GREAT SMOKY MOUNTAINS NATIONAL PARK SCIENCE COLLOQUIUM 2020

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

THURSDAY, MARCH 12, 2020 | 9:00 AM TO 4:00 PM | PARK VISTA HOTEL, GATLINBURG

COLLOQUIUM SCHEDULE

9:00 **WELCOME AND INTRODUCTIONS**
Superintendent's Office (GSMNP) & Todd Witcher (Discover Life in America)

9:10 **The influence of fire severity and urbanization on plant communities in the Great Smoky Mountains**
Mali M Hubert (Ecol & Evol Biology, UTK), Monica Papes

9:30 **Soil macroinvertebrate responses to wildfires in the Blue Ridge Mountains, USA**
Madeline Olliff (Georgia College & State Univ), Bruce A Snyder, Melanie K Taylor, Mac A Callaham

9:50 **Investigation of elevational and wildfire effects on the plethodontid salamander communities of GSMNP**
Andrew Wilk (Ohio State Univ), William E Peterman, Joseph R Milanovich, Daniel J Hocking, John A Crawford

10:10 **15-MINUTE BREAK**

10:25 **Oak regeneration after Chimney Tops II fire is influenced by pine seedling neighbors and soil microbes**
Alexandra Scearce, **Alex Swystun** (Ecol & Evol Biology, UTK), Kendall Beals, Jennifer Franklin, Karen Hughes, Jennifer Schweitzer

10:40 **Impacts of the Chimney Tops II wildfire on soil and stream chemistry within GSMNP**
Salley Reamer (Dept Civil & Environmental Engineering, UTK), John Schwartz, Qiang He, Jen Schweitzer

10:55 **Impacts of fire on soil microbial communities in the GSMNP**
Liu Cao (Dept Civil & Environmental Engineering, UTK), Qiang He, John Schwartz, Salley Reamer, Jen Schweitzer

11:10 **Long-term trends in throughfall deposition and stream chemistry in the GSMNP**
John Schwartz (Dept Civil & Environmental Engineering, UTK), Adrian Gonzalez, Andrew Veeneman

11:25 **LUNCH BREAK (lunch on your own)**

12:45 **Elevation-dependent variation in growth and water use efficiency of red spruce in the Southern Appalachians: Response to rising atmospheric CO_2 and climate**
Chris A Maier (US Forest Service), John Butnor, Justin M Mathias, Richard B Thomas

1:05 **Variation in climate-associated traits of red spruce (*Picea rubens* Sarg.) along elevation gradients in the southern Appalachian Mountains**
John R Butnor (US Forest Service), Brittany M Verrico, Kurt H Johnsen, Christopher A Maier, Victor Vankus, Stephen R Keller

1:25 **Metabarcoding the leaf litter arthropods of High Appalachia**
Michael Caterino (Clemson University Arthropod Collection)

1:45 **Recruitment of large woody debris to streams in GSMNP following the 2016 Chimney Tops 2 wildfire**
Sarah Praskievicz (Univ North Carolina, Greensboro), Rajesh Sigdel

2:05 **15-MINUTE BREAK | workshop attendees break off into separate room**

2:20 **Developing genetic tools to safeguard harvested species in the Great Smoky Mountains**
Jennifer Rhode Ward (Univ North Carolina, Asheville) & **Matt Estep** (Appalachian State Univ)

2:40 **Tall groves of the Great Smokies and the coves that made them**
Steve Norman (US Forest Service), Jitendra Kumar, William Hargrove, Forrest Hoffman

3:00 **Long-term landscape-scale homogenization and decoupling of community-environment relationships following logging in the southern Appalachians**
Margaret Woodbridge (State Univ of New York), Martin Dovciak, Jason Fridley

3:20 **Harnessing the hemlock microbiome: A potential defender against the hemlock wooly adelgid**
Nicholas C Dove (Biosciences Division, Oak Ridge Natl Lab), Timothy J Rogers, Christy Leppanen, Daniel Simberloff, Jim Fordyce, Veronica Brown, Anthony LeBude, Thomas Ranney, Melissa A Cregger

3:40 **Germination ecology of two southern Appalachian winter annuals, *Phacelia purshii* and *P. fimbriata***
Michelle D'Aguillo (Duke Univ)

4:00 **CONCLUSIONS AND FAREWELL**

POSTER **Bringing climate to down to the forest floor: Low-cost, high resolution sensors for microclimate modeling**
Jordan Stark (Syracuse Univ), Jason Fridley

*Affiliation for presenting author (bold) shown here; see abstracts for additional author information. UTK = University of Tennessee, Knoxville; GSMNP = Great Smoky Mountains National Park.

