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T-shirt designed by Sara Schoen entitled
"Exploring biology through screens and machines"

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Member-at-Large
Class of 2021

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PURPOSE

The purpose of this association shall be to promote the advancement of biology as a science by encouraging research, the imparting of knowledge, the application of knowledge to the solution of biological problems, and the preservation of biological resources. The ASB has representation in Section G Committee of the AAAS. Varying types of membership are available to individuals and institutions. See inside back cover.

TIME AND PLACE OF FUTURE MEETINGS

2022 30 March - 2 April, Little Rock, AR
 2023 Winston-Salem, NC

The View from Here: A Message from the President

Great times lie ahead!

I attended my first scientific meeting when a young professor at our small college rented a van and took several students to ASB because he thought it would be a good experience for us. At the 2022 meeting, it will have been 20 years since then and I have returned to the annual meeting almost every year. As a graduate student, I drove a car of lab mates and colleagues to the meeting; as a professor I often took my own van of students; and now as president, I will work to continue providing a friendly platform where students and professionals can disseminate their work and build lasting relationships with other biologists.

In 2009, mere months before earning my PhD, a friend and I asked then president Dr. Pat Cox what we could do to help. This began my long relationship volunteering with ASB. I have since served on the Program Committee, as a Member-at-large on the Executive Committee, as Vice President, and as President-Elect. In my work with ASB, I have met the most incredible people; people who love biology and enjoy helping others love biology too. At that first meeting in Boone, NC, I remember looking down at my printed name badge and seeing other attendees with stickers indicating their position as an officer. I never could have imagined I would be elected President of ASB. I am honored to join the amazing scientists and educators who have served in this position. I am proud of the work we have accomplished so far and look forward to continuing this legacy.

In recent years, we have accomplished great things. ASB committees have expanded membership benefits, increased support for underrepresented and first-generation presenters, worked to heighten the diversity and inclusivity of our meeting and association, increased the caliber of speakers at the meeting, expanded the range of meeting locations, and bolstered the stability and organization of the association. Under the steadfast leadership of Dr. Christopher J. Havran, we made the impossible decision to cancel the 2020 meeting due to a global pandemic. When the pandemic continuing into 2021, we successfully completed our first virtual meeting. We have joined and published with the Alliance to Catalyze Change for Equity in STEM Success (ACCESS). And we have a new relationship with Eagle Hill Publications. I have been honored to be involved in ASB's successes.

My experience highlights how ASB works. We grow through word-of-mouth and dedicated individuals who see the value of our association, who make lifelong friends at the meeting, and who pay it forward by returning with their colleagues and the next generation of southeastern biologists. We thrive by the hard work of volunteers serving on many committees, who help put together the meeting, increase the diversity of representation in the biological sciences, and expand benefits to members. I know that now, as much as ever, monetary and time budgets are strained, but we need YOUR help to continue advancing the importance and value of science in our communities; Keep coming back, bring your friends, and join a committee.



Christopher G. Brown (left) receives an honorable mention certificate from student research award committee member Dennis Haney.

Back when I was honorable at the 2006 Annual Meeting of the Association of Southeastern Biologists in Gatlinburg, TN. (from *Southeastern Biology*, 2006. Vol. 53, No. 3, pg. 341.)

See you in Little Rock!
Christopher G. Brown
ASB President

ASB 2021 R.H. Martin Plenary Session

As leaders around the world grapple with current conversations around diversity, equity, and inclusion, the ASB has instituted a faculty and industry panel discussion on diversity and inclusion to keep us informed and to provide some thought leadership to help address some of those issues in the biology and the natural sciences disciplines. Panelists from diverse backgrounds will also discuss how diverse students can be successful in the biological sciences as well as share the value of diversity and inclusion in academia and insights as to how panelists have excelled in their field of study. All are welcome to engage in the conversation.



Dr. Loretta Ovueraye, Miami Dade College, Moderator

Dr. Ovueraye serves Miami Dade College as the Vice Provost Workforce Programs & Professional Learning. She has managed several Federal grants including a Title V, USDA-NIFA grant, and current S-STEM project. Dr. Ovueraye is an active member of the Association of Southeastern Biologist and currently serves as its secretary and past co-chair of the Human diversity committee. She has contributed to the study of microbial activity in the remediation of Sulphur oxalate containing water and minority student education. In addition to contributions described above, as one deeply engaged in the STEM education field, she worked with a team of collaborators to contribute to the 2014/15 the Southeast Regional PULSE (SERP) Institute report as part of the Vision and Change in Undergraduate Biology Education: A Call to Action [AAAS, 2011]; Funded by the National Science Foundation and the Howard Hughes Medical Institute.



Dr. Edward Moreira Bahnson, University of North Carolina at Chapel Hill, Panelist

Dr. Edward Moreira Bahnson is an Assistant Professor at the Dept. of Surgery and the Center for Nanotechnology in Drug Delivery at UNC Chapel Hill. Dr. Bahnson's research program focuses on the study of arterial disease. He aims to understand how redox dysfunction affects arterial disease progression with the goal of developing redox-based targeted therapies for the vasculature. His personal experiences as a queer Latino immigrant and first-generation college graduate have shaped and fueled an interest in improving equity and inclusion in science and medicine. He has studied how LGBTQ cultural training can impact allyship in physicians with the goal to provide intentionally inclusive care to LGBTQ patients. Dr. Bahnson serves as Interim Chair of the LGBTQ Life Provost Committee at UNC and he is Diversity Equity and Inclusion Chair of the Society of Redox Biology and Medicine.



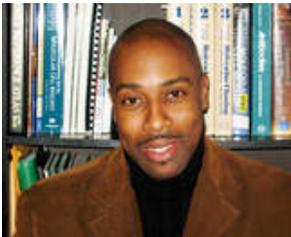
Dr. Kelly Mack, Association of American Colleges and Universities, Panelist

Dr. Kelly Mack is the Vice President for Undergraduate STEM Education and Executive Director of Project Kaleidoscope at the Association of American Colleges and Universities (AAC&U). In this capacity, Dr. Mack provides leadership for the organization's mission level commitments to quality and inclusion through the delivery of world class professional development aimed at empowering our nation's finest STEM faculty to competitively train and educate more STEM students. Prior to joining AAC&U, Dr. Mack was the Senior Program Director for the National Science Foundation ADVANCE Program while on loan from the University of Maryland Eastern Shore where, as a Professor of Biology, she taught courses in Physiology and Endocrinology for 17 years.



Dr. Veronica Segarra, High Point University, Panelist

Dr. Veronica Segarra contributions to science have come in the form of research breakthroughs in the study of budding yeast proteins that coordinate vesicular trafficking pathways, including clathrin, auxilin, and Atg27. Her lab at High Point University (HPU) is not only the home base for her research program, but a place where undergraduate students receive one-on-one mentoring as they strive to develop their identity in science and research. Dr. Segarra is Interim Chair of the Biology Department at HPU and the co-PI on the National Science Foundation (NSF) grants that funded the creation of ACCESS and ACCESS+ (grant numbers: 1744098, 2017953), multi-professional society organizations that advocate for equity and inclusivity in scientific communities.



Dr. Selwyn Williams, Miami Dade College, Panelist

Dr. Selwyn Williams is an Assistant Professor of Biology and the Program Coordinator of the Bachelor of Science in Biological Sciences (BS-BS) program at Miami Dade College (MDC). His teaching interests are centered on the development of innovative high impact pedagogical practices designed to transform STEM education and increase the success of historically underrepresented minorities in STEM careers.

About the R.H. Martin Plenary

Robert H. Martin, founder and owner of Martin Microscope Company from 1946 until his death in 2006, was an avid supporter of ASB and of the sciences in general. He supported ASB for decades as a Patron member and sponsor of the ASB Student Research Award, and, with his passing, his family established what has become the Robert H. Martin Plenary Address fund to help cover the costs of bringing in highly qualified speakers for the ASB annual meeting.

ASB Patrons

Martin Microscope Co, Easley, SC
Dennis, Breedlove, and Associates, Inc., Winter Park, FL

Patron membership is for individuals who choose to support the society beyond annual meeting registration costs. Patron membership includes a one-year membership, one annual meeting registration and two tickets to each of the three evening events at the annual meeting

Virtual Meeting Sponsors

Platinum Level



Gold Level



Patrons



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Associates, Inc.
Winter Park, FL

A Tribute to Michael Edward Held

ASB is saddened to announce that Michael E. Held passed away in 2021. He was a member of the society since 1974 and he served biology profession in several capacities over his many years of membership.

Mike received his AB degree from Thomas More College majoring in Biology, then a M.S. in Biology from Western Kentucky University and finally a Ph.D. in Botany and Ecology (1980) from Ohio University. After several years as an instructor at the University of Tennessee he moved to Jersey City, NJ in 1982 where he had a long career at Saint Peter's College (now a university). While there, he served the university in numerous roles including Chair of the Department of Biology. His teaching skills were varied and included Freshman Biology, Botany, Forestry, Biostatistics, Microbiology, and even Forensic Science. Besides teaching, Mike also served the Saint Peter's well through a variety of appointed and elected committees and leaderships positions.

Research was also part of Mike's academic career, mostly in the area of forest ecology. He worked along with two colleagues Joe E. Winstead and William S. Bryant on ecological studies in Kentucky and Arkansas. His research presentations at conferences totaled over 50 and included the Association of Southeastern Biologists (20), Kentucky Academy of Sciences (10), and Ecological Society of America (5). His presentations at annual meetings spanned subjects including microbiology, teaching, plant physiology, and his passion, forest ecology. He served on the ASB student poster award committee.

Dr. Held also published numerous research papers relating to forest ecology within the pages of such journals as *Annals of Botany*, *BioScience*, *Bulletin of the Torrey Botanical Society*, *Castanea*, and *Journal of the Kentucky Academy of Science*.

Mike was a major factor in the governance of the Southern Appalachian Botanical Society, a affiliate organization of ASB. His leadership capacity was important, he served as President-elect (2003), President (2004-2006) then Past president (2006). While president, Mike championed for a continued strengthening of botanical taxonomy and systematics in the southeast, including a push for new society members, submission of manuscripts to *Castanea*, and an encouragement of members to support the newly formed Society of Herbarium Curators. It was during his term as president that SABS reached their long-term goal of having \$200,000 in its endowment. Finally, Mike served as the Membership Secretary (2008-2019). For all his service to botany, science education, and to SABS, Mike was presented with the Elizabeth Ann Bartholomew Award at the April 2019 meeting. This Award is presented annually by the SABS as the highest honor to individuals that contribute to botany of the Eastern United States.

--Charles N. Horn, Biology Program, Newberry College

ASB PRESTIGIOUS AWARDS PRESENTED AT THE 2021 VIRTUAL ASB MEETING

ASB JOHN HERR LIFETIME ACHIEVEMENT AWARD None awarded

ASB MERITORIOUS TEACHING AWARD **Dr. Ray S. Williams,**
Appalachian State University



ASB LUCRECIA HERR OUTSTANDING BIOLOGY TEACHER AWARD The Lucretia Herr Outstanding Biology Teacher award is usually presented to the recipient of the National Association of Biology Teachers (NABT) Outstanding Biology Teacher Award (OBTA) in the state that the annual meeting is being held. Since we met in a virtual format in 2021, we recognized the OBTA recipients in every southeastern state in which they were awarded.



Mr. Chance Duncan
Russellville High School
Russellville, AR



Ms. Nerissa DeRamus
Thompson High School
Alabaster, AL



Ms. Amber Lawson
Salisbury High School
Salisbury, NC



Ms. Annette Buckner
Dalton High School
Dalton, GA



Mrs. Christina Nicholas-Hurt
Siegel High School
Murfreesboro, TN

ASB SUPPORT AWARDS

THE LAFAYETTE FREDERICK UNDERREPRESENTED MINORITIES SCHOLARSHIP None awarded

SUPPORT AWARD FOR GRADUATE STUDENT MEMBERS OF ASB **Hannah Partridge,** University of North Carolina
Amanda-Jean Blackburn, Western Carolina University

SUPPORT AWARDS FOR FIRST-GENERATION UNDERGRADUATE STUDENT MEMBERS OF ASB **Austin Snide,** Catawba College

ASB RESEARCH AWARDS

ASB STUDENT RESEARCH AWARD – SPONSORED BY ASB PATRON MARTIN MICROSCOPE **Skyler J. Fox** and Ashley Morris, Furman University
“Citizen science platforms as tools connecting communities to research and education: A case study using iNaturalist”

ASB RESEARCH AWARD **John Quinn** and Emma Cook, Furman University
“Patterns of Vertebrate Richness Across Global Anthromes: Prioritizing Conservation Beyond Biomes and Ecoregions”

ASB PRESENTATION AWARDS

ASB STUDENT POSTER PRESENTATION AWARD – ANIMAL BIOLOGY **Sierra Croney**, Western Carolina University
“The effect of canopy openness on saproxylic Coleoptera diversity in the Wilson Creek Watershed”

ASB STUDENT POSTER PRESENTATION AWARD – AQUATIC BIOLOGY **Perla Morales**, Nash Community College
“Geometric morphometric analysis of candidate species within *Desmognathus fuscus*”

ASB STUDENT POSTER PRESENTATION AWARD – CELL AND MOLECULAR BIOLOGY **Jordan Ogg**, Stetson University
“Amyloid- β -Induced chemotaxis behavior and neuronal morphology in transgenic *Caenorhabditis elegans*”

ASB STUDENT POSTER PRESENTATION AWARD – MICROBIOLOGY **Annie Bright**, Campbell University
“Identification and characterization of oil degrading bacteria”

ASB STUDENT ORAL PRESENTATION AWARD – ANIMAL BIOLOGY **Jean Ross**, Elon University
“Multiple functions for multiple signals: the role of sound and vibration in mediating courtship and competition in a Neotropical katydid”

ASB STUDENT ORAL PRESENTATION AWARD – AQUATIC BIOLOGY **James Valentine**, University of Southern Mississippi
“Linking males, females, and nymphs of *Perlesta* species (Plecoptera: Perlidae) in Mississippi using DNA barcoding”

ASB STUDENT ORAL PRESENTATION AWARD – CELL AND MOLECULAR BIOLOGY **Jonathan Black**, University of North Carolina at Charlotte
“Synthesis and Assembly of Functionalized RNA Nanorings”

ASB STUDENT ORAL PRESENTATION AWARD – MICROBIOLOGY **Jonathan Kilroy**, Boston University
“Proposal of Three Models of Extractive-fermentation Bioreactors for the Conversion of Crude Glycerol to Biobutanol by *Clostridium pasteurianum*”

Jessica Wakeman, Campbell University

“Optimization of *Dunaliella salina* growth using commercial fertilizers and salts”

AFFILIATE AWARDS PRESENTED AT THE 2021 VIRTUAL MEETING

- NORTH CAROLINA BOTANICAL GARDEN AWARD** **Emily Oppmann**, Middle Tennessee State University
“Assessing the clonal nature of running glade clover (*Trifolium calcaricum*; Fabaceae)”
- SOUTHEAST CHAPTER OF THE ECOLOGICAL SOCIETY OF AMERICA – EUGENE P. ODUM** **Shannon Walker**, Virginia Commonwealth University
“Belowground characteristics of coastal dune grasses with implications for species-specific effects on erosional resistance”
- SOUTHEAST CHAPTER OF THE ECOLOGICAL SOCIETY OF AMERICA – ELSIE QUARTERMAN-CATHERINE KEEVER AWARD** **Behil Alemu**, Georgia Gwinnett College
“Evaluating mammal diversity across habitats fragmented by a power line cut”
- SOUTHERN APPALACHIAN BOTANICAL SOCIETY – CONFERENCE SUPPORT AWARD** **Sarah Brown**, James Madison University
- SOUTHERN APPALACHIAN BOTANICAL SOCIETY – RICHARD AND MINNIE WINDLER AWARD IN ECOLOGY** **Justin P. Williams and Tracy S. Hawkins**
“Acorn Weevil (Coleoptera: Curculionidae) Predation Dynamics in a Mississippi Bottomland Hardwood Forest” (*Castanea* 85(1): 159-168)
- SOUTHERN APPALACHIAN BOTANICAL SOCIETY – RICHARD AND MINNIE WINDLER AWARD IN SYSTEMATICS** **Elizabeth McMurchie and Andrea Weeks**
“Vascular Flora and Ecological Community Assessment of the Blue Ridge Center for Environmental Stewardship, Loudoun County, Virginia” (*Castanea* 85(1): 42-64)
- SOUTHERN APPALACHIAN BOTANICAL SOCIETY – EARL CORE STUDENT RESEARCH AWARD** **Michelle L. Gaynor**, University of Florida
“Formation and persistence of a co-occurring mixed cytotype autopolyploid system in the Southern Appalachians”
- Noah Dennis Yawn**, Auburn University
“Testing for the hybrid speciation of a fertile population of the sterile fern hybrid, *Asplenium x gravesii* (Aspleniaceae)”
- SOUTHERN APPALACHIAN BOTANICAL SOCIETY – JOHN E. FAIREY SCHOLARSHIP FOR STUDY AT A BIOLOGICAL FIELD STATION** **Luke Sheaffer**, WCU
Brittany Martin, Haywood Community College
Alana Hicks, UT Chattanooga
Brandon Wheeler, WCU
Morgan Gaglianese-Woody, ASU
Neely Millard, UT Chattanooga
Laura Hamon, NCSU
- SOUTHERN APPALACHIAN BOTANICAL SOCIETY – OUTSTANDING STUDENT ORAL PRESENTATION AWARD** **Rebekah Shupe**, Marshall University
“The effect of fire on oak-forest regeneration: A 25-year study”

**SOUTHERN APPALACHIAN BOTANICAL SOCIETY –
OUTSTANDING STUDENT POSTER PRESENTATION
AWARD** **Katie Krogmeier**, Appalachian State University
“Impacts of Polyploidy on the Ecophysiology of
Solidago altissima”

**SOUTHERN APPALACHIAN BOTANICAL SOCIETY –
ELIZABETH ANN BARTHOLOMEW AWARD** **Zack Murrell**, Appalachian State University

**SOUTHEASTERN SECTION OF THE
BOTANICAL SOCIETY OF AMERICA –
OUTSTANDING STUDENT PAPER AWARD
IN PLANT SCIENCE** **Emily Oppmann**, Middle Tennessee State University
“Assessing the clonal nature of running glade clover
(*Trifolium calcaricum*; Fabaceae)”

**SOUTHEASTERN SECTION OF THE
BOTANICAL SOCIETY OF AMERICA –
OUTSTANDING STUDENT POSTER AWARD
IN PLANT SCIENCE** **Regina Javier**, Appalachian State University
“Gas Exchange Characteristics from Differently Colored
Leaves of *Croton petra*”

ASB Presentations

1 - Forest recovery over 19 years following windthrow and salvage logging in a mixed East Gulf Coastal Plain Forest

Callie Oldfield, Chris Peterson

University of Georgia, Athens, GA

Natural disturbance regimes shape forest structure, composition, and function. Though eastern US forests are adapted to large, infrequent disturbances such as windthrows, overlapping anthropogenic disturbances may permanently alter forest dynamics. Although wind disturbances lead to greater heterogeneity, windthrow is often followed by salvage logging, which reduces forest structural complexity. This study examines the compound effect of wind disturbance and salvage logging on forest recovery over 19 years. We examine the change in woody stem density, Shannon diversity, biomass, and species richness. We track community composition and species rank abundance to examine the effect of salvage logging on forest trajectory.

Natchez Trace State Park (NTSP) is in west-central Tennessee, part of the East Gulf Coastal Plain. The forest is composed of hardwoods and *Pinus taeda*. NTSP was impacted by a 1999 downburst; most of the damaged forest was salvaged by 2001. In 2001, 23 30x30m plots were established (15 salvaged, 8 unsalvaged) to characterize tree species and cm DBH for individuals ≥ 5 cm and sapling densities measured. Pre-disturbance composition was reconstructed from stumps in 2001. Tree sampling was repeated in 2020. Forest change metrics were compared using paired t-tests, NMDS, and rank abundance curves.

Nineteen years after wind disturbance, stem density, Shannon diversity, biomass, and species richness had returned to pre-disturbance levels. In plots that experienced windthrow + salvage logging, diversity and biomass did not differ from pre-disturbance levels, while stem density and species richness was significantly higher. *P. taeda* became the most abundant species in salvaged plots, dominating the 5-20 cm DBH size classes. The forest recovered from windthrow within 19 years, but when windthrow was compounded with salvage logging, species abundance and density was altered. We suggest that forest managers weigh the costs salvage logging may have on forests to ensure that ecosystem functioning is not negatively impacted.

2 - Photosynthesis, water use, and biomass allocation of Princess tree (*Paulownia tomentosa*) and Tulip poplar (*Liriodendron tulipifera*) first year seedlings across a light gradients and prescribed fire

Hannah Dinkins

Western Carolina University, East Bend, NC

Forest communities experience disturbances, such as fire and canopy removal, thus creating light gradients and microclimates which affect establishment, carbon gain, and height growth of native and invasive tree species. To test the hypothesis that *Paulownia* has a stronger positive response to post-disturbance in different microclimates compared to *Liriodendron*, I compared early growth of the invasive *Paulownia tomentosa* (princess tree), and native *Liriodendron tulipifera* (tulip poplar). I measured photosynthetic rates, allometry, and biomass of first-year seedlings of both species. The field study had a split-plot experimental design with distributed plots across a forest light gradient (open, edge, canopy), plots were burned or unburned. Environmental variables were measured at the each plot (relative humidity, temperature, soil temperature, soil moisture, soil nutrients (N, P, K)) along with measuring each species individual tree's photosynthetic measurements, transpiration rates, photosynthetic rates, conductance and created photosynthetic curves throughout the growing season. Biomass and allometric measurements were made at the end of the growing season. Preliminary results suggest *Paulownia* had more pronounced allometric growth, biomass accumulation, and photosynthetic responses than *Liriodendron*, which were correlated with plot microclimate. *Paulownia* had a higher photosynthetic rate across all light conditions, with the highest rates in the unburned, full sun plots. Photosynthetic rates of *Liriodendron* varied little across light and burn treatments. Overall, these findings suggest *Paulownia* has greatest growth in a moderate microclimate with lower temperatures, greater soil moisture, and full sun, emphasizing *Paulownia* as an aggressive non-native invasive species following canopy disturbance.

3 - Privet removal increases cover, but not native herb-layer richness in a Georgia wetland.

Michaela Valkenaar, Lissa Leege

Georgia Southern University, Statesboro, GA

Chinese privet, *Ligustrum sinense* is one of the worst invasive plant threats to wetlands in the southeastern U.S. Its prodigious seed production and rapid growth allow it to overtake sites. Once established, it has been found to outcompete native species and halt natural succession. This study examined how privet removal affects the abundance and diversity of native and invasive herbaceous species in a Georgia depression wetland. Our hypothesis was that privet removal would increase native plant species richness and abundance. To test this hypothesis, we conducted vegetation surveys to determine cover, species richness and importance values, and measured light intensity with a ceptometer at the herb level in a wetland partially cleared of privet in 2018 and 2019. 20 randomly-located permanent plots of 10 m² were set up, ten with privet-present area, five in the 2018 cleared zone, and five in the 2019 cleared area (N=20 plots). Inside each permanent plot were four one m² plots for herb layer vegetation, (N=80 plots)

Both native and invasive herb-layer cover in privet-removal plots were triple that of privet-present plots. In 2019 removal plots, invasive species richness was almost double that of 2018 removal and privet plots. In contrast, native species richness did not differ among treatments. Light levels were twice as high in privet-cleared plots compared to privet plots. The species with the highest importance values in both privet and removal plots were *Rubus sp.* (native) and *Microstegium vimineum* (invasive).

In this study, privet removal resulted in a more productive, but not more diverse, herb layer. The same species, native and invasive, that survived under privet, also thrived with its removal. Because of the increase in invasive species and lack of native recruitment, it may be necessary to re-seed the site with native grasses and forbs to withstand invasive over-competition.

4 - Topographic Effects on Damage Severity and Carbon Footprint of Two Southeastern Tornadoes Using High Resolution Aerial Imagery

Rebecca Klee, Chris Peterson

University of Georgia, Athens, GA

Wind disturbances influence forest landscape patterns and can alter structure and function in forested systems across vast areas annually. Among types of wind disturbances, tornadoes have seldom been studied with remote imagery and geographic information systems tools. In this study, we examined high resolution aerial imagery of two tornado tracks in Lee County AL and Monroe County MS. We used supervised classification of the aerial imagery to map damage severity. Using topographic overlays, we test how elevation, side of the tornado track, and aspect influence tornado damage severity. We also relate the total biomass of trees felled to the total carbon transferred from living to decomposing pools to calculate a 'carbon footprint' for each tornado track. Tornado damage severity was greater in lower elevations. On the right side of each tornado track, damage severity was higher for windward aspects. The Lee and Monroe County tornado tracks had estimated carbon footprints of 0.19 and 0.0095 Tg, respectively. The results from this work increase the meteorological understanding of tornado behavior as well as its impact on ecological processes, which can aid in windthrow risk assessment and management practices.

