

**GREAT SMOKY MOUNTAINS NATIONAL PARK SCIENCE COLLOQUIUM  
THURSDAY, MARCH 7, 2024 — 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 Motivational framing increases the efficacy of de(marketing) materials designed to help reduce overcrowding in nature-based destinations**

**Justin M. Beall** (NC State Univ), Lincoln R. Larson, M. Nils Peterson, Whitney Knollenberg, Andrew Binder

**9:30 Park-wide forest change along elevation and topographic gradients, 1935-2019**

**Jason Fridley** (Clemson Univ)

**9:50 Trends in phenology and ozone injury in plants in GSMNP: a case study in longitudinal citizen science data**

**Amy Luo** (UTK), Emmi Felker-Quinn, Susan Sachs, Paul Super

**10:10 15-MINUTE BREAK**

**10:25 Survey of bacteria, fungi, and nematodes from soils across habitat types in GSMNP**

Ivan Emrich, **Seán O'Connell** (Western Carolina Univ)

**10:45 Monitoring amphibian diversity in GSMNP with Environmental DNA**

**Eugenia Naro-Maciel** (New York Univ), Erin Canter, Will Kuhn, Leonardo Maciel, Rob DeSalle, Aaron Aunins

**11:05 A study of the Wears Valley Wetland in GSMNP**

**Madeline Walker** (Maryville College), David Unger, Nathan Duncan, Julie Konkell

**11:25 55-MINUTE LUNCH BREAK**

**12:20 New species in old mountains: uncovering new spider diversity within the Appalachian Mountains**

**Marshal Hedin** (San Diego State Univ), Marc A. Milne

**12:40 Newly described salamander species in the "Salamander Capital of the World"**

**David A. Beamer** (East Carolina Univ), R. Alexander Pyron

**1:00 The Smokies ATBI: a 26-year accounting of the incredible biodiversity of GSMNP**

**Will Kuhn** (Discover Life in America), Todd Witcher, Becky Nichols, Paul Super

**1:20 The GRISLD approach**

**Keith Langdon** (GSMNP, retired), Dan Pittillo, Robert Emmott, Nora Murdock, Tom Howe, Paul Durr, Jason Hollinger, Douglas Bruce, Melissa Fawver

**1:40 15-MINUTE BREAK**

**1:55 Cryptic arthropod diversity in high southern Appalachia**

**Michael S. Caterino** (Clemson Univ), Adam Haberski, Ernesto Recuero

**2:15 Fire and forest history from soil charcoal in Table Mountain Pine stands in GSMNP, USA**

**Sally P. Horn** (UTK), Christopher A. Underwood

**2:35 Population abundance and growth of elk (*Cervus canadensis*) in western North Carolina (2020–2022)**

**Jessica L. Braunstein** (UTK), Joseph D. Clark, Justin McVey, Caleb R. Hickman, Joseph Yarkovich

**2:55 The vulnerability of Appalachian vertebrates to Climate Change: Assessing conservation implications**

**Narayani Barve** (UTK), Emily Brock, Paul R. Armsworth, Xingli Giam, Mona Papes

**3:15 CONCLUSIONS AND FAREWELL**

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

**ALL ARE WELCOME TO TUNE IN!**

Register here for Zoom link: [shorturl.at/gox37](https://shorturl.at/gox37)

More information: [dlia.org/colloquium-2024](https://dlia.org/colloquium-2024)

**Speakers:** No need to register. You'll receive a link via email.

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



# 2024 PARK SCIENCE COLLOQUIUM ABSTRACTS

(by last name of bolded presenting author)

## **The vulnerability of Appalachian vertebrates to Climate Change: Assessing conservation implications**

**Narayani Barve** (*narayani.ku@gmail.com*), Emily Brock, Paul R. Armsworth, Xingli Giam, & Mona Papes

*Dept. of Ecology and Evolutionary Biology, University of Tennessee, Knoxville*

The Appalachian region, a biodiversity and endemism hotspot in the Southeastern United States, faces unprecedented challenges, with climate change emerging as a major threat. Range shifts of species in response to climate change are dependent on dispersal limitations. This predicament poses a threat to their persistence, presenting a complex challenge for conservation practitioners and stakeholders in devising effective strategies.