COLLOQUIUM ABSTRACTS (by last name of presenting author)

Variation in climate-associated traits of red spruce (*Picea rubens* Sarg.) along elevation gradients in the southern Appalachian Mountains

John Butnor *(john.butnor@usda.gov)* [1], *Brittany M Verrico*[2], *Kurt H Johnsen*[3], *Christopher A Maier*[4], *Victor Vankus*[5], *Stephen R Keller*[2]
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Red spruce (*Picea rubens*) is a long-lived tree species that thrives in cool, moist environs. Its ability to adapt to rapidly changing climate is uncertain. In the southern Appalachian Mountains, red spruce reaches its greatest abundance at high elevations, but can also occur across a range of mid and lower elevations, suggesting the possibility of a correlation between genetic variation and habitat. To assess clinal phenotypic variation in functional traits related to climate adaptation, we collected seed from 82 maternal sib families located along replicated elevational gradients in the Great Smoky Mountains National Park, TN (GSMNP) and Mount Mitchell State Park, NC (MMSP). The percentage of filled seeds and seed mass increased with elevation, indicating that successful pollination and seed development was greatest at the highest elevations. Seedlings sourced from GSMNP displayed a strong relationship between elevation and bud set when grown under common garden conditions. High elevation families set bud as many as 10 days earlier than low elevation families, indicating adaptation to local climate. This was not observed at MMSP and may reflect a disruption associated with extensive logging followed by reforestation with planting stock. Across parks, no effect of elevation was noted for bud flush. Our results demonstrate that red spruce in the southern Appalachian Mountains displays clinal variation in bud set that may reflect local adaptation to climate, although this varied between the two parks sampled.

Seed sources from GSMNP are included in an ongoing range-wide study of local adaptation and gene diversity in red spruce gene. Seedlings from 65 sources representing 340 maternal sib families are currently being grown in common gardens in Burlington, Vermont; Frostburg, Maryland; and Asheville, North Carolina. We will monitor variables related to phenology, physiology and growth to better understand the influences of genetics and environmental conditions on phenotypic expression. This information will help inform seed source selection for restoration plantings.

Impacts of fire on soil microbial communities in the GSMNP

Liu Cao[1]*, Qiang He*[1]*, John Schwartz*[1]*, Salley Reamer*[1]*, Jen Schweitzer*[2]
[1]*Dept Civil & Environmental Engineering, University of Tennessee, Knoxville;* [2]*Dept Ecology & Evolutionary Biology, University of Tennessee, Knoxville*

The impact of fire was evaluated by the profiling of soil microbial communities with high-throughput sequencing in both burn and no-burn areas in GSMNP. All study sites, regardless of burn or no-burn status, was found to have *Proteobacteria*, *Acidobacteria*, *Actinobacteria*, *Planctomycetes*, and *Verrucomicrobia* as the dominant populations. However, burnt sites exhibit reduced diversity and variation in soil microbial communities as compared with those in no-burn sites. At the family level, *Gemmataceae* of the phylum *Planctomycetes* was the most abundant bacterial population in burn sites. Soil moisture was shown to have considerable impact on soil microbial community composition, with high moisture content favoring populations associated with *Acidobacteria* while low water content supporting populations of *Planctomycetes*. The significance of other soil physicochemical parameters is currently being studied.

Metabarcoding the leaf litter arthropods of High Appalachia

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

The highest peaks of the southern Appalachian Mountains (USA) harbor a unique and relictual spruce-fir forests that hosts many endemic species. While a handful of arthropod lineages have been examined and found to have diversified in the region, the vast majority have received only cursory study. These communities are threatened by invasive species and habitat loss through climate change. However, the dearth of information on their diversity and uniqueness provides a weak foundation for conservation management. We have undertaken thorough arthropod community inventories using a voucher-based COI plus 16S multiplexed metabarcoding approach. Results to date indicate good success rates and generally high levels of divergence among putatively conspecific populations across peaks. This suggests that levels of endemism and cryptic species richness are much higher than currently supposed.