5 - Differences in phenology, magnitude, and richness of emerging aquatic insects in two headwater valleys

Emily Jones¹, Amy Braccia¹, Jesse Robinson², Michael Croasdaile², Art Parola²

¹*Eastern Kentucky University, Richmond, KY*, ²*University of Louisville, Louisville, KY*

Aquatic insect emergence is an important, but understudied, function of aquatic habitats. Effects of human impacts on the immature stages of aquatic insect assemblages has received more research effort than the adult stages. This study aimed to compare the phenology, magnitude, and richness of emerging aquatic insects at two headwater valleys that have different hydrologic functions as a result of human activities. One valley system had been restored to pre-colonial hydraulic conditions in 2011 and is currently influenced by beaver. The other valley has experienced degradation by channelization for many years. Emergence traps were used to collect emerging insects in the main channels of each valley from May 2020 to February 2021. Insects were identified to morphospecies, counted, and measured. Results suggest that the hydrologically restored site had a larger magnitude (individuals/m²/day and mg/m²/day) of emerging aquatic insects, most likely due to the presence of beaver ponds and flow duration the entire year. Results also suggest a higher richness of emerging aquatic insects from the hydrologically restored site. The phenology of insect emergence differed between locations, probably due to differences in water temperatures and flow duration. This study suggest hydrologically restored sites are more productive and lays the groundwork for future food-web studies.

6 - Evolutionary impact of Wolbachia infection among mosquito species

James E Russell, Rebekah Williams, Michael Saum

Georgia Gwinnett College, Lawrenceville, GA

Inherited bacterial symbionts have played, and are continuing to play, pivotal evolutionary roles in the history of life on earth. One of the most consequential bacterial symbionts in the world currently is an alpha-proteobacterium in the genus *Wolbachia*. Among insects, *Wolbachia* is generally considered a reproductive parasite that manipulates host reproduction to ensure its evolutionary success. The mode of host manipulation has been studied in a large number of host species, and infection phenotypes range from various forms of sex ratio distortion to bacterially induced reproductive isolation. Mosquito species are known to be infected with *Wolbachia* that induce reproductive isolation via a process known as cytoplasmic incompatibility. The evolutionary consequences of *Wolbachia*-induced cytoplasmic incompatibility are potentially extreme for host insect species, and include effects such as reduced genetic variation and speciation. Mosquito species in the Atlanta metropolitan area were sampled and tested for *Wolbachia* infection. Phylogenetic analysis of nuclear, mitochondrial, and *Wolbachia* genes for collected mosquito species suggest several evolutionary effects of infection. Reduced mitochondrial genetic diversity was observed among sampled *Aedes albopictus*. Discordant nuclear-mitochondrial phylogenies among mosquito species was also observed and suggest a possible evolutionary effect of *Wolbachia* infection on patterns of mitochondrial evolution. Statistical analyses of molecular evolution suggest an elevated rate of substitution among certain *Wolbachia*-infected mosquito species.

7 - Exploring Insect Biodiversity and Systematics Using Undergraduate Students at Cypress Grove Nature Park

Darius Mullin, Allaina Armstrong, Preston Buck, Sarah Childress, Hannah Juliussen, Rachel Kuhl, Samuel Ross, Emma Straley, Charisse Walker, Gavin Woodring, Sydney Zemke, Jeremy Blaschke

Union University, Jackson, TN

Insects are crucial to the health of our ecosystems as decomposers, pollinators, and intricate connectors of food webs. Alarmingly, the diversity and abundance of these important creatures has been steeply declining over the last 50 years. A parallel crisis is unfolding in taxonomy as the rate of new workers in insect systematics continues to fall short of the rate at which specialists are retiring. As a small way to combat these

difficulties, an invertebrate biology course at Union University has begun integrating an insect biodiversity and systematics research program into the undergraduate curriculum using a Gressitt-style Malaise trap at Cypress Grove Nature Park (Jackson, TN)—a previously-unsampled hardwood bottomland forest ecosystem. Here, we present results from the first year of collecting (Aug–Oct. 2020). Specimens were collected every ~48 hrs, stored in 90% ethanol, and sorted to Order and Family. Each student then chose a family of interest to study in greater detail, identified individuals to morphospecies, and calculated species accumulation curves to estimate how thoroughly the diversity at Cypress Grove had been sampled. More than 30,000 specimens were collected from 11 orders within class Insecta. Diptera were the most common, followed by Hymenoptera and Lepidoptera. Not including the fungus gnats, the most abundant families were Ichneumonidae, Formicidae, and Tabanidae. Several rare or unusual insects were also identified, including parasitoid rhopalosomatid wasps, mantisflies, and the enigmatic forceps-fly (Merope tuber). This study provides novel baseline insect biodiversity data for Cypress Grove Nature Park, laying the groundwork to track biodiversity changes over time through an intended long-term insect sampling project in the park. Appreciation for biodiversity and an interest in insect systematics was fostered among students and this class has inspired several students to pursue further research opportunities directly related to this project.

8 - Comparison of abundance and diversity of insects using six different colors of Moericke pan traps at Cypress Grove Nature Park, TN

Sarah Childress, Allaina Armstrong, Preston Buck, Hannah Juliussen, Rachel Kuhl, Darius Mullin, Samuel Ross, Emma Straley, Charisse Walker, Gavin Woodring, Sydney Zemke, Jeremy Blaschke

Union University, Jackson, TN

As insect biomass continues to decline globally, it becomes increasingly important to track the abundance and diversity of local insects, particularly pollinators. Colorful pan traps filled with soapy water are commonly used to survey pollinator abundance and diversity. However, different colors often attract different insect species depending on habitat. Here, we report the effects of habitat and pan trap color to attract anthophilous insects from the five most common flower-visiting Orders (Diptera, Hymenoptera, Coleoptera, Lepidoptera, and Hemiptera) at a local nature park in Jackson, TN. Four collecting sites were established, two in meadow habitats and two under the forest canopy. At each site, six pan traps of various colors (white, yellow, blue, red, clear, and ultraviolet) were placed in a circle equidistant apart. Insects were collected every ~48 hrs from Aug–Oct, stored in 90% EtOH, and identified to Order, Family, and morphospecies. Abundance and diversity were measured for each habitat and each color at all three taxonomic levels. White, yellow, and blue pan traps attracted the greatest abundance of insects due to a few particularly numerous species attracted to each individual color. However, the diversity of morphospecies was almost even across all colors. Each color attracted unique morphospecies (e.g. the sap beetle *Conotelus obscura* was attracted to white, and the tachinid fly *Zelia* spp. was attracted to blue). While meadow habitats attracted a greater abundance of insects, there was not a significant difference in diversity between meadow and forest habitats, and some insect families were exclusively found in one or the other (e.g. Apidae in meadows and Tiphidae in forests). This study highlights the importance of diverse habitat sampling and including diverse colors when using pan traps for pollinator surveys as some families and morphospecies were solely attracted to certain colors and habitats.

9 - A New Host Record for the Cricket Assassin Wasp *Rhopalosoma nearcticum* (Brues)

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Union University, Jackson, TN

Rhopalosoma nearcticum (Brues) (Hymenoptera: Rhopalosomatidae) is a rarely encountered wasp with the unusual lifestyle of cricket ectoparasitism. After a single egg is laid on the hind leg of their host, the larva develops rapidly and eventually cripples and kills its prey. Flightless bush crickets (*Hapithus* spp.) are their only known hosts (Family Gryllidae: Hapithinae). During an undergraduate invertebrate biology class, an unknown rhopalosomatid larva was discovered attached to a cricket at Cypress Grove Nature Park in Jackson, TN. Due to the rarity of such specimens, subsequent collections were made each fall for three years (2017–2020). Seventeen larvae and their cricket hosts were collected, including six larvae parasitizing specimens of Say's trig (*Anaxipha exigua* (Say)). Here we report *A. exigua* as a new host record for *R. nearcticum* based on evidence from the barcoding gene *COI*, an analysis of mating call frequencies, and the number of teeth on the stridulatory file. This expands the known hosts of *R. nearcticum* into a new subfamily of crickets (Gryllidae: Trigonidiinae) and provides evidence that these wasps are generalist parasitoids rather than specialists.

10 - Linking males, females, and nymphs of *Perlesta* species (Plecoptera: Perlidae) in Mississippi using DNA barcoding

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Thirty-two species of Nearctic *Perlesta* (Plecoptera: Perlidae) have been described in addition to two putative species described from China. For over one hundred years, these small, brown stoneflies with yellow wing margins and variable head coloration were recognized as a single species, the type species of the genus, *Perlesta placida*. Several additional, overlooked, and obscure species have been described, but because of their similarities and presumably close relationships, they have often been referred to as the *Perlesta placida* complex. These new species were diagnosed/recognized based on male structures (genitalia, paraprocts), egg stalk collars, and female sub genital plates, but many of the nymphs are poorly known and similar morphologically. Although species have been described and delimited using morphological characteristics, two gaps in our knowledge of *Perlesta* can be addressed through use of DNA sequence data: (1) linking nymphs to adults through DNA barcoding using nuclear S16 and mitochondrial COI regions and possibly finding diagnostic morphological features and (2) elucidating phylogenetic relationships of the species following heuristic and Bayesian procedures. This study seeks to address these issues in Mississippi, where two of the

three known species are not represented by molecular data. Filling in the molecular gaps with DNA barcoding will enrich the GenBank database, aid in better understanding of *Perlesta*, and facilitate the identification of unknown stoneflies for future studies and conservation efforts.

11 - Using Embryos of *Xenopus laevis* to Determine the Potential Developmental Effects of Thyroxin

Britney Barker, Kayla Clark, Kabita Kunwar, James Rayburn

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Levo-Thyroxine is the synthetically manufactured medical grade form of one of the two hormones produced by the Thyroid Gland. Thyroxin's main function in the body is to regulate the rate of metabolism, digestion, brain development and bone maintenance, as well as heart and muscle function. There are many indications that excess levels of Thyroxin can cause many cardiac related illnesses, however there are many of these pathways that are still unknown. For this research a teratogenicity assay was conducted with Thyroxin in FETAX solution using *Xenopus laevis* as the model organism. Each developmental toxicity test was conducted for a total of 96 hours, using plastic petri dishes of 10-20 carefully selected embryos in 8 mL of treatment solutions at differing concentrations, each changed at 24-hour intervals. The data from each day of the tests were recorded and statistically interpreted to determine an LC50 and EC50 for each experimental run. The results from two experiments yielded different results possibility due to the age of the thyroxine used. One experiment yielded results that indicated an increase in malformations at low levels of thyroxine including potential effects on cardiac development.

12 - Evidence of non-strike induced chemosensory searching by eastern copperheads (*Agkistrodon contortrix*) during cicada predation

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New evidence of active foraging by eastern copperheads, *Agkistrodon contortrix*, contradicts its description as an envenomation-reliant ambush predator. Recent studies on foraging excursions by *A. contortrix* postulated use of non-strike induced chemoreception to track cicada nymphs during seasonal emergences. Lab evidence of non-strike induced chemosensory searching was previously found in a congener, cottonmouths (*A. piscivorus*), but could not be replicated with *A. contortrix*. We hypothesized that *A. contortrix* does actively forage using chemoreception without envenomation, and that tongue flick rates would be higher for foraging behaviors than for non-foraging behaviors. Behavior of twelve *A. contortrix* were filmed at a campsite in Kentucky during foraging excursions in the summer of 2020. Recordings were analyzed for tongue flick rates and presence or absence of seven behavioral activities. Each minute of recording was assigned to a behavioral category (ground movement, climbing, post-consumption movement, pausing, periscoping, eating, and fighting) based off behaviors within the minute and ecological context of the recording. We found statistically significant differences between tongue flick rates of foraging and non-foraging related behaviors, differences among distinct foraging categories, and no differences in tongue flick rate between non-foraging categories. We also compared predatory movement tongue flick rates between successful events of tracking cicadas to unsuccessful attempts and found a significant difference in tongue flick rates. Our results support our hypothesis that elevated tongue flick rates in movement categories appear to be evidence of active chemoreceptive searching without reliance on envenomation cues. Previous studies evaluating this behavior in *A. contortrix* did not find evidence supporting its use. The increase in tongue flick rates for trials encountering a cicada also suggests that chemoreception may be a discriminating factor for tracking cicada prey items. Documentation of wild instances of non-strike induced chemosensory searching is important for ecological context and laboratory replication.

13 - Using Embryos from The Frog *Xenopus laevis* to Evaluate the Teratogenic Potential of Bupivacaine Hydrochloride

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Local anesthetics are used to anesthetize a specific area of the body during or after a procedure to minimize discomfort. Amino-amide anesthetics like lidocaine or septocaine are commonly used in the dental field for procedures and Bupivacaine HCl is a next generation local anesthetic. With seemingly limited analysis on Bupivacaine HCl's teratogenic potential, the teratogenic hazard was evaluated using the Frog Embryo Teratogenesis Assay-Xenopus (FETAX). In this assay, early stage South African clawed frog, *Xenopus laevis*, embryos were exposed to different concentrations of Bupivacaine HCl for 4 days from small cell blastula to a free living tadpole. The experimental unit consisted of plastic Petri dishes containing 20 embryos in 8 mls of test solution. There were 4 controls and 2 replicates for each concentration being evaluated. At the end of each 24 hour period, dead embryos were removed and solutions were renewed. After 4 days mortality, malformations, and embryo length were recorded. To calculate the teratogenic potential of Bupivacaine HCl the 96-hr LC50 was divided by the 96-hr EC50. The 96-hr LC50 was approximately 70 and the 96-hr EC50 was approximately 10 yielding a teratogenic potential of Bupivacaine HCl of about 7. These results indicate that Bupivacaine HCl would cause an increase risk of developmental anomalies

14 - Differences in morphology and in composition and release of parotoid gland secretion in introduced cane toads (*Rhinella marina*) from established populations in Florida, USA

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Cane toads are highly toxic bufonids invasive in several locations throughout the world. Although physiological changes and effects on native predators for Australian populations have been well documented, Florida populations have received little attention. Cane toads were collected from populations spanning the invaded range in Florida to assess relative toxicity, through measuring morphological changes to parotoid glands, likelihood of secretion, and the marinobufagenin (MBG) content of secretion. We found that residual body indices increased in individuals from higher latitude populations, and relative parotoid gland size increased with increasing toad size. There was no effect of latitude on the allometric relationship between gland size and toad size. We observed an increase in likelihood of secretion by cane toads in the field with increasing latitude. Individuals from southern and northern populations did not vary significantly in the quantity of MBG contained in their secretion. Laboratory-acclimated cane toads receiving injections of epinephrine were more likely to secrete poison with increasing dose, although there was no difference in likelihood of secretion between southern and northern populations. This suggests that differences between populations in the quantities of epinephrine released in the field, due to altered hypothalamic sensitivity upon disturbance, may be responsible for the latitudinal effects on poison secretion. Our results suggest that altered pressures from northward establishment in Florida have affected sympathetic sensitivity and defensive mechanisms of cane toads, potentially affecting risk to native predators.

15 - Role of Interspecific Competition in Spatial Distribution of Two Montane Salamanders

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Biotic interactions such as competition between organisms play an important role in how many species are distributed across landscapes. With recent changes in local climatic conditions, certain species that were previously restricted by abiotic factors have the potential to expand into previously unoccupied areas. These expansions thus give rise to new potential biotic interactions between species that were previously isolated ecologically. For salamanders of the genus *Plethodon*, abiotic factors (e.g. annual rainfall or temperature) play critical roles by directly affecting distribution but also indirectly restrict spatial distributions of species via competitive interactions. Recent research suggests that species in both foothill (*Plethodon yonahlossee*) and montane regions (*Plethodon montanus*) have started expanding to elevations previously unoccupied. To better understand how biotic interactions could shape *Plethodon* communities, we measured performance as change in body condition between inter- versus intraspecific pairings of two salamander species (*Plethodon yonahlossee* & *Plethodon montanus*) in a mesocosm based experiment. We found that the type of competition, whether inter- or intraspecific, resulted in reduction of body condition indiscriminate of species. Our results indicate that biotic interactions between Plethodontid salamanders could play an important role in structuring these novel salamander communities. With future climate conditions becoming less favorable for many species of Plethodontid salamanders, understanding the role of biotic interactions will become increasingly important in predicting salamander persistence.

16 - Harnessing Citizen Science to Address Data Deficiency in Understudied Herpetofauna: Lessons from the Mountain Chorus Frog (*Pseudacris brachyphona*)

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Data deficiency in herpetofaunal conservation is often driven by an abundance of private lands that are inaccessible to traditional surveys, precluding adequate assessments of the conservation status of individual taxa. Citizen science approaches are one avenue that may allow researchers to circumvent landownership issues, although little information exists to date to test such approaches' efficacy, especially when applied to secretive taxa. We used a citizen science initiative to address data deficiency in the Mountain Chorus Frog (*Pseudacris brachyphona*) across an area composed primarily of privately-owned lands in the southern Cumberland Mountains ecoregion. We trained more than 500 citizen observers in performing auditory surveys for this species during 2018 and 2019. Those observers increased the number of known localities of Mountain Chorus Frogs in our study area from 14 to nearly 50 within a single breeding season. We found that breeding habitats for Mountain Chorus Frogs across our study region are primarily pools that are not included in state and federal wetlands inventories, being significantly smaller and more isolated than sites identified in remotely-sensed datasets. These results indicate that data deficiency in this species may be driven in part by breeding habitats that are difficult to remotely identify, many of which occur on private lands and do not meet regulatory thresholds designed to protect wetland habitats. More broadly, our results underscore that citizen science approaches can both enhance the natural history knowledge of understudied amphibian taxa and highlight gaps in conservation policy.

17 - Anuran Breeding in a Small-Town Urban Environment in Northeastern Alabama

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Alabama is geographically and physiographically diverse. The physical variety lends itself to increasing biodiversity. Alabama has the highest biodiversity for states east of the Mississippi River (Duncan 2013). Herpetologically speaking, the state is influenced by the Appalachian Mountains in the NE and the coastal plain to the south. Jacksonville is nestled along the western slopes of the Appalachian Mountains in the Ridge and Valley Province. The Anuran community reflects both these influences as they meet in Jacksonville. The city was divided into 4 quadrats: NE, SE, SW, NW. City streets were driven between dusk and midnight 3-5 times per week over a 2- year period. Ten species representing 4 Families of anurans were observed across the city over that period. Hylid frogs and Ranids dominate the communities. One species, *Hyla chrysoscelis*, was spread nearly evenly across the city. *Anaxyrus americanus* was also broadly spread, but it had a patchier dispersion. Ranids were restricted to a few permanent ponds in the southeastern quadrat. Only one specimen of *Scaphiopus* was found. This species is secretive and

patchy at best. Only one other site for *Scaphiopus* has been recorded in town: both sites were in the NE quadrat. Breeding phenology was compared across years. Patterns varied annually and correlated with rainfall patterns.

18 - Digitizing the Regional Herbarium at Raven Rock State Park (RARO) in Central NC

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Raven Rock State Park is located in Harnett County, North Carolina. The park is home to a small herbarium containing 305 samples of the park's diverse array of flora. Prior to this work, the herbarium had no official records of which plants were represented by its specimens. During the summer of 2019, the herbarium was registered in Index Herbariorum with the code RARO. In August, the specimens were digitized by students and faculty at Campbell University using a digitization rig that was brought down by North Carolina State University faculty. Following the digitization, the specimens were uploaded to the Southeast Regional Network of Expertise and Collections (SERNEC) website, where the label data for each of the specimens were transcribed throughout fall 2019. The herbarium was found to represent over 30 percent of the species that were documented within the park in the official Vascular Plant Checklist for Raven Rock State Park. The majority of the specimens within the park's herbarium were collected from 1980 to 1995 by Paul Hart and Mary Stevens. The presence of this small herbarium serves as an important site of regional vouchers for different species found within the park. Digitizing the herbarium allows the information that has been stored within the park for many years to be shared with the public on a much larger scale.

19 - Predictive niche modeling for the identification of maize pathogens of greatest concern in the US

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Maize is one of the world's most valuable food crops with 717 million metric tons produced annually. Its economic significance worldwide is second only to rice. Given the importance of maize, it is crucial to understand the potential range of pests and pathogens that pose a significant risk to the crop. Ecological niche modeling is used to identify the environmental requirements of these pests and pathogens. Models can be built using existing occurrence data and records of environmental conditions such as vegetative coverage, isothermality, altitude, temperature, and precipitation. In this study, we use pest occurrence location data from the Global Biodiversity Information Facility and bioclimatic variables from WorldClim to create maximum entropy (MaxENT) models and boosted regression trees (BRT) to predict suitable habitat for maize pests and pathogens in the US. Distribution models were made of insect pests of highest concern, including Lepidopterans *Autographa gamma*, *Chilo partellus*, *Helicoverpa armigera*, *Spodoptera litura*, and *Thaumatotibia leucotreta*, Coleopterans *Diabrotica speciosa* and *Heteromychus arator*, and the Hemipteran *Laodelphax striatellus*. Each of these sixteen models were then used to make maps of the potential geographical range that highlights areas that would be most suitable to the greatest number of pests. Coastal areas are susceptible to most maize pests and these maps convey the levels of risk associated with land in close proximity to an ocean. These maps can be used to efficiently direct preventative action to high-risk areas.

20 - What's a Town to Dune: Can Vegetation be Used to Determine the Success of a Constructed Coastal Sand Dune?

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Anthropogenic climate change affects coastal communities around the world, including in coastal Georgia. To combat eroding beaches, Tybee Island, GA constructed large-scale dunes along its beaches, and we conducted a study to evaluate the results of four different planting treatments, focusing on the most effective revegetation methods for sand accumulation. The objective of this study was to assess how well this dune project restored ecological function to Georgia's most visited beach.

We established two planting assemblages in high and low densities across the newly constructed dune. Assemblage 1 applied the planting design created by Tybee, and Assemblage 2 mimicked conditions in pre-existing Tybee dunes, taking into account functional roles of each species. Treatments were compared with each other (4 treatments, each n=6), unvegetated sites on the constructed dune (n=3), and a pre-existing dune (n=6) to establish best practices supporting plant growth and sand accumulation.

Five months after installation, 95% of plants survived, including 99% of large plants (individuals ≥ 10 cm² at planting) and 94% of small plants (<10 cm²). Plants in high density sites were half as likely to suffer mortality as those in low density sites. Canopy cover of small plants increased to almost 5 times their original measure over 3 months, but cover of large plants stayed nearly the same. Bare sites experienced 0.2 ± 0.5 cm of erosion over the 7-month study while the vegetated sites accumulated 3.2 ± 0.2 cm of sand.

Results suggest that vegetation is surviving well and that sand accumulation on vegetated dunes is on par with pre-existing dune sites, but we do not yet have evidence to suggest that planting density or species influences sand accumulation. Data collection will continue through summer 2021, and our findings will advise best practices for planting and monitoring coastal sand dune restoration sites.

21 - Is the interdune grassland swale an optimal habitat for woody encroachment on Hog Island, Virginia?

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Woody plant encroachment into grasslands has rapidly increased worldwide. On barrier islands woody plant encroachment into grasslands can have severe implications on island migration when disturbance reinforcing species (e.g. grasses) are replaced by disturbance resisting species (e.g. shrubs). On Hog Island, Virginia, the expansion of *M. cerifera* has been most acute with a 40% increase in approximately 30 years. *Morella cerifera* adults have a positive impact on their own establishment, while precluding the establishment of other species. Relatively little is known about the establishment of *M. cerifera*. The extent to which abiotic (i.e. light availability, soil characteristics, dune elevation) and biotic (i.e. proximity to adult shrubs, grass density, height and biomass) factors contribute to the success of *M. cerifera* at early stages of development still needs to be examined. The objective of this study was to determine the optimal habitat where abiotic and biotic conditions favor the establishment of *M. cerifera* into grasslands.

Morella cerifera seedlings were identified within distinct communities on the southern end of Hog Island (i.e. edge of shrub thicket, grassy swale, dry grassland, and bare). Along this range 10 cm x 10 cm paired grass only and shrub seedling/grass plots were delineated. Abiotic and biotic factors were quantified by measurements of grass biomass and density, seedling and soil characteristics, and dune elevation. Seedlings were found predominately in areas of relatively low grass density and a narrow dune elevation of approximately 1.5m. Positive correlations were detected between soil organic matter and seedling height, as well as between grass biomass and seedling height. These findings demonstrate that seedlings are favored in interdune grassland swales. Grass density and dune elevation strongly impact the spatial distribution of shrub encroachment on Hog Island. The increase in the spatial distribution of *M. cerifera* could have detrimental consequences for Virginia Barrier Islands.

22 - Understanding the role of Heparan Sulfate Proteoglycan (Hspg2) in brain and behavioral development.

