigate the effects of chytrid. While promising, many unanswered questions remain regarding how amphibians acquire and maintain host-associated microbes. I used four salamander species across three sites and two habitats to address how host ecology and evolution contribute to the microflora found on salamanders.

NEON in the Smokies

Sarah Szito (sthomason@battelleecology.org)¹, **Marie Faust**¹

¹National Ecological Observatory Network (NEON) Program, Domain 07, Appalachian Mountains and Cumberland Plateau, Battelle

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 several years 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 an introduction to resources for access and working with a variety of NEON data for your research or curriculum. It will also provide an analysis of NEON plant community data to show how species richness varies with elevation across GSMNP. Lastly, it will showcase 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 an integral co-benefit of protecting and preserving natural communities.

Assessing the integrated ecohydrological changes in Great Smoky Mountains National Park surrounding the 2016 fire season

Tiffany M Wei (tiffany.wei@duke.edu)¹, Mochi Liao¹, Paul E Super², Ana P Barros¹

¹Dept Civil & Environmental Engineering, Duke University, Durham, NC; ²Great Smoky Mountains National Park, National Park Service, Gatlinburg, TN

In October to December of 2016, a series of wildfires swept through the Southern Appalachian Mountains, causing casualties and devastating infrastructure and natural resources. As extreme weather events and anthropogenic factors contributing to climate change constitute an increasing threat to human life and water resources, quantifying the complex ecohydrological dynamics of areas like the Great Smoky Mountains (GRSM) National Park is crucial for wildfire mitigation and risk assessment.

The ecohydrological response of the West Prong Little Pigeon River Basin in the GRSM is examined during a 5-year period (2015-2019) using a physically-based, fully-distributed hydrology model with dynamic vegetation at high spatiotemporal resolution (250 m, 5-min) after the 2016 fire season. The model is driven by HRRR atmospheric reanalysis and downscaled HRRR quantitative precipitation estimates with inverse rainfall corrections. The temporal evolution of land-cover conditions is specified based on vegetation indices from remote-sensing data. Post-fire ecohydrological changes are examined with a focus on terrestrial water fluxes (streamflow and evapotranspiration), including extreme events. Land monitoring data from AQUA and TERRA are used to support interpretive analysis of model simulations and develop quantitative understanding of the relationship(s) between hydroclimatic variability and ecosystem recovery surrounding wildfires in the GRSM.

Predicting distributions of cryptic species across a landscape with a complex history

Andrew Wilk (wilk.34@buckeyemail.osu.edu)¹

¹School of Environmental and Natural Resources, Ohio State University, Columbus

Fundamental questions of ecology ask where species occur, and why. Recent significant advances have been made in the field of species distribution modeling, but the methods are not without flaws. These techniques usually fail to account for legacy effects of historic land use or disturbance, and rarely account for imperfect detection. By ignoring these factors, resulting predictions may not accurately represent current distributions.

Accounting for imperfect detection is vital when predicting occurrence of cryptic species. Spatially comprehensive databases from museums or government agencies are available, but these data are not typically conducted in a way to estimate detection with traditional methods. Additionally, they rarely include measures of survey conditions, which are vital to estimate detection probabilities. Therefore, to build distribution models with these data, we must employ different statistical frameworks and estimate survey-specific conditions.

Our study takes place in Great Smoky Mountains National Park which, prior to designation, had a mosaic of anthropogenic land use and, since establishment, burned areas have been well documented. This rich disturbance history combined with a park-wide survey for amphibians presents the opportunity to understand how disturbance has shaped current distributions.

In this study we use single-visit occupancy surveys coupled with microclimatic modeling to leverage data lacking survey condition measures to predict distributions for five cryptic, plethodontid salamander species. We also identify whether historic disturbance and fire have observable effects on current distributions.

We found that estimating detection probabilities with downscaled weather data including soil temperature and soil moisture increased model performance for all species, considered both in terms of Akaike's information criterion (AIC) and area under the receiver operating characteristic (AUC). We also found that historic land use and time since fire had species specific importance. Overall, we show the importance of accounting for imperfect detection and landscape disturbance when developing species distribution models.

Winter torpor and arousal activity of four cave-hibernating bat species in Tennessee

Reilly T Jackson¹, Emma V Willcox (ewillcox@utk.edu)¹, Riley F Bernard², John M Zobel¹

¹Dept Forestry, Wildlife & Fisheries, University of Tennessee, Knoxville; ²Dept Ecosystem Science & Management, Pennsylvania State University, State College

In the southeastern U.S., bats susceptible to white-nose syndrome (WNS) frequently arouse from torpor during winter and are often active outside hibernacula. We investigated the torpor and arousal activity of four WNS affected species, two with relatively low (*Myotis grisescens*, and *M. leibii*) and two with relatively high (*M. sodalis* and *Perimyotis subflavus*) WNS susceptibility. We deployed temperature-sensitive radio-transmitters on bats captured outside cave hibernacula during winter to monitor torpor and arousal profiles ($n = 21$) and recorded activity of others at cave entrances by implanting them with passive integrated transponder (PIT) tags ($n = 1,349$). *Myotis leibii* had a higher torpor skin temperature (18.57 ± 0.20 °C) than *M. grisescens* (13.72 ± 0.60 °C) and *P. subflavus* (14.62 ± 0.49 °C; $P < 0.048$). *Myotis leibii* also had a higher arousal skin temperature (32.29 ± 0.67 °C) than *M. grisescens* (29.01 ± 0.64 °C) and *M. sodalis* (28.59 ± 0.38 °C; $P \leq 0.016$). *Myotis leibii* had the highest activity frequency throughout the hibernation period (November–February), with $74.22 \pm 10.62\%$ of tagged individuals detected at cave entrances each month compared to $<30\%$ of tagged individuals from other focal species. Of the 531 PIT-tagged bats active during winter, only 12.60% ($n = 67$), the majority of which were *M. leibii*, were detected at a cave entrance more than once/night. For this species, the time between detections in the same night was 0.87 ± 0.09 hrs. Understanding these differences in torpor and arousal activity will help inform WNS management strategies.