Germination ecology of two southern Appalachian winter annuals, *Phacelia purshii* and *P. fimbriata*

Michelle D'Aquillo *(michelle.d.aguillo@duke.edu)*
Duke University, Durham, NC

The timing of seed germination determines the environment experienced by a plant's most vulnerable life stage, the seedling. Plants can optimize fitness by timing germination such that seedlings emerge when environmental conditions are best. If genotypes or populations differ in the optimal environment for seedling growth, this may exert selection on germination cueing, causing seeds to have different optimal times of germination. This research investigated the relationship between germination cueing, seedling growth rates, and fitness in the field for two southern Appalachian winter annuals, *Phacelia purshii* and *P. fimbriata*. Field matured seeds were collected from 3 *P. fimbriata* and 2 *P. purshii* populations within Great Smoky Mountains National Park, as well as from 8 additional populations outside the park. Seeds were used in laboratory germination and seedling growth assays, by testing for differences in performance as function of population and temperature. Additionally, in August 2019 seeds were dispersed at 3 field sites in western and central NC, and germination phenology and survival have been monitored twice monthly. I found significant variation in germination cueing across species and populations. While this variation was not correlated with seedling growth rates, it did correspond with germination timing and the temperature experienced by seedlings in the field. The implications for fitness in the field and the joint evolution of germination cueing and post-germination traits will be discussed.

Harnessing the hemlock microbiome: A potential defender against the hemlock woolly adelgid

Nicholas C Dove *(dovenc@ornl.gov)* [1], *Timothy J Rogers*[2], *Christy Leppanen*[3], *Daniel Simberloff*[3], *Jim Fordyce*[2], *Veronica Brown*[3], *Anthony LeBude*[4], *Thomas Ranney*[4], *Melissa A Cregger*[1,3]
[1]*Biosciences Division, Oak Ridge National Laboratory;* [2]*Dept Microbiology, University of Tennessee, Knoxville;* [3]*Dept Ecology & Evolutionary Biology, University of Tennessee, Knoxville;* [4]*Dept Horticultural Sciences, North Carolina State University*

The hemlock woolly adelgid (*Adelges tsugae*, HWA) is an invasive insect that is devastating native hemlock populations in eastern North America, and management outcomes have so far had limited success. While many plant microbiomes influence and even support plant immune responses to insect herbivory, relatively little is known about the hemlock microbiome and its interactions with pathogens or herbivores such as HWA. Using next-generation sequencing of the 16S rRNA and ITS gene regions, we characterized the needle, branch, root, and rhizosphere microbiome of *Tsuga canadensis* and *T. sieboldii* supporting low and high levels of HWA populations. We found that both archaeal/bacterial and fungal needle communities as well as the archaeal/bacterial branch and root communities varied in composition in both species relative to HWA population levels. Specifically, high HWA populations were associated with high levels of 23 fungal pathogen sequence variants across the four plant-associated habitats (e.g., needle, branch, root, rhizosphere) compared to trees with low HWA populations. However, host species and plant-associated habitat explained a greater proportion of the variance in the microbiome than level of HWA population. Nevertheless, this work contributes to a growing body of literature linking plant pathogens and pests with the plant microbiome and host health and demonstrates the need to investigate plant microbiome effects across multiple plant tissues.

The influence of fire severity and urbanization on plant communities in the Great Smoky Mountains

Mali M Hubert *(mlubic@vols.utk.edu), Monica Papes*
Dept Ecology & Evolutionary Biology, University of Tennessee, Knoxville