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Heparan Sulfate Proteoglycan 2 (Hspg2) is a highly conserved gene that expresses Perlecan, an extracellular matrix protein implicated in the development of the heart, bones and muscles. Genetic mutations in the human Hspg2 gene are linked to musculoskeletal developmental defects resulting in kyphosis, muscle abnormalities, blepharospasms and joint contractures. Hspg2 gene expression analysis during early embryonic development reveals that the gene is strongly expressed in the developing nervous systems, but its role in the nervous system has not been studied. Zebrafish (*Danio rerio*) offers an ideal vertebrate model organism to understand the role of Hspg2 in early neural development. Hspg2 is expressed in the developing zebrafish brain especially in the retinal ganglions, midbrain and hindbrain regions. Extracellular matrix protein molecules are known to be important in neurovascular and neurocircuit development during the early brain assembly. Preliminary studies have identified that mutations in the Hspg2 gene in zebrafish embryos results in hemorrhaging events within the brain, which would be indicative of defective neurovascular formations. However, the locations and cellular phenotypic defects of these brain blood vessels are yet to be described. Our first hypothesis infers that Hspg2 is required for neurovascular formations during zebrafish brain development, and our second hypothesis states that Hspg2 is required for retinal neuron, circuit and light response behavior development. In order to carry out the experiment, we would need to stain, image and analyze the blood vessels and blood cells in the zebrafish larval brain and cells in the zebrafish retina at different points of development.

23 - TbVps41 regulates trafficking of endocytic cargo to lysosomes of bloodstream forms of *Trypanosoma brucei*

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Trypanosoma brucei is a protist parasite and the causative agent of African sleeping sickness. The parasite life cycle can be simply partitioned into an insect stage and a mammalian stage. The mammalian life cycle stage of the parasite is characterized by its high rate of endocytosis, which is involved in remodeling of its surface coat and parasite survival. Here, using RNAi mediated downregulation, we characterize the role of a TbVps41 protein, a component of the homotypic fusion and vacuole protein sorting (HOPS) complex in the parasite endocytic pathway. Using immunofluorescence microscopy, western blotting and electron microscopy, we present evidence that downregulation of TbVps41, leads to a strong inhibition of endocytosis, vesicle accumulation, enlargement of the flagellar pocket ("big eye" phenotype), and dramatic effect on cell growth. Interestingly, other functions described for Vps41 in mammalian cells and yeasts, such as delivery of proteins to lysosomes, and lysosome-related organelles (acidocalcisomes) were unaffected, indicating that in trypanosomes post-Golgi trafficking is distinct from that of mammalian cells and yeasts. The essentiality of TbVPS41 suggests that it is a potential drug target. Our current and future experiments are aimed towards characterizing the remaining components of this HOPS complex in *Trypanosoma brucei* and other trypanosomatid parasites.

24 - Optimization of a Tamoxifen-Inducible Mouse Model for Studying Glioblastoma

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Glioblastoma (GBM) is a malignant brain cancer that results in patient death within two years following diagnosis. The GBM tumor microenvironment has an important impact on the formation, progression, and drug resistance of this lethal disease. The GBM tumor microenvironment is composed of a variety of cell types that can support tumor growth like microglia. Microglia can switch from a classical, tumoricidal M1 state to an alternative, tumor-promoting M2 state, which encourages tumor growth. However, there are limited studies about the specific effect(s) that microglia have on GBM, thus requiring further research into how these cells affect GBM tumors. Given the importance of the tumor microenvironment to GBM aggressiveness, targeting key signaling pathways in tumor associated cells that are involved in sustaining GBM tumors could be an effective way to reduce tumor progression. One signaling pathway implicated in causing

different cancers involves the nuclear factor-kappa B (NF- κ B) pathway, which has been implicated in M1 to M2 phenotype polarization. Therefore, this study focuses on characterization of a p65^{fl/fl}/CX₃CR1^{creER/+} mouse model, which is an inducible mouse model for studying how inhibition of canonical NF- κ B signaling in microglia affects GBM tumors. After tamoxifen administration, p65, a transcription factor of the canonical NF- κ B pathway, should be deleted in microglia due to the CX₃CR1 promoter. Once tamoxifen binds to the estrogen receptor, cre recombinase will recombine the floxed p65 gene in microglia. Characterization of this particular mouse model is necessary to determine if p65 is effectively deleted in microglia. Preliminary flow cytometry data suggests that p65 deletion in microglia occurred in p65^{fl/fl}/CX₃CR1^{creER/+} mice that received GBM implantations and tamoxifen treatment compared to a vehicle control group. There may be a sex difference in the extent of microglial p65 deletion when comparing the tamoxifen-treated mice to the vehicle control mice, which is still being investigated.

25 - Humanized-zebrafish tumor xenograft identifies critical role for the cell adhesion molecule Integrin alpha 6 (ITGA6) during cancer metastasis

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Present day cancer incidence and mortality rates indicate the need for effective cancer diagnostic tools and targeted cancer therapeutic strategies. Recent studies have focused on the biological pathways of cells and tumor microenvironments to identify putative biomarkers and potential drug targets as diagnostic and therapeutic tools. Human integrins, adhesion receptors, have become the focal points in these studies, specifically Integrin Alpha 6 (ITGA6) which has been implicated in major tumor progression roles: metastasis and angiogenesis. These characteristics make ITGA6 an excellent candidate for potential drug or diagnostic target, however, the mechanism by which ITGA6 facilitates tumor progression remains unclear. Cell culture studies have indicated ITGA6 could be cleaved extracellularly to increase metastasis but, zebrafish with organismal structures and vascular network, present a complete *in vivo* model to track metastasis. Our previous studies indicate that truncated ITGA6 overexpression significantly upregulates tumor metastasis compared to full-length ITGA6 overexpression. Similarly, mutated ITGA6 significantly decreases tumor metastasis. These results suggest that cleaved ITGA6 increases tumor metastasis, potentially aiding in extracellular matrix remodeling. In this study, we aim to identify the cellular role of ITGA6 by transplanting ITGA6 siRNA and DNA transfected PC3 cells into zebrafish tumor xenografts. We anticipate these experiments will help establish the cell and non-cell autonomous roles of ITGA6 during tumor development. Further, we expect to use high-resolution imaging techniques to track the migration of single cancer cells in an *in vivo* system to understand the dynamics of metastasis.

26 - “Winners” among flow mediated interspecific interactions of headwater stream vertebrates

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Due to anthropogenic induced stressors, many ecosystems worldwide are experiencing physical and biological alterations such as increased thermal pollution, increased flashiness of high flow events, and a decrease in stream vertebrate populations in some cases. Among these affected ecosystems are headwater streams which are experiencing more variability in flow and water duration. Competitive interactions among headwater stream vertebrates, such as fish and amphibians, can be influenced by these changes in the surrounding environment. Our study used artificial stream mesocosms to investigate the interactive effects of flow variability and interspecific interactions of two common, headwater stream vertebrates; black-bellied salamanders (*Desmognathus quadramaculatus*) and common creek chubs (*Semotilus atromaculatus*). Individual animals were either paired with a conspecific or heterospecific (e.g. salamander or creek chub). We crossed pairings with one of three flow treatments: (1) high variability, (2) low variability, or (3) no variability. *A posteriori*, salamanders with an increase or the lowest decrease in body condition in the presence of conspecifics were deemed “winners” while “losers” were those with the most decrease in body condition. Our results indicate that flow variability had no statistically significant effect on intraspecific or interspecific competition. However, there was a statistically significant effect of interspecific competition as salamanders decreased in body condition in the presence of creek chubs. Our findings suggest that these two common species have potentially adapted to experiencing variability in flow in their natural environment. Additionally, our results reinforce previous findings that creek chubs could play a role in the distribution of stream salamanders.

27 - Gene Flow Across a Continental Divide

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The Eastern Sub-Continental Divide separates bodies of water in Georgia, leading them east to the Atlantic Ocean, or west to the Gulf of Mexico. This study seeks to answer the question of if/how the continental divide affects gene flow within aquatic species. Since the continental divide separates rivers, our hypothesis is that it would also draw a barrier between fish populations. A paired samples design was used to sample fish from headwater streams in the Chattahoochee and Ocmulgee River watersheds. After collection, tissue samples were assessed via PCR (using mitochondrial and nuclear genes), sequencing, and phylogenetic analysis. The main fish species found in these streams belong to genera *Semotilus*, *Nocomis*, *Notropis*, and *Camptostoma*; all in the family Cyprinidae. Initial results of select gene regions have given some support to the continental divide gene flow hypothesis. However, a mito-nuclear incongruence has been observed in the phylogenetic analyses. Mitochondrial phylogenetic patterns for *Nocomis leptoccephalus* (Bluehead chub) suggest that gene flow within the Chattahoochee watershed may be more limited than between watersheds across the divide.

28 - The influence of environmental parameters on the growth of *Thalassia testudinum* in a field setting

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The seagrass *Thalassia testudinum* is ecologically valuable serving as habitat and food for many organisms. There has been a documented decline in seagrass communities over the past decades and aspects of climate change are predicted to negatively impact seagrass growth. This study sought to understand how environmental variables influence *T. testudinum* communities in Jobos Bay, Puerto Rico. Forty 1 m² quadrats within transects in Jobos Bay were sampled. For each quadrat, percent cover (Braun-Blanquet (BB) score), density, and blade length of *T. testudinum* were recorded along with environmental parameters (depth, temperature, pH, DO, turbidity, and salinity). Additionally, growth rates of *T. testudinum* plants were measured within 12 (25 cm²) quadrats placed at different locations (less turbid and more turbid) and depths (1m and 2m). A Principle Component Analysis (PCA) characterized variation in environmental parameters and community structure for each quadrat. The PCA scores, along with site location and season were used to develop models to predict *T. testudinum*, BB score, blade length and density. The best explanatory models for predicting BB scores included depth, community structure, and location. As depth increased there was a marked decrease in BB score. The best performing models for blade length included the interaction between location and seagrass community structure, with length increasing as the prominence of the invasive seagrass, *Halophila stipulaceae*, increased. The global model (all variables included) was best at modeling density. For the growth study an ANOVA indicated significant differences in growth rate for depth and a significant interaction between location and depth. At the clearer location growth rates were greatest at 2 m but for the turbid location greater at 1 m. This research depicts the importance of understanding location variability on assessing the health and vitality of *T. testudinum* beds when considering estuary conservation strategies and seagrass loss mitigation.

29 - Stream Impoundment Impacts the Life History Traits of Bluegill (*Lepomis macrochirus*)

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Human alterations on natural habitats create selective pressures that can lead to evolutionary change. Stream impoundment causes stream ecosystems to rapidly transform into lentic environments, creating novel selection pressures on the resident fish. Life history traits, such as gonad mass and size at maturity, are often sensitive to changes in environmental conditions. To better understand how natural populations respond to stream impoundment, we measured whether gonad mass and size at maturity in Bluegill were different between reservoirs and streams. Overall, males from streams had larger gonads and matured at a larger size than males from reservoirs. In contrast, gonad mass and size at maturity of females did not differ between habitats. The sex-bias and direction of the differences are consistent with the divergence between lake and stream life histories being attributed to sexual selection as opposed to predation pressure. These results illustrate the potential for a widespread human impact, such as stream impoundment, to alter the phenotypes of fish populations living in these ecosystems.

30 - Interactive Effects of Puma Activity and Habitat Characteristic on Mesocarnivore Diversity

Zach Buddie, Travis Perry

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We investigated the relationship between puma activity and mesocarnivore diversity, as measured by Simpson's diversity index, and whether or not habitat characteristics modify this relationship. Our study area is located in the eastern foothills of the Black Range, bordering the eastern edge of the Aldo Leopold Wilderness, in Sierra County, New Mexico. Photo data were collected, uninterrupted, from 2008 to 2019, from twenty-five remote cameras distributed over 100 km² at a density of 1 camera per 4 Km². Camera locations remained constant over the study period. Puma activity was measured by photo rate and the mesocarnivore diversity was calculated from photo rates as well, essentially providing an index of "diversity of activity". Habitat characteristics associated with remote camera sites were obtained from raster files in ArcGIS. We used quantile regression analysis in R using package qgam and qu set to 0.7. Mesocarnivores recorded in the study area included coyote (*Canis latrans*), bobcat (*Lynx rufus*), gray fox (*Urocyon cinereoargenteus*), ringtail (*Bassariscus astutus*), and badger (*Taxidea taxus*). Puma activity was a significant driver of mesocarnivore diversity ($p < 0.004$). However, this relationship is significantly modified, reversed actually, in riparian habitats ($p < 0.004$). Puma alter the structure of the mesocarnivore community apparently by suppressing coyote and bobcat activity while being positively associated with ringtail activity. There was no significant relationship between puma activity and gray fox activity. It seems that the relationship between puma activity and the mesocarnivore community is different in riparian corridors because coyotes particularly avoid that habitat type in our study area. Our study suggests that removing puma from western ecosystems would have a significant impact on the diversity of the mesocarnivore community.

31 - Effects of Sex and Season on Puma Movement and Predation Rates

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We used GPS collar data from 6 female and 12 male puma (*Puma concolor*) to investigate the effects of sex and seasonality on puma movement and predation rates in southcentral New Mexico. Predation events were identified from GPS collar location data and subsequently investigated on

the ground. We looked at seasonality at two different scales: the two monsoonal climate seasons (six months each) and the traditional 4 temperate seasons (three months each). The two monsoonal seasons were defined as warm-wet (April to September) or cold-dry (October to March). We found significant interactive effects of season and sex on the distances puma traveled, the velocity of their travel, and predation rates. Specifically males traveled further and faster than females and this was most pronounced in the warm-wet season ($t=3.186$; $p=0.001$ and $t=2.931$; $p=0.003$, respectively). Conversely, females killed prey at a faster rate than males and this was most pronounced during the cold-dry season, specifically the winter ($t=-2.51$; $p=0.01$). These relationships are consistent with male puma behavior being driven primarily by access to mates and female puma behavior being driven primarily by the successful rearing of offspring. Our study suggests that female puma may have significantly greater ecological impacts than male puma, given their demonstrably higher predation rates.

32 - Study on the Improved Use of Camera Traps in Wildlife Study

Michael Zarske, Eric Blackwell

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This study used multiple arrangements of motion activated cameras in order to find a more effective deployment method of camera traps. Previous camera studies have had very high false positive rates in photos taken and this study was conducted in hopes to improve the false positive rates of camera studies. Methods tested included paired cameras in vertical and horizontal arrangements. In addition to real paired cameras a dual camera data set was extrapolated to determine if any dual camera set would be more effective than a single camera. Timed camera triggers and various motion sensor sensitivities were tested versus manufacturer default settings. All methods were compared to a baseline taken in the fall of 2019 and to a control camera using manufacturer default settings during this study. A chi-square statistical test was conducted on the results to determine change between control and test sets.

33 - Effects of puma activity, habitat characteristics, and disturbance on coyote activity

Santana Tosi, Travis Perry

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We investigated the relationship between puma and coyote activity and whether this relationship was altered by habitat characteristics or landscape level disturbances. Our study area is located in the eastern foothills of the Black Range, bordering the eastern edge of the Aldo Leopold Wilderness, in Sierra County, New Mexico. Photo data were collected, uninterrupted, from 2008 to 2019, from twenty-five remote cameras distributed over 100 km² at a density of 1 camera per 4 Km². Camera locations remained constant over the study period. Puma and coyote activity was measured by photo rate. Habitat characteristics associated with remote camera sites were obtained from raster files in ArcGIS. In 2013, over 100,000 acres of the Aldo Leopold Wilderness burned in the Silver Fire and provides the landscape level disturbance in our study. We used quantile regression analysis in R using package *qgam* and *qu* set to 0.9 as well as GLM analysis in the R base package. We predicted that coyotes would avoid areas with high puma activity and that this relationship would be more extreme in low visibility habitats. Before the fire, we found that coyote activity decreased significantly with puma activity ($p=0.00352$) and topographic ruggedness ($p=0.00652$), but that there was no significant interactive effect of these predictors. However, after the fire we did find a significant interactive effect of puma activity and topographic ruggedness on coyote activity ($p=0.00169$). The negative relationship between coyote activity and puma activity was increased by topographic ruggedness after the fire. We hypothesize that the fire, adjacent to our study area, created more open habitat for coyotes, allowing them to shun high puma-low visibility habitats with greater frequency. Our study suggests that the relationships between apex predators and individual mesocarnivore species is habitat specific and that disturbance may play a pivotal role in these relationships.

34 - Experimentally comparing the effects of random habitat loss and homogenizing habitat loss on species richness and effective number of species

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Habitat loss is increasing around the world due to urbanization, climate change, and other land-use change. Habitat loss has been shown to negatively impact species richness and other forms of biodiversity. While many predictions of the effects of habitat loss assume random removal of a certain percentage of habitat, land use change or climate change more frequently results in selective habitat loss such that the remaining habitat is homogenized. Understanding how habitat homogenization affects species diversity will allow us to better predict, and thus mitigate, the effects of habitat loss. We experimentally compare the effects of homogenizing habitat loss and random habitat loss on biodiversity. Our experimental design consisted of 45 mesocosms containing a variety of plant species, each assigned to one of three treatments: control (no habitat loss), homogenization (homogenizing habitat loss) and random (random habitat loss). After implementing the treatments, we exhaustively sampled arthropods on each plant in the mesocosms. We found that homogenizing habitat loss causes a decrease in species richness compared to random loss. Effective number of species, however, (a measure of community diversity that takes number of species and evenness of species distribution into account) remained constant between homogenizing loss and random loss. We conclude that homogenizing habitat loss results in more species loss than random habitat loss, but does not affect relative numbers of individuals of each species within the community.

35 - Hard Mast Production: Collaborations to Standardize Regional Indexing Protocols and Forecast Potential Production Using Forest Inventory

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Acorns are important as wildlife food and for oak regeneration. Highly variable acorn production challenges forest managers in gauging crop sizes or estimating yield. Until recently, use of different indexing methods confounded crop comparisons among states. Collaborations between State Agency biologists and US Forest Service researchers lead to a 'toolkit' of methods to simplify and standardize indexing, and tailor acorn production estimates to landscapes. We developed a simple, rapid method to index acorn crop size using visual estimates of the proportion of trees bearing acorns (PBAV) as the independent variable. This replaced labor-intensive, time-consuming acorn crop index methods, and was adopted east-wide by state and federal agencies to standardize indexing for comparable results. Subsequently, we developed models using PBAV to estimate the number of acorns produced within specific years and landscapes, rather than rely on indices. We also used long-term data to develop acorn production capability models based on oak tree dbh, predicted crown area, and average number of acorns per unit crown area. Average production estimates can be tailored to specific stands and different forest management scenarios. Models were implemented into the Forest Vegetation Simulator (FVS-ACORN), the Forest Service's framework for growth and yield modeling. Models allow forest managers to compute average acorn production for their stands through time considering oak decline, mortality, regeneration, and growth, and to analyze trade-offs in forest management alternatives.

36 - Defining Louisiana Freshwater Sponge diversity with COX1-R1, COX1-D2 Barcoding: A Database Development Study for Classroom Curriculum

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DNA barcoding of freshwater sponges has proved to be difficult for students due to the limited sequences found in the NCBI database. This difficulty stems from the inconsistent use of primers in the literature and the lack of dissimilarity in the targeted genome. The primers chosen for this study were COX1-R1 and COX1-D2. These target the cytochrome oxidase gene and an extension intron that provides variability to differentiate organisms at the species level. To contribute to the database, 147 freshwater sponge samples were collected in a Louisiana survey. The sponges were initially identified based on their spicule and gemmule morphology using standard light microscopy and SEM. Forward and reverse sequences were aligned using MEGA software to provide sequences to deposit in the database. This study provides reference sequences for the most commonly found freshwater sponges in Louisiana: *E. fluviatilis*, *E. fragilis*, *H. baileyi*, *R. crateriformis*, *R. ryderi*, *S. alba*, *S. lacustris*, *T. horrida*, *T. leidyi* and *T. pennsylvanica*.

37 - Lessons learned through a regional assessment of long-term fire monitoring data from the Southeastern United States.

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Fire is a natural and key disturbance mechanism in terrestrial ecosystems, especially those that are adapted to regular burning. To fully understand the community-level effects of management actions, such as prescribed fire and alterations to forest structure, appropriate measurements of forest metrics via monitoring are required. Monitoring and quantifying forest parameters such as fuel loading, overstory and midstory density, and understory composition are critical activities for land managers, allowing for the assessment of management activities including the effects of prescribed fire on forest communities. Analyzing nearly two decades of prescribed fire monitoring data, we assessed regional patterns in forest parameters after multiple fire events across the Southeastern United States. Utilizing summarization techniques and numerous statistical models, we found that repeated prescribed fire had beneficial effects on forests. Fire reduced surface fuels, increased understory plant communities, reduced overstory in some forest types, and resulted in increased heterogeneity in fire severity with successive burning. Consistent trends in post-fire responses were most evident after a minimum of three fires, illustrating the importance of not only repeated burning, but continued monitoring efforts after each prescribed fire event.

38 - Reevaluating genetic diversity and structure of *Helianthus verticillatus* (Asteraceae) after the discovery of new populations

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Determining the population genetic structure of isolated or fragmented species is of critical importance when planning a suitable conservation strategy. Knowledge of the genetic composition and differentiation among populations of a rare species can aid conservation managers in understanding how, and which, populations to protect of a threatened species. The whorled sunflower, *Helianthus verticillatus* (Asteraceae), is a federally endangered sunflower endemic to the southeastern United States. The distribution of the species comprises four main populations within three states: Alabama, Tennessee, and Georgia. Recently, new populations were discovered in Marshall County, Mississippi and Franklin County, Virginia. Here, we carry out a population genetic study of these new populations using nuclear microsatellite markers and compare those results to the previously known populations of *H. verticillatus*, as well as to other closely related species. Our results show that both of the newly discovered populations, Mississippi and Virginia, represent novel genetic variation, with Mississippi containing the most private alleles out of all populations tested. The Virginia population is genetically similar to the previously known populations but is under the most conservation concern

given the presence of only two unique genetic individuals found within the population. These results indicate these new populations are worthy of protection and conservation efforts given the unique genetic variation they harbor.

39 - Conservation Genetics of *Nabalus serpentarius* and its Common Congener, *Nabalus trifoliolatus* (Asteraceae)

Steven Ballou

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Nabalus serpentarius (Pursh) Hooker is a species of concern to conservation management on the island of Nantucket in Massachusetts where four populations have been recently observed. Funding and personnel may be limited so it is best to understand which populations need the most attention to construct a management plan that effectively protects the species on the island. Nuclear DNA was extracted from leaf tissue collected from *N. serpentarius* and *N. trifoliolatus* (common congener) on the island. Transferability of *Taraxacum* sp. markers was tested with the samples of the two *Nabalus* species and *Nabalus* specific primers were developed from sequence data for *N. serpentarius*. Both sets of primers were used to genotype individuals of both *Nabalus* species collected on Nantucket. *N. serpentarius* shows no reduction in population genetic variation as compared to the common congener, and the two species demonstrate similar and very low levels of population genetic structure. These data indicate that population genetic threats to the rare species are not an immediate concern. However, given the small numbers of populations and the potential for stochastic demographic threats to them, we recommend protection of all populations. Further, the low levels of population genetic structure among populations could indicate transplants from one population to another would be successful though common garden experiments to investigate the potential for local adaptation would be an important next step.

40 - Modeling Piedmont Prairie Species along Powerline Right of Ways in the Eastern Piedmont of Georgia

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Since European colonization, grasslands across the U.S. have become fragmented and scarce. In recent years, grassland restoration efforts have emphasized utility right of ways (ROWs) as conservation targets. Right of ways are typically maintained using a mowing cycle that mimics historic fire regimes. Their ubiquity, connectivity, and management attention make ROWs excellent candidates for conservation. In central Georgia, thousands of ROW hectares are potential habitat for Piedmont prairies, a diminishing grassland of the southeastern U.S. To determine whether powerline ROWs managed by the Georgia Power Company potentially host Piedmont prairies, we used a resource selection function model to predict occurrence of 11 Piedmont prairie indicator species along company ROWs in Georgia's eastern Piedmont. We developed an initial set of models using herbarium records and citizen science data. We analyzed the location data using seven environmental markers including soil texture, land cover, and soil pH to create a resource selection function model. From this model, we selected 50 ROW sites that we visited during the 2020 field season to assess model predictions. We located seven indicator species across 34 sites. These findings were used to validate our model, which had fair selection success with an AUC of 0.759. Of the species identified, little bluestem (*Schizachyrium scoparium*, Poaceae) was the most common (occurred at most sites) and most abundant (total individuals discovered) while Virginia thyme (*Pycnanthemum tenuifolium*, Lamiaceae) was the least common and least abundant. Using the same habitat predictors and our 2020 field data, we will re-run our models to refine site selection for the 2021 field season.

41 - Leveraging statistical analyses and focused expertise for the assignment of botanical coefficients of conservatism values in Tennessee and Kentucky

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Floristic quality assessments (FQA) are a recognized technique used to create an objective quality assessment of a habitat within a site or region. Pertinent to FQAs is the assessment of all or a few keystone species and their nativity to a location, which are often determined through a coefficient of conservatism value (C-value) assigned by a committee of botanists who are knowledgeable with the floristics of the location. C-values are commonly used to quantify conservational need and ecological tolerance within plant species, by ranking species from 0 to 10 based on their affinity to non-human altered habitat within the same site/region. Despite the assignment of C-values growing among many states and regions, as well as their usefulness in techniques such as FQAs, a comprehensive dataset of C-values has not been created for Tennessee and Kentucky. Due to the large, concerted, and coordinated manual effort needed to assign values for each individual species, two methodologies were developed in order to optimize workflow: (1) statistical estimation methodologies were employed for initial C-value estimation within ~75% of all TN-KY species; and (2) a cost-free, open-source assessment & submission platform was developed to aid to experts for final value assignment. We present the analysis of 48 different publicly-available data sets on C-values from different regions to infer estimated initial values for TN and KY, the pitfalls of these estimated values, and the creation of an online platform to collect and assess expert-submitted C-values. Through this work, we hope to present an alternative, more efficient means to collect C-values for easily assignable species within large regions using readily-available information and technologies.