In our study, we investigated the potential impact of climate change on over 300 species of amphibians, reptiles, birds, and mammals in the Appalachian region. Employing an ecological niche modeling approach, we evaluated the species' potential distributions under current climatic conditions and projected species distributions onto future climate scenarios from four Shared Socioeconomic Pathways (SSPs) and four General Circulation Models (GCMs) across six different future time periods. The models suggest broad regional patterns that might be expected such as latitudinal and elevational shifts in climatically suitable habitats, but they also reveal spatial nuance reflecting the multivariate way in which species respond to climate as well as the complexity of the terrain involved.

Our findings underscore the heightened vulnerability of narrow-range, endemic species with limited dispersal capacities to climate change. These species may require a distinct conservation approach, emphasizing the urgency of species-specific conservation strategies. Conversely, the models suggest some other species may exhibit more resilience to climate change.

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## **Newly described salamander species in the “Salamander Capital of the World”**

**David A. Beamer** (*beamerd23@ecu.edu*)<sup>1</sup>, & R. Alexander Pyron<sup>2</sup>

*<sup>1</sup>East Carolina University, Greenville, NC; <sup>2</sup>Dept. Biology, The George Washington University, Washington, DC*

Great Smoky Mountains National Park has often been referred to as the “Salamander Capital of the World”. This title refers both to the density of salamander populations in the park as well as the high number of different species present. Decades of sampling dusky salamanders across the eastern United States by the research team combined with newly developed next-generation sequencing techniques and analyses have resulted in the description of two new species in the park. This work has also resulted in the description of other new species, some of which are known from very close to the park boundaries and which may yet be discovered in the park. This talk will briefly describe the techniques and methods used to generate the dataset and will summarize the resulting discoveries as well as on-going research efforts to better understand the salamander diversity in the park.

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## **Motivational framing increases the efficacy of de(marketing) materials designed to help reduce overcrowding in nature-based destinations**

**Justin M. Beall** (*jmbeall@vt.edu*)<sup>1</sup>, Lincoln R. Larson<sup>1</sup>, M. Nils Peterson<sup>2</sup>, Whitney Knollenberg<sup>1</sup>, & Andrew Binder<sup>3</sup>

*<sup>1</sup>Dept. Parks, Recreation, and Tourism Management, North Carolina State University, Raleigh; <sup>2</sup>Dept Forestry & Environmental Resources, NC State University; <sup>3</sup>Dept. Communication, NC State University*

Many parks and protected areas around the world are threatened by overtourism – visitation that often creates excessive environmental, social, and economic impacts in tourism destinations. Demarketing strategies that focus on promoting destinations with lower visitation may be effective for relieving pressure on overcrowded parks. However, a gap in the literature remains regarding the most effective ways to promote such destinations. Motivational framings – including appeals to social media use in parks – might enhance the efficacy of promotional demarketing materials. The primary objective of our study was to compare how well demarketing materials using social media motivations and traditional nature experience motivations encouraged Great Smoky Mountain National Park (GRSM) visitors to consider a less crowded alternative site (the Cherohala Skyway). To this end, we surveyed visitors (n = 499) to GRSM in Fall 2022. Using an experimental approach, we randomly assigned participants to one of three brochures marketing The Cherohala Skyway: (1) one emphasizing the nature experience, (2) one focusing on social media opportunities, or (3) a control brochure free of motivational framing. We used three OLS regression models to assess the impact of the framings. Relative to the control, both nature-based and social media framings were effective for enhancing the appeal of the Cherohala Skyway and for intention to visit the Skyway if GRSM became too crowded, but not for influencing intention to visit the Skyway on a return trip to the area. Across the entire sample, 65% found the Cherohala Skyway at least somewhat appealing, 59% were at least somewhat likely to visit on a return trip, and 69% were at least somewhat likely to visit the Skyway if GRSM became too crowded. These findings have implications for destination marketers and managers who wish to enhance the effectiveness of promotional demarketing strategies.

## Population abundance and growth of elk (*Cervus canadensis*) in western North Carolina (2020–2022)

Jessica L. Braunstein (jgiacomini@vols.utk.edu)<sup>1</sup>, Joseph D. Clark<sup>2</sup>, Justin McVey<sup>3</sup>, Caleb R. Hickman<sup>4</sup>, & Joseph Yarkovich<sup>5</sup>

<sup>1</sup>School of Natural Resources, University of Tennessee, Knoxville; <sup>2</sup>USGS, Northern Rocky Mountain Science Center, University of Tennessee, Knoxville;

<sup>3</sup>North Carolina Wildlife Resources Commission, Raleigh; <sup>4</sup>Eastern Band of Cherokee Indians, Fisheries & Wildlife Management, Cherokee, NC; <sup>5</sup>GSMNP, NPS, Gatlinburg, TN