Fire is one of the most powerful disturbances of natural ecosystems because it can reshape existing communities. In the southern Appalachian region of the United States, fires are a re-emerging, yet still largely historical dimension of the landscape. The proximity of human communities to protected areas such as the Great Smoky Mountains National Park (GSMNP) requires forest fire suppression, leading to accumulation of leaf litter and plant biomass and thus the possibility for high severity fires. The urban-wildfire interface and its role in shaping plant communities in this region has not been extensively explored. We investigated understory plant communities affected by the 2016 Chimney Tops 2 fire at 20 plots sites in Gatlinburg, Tennessee, and in the GSMNP. Our goal was to document vegetation changes as the landscape recovers from fire, as well as assess the similarity of the plant species community in the natural and exurban locations during succession after the fire. Overall, we found that the low/medium burn severity sites and exurban locations exhibit the highest plant diversity while the high burn sites and the natural locations have the lowest over the last two years (2018 – 2019). Future work will determine if disturbance across the urban and fire gradients generates new patterns of species dominance over time. The data collected for this study allowed us to evaluate the short-term impact of these disturbance forces on plant communities. This knowledge can be used to improve predictions of plant species composition at sites that are influenced by fire events and recurrent urban development.

Elevation-dependent variation in growth and water use efficiency of red spruce in the southern Appalachians: Response to rising atmospheric CO_2 and climate

Chris A Maier *(christopher.maier@usda.gov)* [1], *John Butnor*[2], *Justin M Mathias*[3], *Richard B Thomas*[3]
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Red spruce (*Picea rubens* Sarg.) is a major component of high-elevation forest ecosystems of the southern and central Appalachian Mountains. It favors cool humid environments, is sensitive to acidic air pollution and is a key indicator species of forest health. Reductions in radial growth were observed in red spruce trees throughout its range during the latter half of the twentieth century. However, in the last twenty years, a broad recovery in tree growth was observed in the central and northern Appalachians. Increased growth was linked to improved air quality, reduced acidic sulfur pollution, increasing atmospheric CO_2, and a positive effect of increasing spring temperatures. Less is known about how improved air quality, warming climate, and rising atmospheric CO_2 (*C*a) have affected growth and physiology of southern populations of red spruce. Being at the southern edge of the species range, red spruce and associated species are threatened by climate change and have a high potential to become maladapted under forecasted climate scenarios.

We combined tree ring width (RW) analysis and carbon isotope discrimination ($\Delta^{13}C$) measurements in mature red spruce at four sites along an elevation gradient (1000-1800 m) to examine how recent environmental change may have effected changes in basal area increment (BAI), gas exchange, and intrinsic water use efficiency (iWUE). The 150+ year chronological record revealed strong spatial and temporal variations in $\Delta^{13}C$, BAI, and iWUE. Averaged over the study period, the high-elevation sites (H) had 33% greater BAI and 18% greater iWUE than the low-elevation site (L). Tree RW and BAI decline throughout much of twentieth century and the H sites experience a sharper decline than the L site. Over the same period, iWUE increased approximately 45%. Breakpoint analysis indicated a distinct increase in iWUE at the H sites beginning in the 1930s that was not observed at the L site. All sites showed a marked increase in BAI and a decrease in iWUE at after 1985. Tree BAI was positively correlated with average monthly minimum temperature measured in April (L) and in August (H) and was negatively correlated with average monthly vapor pressure deficit. In general, temperature explained more of the variation in BAI at H sites than at the L site. Tree BAI was negatively correlated with $\Delta^{13}C$, and the slope of the relationship was steeper for the L site. These results suggest that environmental pressures may be limiting photosynthetic carbon gain at the L sites. However, all sites showed increased growth after 1985, which largely corroborate recent findings of increased growth of red spruce in the northeastern United States.

Tall groves of the Great Smokies and the coves that made them

Steve Norman *(steve.norman@usda.gov)*[1]*, Jitendra Kumar*[2]*, William Hargrove*[1]*, Forrest Hoffman*[2]
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Forest structure contributes to the extraordinarily rich biodiversity of the Great Smokies, but compared to forest composition, the role of structure is less well understood. Above-ground LiDAR provides us with an unprecedented ability to map patterns of forest structure and productivity across this landscape and to begin to understand the reasons for these patterns. In this research, we focus on the tallest groves of the Park to resolve the importance of logging history and topography. We calculated the 95th percentile height of the entire above-ground LiDAR point cloud at both 30m and 10m resolution for the Tennessee and North Carolina sides of the Park. This gave us a robust measure of stand height for each grid cell instead of individual tree heights. We find that the tallest groves of the Park are largely associated with one narrow section of mid to small sized east-west trending coves that are on the lower north-facing slope near water. We further show that this pattern of tall clusters of trees in these coves is largely restricted to areas that had been logged. These differences in height are likely to be artifacts of how logging impacted regeneration since young competitive stands of *Liriodendron* are likely the cause. As we see at nearby Joyce Kilmer on the Nantahala National Forest, such structural artifacts will likely persist for centuries, and this raises questions about the meaning of old growth.