42 - Crowd Mapping: Modeling Species Distributions with Citizen Scientists

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A fundamental goal of conservation is to be able to determine what organisms are extant and, of those extant organisms, predicting where they could occur. Conservationists have traditionally relied on long hours in the field meticulously tracking and recording individuals of species and cross-referencing ecosystem and topology maps to determine new locations for said species. This project sought to speed up the process of modeling species distribution by evaluating the use of a species monitoring app (i.e. iNaturalist©) as a stand in for systematic data gathering by trained researchers. iNaturalist allows untrained individuals to capture images, GPS coordinates, identification, and traits of species and upload the observation to a machine learning database. This study used the software packages QGISv3.1 and MaxEnt to create species distribution models for flowering vascular plants of known ranges and varying ranges of rarity using data only obtained by citizens using the iNaturalist app and bio-climatic maps for the contiguous United States. This study found that data collected from citizens can be used to create accurate species distribution models for plants with large distributions and non-rare statuses. Models created for plants with limited data due to fundamental problems associated with citizen science projects were unreliable or lacked strong support. Citizen science projects are a valuable tool for conservationist to model species distributions within a given range and should be implemented whenever possible. Citizen science projects should also be used in conjunction with more systematic approaches to accurately model the distributions of rarer species. Citizen science apps should be further developed and refined for the purposes of creating species distribution models by implementing strategies suggested by the author.

43 - Assessing the clonal nature of running glade clover (*Trifolium calcaricum*; Fabaceae)

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Trifolium calcaricum, the running glade clover, is one of many uncommon species that are endemic to cedar glades. These rare ecosystems have become increasingly threatened by habitat destruction and fragmentation, which in turn increases extinction risk and decreases genetic diversity within populations. As a result, *T. calcaricum* has been listed as endangered by the states of Tennessee and Virginia. In a conservation project that aimed to preserve *T. calcaricum*, individual plants were relocated from a source site to a secondary location at a Tennessee State Park by a local Tennessee conservationist in 2016. Although the reintroduction project focused on increasing the number of *T. calcaricum* in the field, genetic information was not taken into account when establishing the conservation project. Due to the fact that genetic information, life history characteristics, and habitat requirements are not always available for species with limited protections and funding, baseline studies are more important than ever in the field of conservation science. In the current project, transplanted individuals from the 2016 reintroduction project were assessed to determine the extent of clonality using inter-simple-sequence-repeat (ISSR) markers. Samples were revealed to be moderately clonal, with 46 sampled ramets yielding 14 unique genets. The physical distribution of the largest genet was determined to be approximately 100 meters across. This work provides important baseline information for future studies about a rare and understudied species.

44 - Tennessee-Kentucky Plant Atlas: an online, comprehensive resource for 3600 vascular plant species

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The digitization of herbarium specimens in Tennessee and Kentucky began in 2014 with the National Science Foundation award to the SouthEast Regional Network of Expertise and Collections (SERNEC) entitled: The Key to the Cabinets... (NSF DBI #1410069). Over a five-year period, nearly one million specimens from all herbaria in these states were digitized. Specimen images were taken and at least six fields databased: scientific name, country, state, county, herbarium, and catalog number. Prior to this digitization effort, our understanding of species distributions in Tennessee and Kentucky was based on fewer than half of the specimens available and only those held in the largest herbaria (with one of these, Vanderbilt University having been moved to the Botanic Research Institute of Texas). After nearly the entirety of specimens were digitized, and with funding from the Tennessee Native Plant Society and Kentucky State Nature Preserves Commission, we created a new, two-state atlas within the Plant Atlas family (plantatlas.org). The Tennessee-Kentucky Plant Atlas (<https://tennessee-kentucky.plantatlas.usf.edu/>) produces an atlas map laid over level three and four ecoregions for each of the 3,596 species based on over 300,000 herbarium specimens housed in all Tennessee and Kentucky herbaria. It also includes over 16,000 non-herbarium specimen images of the species from habit shots to magnified dissections. An Advanced Search feature allows users to search the flora for conservation characteristics (e.g., nativity, invasiveness, rarity, wetland status), ecological characters (e.g., phenology, region of origin, moisture requirement, soil characteristics), morphological characters (e.g., habit, duration, phyllotaxis, leaf duration, leaf complexity, flower color), reproductive characters (e.g., flower color, petal number, ovary position), and geographic features. Approximately 50 separate fields may be used to search or sort the 3,596 species. The TN-KY Plant Atlas was developed to be a comprehensive resource for plant enthusiasts, hobbyists, professionals, conservation workers, researchers, teachers, and students of all levels.

45 - Comparative Polymer Composition of Sequential Cell Walls During Motile Gamete Development in Early Land Plants

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Spermatogenesis in land plants with motile gametes (bryophytes and pteridophytes) involves a series of unique morphogenetic changes that profoundly transform the shape, position and internal structure of every organelle. The result is a coiled, streamlined male gamete with minimal cytoplasm and a locomotory apparatus designed to propel the cell toward the female and through the narrow confines of the archegonial neck. Key to this process is the production of a series of four or five unique cell walls that are integral to gamete maturation. While common wall

polysaccharides and callose have been detected during spermatogenesis, very little is known about wall formation and composition during the development of swimming sperm. In this study we compare the polymer distribution in the sequential cell walls that form during male gametogenesis in the fern, *Ceratopteris richardii*, and the mosses, *Physcomitrium* (= *Phycomitrella*) *patens* and *Aulacomnium palustre*. Antheridia at different stages of development were probed using histochemistry in the light and fluorescence microscopes and through immunogold localizations with monoclonal antibodies (MAbs) in the transmission electron microscope. Although the sequence of wall layers produced during spermatogenesis in *P. patens* and *A. palustre* resembles that of *C. richardii*, the wall constituents are remarkably different between the mosses and fern. Most notable is the abundance of hemicelluloses and the absence of callose in the spermatid walls of mosses. Another key finding is that AGPs are abundant in all walls of developing moss spermatids but are only found on the plasma membrane and in the matrix in which gametes reshape and produce flagella in the fern. The results of this study significantly advance our understanding of cell wall composition and dynamics during spermatogenesis in early land plants.

46 - Synthesis and Assembly of Functionalized RNA Nanorings

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Nucleic acids as programmable biomaterials have been designed to form a vast library of nucleic acid nanoparticles (NANPs) which have been demonstrated for broad applications as scaffolds, biosensors, and therapeutics. However, their transition into the clinical setting downstream of therapeutic development has been greatly impeded by their unknown immunostimulatory properties, resulting in adverse side effects. Here, we explore how the designs of hexameric RNA-based nanorings functionalized with therapeutic moieties in various orientations affect immune stimulation and processing in the cell. These therapeutic moieties embedded into the NANP design are Dicer Substrate RNAs which can then be processed for gene knockdown via RNA interference. As a proof of concept, these Dicer Substrate RNAs are designed against green fluorescent protein to explore the efficiency of uptake and silencing in cells. The immune stimulation of various design orientations has been extensively analyzed in human peripheral blood mononuclear cells as well as in reporter cell lines for investigating the link between design parameters of RNA nanoparticles and their immunomodulatory properties. By characterizing patterns in functionalization by immune recognition, NANPs can be optimized for either immunoquiescent delivery or therapeutic adjuvants.

47 - Analyses of cannabidiol and lamotrigine on action potentials of ventral giant fiber in earthworms and the sciatic nerve in frogs

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Cannabidiol causes inhibitory effects on sodium channels, but its action on nerve impulses are not understood. Lamotrigine blocks the nerve impulses, however, it is not known if this action is of extracellular or intracellular origin. With the use of nerve chambers, we are hoping to elucidate this unknown mechanism. We hypothesize that nerve fibers in earthworms may respond differently compared to nerves in frogs. Action potential recording was made possible by the IWork Data Quest system and a nerve chamber. Action potential data was analyzed by looking at two different components—the peaks of depolarization and the difference between the peak of depolarization and the nadir of repolarization. For every fifty minutes of recording, data was divided into three clusters—before chemicals, after 10 minutes of treatment, and thirty minutes after treatment. In frogs, we found the high dosage (1.0 mg/mL) of cannabidiol had no effect on the maximum amplitude of depolarization among the three data clusters—saline, 10-min after cannabidiol, and 30-min after cannabidiol. The high dosage of cannabidiol also had no effect on the repolarization of action potentials when compared among the above three data clusters. In addition, in frogs we found the low dosage (0.1 mg/mL) of cannabidiol showed a significant difference on the maximum amplitude of depolarization when the saline data cluster was compared to the 10-min after cannabidiol cluster. Likewise, there was a significant difference on the repolarization of action potentials when the saline data cluster was compared to the 10-min after cannabidiol cluster and when the 10-min cluster was compared to the 30-min after cannabidiol cluster. Data analyses of lamotrigine on frogs and both chemicals on earthworms are ongoing.

48 - Habitat selection of brooding female eastern wild turkeys

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Resources are located heterogeneously across the landscape, forcing animals to make behavioral tradeoffs and select for patches that best accommodate their energetic and thermoregulatory needs while balancing predation risk. These behavioral tradeoffs manifest as shifts in habitat selection wherein animals change their spatiotemporal use of habitats to meet current and future needs. While some aspects of habitat selection (nest-site, roost-site, etc.) have been extensively studied in wild turkeys (*Meleagris gallopavo*), brood habitat selection is one of the least understood aspects of wild turkey reproductive ecology. Recent research indicates that turkey populations across the southeastern United States are experiencing declines in productivity and recruitment, as evidenced by decreasing poult-to-hen ratios. These declining ratios raise concerns about the availability and composition of quality brooding habitat. Our objective was to evaluate which factors influence brood habitat selection. We quantified arthropod biomass as a measure of forage availability, air temperature as a measure of thermoregulatory stress, and vegetation characteristics as a measure of cover and locomotor hindrance at known locations of brooding and non-brooding female eastern wild turkeys (*M. g. silvestris*) in Georgia and Louisiana, USA during summer 2019-2020. Broods selected sites with greater ground cover vegetation and cooler ambient temperatures than non-brooding females. During daytime, broods selected for sites with greater grass and forb understory vegetation,

greater Orthoptera biomass, and cooler ambient temperatures than random locations. During both daytime and when ground roosting, broods selected for sites with less woody understory vegetation. Collectively, thermal cover, grasshopper availability, and vegetation structure and community all influence brood habitat selection, demonstrating the need for landscape diversity when managing turkeys. Use of cool season disturbance to promote grassy and herbaceous cover in upland systems or chemical/ mechanical removal of understory and midstory woody vegetation may be warranted to increase turkey brood habitat.

49 - Effects of Sea Salt on Frog Embryos, Using the Frog Embryo Teratogenesis Assay: *Xenopus* (FETAX)

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As sea levels rise, salinity will increase into freshwater areas near the coast. Increases in salinity could adversely affect amphibian embryos. Sea salt is produced through the evaporation of ocean water. The chemical composition of the sea salt comprises mostly of sodium chloride and 0.2 to 10% of other salts. It is used as a seasoning in foods, cooking, cosmetics and for preserving foods. This objective of this research was to determine potential developmental effects of sea salts to frog embryos. The effects of the concentration of the sea salt were evaluated using the Frog Embryo Teratogenesis Assay- *Xenopus* (FETAX). The early embryonic stages of South African clawed frog, *Xenopus laevis*, were exposed to the concentrations of the sea salt with FETAX solution for 4 days from small cell blastula to a free-living tadpole. The sea salt was mixed with 20 mL of FETAX solution to make different concentrations of sea salt solution. Five different test solutions were used in sets of plastic petri dishes containing 20 embryos. Two control groups of 4 plastic petri dishes were used, each of 8 mL FETAX solution without sea salt solution. Dead embryos were removed after every 24 hours and solution were renewed. The mortality, malformation and length of tadpole were recorded for all petri dishes at the end of 4 days. The same experiment was repeated three times, and the results were compared individually and combined. The 96-h LC50 ranged from 3.8 to 5.8 ppt. The 96-h EC (malformation)50 ranged from 4.5 to 6.2 PPT. The results show that higher the concentration of the sea salt, the more likely to increase the mortality of the tadpole rather than cause malformation or reduction of embryo growth. These results also indicate that salinities increase to above 3.8 ppt would likely critically impact amphibian reproduction.

50 - The Effect of Nest Size, Placement, and Temperature on Reproductive Success in the Barn Swallow

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In Barn Swallows, coloniality has evolved largely out of necessity due to limited nesting sites. Additionally, Barn Swallows will often reuse nests from the previous and current breeding season, adding new material to the top before nesting. This study was designed to study the effects of coloniality, specifically nest choice, on Barn Swallows' reproductive success. Data was collected during the breeding seasons of colonies at both Warner Park Nature Center (2019) and Equestrian Center (2020) in Nashville, Tennessee. Nests were monitored at least once per week to determine survivorship, and data was collected on nest size, temperature, height, and placement on the building within the colony. We hypothesized 1) high nest temperature would be detrimental due to nestlings unable to regulate temperature, 2) increased height would increase survivorship by lowering predation risk, 3) greater nest density would have a negative effect on reproductive success as risks for predation and disease increased, and 4) small nest cup sizes would decrease number of fledgelings due to size constraints. 2019 results indicated a positive correlation between temperature and number of fledgelings in the first clutch ($R=0.51$) and a negative correlation between temperature and fledgelings in the second clutch ($R=0.33$). A slight negative correlation was also found between nest height and the number of fledgelings ($R=0.13, 0.61$) and nestlings ($R=0.24, 0.53$). Nest distance, visibility, and density did not seem to have an effect. 2020 results show no significant effect of nest cup size. Collectively, this study begins to give insights into the effects that limited nest-site selection may have on survivorship of the Barn Swallow, a significant inquiry for understanding the future of the species.

51 - Multiple functions for multiple signals: the role of sound and vibration in mediating courtship and competition in a Neotropical katydid

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Animals use mating signals to locate potential mates, assess their quality, and compete with other signalers for access to mates. More than one type of signal may be produced during these interactions, and the intended receivers of different signals are not always obvious, particularly when signaling occurs across multiple sensory modalities. For example, male and female Neotropical katydids (*Docidocercus gigliotosi*) duet using vibrational signals (tremulations) prior to mating, and males also produce airborne signals (calls). To determine how each signal type functions in inter- and intrasexual interactions, we quantified behaviors of male and female *D. gigliotosi* during playbacks of both signal types and control stimuli. Playback stimuli were signals from conspecific males, heterospecific males, and silence. We also observed male behavior during playback of female tremulations. Compared to control stimuli, females tremulated and walked more during both calls and male tremulations, and some females located the sources of both these signals. Both sexes tremulated more during playback of tremulations from conspecifics of the opposite sex than those from heterospecifics. Across treatments, males tremulated more in response to signals of the opposite sex than did females, and females walked farther than males. Finally, males called and tremulated more in response to conspecific calls compared with heterospecific male signals or silence, but male responses to male tremulations did not differ across treatments. We conclude that some shared function exists between the two *D. gigliotosi* signal types, as each modality is sufficient for a female to locate a nearby signaling male, and also that males and females can distinguish between calls and tremulations from different species. Additionally, males appear to increase their

signaling effort when competing with a signaling conspecific male. Our findings provide a clearer understanding about how multimodal signaling mediates the complex processes of mate finding and competition for this species.

52 - Small Mammal Community Structure on a North Carolina Old Field Successional Plot

Emmanuela Salecki, Amanda Chunco, Patricia Thomas-Laemont

Elon University, Elon, NC

Old field successional plots of land are an interesting area of study because the diversity of plant and animal life change depending on which period of succession you are studying. While primary succession, such as Mount St. Helens and soils exposed during glacial retreats show the most dramatic changes in biodiversity over time, succession in old farm fields can also bring about a large turnover in biodiversity over a relatively short period of time. Our research focuses specifically on small mammals on old-field successional habitat. We set up a 100 x 90-meter plot with 90 trapping stations arranged at 10m x 10m intervals at Elon University's Loy Farm. Aluminum Sherman Folding Small Mammal Traps were used in order to capture the small mammals. Traps of three sizes (Small, Medium, and Large) were used, with medium traps at every trapping station and small and large traps interspersed throughout the field. Small traps would be either set flush with the ground or elevated on a wooden stake. These traps were placed as such in order to catch field mice, which generally jump or climb. The bait used in the traps was a mixture of creamy peanut butter and horse feed oats wrapped in wax paper into a "kiss" and hung at the back of the trap. On trap days, traps would be opened at approximately 0800 and then subsequently checked for mammals at approximately 1400 the same day. Trap number, weight, length, sex, mating condition, unique individual details, and tag number if present were recorded for each small mammal captured. New captures received an ear tag. The goal of this research was to examine the small mammal community in a secondary successional field in the Piedmont of North Carolina.

53 - Biofilm inhibition via the application of novel lead compounds in *Cryptococcus neoformans*, *Enterococcus faecalis*, *Enterobacter aerogenes*, *Candida parapsilosis*, *Candida albicans*, *Vibrio fischeri*, and *Proteus mirabilis*

Natalie Yaeger, Jeff John

Mercer University, Macon, GA

Biofilm formation is among the most prevalent virulence factors for both prokaryotic and eukaryotic organisms. Understanding the mechanism behind biofilm formation could lead to novel treatments of bacterial and fungal infections via the inhibition of biofilm rather than bactericidal or bacteriostatic methods. By decreasing the need for bactericidal or bacteriostatic methods, the prevalence of antibiotic resistance would decrease thereby protecting the normal flora of the body. Preliminary research has been conducted on five species of bacteria: *Bacillus subtilis*, *Escherichia coli*, *Staphylococcus aureus*, *Streptococcus mutans*, and *Pseudomonas aeruginosa* that show growth of biofilm production. Over 300 novel lead compounds resembling quorum-sensing signaling molecules have been synthesized and tested to find biofilm inhibition compounds. It has been discovered that 28 of these compounds inhibit biofilm formation in one or more of these species. This project extends our current database by expansion of analyses for seven additional species including *Enterococcus faecalis*, *Enterobacter aerogenes*, *Candida parapsilosis*, *Candida albicans*, *Vibrio fischeri*, and *Proteus mirabilis* as well as the first eukaryotic species to be studied within this lab, *Cryptococcus neoformans*. The addition of a eukaryotic organism, *Cryptococcus neoformans*, will not only broaden our research but also allow us to see the impact eukaryotic biofilm formation could possibly have on subsequent eukaryotic species. Through the exploration of biofilm created via more complex organisms, the ability to find definitive links to real world implications increases exponentially as results garnered from *C. neoformans* can act as a baseline by which other eukaryotic biofilms can be compared. The research gathered pertaining to the bacterial species and eukaryotic species above has been associated with numerous diseases, including cancer. This showcases the true importance and impact of this research.

54 - Proposal of Three Models of Extractive-fermentation Bioreactors for the Conversion of Crude Glycerol to Biobutanol by *Clostridium pasteurianum*

Jonathan Kilroy

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Crude glycerol is produced as a major waste product of the biodiesel industry. Purification of glycerol is difficult and costly due to toxic impurities. The accumulation of crude glycerol hampers the efficiency and economic viability of biodiesel production, leading to a phenomenon known as the "glycerin glut". Fortunately, the species of bacteria *Clostridium pasteurianum* provides a potential solution. *C. pasteurianum* can rely on glycerol as its sole carbon and energy source while tolerating many of the toxicities inherent in crude glycerol. This species is capable of converting glycerol into butanol, a useful fuel additive. In order to optimize this conversion, a continuous culture chemostat is used to improve cell growth and fermentation. Continuous culture of *C. pasteurianum* was found to induce a steady state which consistently increased butanol yield by approximately 10% over that of batch cultures and decreased production of 1,3-PDO by at least 11% and minor fermentation products by at least 6.7%. Preliminary experiments suggest that separation of butanol from this continuous culture may be feasible via diffusion across a semi-permeable membrane. Three models of a bioreactor which facilitate *in situ* extractive fermentation are proposed based on these findings. Two employ an extraction column containing a hollow fiber membrane connected either to the collection reservoir or the reactor which houses the culture. The third employs a membrane submerged in the reactor, separating the live culture from an extraction solution.

55 - Microbial Diversity of Campbell University Ants

Caitlyn Vester, Stephanie Mathews

Campbell University, Buies Creek, NC

Ants are social insects that live in symbiosis with their environment. Dense ant colonies means higher risk of infection; therefore, ants have adapted a defense system against parasites and pathogens through the production of antimicrobial secretions from their metapleural gland. This study aims to evaluate the microbial diversity of worker ants in the built environment of Campbell University. *Solenopsis invictica* ants were collected from Campbell University and bacteria were isolated using culture-based methods, identified using 16S rRNA sequencing, and assessed for antibiotic production. Approximately 1.2×10^3 CFU/ant were cultured from ants collected on campus using Luria Bertani Agar incubated at 25°C. Based on colony morphology, 32 bacteria were isolated to be identified. Of these isolates, 17 were sent for sequencing after successful 16S rRNA amplification by PCR. DNA sequencing identified 9 isolates at the genus/species level and 8 at the genus level. Antimicrobial assays of some isolates demonstrated activity against *Staphylococcus epidermidis* and *Escherichia coli*. Most of the isolated bacteria exhibited antimicrobial properties. A comparative study to outside environments will determine if the bacteria isolated from Campbell ants are carrying are unique to ants in other environments.

56 - Linoleic acid affects membrane permeability and antimicrobial activity of fish piscidins on *Vibrio cholerae*

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Antimicrobial peptides are found in all organisms and have gained notoriety in recent years for their effectiveness against a variety of pathogens. Piscidins, first isolated from the mast cells of vertebrates, comprise a family of these host defense peptides. Piscidins 1 (P1) and 3 (P3), found in sea bass and other fishes, are isoforms with different modes of action. P1 induces membrane perturbation, while P3 binds DNA to exert antibacterial activity. Each has the ability to bind Cu^{2+} (P1Cu and P3Cu) which dramatically impacts their antimicrobial characteristics. The purpose of this study was to investigate the activity of metallated and nonmetallated P1 and P3 on *Vibrio cholerae*, a Gram-negative bacterium of medical importance that normally inhabits an aquatic environment, often associating with fish and other marine life. Known to assimilate exogenous fatty acids into membrane phospholipids, *V. cholerae* possesses the ability to modify membrane permeability depending upon environmental fatty acid availability. Herein we investigated both permeability and antimicrobial effects of P1, P1Cu, P3, and P3Cu on *V. cholerae* grown in the presence and absence of linoleic acid (18:2). Membrane permeability was assessed using a crystal violet assay. These experiments observed a marked decrease (~15%) in permeability when the bacteria is provided 18:2. All piscidins elicited heightened permeability, with 18:2 decreasing the effect for nonmetallated forms of the peptide. Furthermore, some piscidins displayed concentration dependence with regard to permeability effects. The minimum inhibitory concentrations (MICs) for P1 and P1Cu were increased 2-fold when 18:2 was supplemented. The MIC of P3 was significantly decreased (4-fold) in the presence of 18:2, while no difference was observed with P3Cu. Not only do piscidins alter bacterial membrane permeability and display promising antimicrobial capabilities, but the observed effects of exogenous fatty acid supplementation could also hold potential for targeted treatment of infectious disease.

57 - Initial Assessment of Potential Relationships Between Plant Communities and the Soil Microbiome in Closed Forest and Longleaf Pine Restoration Sites.

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Longleaf pine is an endangered ecosystem characterized by high levels of biodiversity. Our study took place in the Sheffield Wildlife Management Area located in the Piedmont ecoregion of Georgia in Paulding County. Fifty plots of $10 \times 30 \text{ m}^2$ were setup on south or north facing slopes, some in covered forest, and some in an area actively being restored for the longleaf pine. All trees above 1.37 m were identified and had their diameter measured, and species diversity, relative density, dominance, and frequency were determined. Herbaceous plant cover percentages were recorded in select plots. Soil samples were also collected in sterile plastic tubes in six of the above-mentioned plots, at the center and 10 m above and below the central point of each plot. Plant species diversity was slightly higher in south facing compared to north facing slopes, and the soil microbiome suggests high levels of bacterial diversity and differences in fungal microbiome among plots. Our aim is to begin to determine potential associations between below and above-ground communities. For this presentation, we examine the associations that exist in study plots between tree and fungi taxa.

58 - Geospatial Analysis of an Old-Growth Forest in Southwest Georgia Landform Transformation and Species Distribution

Elizabeth Harrell

Thomas University, Thomasville, GA

The unique diversity in Lost Creek Forest is attributed to its status as an Old-Growth forest. Approximately 117 acres of the 207-acre plot has not been harvested at any point in historical records. The lack of habitat disruption leads to a unique diversity in plant species that can rarely be found in the South Georgia area. Florida milkvine (*Matelea floridana*) is commonly found in the light gaps of Lost Creek Forest, and is an endangered herbaceous, twining, perennial, vine of the Asclepiadaceae family. Eight species locations have been documented in the state of Florida, where it is listed as imperiled, and 2 species locations in the state of Georgia where it is listed as critically imperiled. This study spatially analyzed the distribution of *Matelea floridana* in relation to geographical habitat fragmentation, light gap distribution, and light gap diameter within Lost

Creek Forest. The correlation relates the role of natural disruption through the use of light gaps, and plays a crucial role in the distribution of this critically imperiled species.