In an effort to restore extirpated elk to their previous range, 52 elk were reintroduced to Great Smoky Mountains National Park (GRSM) in North Carolina during 2001 and 2002. Since their reintroduction, elk numbers have increased, and their range has extended beyond GRSM boundaries. Our research objectives included estimating population abundance, apparent survival, per capita recruitment, and population growth rate of elk in North Carolina. We used spatially explicit capture-recapture (SECR) models based on fecal DNA to identify individual elk and estimate population abundance and growth in the region. We walked a series of transects throughout the region over 3 winter field seasons (2020–2022) and collected elk pellets encountered along these transects. These data were incorporated into both closed and open population SECR models to estimate elk densities, abundance, and population vital rates over the three-year period.

The top performing single-sex closed SECR models for males and females estimated density separately by year and as a function of the scaled distance to primary field with densities decreasing as the distance to field increased. The total realized abundance estimates of combined males and females in the study area were 179 elk (95% CI = 149–215) in 2020, 220 elk (95% CI = 188–256) in 2021, and 240 elk (95% CI = 207–279) in 2022.

The top open population SECR model estimated both apparent survival ( $\phi$ ) and population growth rate as functions of sex and year. Mean  $\phi$  for males were 0.682 (95% CI = 0.317–0.908) for 2020–21 and 0.339 (95% CI = 0.152–0.596) for 2021–22. Mean  $\phi$  for females were 0.953 (95% CI = 0.830–1.000) for 2020–21 and 0.829 (95% CI = 0.601–1.000) for 2021–22. Mean population growth rate estimates ( $\lambda$ ) for females were 1.559 (95% CI = 1.162–2.091) for 2020–21 and 1.122 (95% CI = 0.876–1.437) for 2021–22. Mean  $\lambda$  for males were 1.127 (95% CI = 0.806–1.575) for 2020–21 and 0.811 (95% CI = 0.566–1.163) for 2021–22.

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## Cryptic arthropod diversity in high southern Appalachia

Michael S. Caterino (mcaterini@clemsun.edu), Adam Haberski, & Ernesto Recuero

Dept. Plant & Environmental Sciences, Clemson University, SC

Recent work collecting, identifying, and DNA barcoding leaf litter arthropods from the higher parts of the southern Appalachians has revealed considerable cryptic species diversity. Our lab's work has particularly focused on beetles, where a combination of molecular and morphological work has discovered numerous new species, several endemic to the Smokies. However, patterns of cryptic endemism in allegedly widespread species appear to pervade many other arthropod groups, including isopods, springtails, pseudoscorpions, and others.

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## Park-wide forest change along elevation and topographic gradients, 1935-2019

Jason Fridley (fridley@clemsun.edu)

Dept. Biological Sciences, Clemson University, SC

Large environmental and biotic changes have occurred throughout the Park since its establishment in the 1930s, but attempts at evaluating their impacts on forest composition have been stymied by patchy survey data in space and time. Using a new ~1000-plot vegetation database surveyed under the NPS vegetation mapping program (2017-2019), I compare modern tree species distributions with those from the 1930s, as surveyed by a CCC field crew led by Frank Miller (1380 plots, 1935-1938). With a nod to R.H. Whittaker, I use joint species distribution models to quantify how canopy and understory tree occurrences have shifted along gradients of elevation and exposure, the latter focusing on a single composite index involving both topographic position and radiation load. As documented for much of the Eastern U.S., results indicate fire suppression as among the largest drivers of Park forest change, with oak-hickory recruitment failure a dominant feature of modern forests, particularly in low-elevation sites of high exposure and regardless of disturbance history.

## **New species in old mountains: uncovering new spider diversity within the Appalachian Mountains**

**Marshal Hedin** ([mhedin@sdsu.edu](mailto:mhedin@sdsu.edu))<sup>1</sup>, Marc A. Milne<sup>2</sup>

<sup>1</sup>Dept. Biology, San Diego State University, CA; <sup>2</sup>Dept. Biology, University of Indianapolis, IN

The southern Appalachian Mountains are one of the most ancient and biodiverse parts of eastern North America. This biodiversity extends into the invertebrate world as well as vertebrate, as this region is one of the most regionally biodiverse for millipedes, beetles, and spiders among other arthropod taxa. One of the most biodiverse taxa in these mountains are the cave and karst-loving spiders of the genus *Nesticus* (Araneae: Nesticidae). Spiders within this genus are taxonomically diverse though understudied with the latest major revision of the group occurring 40 years ago. By combining morphological observations and measurements with genetic data in the form of ultraconserved elements, we constructed robust, highly supported phylogenies to inform species delimitation. This integrative taxonomic method resulted in the discovery of 10 new species. Additionally, we described the previously unknown sexes of four additional species. Compelling biogeographic patterns and important conservation implications emerged from these analyses as several species seem to be microhabitat specialists that deserve monitoring to ensure their future survival.