Soil macroinvertebrate responses to wildfires in the Blue Ridge Mountains, USA

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Wildfires are of increasing concern in light of climate change, more frequent late summer droughts, and increasing incidence of human ignitions. There have been few studies examining the effects of wildland fires on soil macroinvertebrates in the Blue Ridge Mountains, in spite of the importance of these animals to soil processes, and their contributions to the biodiversity of these ecosystems. During November and December of 2016, the southeastern USA experienced numerous, large wildfires. These fires offered an opportunity to study the effects of wildland fire on soil macroinvertebrates. We sampled plots from three different wildfires in North Georgia and Tennessee, each plot with five burned plots and five unburned plots. These sites were sampled seasonally from 2017 through 2020. At each plot, on each date, we collected macroinvertebrates by hand sorting both litter (4 m diameter plots); at the North Georgia sites we also hand sorted mineral soil monoliths (30 x 30 x 30 cm) for 30 person-minutes each. All macroinvertebrates were identified to morphospecies. Two focal taxa, earthworms and millipedes, were identified to species. Abundance, species richness, and several diversity metrics were calculated to compare the macroinvertebrate communities of the burned areas to those in the unburned areas to better understand their response to fire. In addition, a subset of individuals from the focal taxa will be selected for sequencing of several genes (COI, 16S, 18S, and 28S) to establish baseline diversity measures for future studies.

Recruitment of large woody debris to streams in GSMNP following the 2016 Chimney Tops 2 wildfire

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Large woody debris (LWD) is a significant driver of physical and ecological processes in river systems, but the relative roles of continuous individual mortality versus episodes of mass mortality in LWD recruitment are not well understood. Here, the 2016 Chimney Tops 2 wildfire, a rare severe wildfire in the eastern US, was used as a case study for examining the role of mass mortality in LWD loads of streams in Great Smoky Mountains National Park (GSMNP), Tennessee. LWD surveys were conducted on four reaches in two drainage systems affected by the fire in order to ascertain the total frequency and volume of wood pieces and jams. In addition, the condition of LWD was assessed for burn marks so that the frequency and volume of fire-recruited wood could be estimated. Assuming that unburned wood represents the background rate of individual mortality, the Chimney Tops 2 fire resulted in a large influx of LWD to the study reaches, with large percentages of individual pieces (average of 47% by frequency, 48% by volume) and jams (average of 72% by frequency, 93% by volume) exhibiting burn marks. On average, burned LWD pieces had a larger diameter than unburned pieces in three of the four study reaches. Results suggest that rare mass-mortality events like the Chimney Tops 2 wildfire could play a major role in LWD dynamics of GSMNP streams.

Impacts of the Chimney Tops II wildfire on soil and stream chemistry within GSMNP

Salley Reamer *(sreamer47@gmail.com)*[1]*, John Schwartz*[1]*, Qiang He*[1]*, Jen Schweitzer*[2]
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The Chimney Top 2 (CT2) fire began in November 2016 and burned nearly 18,000 acres, with 11,000 acres burned within the Great Smoky Mountains National Park (GRSM). The fire spread due to strong, dry winds in the area and extreme drought conditions. Within the burn area, 55 stream miles were affected; it is typical to see a pulse of sediment move into waters after a fire. The impacts of wildfire are typically short term.

A soil and water characterization of the burn area will be produced, with a battery of parameters being tested. These parameters will be tested on soils collected in 2018 and 2019, at locations in all levels of burn: no burn, low/medium and high burn. Additionally, samples will be collected at sites near the burn, that were not impacted as a control. Sites will be selected away from major roads in the park to avoid contamination from sources such as road chat applied in the winter and exhaust from vehicles.

We have a unique opportunity to analyze the impacts of the CT2 fire as a result of continuous monitoring efforts in the park over the past two decades, including site characterization at 15 to 20 sites in and near the burn area. Additionally, there is little known about the impacts of wildfire on East Coast natural environments.