59 - The Biotic and Abiotic Correlates of the Abundance and Distribution of Seagrasses in Lake Worth Lagoon, Palm Beach County, Florida

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Seagrass is a flowering plant found in tropical and sub-tropical marine systems and is common along the coasts of Florida, including Lake Worth Lagoon (LWL – Palm Beach County, FL). Over the past 10 years, seagrass beds have been decreasing rapidly and as an indicator species its decline has brought to light other issues in the ecosystems, such as harmful algal blooms and declines in estuarine health. The goal of this study is to model potential patterns of environmental parameters and community structure that may correlate with the decline of seagrass populations in LWL over a 12-year period from 2007 to 2019. Nine transects throughout the LWL were visited annually (May – August) and environmental parameters (e.g., temperature, dissolved oxygen, and salinity), seagrass Braun-Blanquet (BB) scores (a record of coverage), and macroalgal BB scores were recorded. A preliminary multivariate analysis of variance indicated significant differences in annual variability of environmental parameters within the LWL watershed over the 12-year period. Major drivers of the variability included changes in dissolved oxygen content, total nitrogen, total phosphate, salinity, and pH. An analysis of variance (ANOVA) investigating the annual variability in mean seagrass BB score showed an abrupt decline in 2013, with seagrass cover remaining very low throughout the rest of the dataset. A separate ANOVA conducted on the annual macroalgal BB scores displayed a similar pattern, with macroalgal coverage declining abruptly in 2013 and remaining low. Interestingly, initial analysis of this dataset suggests that abiotic, rather than biotic, factors may dictate the stability of seagrass communities in Lake Worth Lagoon. Continuing analyses include the development of models utilizing combinations of environmental parameters, community structure, temporal variables, and spatial variables that predict specific seagrass species' presence/absence and BB scores in this watershed, with those models being evaluated by Akaike Information Criterion.

60 - Belowground characteristics of coastal dune grasses with implications for species-specific effects on erosional resistance

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Coastal dune systems are vulnerable to accelerated rates of erosion due to sea-level rise. Vegetation can facilitate dune creation and resilience through the growth of aboveground parts, which trap and stabilize aeolian transported sediments. Recent studies have demonstrated that belowground biomass may also be important for stabilizing sediments under different wave erosional regimes, with species having different effects. A gap in knowledge remains about whether other aspects of belowground structures, such as root traits, may inform our understanding of species-specific effects on dune erosional resistance and how these differ among key species. Our objective was to evaluate belowground characteristics of four prominent dune grass species (*Ammophila breviligulata*, *Spartina patens*, *Uniola paniculata*, and *Panicum amarum*) that may be important for understanding dune erosional resistance. Whole plant samples of each species were collected from the foredune at the USACE Field Research Facility in Duck, NC. Samples were evaluated for biomass, mycorrhizal percent infection, and several root traits and characteristics.

Species exhibited unique suites of belowground characteristics. *A. breviligulata* and *U. paniculata* had similar amounts of total belowground biomass but differed in factors such as root surface area distribution, rhizome biomass and length, root tissue density, and specific root length. *Spartina patens* and *A. breviligulata* exhibited the highest maximum root tensile strength (the amount of pulling pressure roots can withstand before breaking) values while *U. paniculata* had the lowest. Species also differed in mycorrhizal percent infection, which may be important for understanding mycorrhizae-mediated erosional effects. This study demonstrates that prominent dune species possess unique combinations of belowground features that may be important for understanding species-specific effects on dune erosional resistance.

61 - Using multispectral canopy reflectance as a measure of tree stress in a bottomland hardwood forest (BLHF)

Paurava Thakore, Joydeep Bhattacharjee

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Forest pests and disease continue to be one of the largest drivers of forest loss both ecologically and commercially. Enhanced vulnerability from irregular climate patterns, extreme weather, and range expansion further exacerbates this problem. Monitoring and evaluation of these disturbances have long been a function of integrated forest management. We attempt to increase monitoring capacity using novel methods of image acquisition, processing, and analysis. We will use a time series of high-resolution multispectral imagery sourced from Unmanned Aerial Systems (UAS) in combination with multi-modal image segmentation using a neural network to conduct analysis at stand, individual, and sub-canopy scales. The U-Net model architecture chosen for this study facilitates segmentation while preserving topological associations of imagery in contrast to many object or pixel based classification methods. Four one hectare plots located at Russell Sage Wildlife Management Area in northeast Louisiana representing a mature mixed BLHF will be surveyed over the entire leaf phenophases. Ground-truthing of sixteen intensive subplots within the survey area using a standardized Forest Inventory Assessment methodology will support observations for supposed variations in canopy reflectance across seasons. We hypothesize particular plant stress (ex: Oak Leaf Blister, Crown Galls, water, etc.) will have unique spectral signatures given the physiological effect spatially on an individual (ex: leader dieback, patchy diffuse reduction in reflectance, etc.). Through this study we hope to develop tools that will inform broader assessments of forest health in an automated and scalable manner, while taking into account the scenarios of a changing climate.

62 - Determining the Impacts of Freshwater Inundation Duration and Depth on Coastal Marsh Vegetation Species

Coral Foster, Dr. Jonathan Willis

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Coastal Louisiana is experiencing wetland loss due to a number of factors, including the reduction of marsh elevation through the subsidence of deltaic sediments. River sediment diversions, which reconnect sediment deficient marshes with the Mississippi River, are one of the large-scale tools planned for restoring these impacted coastal environments. Routine inundation is an important component of coastal marshes providing suspended sediments to enhance marsh accretion and consequently marsh elevation. However, prolonged inundation will occur in diversion outfall areas during operation, potentially resulting in increased flooding stress on marsh vegetation. Although routine inundation is an important component of coastal marsh sustainability, the effects of extended freshwater inundation, typical of sediment diversion operation, on the growth of key marsh vegetation species need further investigation. A large-scale mesocosm study has therefore been initiated at the Nicholls State University Farm Facility to determine the effects of sediment diversion-relevant inundation depths and durations on the growth responses of four key marsh vegetation species. Specifically, four species, *Spartina alterniflora*, *Spartina patens*, *Sagittaria lancifolia*, and *Typha latifolia*, were subjected to differing inundation depths (0 cm, 20 cm, and 40 cm above the soil surface) and durations (2 weeks, 4 weeks, 8 weeks, and 12 weeks) and compared to reference conditions (constant water depth 10 cm below the soil surface) in regards to non-destructive and integrated growth metrics. Preliminary data analysis revealed similar rates of net CO₂ assimilation across treatments at week 16, 4 weeks after all experimental units were returned to reference conditions. These findings suggest that even when exposed to 40 cm deep flooding for 12 weeks, the marsh species tested in this study will likely exhibit levels of photosynthetic activity similar to reference levels when returned to mesic conditions.

63 - Phylogenomics and population genetic study of *Centrapalus pauciflorus*, a potential novel industrial oilseed cropRamhari Thapa¹, Jennifer Mandel^{1,2}¹University of Memphis, Memphis, TN, ²Center for Biodiversity Research, Memphis, TN

Epoxidized oils, oils rich in epoxy fatty acid, find many industrial applications such as in the manufacturing of plastics, paints, adhesives, cosmetics, and other oleochemical products. *Centrapalus pauciflorus*, an annual drought tolerant plant native to tropical Africa including Ethiopia, Kenya, and northern Tanzania, produces naturally epoxidized oil. Seeds of *Centrapalus pauciflorus* contain an unusual C18 epoxy fatty acid (12, 13 epoxy-cis-9-octadecenoic acid), also known as vernolic acid, which is environment friendly, less viscous, less expensive, and has better polymerizing characteristics compared to artificial epoxy oils produced by modifying petrochemicals or artificial epoxidation of linseed and soybean oils. Attempts to grow *C. pauciflorus* as an oilseed crop in Ethiopia and North America, which can serve as a renewable source in the industries, have not been successful. Much research has been done regarding genetic variability, agronomic traits, and vernolic oil contents of the *Centrapalus pauciflorus* species; however, information from a robust backbone phylogeny of the *Centrapalus* and other closely related species useful for improving domestication, breeding successes, and other evolutionary studies has been lacking. We performed a phylogenetic study of the genus *Centrapalus* and closely related species using a Hyb-Seq method and assessed the population genetic studies of the *Centrapalus pauciflorus* accessions available in the USDA seed bank. Both the concatenated and coalescent-based analyses of DNA sequence data from hundreds of nuclear loci recovered the genus *Centrapalus* as a monophyletic group. The genus was further resolved into two distinct clades, one consisting of *C. pauciflorus* subspecies *pauciflorus* and the other consisting of other subspecies of *C. pauciflorus*. The result also correlated in the population genetic studies performed by using ten highly transferrable microsatellite markers developed specific to *Centrapalus* species. Population genetic studies also showed that *C. pauciflorus* ssp. *pauciflorus* has higher genetic diversity compared to the other subspecies of *C. pauciflorus*.

64 - An Examination of Introgression in the *Trillium erectum* Species Complex Using Microsatellite Analysis

Austin Brenek, Kathy Mathews

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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 Principle 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.

65 - Citizen science platforms as tools connecting communities to research and education: A case study using iNaturalist

Skylar Fox, Ashley Morris

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iNaturalist is a popular citizen science platform among biologists as well as the general public. This application has the ability to foster communication and discussions between those with a lot of experience identifying and working with organisms and with those who simply like to observe nature in their free time, as well as anyone in between. However, iNaturalist has many wide-reaching applications that increase knowledge of biodiversity. iNaturalist has been used increasingly in the world of research, especially through publication of observations to the Global Biodiversity Information Facility (GBIF). Additionally, iNaturalist has been incorporated into the classroom in for students K-12 as well as for undergraduates. There are many features of this application that educators can use to enhance their students' understanding and provide them with in-the-field biological and ecological experience. iNaturalist is just one of the many citizen science platforms that are used in the world of science today. In order to recruit volunteers for specific iNaturalist projects, it is important for the project curators to understand the motivations of their volunteers so that they can make sure the project is appealing. Speaking more broadly, creators of citizen science platforms and projects must in general understand participant motivations to continue to retain and recruit volunteers so that the platform and/or project can be successful. It is also vital that curators recruit a diverse group of participants for projects in order for the project to be as effective and wide-reaching as possible.

66 - Comparing the Effect of Four Propagation Techniques on Hybrid Chestnut Seedling Quality

Taylor Evans, Heather Griscom

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Successful restoration of chestnut hybrids is reliant on both genetic resistance to chestnut blight (*Cryphonectria parasitica*) and the long-term survival and reproduction of resistant individuals. Producing field-ready seedlings able to survive abiotic stresses and compete effectively with existing vegetation will require a renewed focus on seedling quality assessment. Seedling quality is important for successful restoration projects and nursery propagation techniques can affect seedling morphology to increase the likelihood of survival. Four production methods, bare-root seedlings, seedlings grown in containers, an air-pruning raised bed, and the Root Production Method® (RPM®) will be compared across several measures of seedling health in order to determine which technique produces seedlings most likely to survive out-planting. Propagation techniques that utilize air-pruning, such as the raised-bed and RPM®, have been shown to increase the number of first order lateral roots and overall root volume when compared with bare-root seedlings. Additionally, RPM® has been shown to produce seedlings with greater basal diameter, height, and a lower age at first fruiting than bare-root stock of the same age, though at many times the cost of bare-root seedlings. After one year, seedlings ($n \sim 375$) were removed from their growing treatment and measured for height, root collar diameter, number of first-order lateral roots, and root volume to determine overall seedling quality of each treatment. Total cost per seedling will be to provide additional information for nurseries and practitioners who would like to produce their own chestnut hybrid seedlings for restoration plantings.

67 - Patterns of vertebrate richness across anthromes: prioritizing conservation beyond biomes and ecoregions

John Quinn, Emma Cook

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There is a clear need to refocus the way we prioritize conservation actions at a global scale to incorporate human systems. Anthromes have been suggested as one tool for integrating anthropogenic effects on ecosystems, but spatially explicit comparisons of biodiversity patterns are limited at a global extent. To address this gap, we used global data sets of anthromes and terrestrial vertebrate richness. We ranked anthromes by richness to all and threatened species at a global scale, temperate and tropical extents, and within major geographic regions. We tested for correlations between overall richness and count of threatened species, between taxonomic groups (birds, mammals, amphibians), and between taxa and conservation actions. At the global scale, there is high variation in vertebrate species richness by anthrome with low species richness in barren and wild lands and higher richness in villages, rangelands, and woodlands. Threatened species distribution follows a similar pattern with high numbers of threatened species in village and remote seminatural woodland anthromes. Analyses at regional extents help to explain some of the patterns seen at the global scale. Regional heterogeneity is clear across regions. Protected areas are not aligned with richness patterns in anthromes though anthromes and hotspots are spatially aligned. Human modified ecosystems provide opportunities for conservation and global and regional ranking of anthromes helps identify priorities that can complement biome and ecoregion-based prioritization. Currently, much of conservation research and prioritization is in wildlands or perceived natural landscapes, however this data shows a clear need to focus conservation efforts on seminatural, managed, and residential lands. These data would be helpful for global conservation organizations as an updated framework that can be used to prioritize global resource allocation while considering both ecological and social systems.

68 - Implications of UNESCO World Heritage Site Classification on Buffer Zones

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Protected areas (PA) are a common biodiversity conservation tool used to protect a landscape, its ecosystem services, and the species that rely on that habitat. However, the classification of a PA may have unanticipated or considered effects on the landscape buffering the PA. Previous research has uncovered the benefits and drawbacks of PA establishment for the surrounding communities, but this literature does not often consider how globally recognized protection methods, like UNESCO World Heritage Sites, may impact the communities around PAs at a global

scale. A World Heritage Site (WHS) is a location that possesses heritage deemed to have universal value that requires protection for current and future generations. Likewise, these efforts have only considered a very narrow band of spatial proximity. The aim of this study is to determine global patterns of change for four indicators over different spatial extents in the buffer zones of WHS. We conducted a spatial analysis of the four indicators, human footprint (HF), human appropriated net primary production (HANPP), forest landscape integrity index, and forest loss, in the buffer zones of 720 WHS globally over three buffer zone distances, 1, 11, and 100 km. The study determined that the classification does affect human and natural systems in the buffer zones, but at different intensities and spatial extents for each indicator. For instance, HF experienced its greatest change of a 79.28% increase between the 1-11km buffer zones, whereas HANPP experienced its greatest change of a 18.54% increase between 11-100 km. These results show that the relationship between the WHS classification and the adjacent surrounding landscape is complex and dynamic. This relationship, therefore, requires additional consideration on a case specific scale to understand if a WHS classification is an appropriate conservation tool for protecting the heritage while also allowing the surrounding communities to meet their needs.

69 - The effect of fire on oak-forest regeneration: A 25-year study

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In the Eastern US, fire is a natural process in *Quercus* (oak) forests. Fire promotes oak regeneration by reducing competition, preparing a suitable seedbed, and decreasing soil moisture. However, oak regeneration has declined since the early 20th century due to fire exclusion. In this study, we examined the effects of fire on tree regeneration over 25 years and asked: (1) Does tree regeneration vary under different fire regimes?, (2) Do the outcomes of prescribed fire differ on xeric, intermediate, and mesic sites? and (3) Which limiting resources affect regeneration the most? From a study initiated in 1994, we re-sampled 45 1250m² permanent vegetation plots across three fire treatments (unburned, annually burned, burned every three years) in the Wayne National Forest, Ohio. Pretreatment data was collected in 1995 and low-intensity prescribed burns were conducted during 1996-1999 followed by a mostly fire-free period. Tree seedlings were tallied and identified in sixteen 2m² quadrats and saplings were tallied and identified in 312.5m². Using linear mixed effects models and model selection using AIC, we examined if seedling and sapling density changed from 1995 to 2019 and 2002 to 2019 in relation to fire, light availability, soil nutrients, and soil moisture. Through time, *Quercus* saplings increased on burned areas while *Acer* seedlings and saplings decreased throughout ($p < 0.01$). From 1995 to 2019, *Quercus* saplings increased on xeric soils ($p = 0.01$) while *Acer* seedlings and saplings decreased in all soil moisture types. Soil texture, forest structure, IMI, and soil macronutrients were most related to the change in (Δ) *Quercus* sapling density from 1995 to 2019. Δ *Quercus* sapling density from 2002 to 2019 was related to shrub cover and ammonium. Our results indicate that prescribed fire positively influenced *Quercus* regeneration especially on drier sites, while *Acer* has decreased throughout all soil moisture categories and fire treatments.

70 - The Spring Wildflower Pilgrimage in the Great Smoky Mountains National Park, at 70 years old, is among the oldest and largest public outreach events for biology, ecology, conservation, and land management.

Joey Shaw

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71 - Elevational Range Specialization of Neotropical Bees of the Seasonally Dry Pacific Slope Forests of Costa Rica

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There is an urgent need to document the distribution of bee assemblages along tropical mountains to understand how these ecologically and economically important pollinators may respond to climate change and other global change impacts. Here, we quantified bee abundance at 100m elevation intervals across a narrow elevation gradient on a short mountain (1800m peak) in the seasonally dry Pacific slope forests of Costa Rica. The study area is characteristic of the tropical countryside and includes smallholder farms, home gardens, live fences, windbreaks, pasture and forest patches. We focused on the honey bee, *Apis mellifera* and 25 other bee species representing two tribes: the economically important social, stingless bees (Tribe Meliponini) and the small carpenter bees (Tribe Ceratinini).

We found that 15 of 26 bee species showed abundance differences by elevation, suggesting that many species in these tribes exhibit elevational range specialization. Differences in the relative abundance of bees by elevation was evaluated using a CCA ordination. Elevation and site together explained ~42% of the variation in the bee community composition ($F_{pseudo(3,8)} = 1.91$, $p = 0.002$).

Mountain-dwelling species are expected to shift ranges upslope to higher elevations and cooler temperatures over time due to global temperature increases. Our results indicate that bee species of tropical montane landscapes could be at high-risk to warming temperatures or changing patterns of precipitation, as elevation is a strong factor in shaping bee communities, and species with narrow elevational ranges or specialization within a narrow portion of their elevational range are predicted to be more vulnerable to range shifts.

72 - Prevalence of the parasite pathogens that cause Lyme disease in Southwestern Georgia and Southeastern Alabama.

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The occurrence of Lyme disease is on the rise in the United States. Lyme disease is caused by infection from the *Borrelia burgdorferi* bacteria. The bacteria are spread through the bite of the black-legged deer tick, *Ixodes scapularis*. At present, the majority of cases of Lyme disease are located in the Northeastern United States. The lack of prevalence in the southeastern United States has been attributed to variations in habitat. However, several cases of Lyme disease in the Southeastern United States have been misdiagnosed. The prevalence of *Borrelia burgdorferi* in Southwest Georgia and Southeastern Alabama has not been addressed.

We collected 270 ticks in December 2018, 2019 and 2020 in Southwest Georgia and assessed the presence of *Borrelia burgdorferi* s.s. through real-time PCR methods. Of the 41 sampled to date, one of them tested positive for *Borrelia*, although not *B. burgdorferi*. Further research will include sampling the other 229 ticks for the presence of this bacteria. Possible explanations for such a low occurrence may include the presence of antibacterial properties of deer blood, as well as dry conditions due to large amounts of pine forests in the region. These may hinder the amount of biting ticks, therefore the occurrence of Lyme disease.

73 - Insect Preference of Terpenes in *Solidago altissima*

Faith Weaver, Ray Williams

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Phytochemicals such as terpenes act on insects in many ways, including possibly as attractants to plants. We are investigating if insect herbivores and pollinators are recognizing and preferring different terpenes produced by *Solidago altissima* (tall goldenrod). Previous data found that both aphids and pollinators choose different genotypes of *S. altissima* and those genotypes contain different concentrations of some terpene compounds. The importance of this study is to discover phytochemical factors resulting in the preference of insects in a genetically variable plant species thus furthering the knowledge about these plant-insect interactions. The investigation uses a combination of preference and field studies examining terpenes found in the different genotypes of tall goldenrod found in Watauga CO, NC. A 3.5 ha old-field dominated by *S. altissima* was sampled for pollinator abundance and diversity, and flowers sampled for terpenes in order to examine possible effects of varying terpene chemotypes. In 9 1m² plots, separated by 35 m to ensure each plot was different a genotype, pollinator visitations were visually observed over four 15-minute periods during peak flowering in September-October 2020. Two flower samples from 3-4 individual plants on each plot were taken. Flowers were placed in pentane for several weeks and terpenes analyzed using GC protocol. Splitting the plots into three categories; upper, middle, and lower region, a difference in *Bombus* sp. visitations were observed. The upper region totaled 6 *Bombus* visitations, the middle 26, and the lower had 23. Resulting in a 125% increase in *Bombus* visitations in the middle region compared to the upper and 12.2% between the middle and lower. Linear regression analyses will be used to analyze pollinator response using mean terpenes values of each plot. If the pollinator data relates to specific terpene compounds, this is suggestive of preference, which will be further explored in controlled laboratory trials.

74 - An Inventory of Syrphid Flies (Family Syrphidae) of the Blue Ridge Parkway

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Flies of the family Syrphidae (a.k.a. hover flies or flower flies) may be second only to native bees as important pollinators of native plants. There are over 6,300 described species in this family world-wide and about 300 possible species in the Southern Appalachians. Despite their importance there have been few syrphid fly inventories conducted, leaving questions regarding geographic distribution, species diversity, and proper sampling methods. To address these questions, I identified samples belonging to the family Syrphidae collected in passive traps and netting efforts at 60 sites spanning nearly 500 miles along the Blue Ridge Parkway (NC and VA) during a larger pollinator inventory. This inventory was a component of the All-Taxa Bioinventory (ATBI) in the region. Samples stored in ethanol-filled whirlpaks were washed, dried, pinned and then identified using the *Field Guide to the Flower Flies of Northeastern North America*. In total, there were 40 species identified among 344 syrphid flies captured at 26 mileposts along the Parkway. The data will be used to compare species richness among sites and most effective survey techniques. This project serves as a valuable assessment of an underreported group of pollinators and should provide ample practical information for conservation efforts and the efficacy of typical sampling methods.

75 - An exploration of the foraging behavior of a hawkmoth in response to floral textures

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Manduca sexta are large, nocturnal hawkmoths that search for nectar by hovering at a steady distance from a flower while tapping its surface with their long, thin proboscis. Hovering is energetically expensive, so it is reasonable to expect that the efficiency of this searching behavior is under selective pressures. We and others have previously shown how, upon tactile detection of floral features such as grooves on the corolla, *M. sexta* orient their body parallel to the grooves and rapidly run their proboscis back and forth (BnF) through them. Here, we used this behavior as an indicator to explore the spatial resolution of the proboscis's tactile sense. Using 3D-printed surrogate flowers with varying groove widths (1.0, 0.1, 0.05, and 0.0 mm), we found that *M. sexta* can detect grooves as small as 0.1 mm but not 0.05 mm, so our next step is to improve the precision of our estimate by using groove widths between this range.

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

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Widespread logging had 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, 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 important considering biotic homogenization, 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.

77 - Dry-mesic longleaf pine vegetation of the Atlantic and East Gulf Coast Coastal Plain: Vegetation classification and biogeography

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Description and classification of natural communities are critical for both theoretical and applied vegetation science, including conservation planning and restoration. The US National Vegetation Classification (USNVC) is a hierarchical system for documentation of natural vegetation within the US. Our goal was to employ an approach consistent with USNVC standards to revise the Associations within the Dry-Mesic Loamy Longleaf Pine Woodland Group (G009), which contains subxeric and mesic longleaf pine (*Pinus palustris* Mill.) vegetation. We asked: (1) What are the vegetation types that constitute G009 longleaf pine woodlands? and (2) How does species composition of these types vary with soil properties and geography? Beginning with the existing USNVC, based primarily on best professional judgment of vegetation scientists and existing literature, we employed quantitative methods with plot-based vegetation data. We used hierarchical clustering with flexible β on 325 vegetation plots that span the range of variation within G009 longleaf pine woodlands. Misclassified plots were reassigned using silhouette width and fuzzy clustering. Thereafter, clusters were mapped onto existing USNVC Associations based on floristics, environmental conditions, and geography, or new Associations were described. Our analytical framework resulted in identification of 29 vegetation types that span NC, SC, GA, FL, and AL. Of these, 22 were mapped to existing Associations, while seven represented new types. Key environmental variables that relate to compositional differences across Associations include soil texture, soil moisture, soil base cations, and geographic position along north-south and near coast-inland gradients. We documented geographic gradients in community composition that reflect the turnover of dominant taxa, high levels of local endemism and restricted-range taxa, and broad-scale edaphic gradients. Our classification is an improvement on the previous scheme as it provides more detailed information on environmental conditions, geographic extent, and diagnostic taxa for each type, and it describes distinctive, previously unrecognized types.