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## **Fire and forest history from soil charcoal in Table Mountain Pine stands in GSMNP, USA**

**Sally P. Horn** ([shorn@utk.edu](mailto:shorn@utk.edu))<sup>1</sup>, & Christopher A. Underwood<sup>2</sup>

<sup>1</sup>Dept. Geography & Sustainability, University of Tennessee, Knoxville; <sup>2</sup>Dept. Environmental Sciences & Society, University of Wisconsin, Platteville

Table Mountain Pine (*Pinus pungens* Lamb.) is a fire-dependent species whose importance in the Appalachian Mountains has been reduced by fire exclusion. Armbrister (2002) examined fire-scarred pines in five Table Mountain Pine stands in Great Smoky Mountains National Park (700–1200 m elevation) to examine recent fire history. He found that most fires occurred during the dormant season, with a Weibull median fire interval of 6.75 years prior to park establishment. To document earlier fires in these stands, we recovered and analyzed soil charcoal. Soil charcoal records are of lower temporal resolution than tree-ring records of fire history but provide spatially explicit evidence of fires for periods beyond the reach of tree-ring records. Cores were recovered in 10 cm increments to the depth of refusal (25–90 cm) in the five stands (6 cores per stand) using a root corer, and wet-sieved through 2 mm mesh screens to recover charcoal. Nearly every depth interval of every core contained charcoal, indicating repeated local fires. Following initial radiocarbon dating of 7 charcoal samples, we randomly selected an additional 25 fragments for identification and dating. AMS radiocarbon dates on individual charcoal fragments ranged from 5160 years before present to modern, with most ages in the last millennium. Yellow pines were the source of most of the charcoal, but we also identified charcoal from white pine, chestnut, and red maple.

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## **The Smokies ATBI: a 26-year accounting of the incredible biodiversity of GSMNP**

**Will Kuhn** ([will@dlii.org](mailto:will@dlii.org))<sup>1</sup>, Todd Witcher<sup>1</sup>, Becky Nichols<sup>2</sup>, & Paul Super<sup>2</sup>

<sup>1</sup>Discover Life in America, Gatlinburg, TN; <sup>2</sup>GSMNP, NPS, Gatlinburg, TN

Great Smoky Mountains National Park is teeming with biological diversity. Here, we describe the All Taxa Biodiversity Inventory, a massive effort to catalog every species living in the park. Managed by park nonprofit partner Discover Life in America, the ATBI is a partnership with the National Park Service, regional and international scientists, volunteers, and community partners. Nearly 21,800 species have been documented in the Smokies, of which more than 12,000 have been added through this effort, and among them an astounding 1,079 that are new to science. We will discuss the past, present, and future of this ongoing effort.

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## The GRISLD approach

**Keith Langdon** (*krlangdon@gmail.com*)<sup>1</sup>, **Dan Pittillo**<sup>2</sup>, **Robert Emmott**<sup>3</sup>, **Nora Murdock**<sup>3,4</sup>, **Tom Howe**<sup>5</sup>, **Paul Durr**<sup>6</sup>, **Jason Hollinger**<sup>7</sup>, **Douglas Bruce**<sup>8</sup>, & **Melissa Fawver**<sup>9</sup>

<sup>1</sup>retired Supervisor Biology, GSMNP, NPS, Gatlinburg, TN; <sup>2</sup>retired Botany/Ecology Professor, Western Carolina University; <sup>3</sup>retired Ecologist, Appalachian Network, NPS; <sup>4</sup>retired, Endangered Species Office, USFWS; <sup>5</sup>retired, private industry & former president, TN Ornithological Society, Knoxville; <sup>6</sup>Chief Wetland Scientist in private industry; <sup>7</sup>Herbarium, Western Carolina University; <sup>8</sup>Group Leader, Metrology group, Nucelar Spallation Facility, ORNL; <sup>9</sup>commercial (macro-)photographer