Soils were collects in 2017-2019. Each sample was air dried and sieved to remove debris. The air-dry, sieved soils were used to test the following parameters: pH, moisture content, organic matter content, total carbon, sulfur and nitrogen, exchangeable base cations, exchangeable aluminum and iron, exchangeable sulfate, nitrate and chloride, exchangeable acidity, cation exchange capacity, and total base saturation. The water sample collection began just days after the fire ended and has continued. These samples will be tested for conductivity, pH, major anions and cations, as well as metals including aluminum, iron, copper and zinc.

Oak regeneration after Chimney Tops II fire is influenced by pine seedling neighbors and soil microbes

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Background: Natural fire in the southeastern US has been rare over the last 100 years due to fire suppression policies, yet fire frequency is thought to be an important mechanism for oak forest regeneration. The proximate reasons for this phenomenon remain largely unknown. Identifying the ecological mechanisms that influence oak response to fire may improve management efforts to enhance oak regeneration. Findings from foundational soil science combined with more recent research show that the vast diversity of microbial life in soil can greatly influence plant growth by altering nutrient availability as well as directly altering specific plant traits related to growth. As such, it is likely that soil microbes play a role in oak recovery after fire disturbance. Additionally, recent observations of high abundance of pine seedlings in highly burned sites from the Chimney Tops II fire have sparked concern that oak regeneration success post-fire may be inhibited by competition with pine seedlings. To address the questions of if and how soil microbes and interactions with pine seedlings mediate oak success following fire, we examined microbiome diversity and composition from soils collected from the Great Smoky Mountains National Park (GSMNP) that were burned in the 2016 Chimney Tops II fire. Using the collected field soil, we then conducted a greenhouse experiment to examine oak seedling growth in treatments of soil burn severity and plant community (oak seedling as neighbor vs. pine seedling as neighbor). We hypothesized that fire has a strong influence on soil microbiome diversity and composition, and that fire-induced differences in soil microbial communities subsequently alters oak seedling growth traits. We also hypothesized that the strength of soil microbial influence on oak seedling is dependent on plant neighbor.

Results: Analysis of soil microbial community composition from the collected field soils find that microbial diversity is greatly reduced in high burned soils compared to unburned soils. Results from the greenhouse experiment show that some growth-related traits of oak seedlings are influenced by fire-induced changes to the soil microbiome. Seedlings Produced on average 40% more root biomass when grown in a burned soil microbiome compared to seedlings grown without a field soil microbiome. This effect was not influenced by plant neighbor. However, across soil burn severity treatments our results show that oak seedlings generally grow better near pine seedlings as opposed to other oak seedlings. Oak seedlings grown with a pine seedling neighbor produced 23% more root biomass, and 20% more total biomass than those grown with an oak neighbor. Oaks also grew nearly 90% faster when grown with a pine seedling neighbor compared to an oak neighbor. This trend of enhanced growth with pine is likely due to lack of competition for soil nutrients because of difference in rooting strategies between oaks and pines.

Long-term trends in throughfall deposition and stream chemistry in the GSMNP

John Schwartz *(jschwart@utk.edu), Adrian Gonzalez, and Andrew Veeneman*
Dept Civil & Environmental Engineering, University of Tennessee, Knoxville

Significant declines in acid deposition has been reported in the eastern United States, particularly sulfate since the mid-2000s, and this has been observed in the Great Smoky Mountains National Park (GRSM). In part, this is likely attributed to federal regulations and TVA power plant operational improvements. Throughfall deposition and stream chemistry has been monitored at Noland Divide, the high-elevation monitoring site within the GRSM. Long-term trends record significant declines in sulfate deposition. A complete ion balance will be presented and compared to ion mass export from the watershed. In addition, the last park-wide deposition mapping conducted was by Weathers et al. in 2000. In that study, elevation was a dominant factor to the levels of acid deposition. In 2016 a park-wide survey of through deposition was conducted to update our understanding of changes that has occurred. One result that needs further investigation is that sulfate deposition has declined at all elevation, however the pH remains the same at the high elevation sites. Some hypotheses will be proposed.