78 - Isolating, purifying, and investigating Mycobacterial lysogens

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Bacteria have shared an entangled evolutionary history with bacteriophages (viruses that specifically infect bacteria) for the past three billion years. Some bacteriophages (phages) use a specific type of infectious pathway that helps maintain their host's viability and hence enable a mechanism of co-existence. To investigate this further, two temperate mycobacteriophages (ExplosioNervosa and Rhynn) were selected. Both these phages are able to form lysogens and exist in the host cell's genome indefinitely as a prophage. Annotation of their genomes revealed the presence of immunity related genes. These particular genes potentially explain how some phages are able to protect their host and resist superinfection by other related and non-related phages. Bacterial lysogens were created by incubating bacterial host cells with the phages. Any resulting lysogens were a sign that host cell growth had taken place in the presence of a prophage, so provided a sample of lysogenized bacteria. The lysogens were purified and tested against their original infecting phage as well as an unrelated bacteriophage (Haimas) to see if they were able to resist superinfection. Tests showed that both Haimas and the original viruses were still able to infect the lysogens and cause them to lyse. Infections of these phages on their own lysogens raised the idea of spontaneous reversion; the prophages could have reverted to the lytic cycle due to a triggering condition in their environment. The ability of the host-phage relationship to respond to certain environmental signals warrants further investigation, as does manipulation of the genes linked with immunity and infection. Investigating the triggers and unraveling the mechanisms that fuel coevolution helps further our understanding of the host-parasite equilibrium that exists today and highlights opportunities for future applications.

79 - Polyunsaturated fatty acid-mediated effects on membrane remodeling, virulence phenotypes, and cyclic peptide resistance in *Vibrio alginolyticus* and *Vibrio fischeri*David Smith¹, Allycia Lee¹, Carina Houck¹, Timothy Simmons¹, Ayanna Esdaile², Steven Symes¹, David Giles¹¹The University of Tennessee at Chattanooga, Chattanooga, TN, ²Millsaps College, Jackson, MS

Vibrio alginolyticus and *Vibrio fischeri* are Gram-negative bacteria found globally in marine environments. Studies have shown that certain bacteria (i.e. *Escherichia coli* and *Vibrio cholera*) are capable of using exogenous polyunsaturated fatty acids (PUFAs) to modify the phospholipids of their membrane. Moreover, exogenous PUFAs have been shown to affect certain phenotypes that are important factors of virulence. The purpose of this study was to investigate whether *V. alginolyticus* and *V. fischeri* are capable of responding to exogenous PUFAs by remodeling their membrane phospholipids and/or altering behaviors associated with virulence. Thin Layer Chromatography (TLC) analyses of extracted phospholipids following exposure to individual PUFAs provided qualitative data supporting fatty acid incorporation. Exogenous fatty acid assimilation was confirmed by Ultra Performance Liquid Chromatography / Mass Spectrometry (UPLC/MS). Several growth phenotypes were identified when individual fatty acids were supplied in minimal media and as sole carbon sources. Interestingly, several PUFAs inhibited growth of *V. fischeri*. Significant alterations to membrane permeability were observed depending on fatty acid supplemented. Strikingly, arachidonic acid (20:4) reduced membrane permeability by approximately 35% in both *V. alginolyticus* and *V. fischeri*. Biofilm assays indicated that all fatty acids except 18:3 γ decreased biofilm formation in *V. alginolyticus*, while two omega-6 fatty acids (18:2 and 20:4) increased biofilm formation in *V. fischeri*. All fatty acids caused decreased swimming motility in *V. alginolyticus*, while only one fatty acid (linoleic acid [18:2]) significantly increased swimming motility in *V. fischeri*. Finally, exogenous PUFAs significantly altered the minimum inhibitory concentration of the cyclic peptides polymyxin B and colistin, but not the β -lactam antibiotic imipenem, in both species. In summary, exogenous fatty acids cause a variety of changes in *V. alginolyticus* and *V. fischeri*, thus adding these bacteria to a growing list of Gram negatives that exhibit versatility in fatty acid utilization.

80 - Optimization of *Dunaliella salina* growth using commercial fertilizers and salts

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The halotolerant algae *Dunaliella salina* produces high levels of carotenoids, antioxidants, and fatty acids, which are required components of aquaculture feed, particularly in brine shrimp rearing. Obtaining high biomass in a low-cost medium is essential in the process of feed production. For future enhancement of *Dunaliella* biomass production, low-cost media using combinations of commercially available salt and fertilizer was compared to the medium used in current culturing methods. *D. salina* growth was observed over a range of salinities in commercial fertilizer and quantified using automatic cell counting and UV-vis spectrophotometry. Growth was then observed in an all-commercialized salt and fertilizer medium, followed by a commercialized salt and custom fertilizer medium, and characterized by UV-vis spectrophotometry. *D. salina* exhibited an optimum growth rate and cell density in 0.25M commercialized salt media with a custom fertilizer mixture. When grown with Miracle-gro fertilizer, growth rates in NaCl and commercialized salt media were equivalent and optimal at 0.50M, but with a lower cell density. The primary results of biomass, cell density, and growth rate indicate that a commercial salt and fertilizer medium shows promising potential for low-cost mass culture of *Dunaliella salina* in the aquaculture industry. Future work includes lipid and protein content analysis of algae grown in optimized salt and nutrient conditions.

81 - Ecophysiology of Toxic Bloom-Forming Cyanobacteria and their Symbionts

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Toxic cyanobacteria blooms are a global problem causing adverse effects to numerous lakes and rivers. Combating these blooms are difficult because the plethora of factors contributing to the success of bloom-forming cyanobacteria are not fully understood. Here we focus on biotic factors driving blooms of toxic *Microcystis* by describing potential interactions with heterotrophic bacteria within the phycosphere. First, we identified and characterized over 100 different bacterial isolates from *Microcystis* blooms in Lake Tai, China (August 2018) and Lake Erie, Ohio (July 2017). Three of these isolates were shown to have beneficial effects on *Microcystis* when grown in co-culture with axenic *Microcystis aeruginosa* NIES 843. One of these isolates (from Lake Tai) was chosen for further study. Briefly, co-cultures were set up to examine how *Microcystis* cellular processes were impacted by the presence and absence of the isolate using an RNA-seq approach. Time points for RNA-seq analysis were taken at mid-log and early stationary phase of *Microcystis* growth. Another time point was taken 12 hours after the mid-log phase to tease apart processes that may be differently affected over a diel cycle. These data provide new insight into the molecular mechanisms that drive interactions in the *Microcystis* phycosphere.

82 - Plant-Pollinator Network Dynamics of the Little Fork Shale Barren

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Shale barrens are steep sloping mountainside ecosystems characterized by rocky Upper Devonian age shale substrate, high light, and low water availability. They form an array of biogeographical “islands” throughout Mid-Appalachia whose niche dynamics, response to disturbance, and pollination ecology remain to be investigated. This project addresses information gaps of shale barren pollination ecology by using a network analysis approach, a set of statistical techniques used to display relationships, and quantifying within-season turnover of plant-pollinator interactions. Plant and pollinator data were collected via pollinator and vegetation surveys conducted during 10-day monitoring periods through the full growing season of a shale barren site in West Virginia. Monitoring period data revealed moderately specialized plant-pollinator networks that experience high within-season interaction turnover dictated by interaction rewiring. Simulation models confirmed that species abundance and phenology constrain interaction turnover and interaction rewiring. Linear regression analysis of weather conditions and pollinator activity found median temperature to have the strongest relationship with higher pollinator activity at greater median temperatures. Our findings expose the depth and dynamics of biodiversity present in a superficially understood “barren” ecosystem as well as hints to interaction variation indirectly tied to weather conditions.

83 - Recent discoveries and a way forward to assess invasive species risk from hitchhiking propagules at international seaports

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Humans have access to a vast array of commodities through global trade. As frequency and volume of trade increases, risks associated with trade must be measured to inform effective policy implementation. The biotic risk of the exchange of nonnative, potentially invasive, plant species increases with trade trends, threatening natural ecosystems and agriculture. Research conducted at international points-of-entry, such as seaports, requires collaboration among private, academic, and governmental sectors. Here, we demonstrate the importance and feasibility of these cross-sector collaborations with our study of the industrialized flora at the Port of Savannah, Georgia, USA. The flora demonstrated that the proportion of nonnative plant species richness was higher at this industrial site than any of the 19 comparison floras conducted in Georgia and South Carolina over the last 30 years. Further research taxonomically classified and quantified hitchhiking seeds that accumulated on refrigerated shipping containers and were transported inadvertently from overseas to the USA. We identified thirty taxa hitchhiking on shipping containers that carried a single commodity sampled over two years, primarily wind-dispersed members of the grass (Poaceae) and sunflower (Asteraceae) families. The most abundant species collected was the Federal Noxious Weed, wild sugarcane (*Saccharum spontaneum*). We estimated propagule pressure from these collections and further conducted controlled viability and survivorship trials. Based on these empirical data, process-based simulation models indicated high invasion risk for hitchhiking species, even with exceedingly low escape rates. To facilitate more rapid identification of propagules, we trialed DNA barcoding, and due to complications associated with obtaining clean gDNA directly from seed and lack of species-level identity from two standard cpDNA barcodes, we determined that development of other genetic-based species identification of propagules is necessary. We continue this collaborative initiative to better understand the risks associated with invasive species introduction through global trade and to inform strategic management efforts.

84 - Invasive Ants and their Invasive Plant Diets: Implication for Mutualism in Biodiversity Hotspots?

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Mutualisms have been proposed as mechanisms by which invasive fire ants (*Solenopsis invicta*) successfully exploit new environments. As generalist consumers, fire ant diets include sugary plant juices, which are accessed indirectly through mutualisms with honeydew insects. Fire ants are now established in protected, fire-managed savannas dominated by longleaf pine. Savannas are biodiversity hotspots and important refugia for numerous noteworthy and rare taxa. We explored plant diets of fire ants collected from longleaf savannas in Brunswick County, North Carolina, by amplifying DNA extracted from whole ants. Next-generation sequencing, based on *rbcL* amplicons, detected non-native *Lolium* spp., although native species of plants generally had greater numbers of sequence reads. We used Sanger sequences from *ITS2* amplicons to further explore the dietary importance of plants. Sanger sequencing, which creates nucleotide sequences from single DNA templates, can be problematic for mixed diets. Nevertheless, Sanger data implicated the invasive ryegrass *Lolium rigidum*, as the most common plant food. Ryegrass is ubiquitous in North Carolina but has not been observed in intact longleaf savannas. We hypothesize that fire ants consumed ryegrass indirectly; they did so by consuming honeydew from insects that dispersed into the savannas after feeding on ryegrass growing elsewhere. This hypothesis has yet to be tested. If correct, it has important bearing on the long-term integrity of longleaf pine ecosystems, which are managed as habitat islands surrounded by altered landscapes that are “reservoirs” for numerous invasive species. Mutualisms between fire ants and other invasive species could facilitate future introductions and may help to explain the success of fire ants in longleaf savannas.

85 - Challenges and opportunities associated with co-advising research students in a classroom setting

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Conducting interdisciplinary research with students can be difficult for faculty without expertise in multiple disciplines. To address this, co-advising of students by multiple faculty members can help students gain experience in disparate fields of study and increase their understanding of how different fields are linked. Here, we present our findings from a semester-long research course that was taught by two science faculty members with different areas of expertise. We highlight the benefits and challenges for students who were co-advised and present the results of surveys that assessed student’s understanding of disciplinary techniques and how to conduct interdisciplinary scientific research.

86 - Should we require all Biology students to take an entire semester of calculus? A former math major and math lover says "NO"!

Howard Neufeld

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Appalachian State University requires all of our majors to take a semester of calculus, a mandate that has been in place for over 40 years, but which has not engendered much serious discussion as to whether or not it makes sense to do this. Herein I argue that few of our majors will ever need to use calculus over the course of their careers (when did your doctor ever require calculus?) and that we should abandon this requirement. We should replace it with a quantitative skills set course that places greater emphasis on the mathematics that students might eventually use, such as arithmetic, algebra and modeling, and couple this with a greater emphasis on statistical analyses, which I suggest all students will need after graduation. Andrew Hacker, professor of mathematics and author of *The Math Myth*, argues similarly. He exposes the fact that various assumptions about the utility of a mathematical education are just myths, including, for example, the idea that a good grounding in mathematics improves performance in other academic areas. For example, of the 5% of students who scored over 700 on the math portion of the SAT, only 36% of them scored as high in the critical reading section. But of those who scored over 700 on critical reading, 44% scored 700 on the math portion! We should not be basing our curriculum on falsehoods! I propose a revised quantitative skills requirement where students choose between calculus or a mathematics-for-the-life-sciences, coupled with either basic or accelerated statistics, for a total of 7 credit hours of course work. This curriculum would give our Biology majors more flexibility and remove obstacles for students who do poorly in calculus, enabling them to graduate without having their dreams dashed by a requirement that is both cruel and unnecessary.

87 - Credentialing and Careers in the Bioscience Industry

Tamara Mandell

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Biotility, the education and training arm of the University of Florida's Center of Excellence for Regenerative Health Biotechnology (UF CERHB) was established to enhance Florida's competitive ability to attract and grow a world class biotechnology industry; building on the availability of responsive and relevant education and training programs which provide a multi-tiered source of workforce talent. The *Biotechnician Assistant Credentialing Exam* (BACE) was established in 2012 at Biotility to support economic development and provide skilled workers for Florida's expanding Biotechnology Industry. The opportunity to earn industry-recognized credentials is becoming increasingly important in programs designed to prepare students for careers, and as a result the BACE is now utilized nationwide. We invite you to learn about the development of the credentialing exam, the involvement of the bioscience industry for its recognition, and outcomes. We will also discuss strategies for success when preparing for the BACE.

- Learn specifics relating to industry involvement in the development of the BACE, and the positions to which it aligns.
- Discuss Biotechnological/Biomedical Science program content and skills in the context of bioscience industry knowledge and skill sets, as represented on the BACE. Participants will also identify strategies and best practices for success.
- Participate in discussions about the bioscience industry work environment, and career options.

88 - Thinking Routines, Graphic Organizers, and Guided Journaling on a Short-Term STEM Study Abroad Course

Darlene Panvini

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Short-term study abroad courses typically span 2-3 weeks and can pose pedagogical challenges for STEM faculty needing to cover a full course of content in a short amount of time. Challenges include: lack of pedagogical resources and research on teaching science abroad; the need to intentionally intervene to structure learning so students have time to process, connect, and reflect to promote deeper thinking; little time for preparation, grading, or content front-loading; and finding balance between class-based instruction and experiential activities. Thinking routines and graphic organizers were incorporated into Guided Journaling Worksheets to address these challenges during a short-term STEM course taught in Costa Rica during a Mayterm. The course, "Conservation and Sustainability in Costa Rica," was developed for both science and non-science majors. The thinking routines and graphic organizers fostered intentional writing that: sharpened student focus, connected experiences with concepts, encouraged thinking and learning, promoted student reflection, and elucidated student concerns. During the trip, the journaling helped students stay attentive to the learning aspects of the trip. The worksheet format of the journal resulted in manageable student and faculty workloads. In addition to study abroad courses, these tools can be a helpful resource for faculty teaching other types of experiential learning courses, including internships, community engagement, field trips, and laboratory activities.

89 - Seeing Trees Without the Forest: Teaching Dendrology Online during a Pandemic

Stephanie Jeffries

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Dendrology, a core class for several undergraduate programs, teaches students how to sight-identify 160-180 trees in a single semester. When classes pivoted online after two weeks of field instruction, we created a number of different ways for students to learn and practice identification remotely. Learning tools included synchronous online labs with teaching slide decks, a self-guided campus tour, and weekly playlists on our YouTube channel. Practice tools included weekly synchronous quizzes, online and in-person study sessions, and the Visual Learning – Plant Identification tool. Student demonstrated their proficiency using an online midterm and final as well as a digital plant collection. Students appreciated the variety of pathways that enabled them to learn identification, but their preferences varied. Some students perceived access inequity with many students off-campus who felt that learning was facilitated by being on campus. With the help of an instructional development grant, I plan to revise the most useful tools for the course, offer greater flexibility, and use reflective metacognition practices to enhance student success in learning identification.

90 - Ancient Pink and Purple Microbes for Research and Education: Making Microbiology Manageable

Priya DasSarma, Shiladitya DasSarma

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Biology course leaders often find approaching microbiology in the laboratory somewhat daunting, citing both a dearth of available activities, as well as concerns about the potential pathogenicity of many common microbes. In response, using the extensive research and outreach resources from our laboratory, we have developed a series of inquiry-based teaching modules using salt-loving halophilic Archaea (Haloarchaea), which are safe (BSL-1) and easy for cultivation, experimentation, and disposal. The modules are readily available and cover topics such as basic microbiology, antibiotics, life in extreme environments, genotype and phenotype, genomics, bioinformatics, as well as biotechnological and biomedical applications.

In addition to these laboratory modules, we have also developed a series of online resources that may be used for remote learning, including [HaloWeb](#), a facile resource for exploring genomes and proteomes, [MolGenT](#), a web-based molecular genetics self-guided tutorial site (featured by both [NASA](#) and [NSF](#)) and [HaloEd](#), for enrichment of laboratory experiences with discussion questions and published literature.

Using these resources, students are able to effectively engage in learning microbiology, molecular genetics and biology, and explore subjects as diverse as vaccine development to astrobiology. Our approach has led to successful experiential learning and extension activities from basic laboratory to in-depth honors and capstone projects.

91 - The effect of Staphylococcus aureus exposure on white-tailed deer trabecular bone stiffness and yield

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Osteomyelitis is an infection of the bone or bone marrow caused by the infiltration of bacteria, resulting in destructive inflammation, bone necrosis, and abnormal bone remodeling. With a growing number of osteomyelitis diagnoses, many of which are linked to *Staphylococcus aureus* (*S. aureus*), it is imperative to understand the pathology of *S. aureus* in relation to bone to provide better diagnostics and patient care. While the cellular mechanisms of *S. aureus* and osteomyelitis have been studied, little information exists on the biomechanical effects of such infections. We postulated that exposure to *S. aureus* for 72 hours would significantly decrease both the stiffness and yield of trabecular bone tissue. One hundred and three trabecular cubes (5 x 5 x 5 mm) from the proximal tibiae of *Odocoileus virginianus* (white-tailed deer) were used in this experiment. Bone cubes were sterilized and then swabbed to confirm sterilization before inoculation with *S. aureus*-ATCC-12600 (test group) or sterile nutrient broth (control group) for 72 hours. All cubes were then tested in compression until yield using an Instron 5942 Single-Column machine. Structural stiffness (N/mm) and yield (MPa) were calculated and compared between the two groups. Our results reveal that acute exposure to *S. aureus* does not significantly decrease trabecular bone stiffness or yield.

92 - Fishing for New Antimicrobials: Synergism between Fatty Acids and Piscidin Treatment

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A promising avenue for discovery of therapeutic agents involves studying host defense molecules produced by all known species on Earth: antimicrobial peptides. These members of the innate immune response, by virtue of structure and charge, destabilize biological membranes and potentiate killing of bacteria, viruses, fungi and yeast. The first antimicrobial peptides isolated from vertebrate mast cells were the fish piscidins P1 and P3, whose contrasting antibacterial activities involve Cu²⁺ binding. Other recent reports have uncovered the varied effects of exogenous polyunsaturated fatty acids (PUFAs) on bacteria, inducing changes in membrane permeability and altering resistance to antimicrobials that target membrane dynamics. The current study explores the activity of P1 and P3 against *Vibrio cholerae* independently and in combination with fatty acid supplementation. To accomplish this, we assessed membrane permeability and antibiotic resistance in fatty acid-exposed *V. cholerae* treated with P1 and P3. Using four physiologically relevant fatty acids (linoleic, arachidonic, eicosapentaenoic, and docosahexaenoic acids), we observed significant decreases in membrane permeability following fatty acid exposure. When P1 and P3 were administered, their antimicrobial effectiveness was changed depending upon fatty acid supplied in the media. The MICs of P1 and P1Cu were decreased when 18:2 and 22:6 were available and increased when 20:4 was present. The influence of fatty acid exposed *V. cholerae* depended on the Cu²⁺ binding status of P3. Subinhibitory P1 and P3 were also applied for measuring their impact on membrane permeability in the absence of PUFAs. Taken together, our results defined the antibacterial effects of two piscidins on *V. cholerae*. Furthermore, we observed synergistic and antagonistic piscidin susceptibility patterns elicited by dual treatment with exogenous PUFAs. The findings further highlight the potential for cationic antimicrobial peptides as therapeutic agents, as well as the intriguing possibility that PUFAs can augment bactericidal activity.

93 - Assessing the threat posed by antibiotic resistant bacteria in an urban river

Matt Heard, Chris Barton, Rachel Hongo

Belmont University, Nashville, TN

The emergence of antibiotic resistant bacteria in urban rivers poses a significant threat to ecosystem and human health. However, in most urban rivers, we lack an understanding of how common resistance is, how this threat changes spatially and temporally, and how bacterial genetic diversity effects the emergence of resistance. In this study, we aimed to address these issues by examining how antibiotic resistance varied in a common fecal indicator organism – *Escherichia coli* (*E. coli*) – across the Cumberland River in Nashville, TN over a two-month period in 2019. To carry this out, we collected 160 water samples from eight locations along the Cumberland River in January and February and assessed these samples for the presence of *E. coli*. Using samples that tested positive for *E. coli*, we determined whether isolates showed resistance to eight common antibiotics: Chloramphenicol (30 µg), Erythromycin (15 µg), Kanamycin (30 µg), Neomycin (30 µg), Novobiocin (30 µg), Penicillin (10 units), Streptomycin (10 µg), and Tetracycline (30 µg). Furthermore, we used phylogrouping to determine whether different isolates of *E. coli* varied in resistance levels to different antibiotics. Across our sampling effort, we found 140 isolates of *Escherichia coli* and we determined that 100% of isolates were resistant to at least five types of antibiotics. We also found no significant differences in the mean number of colony forming units of *E. coli* between our two sampling times. However, we did find that the presence of *E. coli* and the types of antibiotics that isolates showed resistance to varied depending on where the samples were collected and depending on what phylogroup the isolate was from. Ultimately, our findings suggest that the emergence antibiotic resistant bacteria may pose a growing threat in the Cumberland River and that more information is needed to determine the causal factors driving these trends.

94 - The Toxicology of the Trumpet Vine (*Campsis radicans*)

Katie Zinke

Elon University, Elon, NC

The Montagnard community represents dozens of tribes from the Central Highlands of Vietnam, some of whom now live in Greensboro, NC. Since some Montagnard community members are food insecure, they collect and consume large quantities of a native North Carolina vine, *Campsis radicans*. Montagnard community members chose to eat *C. radicans* because it resembles an edible plant native to Vietnam, *Oroxylum indicum*, and both species are in the *Bignoniaceae* family. As *C. radicans* is not readily consumed in its native range, there is little data available on the toxicity of its consumption. Extracts from *C. radicans* leaves and flowers were created following the preparation methods of many Montagnard community members, which includes boiling and cooking the plant matter. After collection, the extracts were diluted by a power of 10 (100%, 10%, 1%, 0.1%, 0.01%). Using *Daphnia magna* to observe mortality, four trials were performed with these extracts. Additionally, preliminary developmental and mortality assays were performed on *Danio rerio* embryos through exposure to various leaf extracts (100% boiled, 100% cooked, 10% boiled). The *D. magna* assays show that *C. radicans* leaves are more toxic than the flowers, and that boiled leaves are more toxic than cooked. Within the leaf extracts, the higher concentrations are more toxic than the lower concentrations. There are signs of developmental abnormalities, underdevelopment, and premature hatching in *D. rerio* embryos when exposed to the leaf extract. These findings suggest that *C. radicans* leaves are toxic and that consuming them may also cause possible developmental abnormalities. Based on this research, it is advised that the boiled water be discarded after the first cooking, the plant be consumed only in moderation and children and pregnant women avoid consumption all together.

95 - Finding herbarium specimens that could be used to trace heavy metal pollutants and compare them pre- and post- 1960s in the most polluted city in the United States, Chattanooga, Tennessee

Megon Stepaniuk

University of Tennessee at Chattanooga, Chattanooga, TN

Here we use herbarium specimens collected throughout the last 100 years from the greater Chattanooga area to screen them for the presence and concentration of metals. Chattanooga was declared the most polluted city in America in 1969 from the years 1961-1965 due to unchecked industrial emissions. Factories, railroads, coal furnaces, and iron making were only a few of many industrial operations releasing metal particulates and toxicants into the atmosphere. Metals can be deposited atop plant surfaces or soil when they find a sink there. Living plants have been used to assess metal pollution concentrations, though assessing historical pollution concentrations with herbarium specimens has recently been shown to be a valuable tool to science as well. The aim of this study is to use online digital repositories (SERNEC portal link) of herbarium specimens to identify candidate specimens that may be used in the future to chronicle airborne metal concentrations in the greater Chattanooga area: Hamilton County, Tennessee as well as Walker, Dade, and Catoosa Counties, Georgia. To be useful to a potential study of this kind, these specimens must meet the following parameters: there must be multiple specimens of each species from pre-, during, and post- 1960s; each specimen must have enough biological plant material to remove some without destroying the integrity of the specimen; and the species must be one with metal-accumulating properties or morphological characteristics that increase the chances of deposition upon the leaf surface.