The Gang of Retirees In Search of Life's Diversity (GRISLD) is a group of retirees who have a serious interest in species diversity, inventories, biology and ecology, in general - the Smokies in particular. Our approaches try to complement historic inventories of species in the park, by filling in perceived gaps in time, space and taxa sampled. We concentrate on learning different species groups in order to efficiently record species in park locales and better detect unusual occurrences. Individual GRISLD members may be developing skills in multiple species groups or focusing on a single group. Vascular plants, lichens, land snails, bees and several other insect groups are areas of high interest, but any reliably identified species may be documented while in the field. We peer review identifications amongst ourselves and refer difficult taxa to authorities. Documentation is in park-provided databases, with any specimens deposited into the park museum. We work with the park staff and DLiA. These data are used to generate species checklists, relative abundances, discovery of rare species, newly detected exotic species, ecological connections between species, and augment the park's species mapping project.

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## Trends in phenology and ozone injury in plants in GSMNP: a case study in longitudinal citizen science data

**Amy Luo** (*aluo@vols.utk.edu*)<sup>1,2</sup>, **Emmi Felker-Quinn**<sup>2</sup>, **Susan Sachs**<sup>2</sup>, & **Paul Super**<sup>2</sup>

<sup>1</sup>Dept. Ecology and Evolutionary Biology, University of Tennessee, Knoxville; <sup>2</sup>National Park Service

Citizen science projects are a powerful tool for monitoring long-term ecological trends. Great Smoky Mountains National Park hosts multiple decades-long citizen science projects that have tracked changes plant phenology and ozone-related foliar injury. For the plant phenology projects, volunteers have monitored annual phenology in herbaceous garden plots since 2000 and in tree plots since 2012, representing sites across the park. These monitoring efforts have found a variety of responses across species and elevation bands. Notably, spring green up for trees is advancing in lower elevations, but is occurring later at higher elevations. The ozone biomonitoring dataset has been collected by student groups since 2003. Using these data, we have found that ozone-related damage to plants has improved since 2012; metrics of foliar injury were stable or increasing up until 2012 but have been decreasing since then. The marked reduction in ozone-related injury in the park may highlight a success in recent air pollution regulatory efforts.

## Monitoring amphibian diversity in GSMNP with Environmental DNA

Eugenia Naro-Maciel (enmaciel@nyu.edu)<sup>1</sup>, Erin Canter<sup>2</sup>, Will Kuhn<sup>3</sup>, Leonardo Maciel<sup>4</sup>, Rob DeSalle<sup>5</sup>, & Aaron Aunins<sup>6</sup>

<sup>1</sup>Liberal Studies, New York University, NY; <sup>2</sup>Great Smoky Mountains Institute at Tremont, Townsend, TN; <sup>3</sup>Discover Life in America, Gatlinburg, TN; <sup>4</sup>New York University; <sup>5</sup>Institute for Comparative Genomics, American Museum of Natural History, New York City, NY; <sup>6</sup>USGS Eastern Ecological Science Center, Kearneysville, WV

Amphibians are suffering alarming declines globally due to disease, pollution, habitat loss, climate change, and other factors. Great Smoky Mountains National Park (GSMNP) provides refuge for numerous species, but understanding of these often cryptic taxa remains insufficient. To advance knowledge of their occurrence and distribution, and to complement long-term traditional surveys, an environmental DNA (eDNA) study of key habitats was conducted in 2022 (July) and 2023 (January, March, and May). Underwater surface sediment, and, where available, vernal pond surface water samples and negative controls, were collected at five sites in the Tennessee region of the GSMNP, with each containing 1-3 sampling locations. Additionally, water surface temperature and pH were measured. Following collection, samples were stored frozen until eDNA was extracted using Qiagen DNeasy PowerWater and PowerSoil Kits following manufacturer instructions and quantified with a Qubit that also confirmed clean negative controls. Soil samples yielded substantially more eDNA than water, due to turbidity-related limitations of water filtration. eDNA from four sediment samples each collected at Finley Cane and Methodist ponds over the study year, as well as one positive control containing a mix of GSMNP amphibian DNA, were sent out for amplification and sequencing. Two of the three primers, amplifying Cytochrome Oxidase I and 16S, yielded satisfactory results, but 12S performed poorly. Of the anuran (*Rana/Lithobates sylvatica*) and amphibians in the positive control (*Ambystoma jeffersonianum*, *A. maculatum*, *A. opacum*, *A. talpoideum*, *Desmognathus imitator*, *D. wrighti*, *Plethodon jordani*, and *P. metcalfi*), *R. sylvatica* was the only species additionally found at both field sites for both markers. Most *Ambystoma* species were detected in the positive control as well as the field, but *A. jeffersonianum* was not found at all because corresponding reference sequences are not yet on GenBank. *Desmognathus* and *Plethodon* results were similar, despite being less commonly detected than *Ambystoma*. Though traditional surveys offer the opportunity for in situ *quantification* of target species, eDNA allows for *detection* of cryptic species often undocumented in visual surveys in these habitats, including *A. talpoideum*. Once complete, this work combining amphibian genetic data with ongoing traditional surveys will provide complementary information important for managing vulnerable amphibians in the Great Smoky Mountains, with applications for other taxa and sites.