Bringing climate to down to the forest floor: Low-cost, high resolution sensors for microclimate modeling [POSTER]

Jordan Stark *(jordan.r.stark@gmail.com), Jason Fridley*
Dept Biology, Syracuse University

Organisms can experience environmental conditions that differ dramatically from those measured at weather stations or modelled over coarse spatial areas due to a range of topographic factors and biological interactions. Globally, this variation in microclimate conditions may buffer organisms from the most severe effects of climate change. Conversely, if microclimate conditions are strongly driven by ecosystem structure, disturbance may exacerbate impacts of climate change on the local scale. While theoretical frameworks for microclimate variation exist, high costs have limited the scope of on-the-ground measurements, especially for variables other than air temperature. Here, we have developed new low-cost, low-power sensors and dataloggers ($20-$30) that can measure soil temperature and moisture at dispersed sites. Initial deployments of these sensors in the Smokies in August-October 2019 indicated that they can detect precipitation events and showed strong differences among sites. Current and future deployments of a network of these sensors across gradients of topographic and biological conditions in the Smokies will allow development of new detailed models of microclimate conditions and their drivers.

Developing genetic tools to safeguard harvested species in the Great Smoky Mountains

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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 these: 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 in these and six other species of conservation interest. 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.

Investigation of elevational and wildfire effects on the plethodontid salamander communities of GSMNP

Andrew Wilk *(wilk.34@osu.edu)*[1], *William E Peterman*[1], *Joseph R Milanovich*[2], *Daniel J Hocking*[3], *John A Crawford*[4]
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Climate change and altered disturbance regimes are expected to shape future wildlife distributions and population dynamics. High latitude and elevation ecosystems are predicted to be most impacted, including Great Smoky Mountains National Park. Additionally, ectothermic species with low vagility, such as salamanders in the family Plethodontidae, are at greater risk from these changes. Along with projected increases in temperature and precipitation variation, future fire potential for the southeast United States is projected to increase. Longer fire seasons, increased drought severity, and changing vegetation communities, may alter habitat conditions in the park. To effectively manage wildlife in the future, an understanding of their potential responses to changing climate and wildfires is needed. In 2016, the Chimney Tops 2 fire burned a swath along an elevational gradient on the Tennessee side of the park. Unfortunately, historic data is sparse in this area, but distribution models can identify what species likely occupied the area before it was burned. Intensive sampling of burned and adjacent unburned areas will provide us with an understanding of how salamander communities may respond to future potential wildfires while baseline data and long term monitoring of salamander populations along 441 will elucidate responses to changing climate.

Long-term landscape-scale homogenization and decoupling of community-environment relationships following logging in the southern Appalachians

Margaret Woodbridge[1], *Martin Dovciak*[1], *Jason Fridley*[2]
[1]*State University of New York College of Environmental Science and Forestry, Syracuse;* [2]*Syracuse University, Syracuse, NY*

Widespread logging occurred throughout the eastern United States by the early 20th century. Despite the extensive nature of logging, studies addressing questions about the long-term impact of logging have been limited by scarcity of historical land-use data and rarity of forests without a history of intensive human disturbance. But how has this widespread disturbance changed how forests are structured on the landscape? It is well known that climatic and topographic factors have a strong influence on community composition and structure in forests in this region, but the logging signature on these relationships is unclear.

We explored this question using the documented land-use history of Great Smoky Mountains National Park (GSMNP), which maintains some of the largest tracts of old growth forest in the eastern US. We used Generalized Dissimilarity Modelling (GDM) and data from several vegetation studies to address questions about the relationship between beta diversity and logging history. Measuring beta diversity is particularly important considering biotic homogenization, the increased similarity of regional biota, can occur for decades following human disturbance. Beta diversity also provides important insights into the processes that shape communities and patterns of biodiversity, which is particularly important in the southern Appalachians given the highly variable communities in the region.

We found that logging changes the long-term relationships between space/the environment and vascular plant species turnover (one aspect of beta diversity). Specifically, logging increased the importance of spatial factors, and decreased the importance of environmental/topographic factors in structuring communities. Additionally, logging resulted in long-term homogenization of forest communities on a landscape scale. Our results provide information on the specific drivers of differences between old growth and logged forests which is invaluable for informing forest management, conservation and, remediation.