96 - The soil seed bank in Elon University Forest

Austin Burnett

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The soil seed bank is extremely important for subsequent generations of plants during secondary succession. However, with the addition of invasive species into these forests has caused a decrease in biodiversity as plants compete for limited resources. This study aims to look at the soil seed bank in the Elon University Forest to determine the diversity of vascular plants and to determine the presence of invasive species present in the soil. Soils from ten different plots were collected and placed in pots to allow the seeds within the soil to grow. The pots were kept in a greenhouse and the soils were watered as necessary. Once plants had grown to a size where they could be identified, they were removed from the pots and the soil was removed to facilitate the germination of other seeds that might be in the soil. We found that there was a significant presence of invasive species within the soil seed bank. These results suggest that invasive vascular plants will continue to be a potential problem in Elon University Forest. The long-term ramifications of this will be discussed.

97 - Aging the unageable: using parasite size modes to age a crustacean host

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Populations of the native northeast Pacific intertidal blue mud shrimp, *Upogebia pugettensis* (Dana, 1852), are in steep decline rangewide. These declines are directly associated with intense infestations of the introduced Asian bopyrid isopod parasite, *Orthione griffenis* (Markham, 2004). Infestations lead to effective castration and total reproductive losses among female *U. pugettensis*. The nonindigenous origins of *O. griffenis* in North America and the absence of refuges for *U. pugettensis* preclude assumptions of host resilience, equilibrium domains or otherwise long-term co-existence. Intervention by delaying or reversing the decline of *U. pugettensis* will only be possible through understanding the ecology, energetics and population dynamics of this new host/parasite interaction, that has not been resolved for any marine bopyrid isopod in the world. Bopyrid isopod parasites effectively castrate their female decapod hosts by hemolymph extraction. However, even though host biomass can only be lost to *O. griffenis*, *U. pugettensis* weight per length does not decline with increasing parasite load. The energetics of this interaction, that are critical for understanding the population dynamics of this system have therefore remained an enigma. We therefore examined the energetics and population dynamics of this host/parasite interaction by analysis of the spatial and temporal variations in size and weight frequencies of *U. pugettensis* and their *O. griffenis* parasites. We compared the ages and growth rates of *O. griffenis* among hosts to infer energetic losses and then compared infested and uninfested host population size structures over time to estimate the effects of these energetic losses on host growth, reproduction and survival.

98 - An analysis of the effects of temperature on microbial productivity using long term data gathered from various LTER and iLTER sites

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Global climate change currently leads to increased global temperatures, more extreme weather patterns, habitat destruction, shuffled species distributions, and altered biological productivity. Though many of the global climate changes are most obvious at the macroscopic level, the changes begin at a much smaller spatial scale and accumulate. These smaller effects range from the loss of species diversity in areas to a change in microbial productivity at different latitudes. Microbes represent the underlying backbone of many ecosystems around the world by recycling nutrients and serving as food that fuels trophic levels. Therefore, by examining the effects of global climate change on some of the smallest denizens of the planet we can better understand the consequences of climate change on a larger ecological scale and take action to mediate the effects in the short term and plan for the future. In this study, I will examine the effects of global climate change, by quantifying the relationship between temperature and microbial productivity at different spatial scales at different latitudes in marine ecosystems. I will be using long term ecological data gathered from the various Long-Term Ecological Research and International Long-Term Ecological Research sites, (LTER and iLTER), from around the world. By using data gathered from multiple sites and across a relatively long span of time we can build a greater understanding of the widespread effects of global climate change across the planet as it relates to microbial productivity.

99 - Phenotypic plasticity in geographically central and peripheral populations of Jefferson salamanders (*Ambystoma jeffersonianum*) in response to simulated climate change

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Climate change is expected to negatively impact species worldwide, with varied ecological and evolutionary responses. Relatively sessile taxa, such as amphibians, will likely be precluded from large-scale migration in response to climate change, thus necessitating evolutionary and/or developmental responses “in place”. Phenotypic plasticity may assist in mitigating climate change effects under such circumstances by allowing populations to “track” changing climate with appropriate phenotypic responses. However, geographically marginal populations may exhibit reduced capacities for phenotypic plasticity in response to climate change, though this relationship has not been directly tested. To determine how geographically central and marginal populations respond to climate change via phenotypic plasticity, we monitored the growth and development of larval Jefferson salamanders (*Ambystoma jeffersonianum* (Green 1827)) under current, and predicted future, climate scenarios using a mesocosm design. Although phenotypic plasticity occurred in both edge and core populations, there was no statistically significant difference in

larval growth, survivorship, time to metamorphosis, or size at metamorphosis between core and edge populations under reduced hydroperiods. These results do not support assumptions of the abundant center distribution, which assumes populations in closer proximity to edges of species' geographic ranges exhibit reduced genetic diversity due to smaller population sizes than core populations, thereby limiting plastic responses in marginal populations. Our results could be explained by high habitat heterogeneity at range edges, which may prime peripheral populations for more varied responses. Future genetic studies may be beneficial in explaining possible differences between core and edge populations that may account for equivalent responses to climate change, such as gene flow between populations or genetic swamping. Factors such as these could subsequently impact the plastic responses of differing populations across species' geographic ranges.

100 - Toward a trait-based understanding of heterogeneous winter range shifts in eastern North American birds

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Many species' distributions are shifting in response to climate change. In the northern hemisphere, most distributional shifts are northward, but there is heterogeneity in the rate and direction of these shifts both within and between species, likely related to species traits. We used a large citizen science data set to quantify the rate and direction of latitudinal winter range shifts over four decades for 65 mostly passerine birds in North America, both regionally in eastern North America as a whole, and more locally for the Atlantic and Mississippi flyways separately. Most species showed northward range shifts, but many showed no latitudinal shift, and some shifted southwards. We documented differences in the rate and timing of shifts in the two eastern flyways (flyway asynchrony). We tested whether species traits (winter geography, movement strategy, and winter diet) could explain any of the regional or local variation in range shifts. We found that short-distance migrants and residents shifted northward at a higher rate than other types of migrants. Omnivores and feeder birds more consistently shifted northwards, whereas dietary specialists showed strong variation in the rate and direction of winter range shifts. Winter geography explained some differences between flyways, and movement strategy and diet explained some differences within flyways. Though documenting large-scale patterns of species responses to climate change has been dominant in the literature, variation in range shifts within and among species with differing ecological and biogeographic traits can help us better understand the mechanisms that mediate differing responses to climate.

101 - Factors influencing fatal bird-window collisions on the University of North Carolina Asheville campus

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It has been estimated that up to one billion birds fatally collide with glass windows in low to medium height buildings across North America every year. This research sought to quantify fatal bird-window collisions on the University of North Carolina Asheville campus. During the 2020 fall migration season, from September 28th to October 30th, four standardized surveys per week were conducted to determine the number of fatal collisions occurring at eight buildings across campus (representing 18% of campus buildings). Ad hoc collision data was collected from students and staff of the university during the survey period through a google form. Birdcast scores were used to determine if there is a correlation between window collisions and the number of birds migrating over the area. Building aspect and nearby vegetation structure were also measured to test if the surrounding foliage or aspect of the building influences collision frequency. A slight positive correlation between window collisions and Birdcast scores ($R^2=0.0763$) was observed. Windows located at eastern and southern aspects produced the greatest percentage of mortalities (28% and 26%, respectively). Buildings with surrounding vegetation structure of 1m-3m in height accounted for 63% of collisions. Ongoing surveys throughout the winter and spring of 2021 will be used to determine if there is a difference in collision frequency between the major migratory seasons. Life stages of carcasses collected across all surveys will be evaluated to determine if certain aged birds are more likely to collide with windows, despite the differing distributions of ages across local and migratory bird populations at various points in the year. An ongoing wildlife camera survey will be used to determine the frequency of carcass scavenging by wildlife. The findings of this research will be used to encourage UNCA to adopt mitigation strategies to reduce bird-window collision fatalities on campus.

102 - Spatial distribution of wildlife-vehicle collisions in southwest Virginia, USA

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Wildlife-vehicle collision (WVC) mitigation is important for wildlife conservation due to high wildlife mortality rates. Understanding the spatial patterns of WVCs can help wildlife managers and transportation planners develop measures to mitigate negative impacts on wildlife. We apply a kernel density estimation and Monte Carlo significance method known as KDE+ to data from a 2015 WVC study in the Appalachian Mountains of Virginia, USA in order to identify WVC hotspots and rank them according to strength and stability. Overall, 70 significant hotspots were identified among all species with 61, 53, 31, 17, and 21 significant hotspots, respectively, for each of the 6 species encountered most frequently as road kills: Virginia opossum (*Didelphis virginiana*), raccoons (*Procyon lotor*), woodchuck (*Marmota monax*), eastern cottontail (*Sylvilagus floridanus*) and striped skunk (*Mephitis mephitis*). Our approach provides a mechanism for managers to identify species-specific WVC hotspots and better refine mitigation approaches.

103 - The Oak Conservation Alliance: Forming an interdisciplinary network of allies to help prevent and monitor pathogens in the oak family (Fagaceae) such as sudden oak death, oak wilt, and beech bark disease

Ryan Huish, Megan Roark, Kaleigh Still, Skylar Mathieson, Isabelle Johnson, Samantha Hill, Ashleigh Nalls, Dylan Mullins

The University of Virginia's College at Wise, Wise, VA

The oak family (Fagaceae) represents many ecologically, ethnobotanically, and economically important species, including the oaks, chestnuts, and beech. However, multiple pathogenic diseases—such as sudden oak death, oak wilt, and beech bark disease—are threatening their long-term health and conservation. Synergistic, interdisciplinary, and cross-agency collaborations will be required to effectively monitor and plan for these threats. To this end, we have organized the Oak Conservation Alliance and have made (and are seeking more) allies from research and academic institutions, state agencies, non-governmental organizations, tribal organizations, private sectors, community scientists, and other groups to help carry out our goals. Forming this alliance is helping to provide a stronger framework for dynamic collaboration, educational outreach, and funding opportunities. Community forum discussions have been held, representing stakeholders from various backgrounds that have provided valuable insights to address concerns. Monitoring and educational methods include the use of mapping technologies, remote sensing, tissue sampling, community scientist applications, and various online platforms, merged with various approaches from the humanities. One methodological approach utilizes a delineated project nested within the iNaturalist social networking service where anyone—using their iNaturalist smartphone app—can take georeferenced and annotated photos of suspected symptomatic plants, which will then be stored in a database for plant pathologists to view, organize, and follow up with on-site if the symptoms appear diagnostic. The resulting data will be funneled into databases for use in future research, including spatial analyses, risk assessments, and ecological impact studies to help understand and preserve our valuable ecosystems and heritage in eastern North America.

104 - Interaction of freshwater wetland plant species with two size classes of microplastics in surface waters

Alexandra Woods, Dr. Jonathan Willis

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Microplastic contamination is pervasive throughout the environment, particularly in aquatic ecosystems. Extensive research has been performed regarding microplastic prevalence and impacts in marine environments, while microplastic effects in freshwater ecosystems is a comparatively new research field. Utilizing the natural filtration processes that occur in wetlands might provide a cost-effective technique for microplastic reduction and water quality improvement. Wetlands are frequently employed to address surface water pollution, but understanding is limited regarding how wetland systems may interact with microplastics. A series of mesocosm studies were initiated at the Nicholls State University Farm facility to address these data gaps. The first controlled-condition study assessed retention of two microplastic size classes by vegetative surfaces of *Panicum hemitomon*. The study duration was 2.5 months, during which cumulative stem height and stem density of *Panicum hemitomon* were measured monthly. Aboveground tissues were harvested and the abundance of microplastics remaining in surface water as well as that retained on submerged tissues was determined. Significant retention of microplastics by *Panicum hemitomon* was observed in both 43-250µm and 250-500µm size classes at dosages ~250,000 particles m⁻³ and ~170,000 particles m⁻³, respectively. This retention is likely mediated through biofilm processes on the submerged plant tissues. Importantly, no impacts to *Panicum hemitomon* survival or growth responses were found at any microplastic size class or dosage. A companion mesocosm study evaluated the impact of surface water microplastic concentrations up to 770,000 particles m⁻³ on the photosynthetic processes on various freshwater wetland species, with no reduction in either net CO₂ assimilation or stomatal conductance detected for any of the species assessed. Although further research is necessary, these results point to the potential efficacy of common wetland vegetation in the amelioration of microplastics in surface water.

105 - Effects of hemlock woolly adelgid on mesic understory tree community composition in the old growth forest of Lilley Cornett Woods

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Lilley Cornett Woods (LCW) is one of the best examples of an old growth, mixed mesophytic forest left in Kentucky. The forest composition has been well-characterized since Bill Martin established plots in 1971 that have been surveyed every 10 years. While the forest has been protected from many anthropogenic disturbances, it is still vulnerable to invasive species such as hemlock woolly adelgid (HWA, *Adelges tsugae*). This study compares data collected in 1999 (pre-HWA invasion) and 2010 (post-HWA invasion) to data collected in May to August of 2020 to determine how HWA has affected the understory populations of the beech (*Fagus grandifolia*) and hemlock (*Tsuga canadensis*) communities at LCW. Eleven hemlock dominated plots and eighteen beech dominated plots were surveyed across two different areas of the forest. The data collected in each plot includes tree species identity and diameter at breast height, with the understory composed of all trees 2.5 cm dbh to 12.5 cm dbh. Importance values, species richness, and total density were calculated to show change over time. There was an overall decrease in species richness and total density in each community, as well as an increase in the importance values of beech within each community. The overall increase in importance values of beech shows that beech trees are becoming more dominant in the understory of both communities. Importance values from the two areas show that understory composition is changing more rapidly in one area (Shop Hollow), while the other surveyed understory (Whittaker) is staying more stable.

106 - Observations of northern migration in the tropics, an Herbarium and citizen science approach

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Warming temperatures are affecting plant distributions globally. In the northern hemisphere, tropical plant species could move their ranges northward. This northward expansion has previously been documented in several cases, such as the northward expansion of mangrove species along the northeastern coast of Florida. Using herbarium specimens and the citizen science observation platform, iNaturalist, we note tropical plant species that may have recently advanced northward in Florida due to rising temperatures. Anthropogenic-assisted spread through cultivation or inadvertent movement of propagules may be partly responsible. The possibility also exists that these species have long been present but went unnoticed in these areas.

107 - Sandmyrtle (*Kalmia buxifolia*, Ericaceae) biogeographic history supports the Cape Fear Arch as a Glacial Refugium

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Sand myrtle, *Kalmia buxifolia* (Bergius) Gift & Kron, exhibits a disjunct distribution in eastern North America, ranging from the NJ Pinelands (NJP) to the Sandhills/Cape Fear Arch (SCFA) and westward into the Southern Appalachian Mountains (SAM), with no present-day geographic connection between NJP and southern populations, and very little between the SAM and SCFA populations. This species exhibits considerable morphological variability, leading experts to recognize between one (current consensus) and three species historically. Here, we update efforts to understand the biogeographic history and genetic structure of this species within the context of southeastern biogeography. We developed microsatellite markers using populations from each of the three regions and then applied these markers to a total of 11 populations of Sand myrtle and its closest relative, *Kalmia procumbens* (L.) Gift, Kron & P. F. Stevens ex Galasso, Banf. & F. Conti and evaluated various measures of population diversity and divergence. We evaluated phylogenetic signal using both chloroplast and nuclear markers and compared this to signals within the microsatellite data. Our updated dataset continues to reveal striking inter-population divergence in the south. Our analyses provides support for the hypothesis that the Cape Fear Arch of the Carolinas was a glacial refugium, from which Sand myrtle migrated northwestward into the SAM and northward into the NJP. Intermittent genetic connectivity between the NJP and SCFA populations appears to have continued for some time, but SAM populations have diverged considerably during the same period, raising new questions about the mechanism of divergence in the mountain populations.

108 - Update on the distribution of *Rhododendron eastmanii* (May-white azalea, Ericaceae) in South Carolina

Charles Horn

Newberry College, Newberry, SC

Rhododendron eastmanii (May-white azalea) was first described in 1999 and at that time was known from only two locations in South Carolina. In the subsequent 20 years, much field work has resulted in the documentation of 62 populations in 13 counties, all within South Carolina. Recent work has emphasized revisitation of populations within the Sumter National Forest to assess the status of previously populations, some not visited since 2000. Additionally, attempts to fill in distributional details along the Congaree Bluffs area of Calhoun and Orangeburg counties has continued. During field trips, more accurate population surveys have been completed to document population size, geographical range, and reproductive success. Most individuals are found on slopes of ravines at stream headwaters. As expected, some populations have declined, and some have expanded. Invasive species are apparently becoming more common and are negatively impacting azaleas, especially *Lonicera japonica*, and *Elaeagnus umbellata*. On a positive note, surveys of ravines adjacent to known populations have been fruitful in locating additional plants.

ASB Symposia

SYMPOSIUM 1: Integrating Virtual Mentoring and Professional Development Experiences with Field-Based Summer Undergraduate Research

Organizers: David Brown¹, Dustin Angell², Nick Koenig¹, Kelly Watson¹, Stephen C. Richter³, Melissa Pilgrim⁴

¹Eastern Kentucky University, ²Archbold Biological Station, ³Division of Natural Areas, ⁴University of South Carolina Upstate

Field-based research experiences provide multiple levels of training and bring together faculty and students to develop strong mentoring relationships. This process is challenged when in person interactions are limited. This symposium explores best practices and provides examples of virtual training experiences that augment research experiences when field interactions are limited. Virtual activities can include team building, professional development workshops, and panel discussions with professionals. A variety of platforms can be used to build and maintain training relationships, including video-conferencing, group chats, and other social media. The presenters in this symposium overcame substantial challenges to administer or participate in undergraduate research programs during the Covid-19 pandemic. They will share mentoring and training approaches that were effective in remote training situations and that either worked better or as well as in-person activities. The symposium will also explore how adopting virtual training practices can enhance participation of groups underrepresented in the sciences by creating opportunities that would otherwise not be available, regardless of the reason for limited in person interactions.

109 - Utility of Virtual Symposia in the Undergraduate Research Experience

Melissa Pilgrim

University of South Carolina Upstate, Spartanburg, SC

Undergraduate research is a high impact practice that addresses NACE core competencies. Symposia help to close the loop of the research process, as students gain experience communicating the results of their work. Virtual symposia can provide one alternative to the classic conference model, particularly as we all face travel issues caused by the pandemic. One of my responsibilities as Director of Research at the University of South Carolina Upstate is to organize an annual research symposium. The event is interdisciplinary and regional in scope. The symposium is traditionally an in-person event, but in response to the pandemic we transitioned the 2020 event to a virtual format using Microsoft Teams as our platform. One goal of oral and poster presentations at professional conferences is to have students experience interacting with a live audience; thus, we kept the virtual event synchronous (i.e., occurring in real time). Over thirty universities participated in the event and we were reasonably able to capture the spirit of an in-person symposium. I plan to discuss the pros and cons associated with hosting the symposium as a synchronous virtual event, what we learned about helping students prepare for virtual presentations, and the utility of Microsoft Teams as a platform for virtual symposia.

110 - Learning Outcomes of Research: Pre & Post-COVID-19

Nick Koenig

Eastern Kentucky University, Richmond, KY

As an undergraduate at Eastern Kentucky University, I have had the opportunity to participate in various research projects ranging from floristic surveys and invasion ecology, to genomic analyses and literature reviews. These projects have been prior to and after the COVID-19 pandemic as well as transitioning between the two. Overall, I will go into the learning outcomes (from a student's perspective) of research and how some of these skills lend themselves to a virtual setting over others. In particular, I will be going in-depth on three projects: canopy assessment and niche modeling of an invasive grass in an old-growth forest; a vascular flora of the Central Kentucky Wildlife Management Area in Madison County, Kentucky; and a literature review of the species concepts reference in newly described pteridophyte species. All three projects are in different fields of plant science and at different phases of research. Specific learning outcomes that will be discussed are species identification, canopy assessment, and field techniques which do not transfer well to a virtual setting while statistical analyses, coordinating meetings with collaborators, and conference presentations are much more accommodating.

111 - The Virtual Field: new remote learning experiences at field stations and marine labs

Dustin Angell

Archbold Biological Station, Venus, FL

In response to the academic shutdown caused by COVID-19 pandemic, the Organization of Biological [Field Stations](#) (OBFS) launched an emergency grassroots effort to create and distribute virtual learning resources from field stations and marine laboratory (FSMLs) to support faculty, students, and others. The initial effort resulted in a coalition of 50+ member organizations from across the world that began developing

virtual content for students of all ages. This talk will explore OBFS's "The Virtual Field" website and highlight the virtual education programs from one field station, Archbold Biological Station in Venus, Florida.

112 - Introductory Comments: Finding the Right Mix of Virtual and Field Experiences

David Brown

Eastern Kentucky University, Richmond, KY

Most ecologists conduct research in outdoor field settings, so it is seemingly essential that undergraduate students training to become ecologists work directly in the field. Although it is likely that students who have missed opportunities to conduct field research alongside mentors can make up for those lost experiences, they can take advantage of a variety of opportunities to continue to develop as scientists. We will hear from an undergraduate student who has research experience from before and during Covid-19 how he adapted to collaborating with faculty and his peers. We will also learn how the lost opportunities for field-based learning were buffered by a collaborative effort of the Organization of Field Stations to develop virtual field experiences. In addition to virtual meetings with mentors, some technologies, such as ArcGIS Online and iNaturalist are well suited to support students conducting field based research with primarily virtual mentoring. Presentations at conferences are often the culminating experience of undergraduate research, so we will also explore formats for virtual delivery of undergraduate symposia. Our panel discussion will explore how some virtual experiences may continue to be valuable and what aspects of being in the field are indispensable. We will also discuss how virtual activities can supplement and substitute for in person interactions in ways that may broaden participation in the sciences and ultimately increase the frequency of different types of collaborative interactions for students.

113 - Field-based technologies and virtual experiences for undergraduates: research, team building, and mentoring

Kelly Watson¹, Melanie Link-Perez²

¹*Eastern Kentucky University, Division of Natural Areas, Richmond, KY*, ²*Eastern Kentucky University, Department of Biological Sciences, Richmond, KY*

A variety of virtual and field-based technologies provide opportunity to deliver meaningful field-based research experiences for undergraduates despite challenges with in-person interactions due to Covid-19. We describe several technologies and virtual activities used to enhance and support field-based research, team building, and virtual mentoring during a Research Experience for Undergraduates focused on disturbance ecology at Eastern Kentucky University, which ran a hybrid in-person and virtual program during the summer of 2020. Technologies discussed will include ESRI's Collector and ArcOnline platform for field-based mapping and spatial analysis, the deployment of iButtons to enhance understanding of microclimate variations, encouraging iNaturalist activities and challenges for team building, creating field-based videos and presentations using GoPro cameras and Youtube, and virtual interactive experiences with the ThingLink image platform. Methods for delivering effective training on these technological platforms in a virtual setting will also be discussed.

SYMPOSIUM 2. A CURE for your Curriculum: Implementing Course-embedded Undergraduate Research (CUREs) into your Curriculum

Organizers: Judy Awong-Taylor, Clay Runck, Allison D'Costa

¹Georgia Gwinnett College

How effective are Course-embedded Undergraduate Research Experiences (CUREs)? There is a growing body of evidence that shows a link between student research and lasting learning, and that research experiences increase students' interest in careers in STEM (National Research Council 2003; Lopatto 2007; Lopatto 2009; Laursen et al. 2010). Lopatto (2007) also point out that even a short immersion experience in undergraduate research is enough to effect long-term gains in student motivation for learning, independence, understanding of science. More recently, Awong et al. 2016 showed that CUREs increase students' attitude about STEM, research skills and experience, and scientific literacy. These experiences also play a significant role in alumni getting into graduate school, being employed, or both (Schmitz and Havholm 2015). This symposium will provide information and activities on how to implement effective CUREs into the curriculum. The symposium will include faculty speakers from Georgia Gwinnett College, Clayton State University, Savannah State University, and University of Louisiana Monroe who have designed and implemented CUREs in a variety of biology courses (introductory and advanced levels). The symposium will introduce key components (STEM skills, assessment, etc.) of effective CUREs. Speakers will describe their CUREs, address key successes and challenges of their CUREs, and how instructors have addressed these challenges (including the Covid-19 impact). Assessment of CUREs will also be discussed. The symposium will include eleven CURE talks and will end with a live question and answer session with our panel of speakers. A live panel discussion/ Q&A session will be held at the completion of the CURE Symposium. Join faculty speakers from Georgia Gwinnett College, Clayton State University, Savannah State University, and

University of Louisiana Monroe who have designed and implemented CUREs in a variety of biology courses (introductory and advanced levels) for a general question and answer session.