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## Survey of bacteria, fungi, and nematodes from soils across habitat types in GSMNP

Ivan Emrich, & Seán O'Connell (soconnell@email.wcu.edu)

Dept. Biology, Western Carolina University, Cullowhee, NC

The smallest organisms in Great Smoky Mountains National Park account for tremendous diversity in the soil environment and are understudied due in part to the difficulty of observing them directly. A total of 22 sites were sampled from All Taxa Biodiversity Inventory (ATBI) plots and other areas of interest in summer and fall of 2023 to add to the known microbial taxa in GSMNP. This work included surveying bacteria and fungi based on extracting DNA from soil and examining rRNA genes via high throughput DNA sequencing. Other samples were probed for 53 nematode taxa using quantitative PCR (qPCR) approaches. Bacterial taxa observed in the sites ranged from 1,267 to 3,298 (average = 2,390) operational taxonomic units (OTUs) while fungi ranged from 15 to 125 (average = 51) taxa per site. Bacterial taxa were distributed most commonly among the phyla Acidobacteria and Proteobacteria with Planctomyces, Verrucomicrobia, and Chloroflexi also being common. Fungi in each site were often dominated by either Ascomycota or Basidiomycota with Mucoromycota in lower abundances. Nematodes were collapsed into their feeding preferences and omnivores were clearly dominant across the samples with fungivores and herbivores next most abundant followed by bacterivores. Prominent nematode genera included *Microdorylaimus*, *Eudorylaimus*, *Filenchus*, *Heterodera*, *Labronema*, *Mylonchulus*, *Acrobleoides/Cephalobus*, *Tylencholaimellus*, *Prismatolaimus*, *Mesocriconema*, *Gracilacus*, and *Basiria*. Ongoing work is underway to better define each taxon encountered in this study and to use networking models to link taxa to each other to form hypotheses about ecological interactions. While microorganisms and tiny animals are often difficult to catalog, they are some of the most important drivers of ecosystem functions, including nutrient cycling. Understanding which species are present in GSMNP, no matter how small, can lead to a better appreciation of the role they play at larger scales.

## **A study of the Wears Valley Wetland in GSMNP**

**Madeline Walker** (*madeline.walker@my.maryvillecollege.edu*), David Unger, Nathan Duncan, & Julie Konkel

*Maryville College, Maryville, TN*

The Wears Valley Wetland (WVW), one of the largest wetlands within the Great Smoky Mountains National Park, has a history of human altered landscape in the form of tourism, agriculture, and the construction of the Foothills Parkway. The WVW is a palustrine wetland connected to a section of Cove Creek, a perennial stream situated at the boundary of the Great Smoky Mountains National Park (GSMNP). The purpose of this study was to collect baseline data to assess the functioning condition of the WVW and its influence on the adjoining reach of Cove Creek. Quantitative and qualitative data were collected between June and October of 2023. Line-point intercept vegetation surveys confirmed that the 25-meter riparian buffer is dominated by 75% facultative plant species. Water quality analyses showed a difference in water quality between the WVW and Cove Creek. Ion concentrations and conductivity were higher in WVW; however, pH, turbidity, and dissolved oxygen were higher in Cove Creek. Results showed that water inflow from WVW reduced *E. coli* concentration in Cove Creek at the confluence of the two systems suggesting WVW has the capacity for the reduction of pollutants. The Proper Functioning Condition qualitative assessment indicated that WVW appears to be functioning whereas Cove Creek is functional at-risk. None of the wildlife observed in opportunistic surveys was listed as threatened or endangered. This baseline data and analysis can provide insight necessary to create management and monitoring plans that address the concerns of all stakeholders.

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