114 - Effect of CURE Projects on Written Communication Skills in Gateway Biology Course

Takayuki Nitta, Xiaorong Zhang, Andrew Methven, Andrea L. Moore

Savannah State University, Savannah, GA

Savannah State University (SSU) is a public historically black university in Georgia. The department of Biology at SSU introduced two CURE projects, (i) Quantitative Analysis of Organic Molecules in Foods and (ii) Algal Growth Experimentation to transform traditional organic molecules and lab into a mini-research project in the BIOL 1107L – Principles of Biology I Lab. These CURE projects were designed to reinforce theory related to organic molecules and photosynthesis, engage students in experimentation and data analysis, and provide inquiry-based activities to bridge several core ideas in BIOL 1107, which would aid in student success and retention rates. The first CURE project, organic molecules lab, requested our students to hypothesize types and amount of organic molecules they selected, implemented the research protocol and analyzed experimental data to determine the protein and carbohydrate content of each food. The second CURE project was adapted from the Algae to Energy: Optimizing Systems lab by Boyce Thompson Institute. In the project, students designed and conducted an experiment that manipulated one or more variables involved in growing algae (CO₂, light and/or nutrients) and measured algal growth with a spectrophotometer and/or hemocytometer. The SSU CURE team assessed students' ability to apply the process of science, specifically, to design experiments using the Experimental Design Ability Test (EDAT) and their description of the experiment in lab reports across control (traditional labs) and experimental (CURE) groups. We here analyzed and assessed the two reports that were written through the projects. The reports are expected to describe some fundamental factors in science written communication (e.g. statement of questions, hypothesis, methods, data presentation, interpretation). The data analyzing the reports with our rubric and how our CURE projects influence students' skills in written communication will be presented in the conference.

115 - Learning Assistants Support Success in CUREs Courses

Barbara Musolf, Ann Showalter

Clayton State University, Morrow, GA

We have approached increasing student success in our introductory course undergraduate research experience (CURES) courses by teaching the process of science through careful scaffolding and by embedding learning assistants in our labs. Learning assistants are near peers who have recently succeeded in one of our introductory CURES courses. They receive pedagogical training and faculty mentoring so that they can guide students in thinking critically about material introduced in class, help students monitor their learning through use of reflections, facilitate group work, and help create a sense of belonging to our biology community. In teaching the process of science, faculty provide practice assignments that are used by students to have conversations with their class learning assistants about their understanding of the material. Learning assistants use their understanding of metacognitive practices by encouraging students to examine their learning successes and failures in the CURES labs. Each week, students write reflections on their learning and that feedback is used by faculty and learning assistants to address difficulties in comprehension that may arise in class. Over the semester, students become more adept at evaluating their learning. The CURES labs require that students work in groups to carry out experiments that they design together. Learning assistants weekly check in with groups to facilitate collaborative behavior and troubleshoot problems that may arise among group members. Students report that they are more comfortable engaging with Learning Assistants about problems they encounter in class and in group work. The relationships that students form with their learning assistant often persist beyond the CURES course and provide a bridge for students to more easily imagine themselves as future scientists.

116 - Biotechnology Applications in the Detection of Genetically Modified Foods

Ernest Ricks, Jr., Cindy Achat-Mendes, Jennifer Hurst-Kennedy, Robert Haining

Georgia Gwinnett College, Lawrenceville, GA

This CURE provides students the opportunity to learn and use leading techniques in biotechnology, while strengthening their understanding of the central dogma of biology during an authentic research experience. In one module, students can use PCR to detect the presence of common genes found in genetically modified (GM) foods. In a second module, students can isolate messenger RNA, synthesize cDNA, and employ real-time quantitative PCR to investigate the expression of GMO genes. The last module utilizes Enzyme-Linked Immunosorbent Assay (ELISA) to detect the presence of GM proteins. Students receive training in lab research/STEM skills including troubleshooting equipment, experimental design, maintaining a lab notebook, writing manuscript-style lab reports, and oral presentation of research findings. Students are required to know the purpose of reagents and procedures rather than follow cookie-cutter recipes. They learn theory and application of PCR, real-time PCR, and ELISA to investigate the relationship between genes, RNA and proteins, respectively, in GM foods. This CURE resulted in 20+ conference student presentations. Its effectiveness was assessed by evaluating gains in *student learning and student attitudes* towards research and STEM careers. Assessment tools included: *pre- and post- content surveys* (multiple choice questions linked to course learning objectives), *4-year URE student survey*, and *lab report rubric designed by Biology Faculty*. The attitudinal survey data suggest that following participation in the GM foods lab design, students: 1) Became more knowledgeable about genetically modified food testing and central dogma; 2) Appreciated taking ownership of their own research project; 3) Expressed better understanding of research in the biotechnology field. Significant outcomes of this lab curriculum include student-initiated hypothesis-driven authentic research projects, troubleshooting and critical thinking as students worked through technical challenges. Despite the COVID-19 pandemic, students were still able to successfully participate in the CURE, through the use of video-recorded training, on-line meetings, and virtual research conferences.

117 - Research for ALL: CURE the undergraduate curriculum

Allison D'Costa, Clay Runck, Judy Awong-Taylor, Cindy Achat-Mendes, Tirza Leader

Georgia Gwinnett College, Lawrenceville, GA

Unlike traditional apprentice-style research that is highly selective, Course-embedded Undergraduate Research Experiences (CUREs) increase inclusivity because they offer research experiences to all students enrolled in the course irrespective of their background and skills. For institutions that attract a diverse population of students, especially from groups that are underrepresented in STEM, a CURE in a freshman science course might be a student's first exposure to research. While all CUREs have been designed to help students develop STEM skills and competencies, some CUREs, especially those designed for freshman, offer more guided-inquiry and research that is novel to the students, while others offer authentic research experiences. We have developed a model in which CUREs are offered to all STEM majors during all four undergraduate years, so as students progress towards matriculation, they are exposed to multiple CUREs, repeated research experiences, and scaffolding of STEM skills, and, as a result, build confidence to conduct independent research and enter the STEM workforce. We have conducted a longitudinal study to determine the impact of CUREs on student attitudes towards STEM, gains in STEM skills, GPA, gender, ethnicity, and retention rate. In this presentation we will describe the development, implementation, assessment, and results to date of our four-year CURE model.

118 - Novices and Nerds: Data validity in the study of birds

Bill Ensign

Kennesaw State University, Kennesaw, GA

Increased interest in Course-Based Undergraduate Research Experiences (CUREs) has led many faculty to incorporate CUREs into their classroom. A perceived advantage of using CUREs is that they allow faculty to leverage their limited time, effort, and resources by combining teaching and research into a single experience. Ideally, data gets collected, students learn by doing, and over the course of multiple iterations the faculty member gets a publication. For these benefits to be fully realized the validity of the data generated by students needs to be equivalent to that of any other well-constructed scientific investigation. To assess the quality of student generated data, I designed a 4-week lab module where students (novices) used a well-defined protocol to collect presence/absence data on bird species at four fixed stations around a lake on the Kennesaw State University campus. During the same period of time, an expert (the nerd) also collected data using the same protocols at the same stations. Novice and nerd data were compared in two ways. First, species accumulation curves and asymptotic species richness for each location were generated for both data sets to assess the reliability of novice data for studies of bird community composition. Second, detection probabilities of selected species for both data sets were estimated to assess novice data reliability for studies of bird species ecology. Results indicated that asymptotic species richness was similar for both data sets, but the nerd rate of species accumulation was much more rapid. Detection probabilities of visible, vocal species were similar between novices and nerds but detection probabilities of smaller, cryptic species were much lower for novices. These results suggest that execution of a well-designed pilot study with potential to reveal inconsistencies in data between novice and expert researchers is essential to successful implementation of CUREs in field-based studies.

119 - Designing CURE Assessment

Tirza Leader, Judy Awong-Taylor, Cindy Achat-Mendes, Clay Runck, Allison D'Costa, Chantelle Anfusio, David Pursell

Georgia Gwinnett College, Lawrenceville, GA

Assessment is a crucial piece of any experimental design, classroom experience, or innovation. We will walk through the process of designing assessments pertinent to CUREs. Strengths and weaknesses of different forms of assessment will be discussed. Participants of this presentation will learn to integrate different forms of assessment to track student learning, and evaluate CUREs.

120 - Implementing CUREs in the Curriculum: Results of Experimental Design Ability Test (EDAT)

Andrea L. Moore, Takayuki Nitta, Xiaorong Zhang, Andrew Methven

Savannah State University, Savannah, GA

As a part of the Vision and Change movement, a team of biology faculty at Savannah State University have begun to redesign the introductory biology labs to include a component where students apply the process of science through CUREs. The team has developed and implemented two CUREs that transform the traditional cookbook labs into two short mini-research projects designed to answer real world questions. The first, Quantitative Analysis of Organic Molecules in Foods and the second CURE entitled, Photosynthesis: Algal Growth Experimentation, are aligned to the student learning outcomes for the lecture class and provide skills that will be used in successive courses. The organic molecules CURE allows students to measure the protein and carbohydrate concentration of foods to address the claim that vegans can get the necessary components for a healthy diet. The photosynthesis CURE is a modification of Algae to Energy: Optimizing Systems lab by Boyce Thompson Institute and allows students to manipulate variables (CO₂ or wavelength of light) to optimize the growth of *Chlorella*. The CUREs allow students to apply the scientific process, analyze data, and write for the sciences. We assessed students' ability to apply the process of science by designing experiments. The Experimental Design Ability Test (EDAT) was administered as a pre- and post-test with one formative assessment for the CURE sections. Results of the first two years of implementation, challenges, and concerns will be shared.

121 - Implementation of a semester-long, cell culture and fluorescence microscopy CURE with an underrepresented STEM student population

Jennifer Hurst-Kennedy, Michael Saum, Cindy Achat-Mendes, Allison D'Costa, Elisabeth Javazon, Shoshana Katzman, Ernest Ricks, Jr., Alessandra Barrera

Georgia Gwinnett College, Lawrenceville, GA

Georgia Gwinnett College (GGC) is an access institution with a diverse student body, located in metro Atlanta. To strengthen research skills, teach employer-valued cell biology laboratory techniques, and increase student engagement; a semester-long, inquiry-based CURE was developed and implemented in Cell Biology with Laboratory (BIOL3400K), a sophomore-level course, which serves as a “gateway” to all upper-level Biology courses. This CURE centers on the investigation of a student-chosen experimental factor on the viability of cultured, mammalian cells. Through participation in this CURE, students gain experience in cell culture, fluorescence microscopy, and viability assays, and strengthen important research skills, such as literature searches, graphing, and data analyses. The impact of this CURE on student learning gains and attitudes was assessed using a pre-/post- content exams and the Colorado Learning Attitudes about Science Survey (CLASS). Our data show that all students made significant content gains. Female students made larger learning gains than male students. Additionally, minority students performed better than majority students in some content areas. Student attitudes did not change, or in some cases were slightly more negative after the CURE. Overall, this CURE had a positive impact on students by engaging them in an inquiry-based laboratory experience.

122 - Development of a Novel Online SARS-CoV-2 CURE for an Introductory Genetics Course

Adrienne Cottrell-Yongye, Elisabeth Javazon, James Nolan, Jill Penn, Jennell Talley

Georgia Gwinnett College, Lawrenceville, GA

In order to retain high impact lab practices while following social distancing requirements of the COVID-19 pandemic, we created a multi-week lab module that allows students to participate in a course-embedded undergraduate research experience (CURE) about SARS-CoV-2, the virus that causes COVID-19. The research project can be completed online and teaches students multiple techniques used in Bioinformatics, an emerging and lucrative field that combines Biology and Computer Science. Students first learn the history and biology of the SARS-CoV-2 virus, develop hypotheses and design their own experiments to analyze and compare various aspects of the SARS-CoV-2 virus. Additionally, students present their findings in either oral or written form, thus engaging in all aspects of the scientific method. Research projects ranged from students analyzing how the virus spread to a specific geographical area while others investigated various mutations in the viral genome and possible implications of the mutations. The spread of the recently identified UK and South African variants will be a new area of interest. During their investigations, students actively engage with collaborative databases such as NCBI and GISAID, which as of January 21st, 2021, has collected more than 400,000 SARS-CoV-2 sequences worldwide since the pandemic began. Students have access to the same data as leading epidemiologists and virologists and have potential to discover new information about the virus. In August, researchers from the US and UK published an article about a mutant version of the Spike protein using the same tools as the student independent research projects.¹ Students are excited by the challenging project because it incorporates practical and relevant scientific information. Preliminary assessment of this CURE is presented in a poster titled: Preliminary Assessment of a Bioinformatics CURE in an Introductory Genetics Course about SARS-CoV-2.

1. Korber et al. 2020. *Cell*:182, p. 812-827.

123 - Using NSF's NEON data in the undergraduate ecology classroom

Jennifer Kovacs

Agnes Scott College, Decatur, GA

Bringing meaningful and authentic research experiences into the ecology classroom during a regular semester is challenging. There are very real constraints on completing a student-driven research project, from conception to data analysis to presentation, within a thirteen week period. One way to enable students to fully partake in a very authentic student-driven research project is to use publicly available databases. However, very often these datasets have already been analyzed or are incomplete and hard to work with. NSF's National Ecological Observation Network (NEON) database provides high quality, research grade datasets that in many cases have not been previously analyzed. While some of these data products can be large and over-whelming to beginning researchers, with some assignment scaffolding and some basic data wrangling students can quickly begin to ask exciting research questions and perform their own data analysis. This semester I taught an ecology CURE which paired the open source project-based textbook "Passion Driven Statistics" with NEON datasets. Students asynchronously worked through 15 online modules including videos which introduced them to topics that ranged from how to ask a scientific research question to how to perform univariate and multivariate statistical analyses using either in R or Python (student's choice). Most students had not used either programming language prior to starting the course, and 7 out of the 13 students had no research experience. By scaffolding the research experience and slowly introducing students to these large and comprehensive NEON data products, students were able to gain valuable research, data wrangling, and data analysis experience in the undergraduate classroom during a single semester.

124 - Microbial diversity in a “Pond in a Jar” ecosystem-A CURE at the University of Louisiana Monroe

Chris Gissendanner, Tom Sasek, Srinivas Garlapati, Timothy McMahan

University of Louisiana Monroe, Monroe, LA

Microbial diversity is an important component of all ecosystems. In humans, disruption of the microbial ecosystem of the gut can lead to serious health consequences. We have designed a CURE that investigates the effects of environmental disruption on the microbial diversity of a laboratory “pond” ecosystem. This CURE is an update of a “Pond in a Jar” project that has been a part of the introductory biology lab course at ULM for over 15 years. In the updated CURE, students utilize microbiological techniques to quantitatively and qualitatively assess microbial diversity following chemical disruption of the ecosystem. We intend for this CURE to address the following STEM skills: 1) Ability to apply the process of science; 2) Scientific communication; and 3) Data analysis. Experience from the initial implementation of the CURE led to revisions to better guide students in quantitative analysis and interpretation of results. The current version also incorporates identification of bacteria by 16S rDNA sequencing. We will present the results of this ongoing effort.

125 - Pandemic-Induced Improvements to the Scaffolding of CUREs for Introductory Biology

Ann Showalter, Michael Sitvarin, Vivian Padin-Irizarry, Barbara Musolf

Clayton State University, Morrow, GA

For the last several years, we have been transforming the curriculum of our major’s introductory biology laboratory courses by including course-embedded undergraduate research experiences (CURE) and other high-impact teaching practices. In response to the pandemic, these courses were converted to a hybrid format with shortened class times, which required substantial adjustments in how the courses were scaffolded. Our CURE courses emphasize scientific thinking through the process of science and data analysis. To develop these skills, students need ample practice and instructional feedback. To support this, we created video lectures for all aspects of the courses, and developed pre-lab assignments that are discussed in groups during the synchronous lab times. We also make use of video demonstrations during class to train students on observing animal behavior and developing procedures. We have found many of these instructional tools developed in response to the pandemic to be substantial improvements over what we did pre-pandemic. This presentation will outline the structure of our CURE courses and our new strategies for scaffolding student learning.

126 - A curriculum embedded undergraduate research experience that utilizes the antlion feeding and behavior

Patrick Cain, Mark Schlueter

Georgia Gwinnett College, Lawrenceville, GA

We created a CURE project that utilizes antlions, which are also sometimes referred to as doodle bugs. Antlions are insects in the Family Myrmeleontidae and are best known for the fierce prey-capturing behavior exhibited by their larvae. The main goal of the following proposal is to create a CURE project that utilizes antlions in the introductory BIOL 1108K course to help increase student engagement. In this project, we introduced BIOL 1108 students to the biology and behavior of antlions. The specific focus of the project initially was the predatory behaviors and feeding habits of the antlion larvae. Students in each class were divided into groups of three or four to complete the initial project, after which the students developed a second experiment of their own design. We compared survey data covering basic biology, experimental design, and antlion biology between three BIOL 1108 sections that used antlions and two sections that conducted corn growth experiments (control groups). BIOL 1108K has three STEM skills assigned to it (data analysis, effective communication, ability to apply evolutionary concepts). Thus, during this research project, students gathered raw data in their experiments and then used t-tests and ANOVA to compare, contrast, and interpret data. Students also practiced their “effective communication” by writing a scientific paper. Evolutionary concepts will be explored, discussing the ecology and evolutionary principles behind the predatory tactics of the antlion larvae. While antlions are generally easy to work with, observing predatory behavior is always challenging.

127 - Genetics course-based undergraduate research experience (CURE) exploring disease utilizing bioinformatics & nematodes in hybrid learning

Natalie Forte¹, Anil Challa², Katelyn Cooper³, Ashley Turner¹

¹*Jacksonville State University, Jacksonville, AL*, ²*University of Alabama at Birmingham, Birmingham, AL*, ³*Arizona State University, Tempe, AZ*

Genetic and evolutionary conservation analysis in model systems can provide insight for conceptual understanding of gene structure, function, and evolution. We developed a semester-long course-based undergraduate research experience (CURE) in a hybrid (online and in-person) learning environment with the intent to engage students in an authentic research experience focused on bioinformatics using the genetic model organism *Caenorhabditis elegans*. Using a combination of bioinformatics and ‘wet lab’ tools, students analyzed the conservation of a gene and structure-function analysis of disease-associated variants of unknown or likely pathogenic clinical significance. The course was offered fall 2020 with 39 students enrolled. Embedded in the course were a series of workshop-style research sessions, tutorials, and ‘wet lab’ sessions. Each student selected a human or animal disease of interest and worked through a series of tools to identify a disease-associated gene with a corresponding orthologous gene in *C. elegans* and disease-associated variants for analysis. Students took these identified conserved variants into ‘wet lab’ sessions to design and test a polymerase chain reaction-based assay to serve as a genotyping assay in downstream CRISPR-Cas9 experiments. Discussions, responsible conduct of research training, electronic lab notebooks, iterative project reports, quizzes, and group oral presentations were assessed for mastery of learning objectives and research progress. We assessed the impact of the CURE on students’ cognitive and emotional ownership using a closed ended survey administered at the end of the semester. We also examined to what extent students’ reasons

for choosing their disease of interest influenced their cognitive and emotional project ownership. We found that students developed notably high cognitive and emotional ownership, comparable with CUREs taught in-person. Early analyses also suggest that students with more personal reasons for choosing their disease demonstrate higher cognitive and emotional ownership compared to students without a personal reason for choosing their disease.

ASB Posters

P1 - The Effect of Hand Dominance on Nerve Conduction

Kassandra Myers, Heather Evans Anderson, Michele Skelton

Stetson University, Deland, FL

There is limited research on how hand dominance relates to the speed of nerve conduction. Research on the relationship between handedness and nerve function may be beneficial in rehabilitation of cerebrovascular accident patients. In stroke patients, loss of strength and mobility occurs when nerve function decreases. Stimulation of sensory nerves in stroke patients promotes recovery and handedness may be an important consideration in treatment plans. Hand dominance occurs due to persistent overuse of one hand, which creates stronger neural pathways in comparison to the non-dominant side. The purpose of this study was to determine if differences in nerve conduction strength could be measured between dominant and nondominant hands in healthy subjects in order to establish a baseline to which measurements from stroke patients could be compared. Twenty-four, college-aged males and females were recruited for this study. An iWORX 214 lab kit was used to measure nerve conduction velocity by administering median nerve stimulation through electrodes. Electrodes were placed in 5 locations on the hand and lower arm. Stimulation began at 0.0 volts, then increased 0.5 volts up to a maximum stimulation of 1.5 volts in order to measure the amplitude of muscle response. LabScribe 4 Data acquisition and Analysis software was used to collect data. A paired samples t-test compared data from dominant to nondominant hands. Dominant hand nerve conduction velocity was $0.0029 \text{ volts} \pm 0.0014$ and non-dominant hand nerve conduction velocity was $0.0023 \text{ volts} \pm 0.0012$. Preliminary results showed a statistical significance ($p \leq 0.05$) between dominant and non-dominant hands. Further research will include measurement of both motor and median nerve conduction velocity.

P2 - Effects of bisphenol-A on nerve activity in *Lumbricus terrestris* and *Procambarus clarkii*

Destiny Sciuva, Todd Wood, Abigail Kruger, Julie Wilson, Madison Chen, Claud Bugheni, Jaleesa DeJesus, Meenal Joshi, Erin Perry, Justin Rush, Skylar Smith, Jordan Spires, Nicholas Wilson, Katey Hughes

Columbus State University, Columbus, GA

Bisphenol A (BPA) is a widely used plasticizer that has gained controversy in recent decades due to increasing concern of biological and ecological disruption. Research has shown that BPA produces a wide variety of adverse effects on processes related to development, metabolism, and general survival. Scientific findings on the effects of BPA as an environmental contaminant are fragmented in regards to regulatory implications and overall ecosystem disturbance. Previous studies show measurable harm from BPA exposure in organisms at environmentally-relevant concentrations defined as equal to or less than $12 \mu\text{g/L}$. For the purposes of this study, we exposed both an aquatic and a terrestrial invertebrate to $10 \mu\text{g/L}$ BPA to determine the effects on key features in nerve activity in separate trials. Results displayed a statistically significant decrease in both frequency and amplitude of nerve activity across all treatments at increasing voltage levels along with other morphological changes in the common earthworm, *Lumbricus terrestris* (2-way ANOVA, $F_{36,324}=32.18$, $P<0.0001$). For the crayfish, *Procambarus clarkii*, there was no significant difference between control and BPA groups in regards to frequency and/or amplitude of action potential, but there was significance from the mean, showing progression toward potential change if more trials were tested. The results of this study indicate that BPA does have an effect on nerve activity in the invertebrates tested. Further studies on the effect of such toxicants can provide recommendations for updated and more frequent environmental contaminant testing for better regulatory and conservatory management.

P3 - Longitudinal change in fish size in a central Florida spring

Tabor Filippello, Tessa Barnard, Kirsten Work

Stetson University, DeLand, FL

Flowing water produces longitudinal zonation; in streams, upstream areas may be more turbulent and have higher dissolved oxygen than downstream areas. In contrast, freshwater springs may be very turbulent at the headspring, but the dissolved oxygen may be quite low. As a result, many spring runs exhibit zonation of fish species, with small species tolerant of low dissolved oxygen (e.g. poeciliids) at the headspring and much larger species downstream (e.g. large centrarchids). However, for species balancing metabolic need and predation risk, this species zonation may be further complicated by longitudinal changes in size. Volusia Blue Spring provides a good of this zonation; the water leaving the headspring contains approximately 0.1 mg L^{-1} of dissolved oxygen. Given the potential zonation of large predatory fish, we compared the upstream and downstream sizes of three species of fish vulnerable to predation: *Gambusia holbrooki*, *Lepomis macrochirus*, and *L. microlophus*. At one upstream and one downstream site, we seined for and measured all *G. holbrooki* and small *Lepomis* individuals captured. For the larger *Lepomis* individuals, we snorkeled each site entirely, counted the fish that we observed, and photographed representative fish with a GoPro outfitted with two underwater lasers mounted with parallel beams 7 cm apart. We measured the fish on the photographs and calculated their length using the 7 cm reference points on the side of each fish photographed or on the substrate next to the fish. The sizes of all three species differed between upstream and downstream sites, with larger *G. holbrooki* and smaller *Lepomis* individuals upstream than downstream. Predators may be rare upstream, so fish populations may be more vulnerable downstream. To avoid predation downstream, the small *G. holbrooki* may avoid detection, whereas the large *Lepomis* may exceed the gape width of the predators.

P4 - Correlation Between Obesity, Diabetes, and Inactivity in Southwest Georgia

Morgan Smith

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Studies have shown that areas with lower walkability index scores have a higher rate of obesity and diabetes among their population. The goal of this study is to analyze the correlation between walkability and obesity, inactivity, and diabetes for Thomas, Grady, and Brooks County, GA. When comparing Grady, Brooks, and Thomas County, Grady County has the highest inactivity rate (32.1 %), a similar obesity rate (33 %) when compared to the other two counties but has the lowest prevalence of diabetes (12.1 %).

P5 - The local and landscape features associated with roost site selection and nesting success in urban black vulture (*Coragyps atratus*) and turkey vulture (*Cathartes aura*) populations

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Landcover changes resulting from increasing urbanization alter habitat type, structure, and resource availability on local and global scales. For vultures, urbanization may have both positive and negative impacts, such as increased foraging opportunities due to roadkill presence and decreased nesting success due to human presence, complicating our understanding of the effect of urbanization on these essential species. We examined how landscape and local features affect roost site selection and nesting success of black vultures (*Coragyps atratus*) and turkey vultures (*Cathartes aura*) in the Charlotte Metropolitan Area, North Carolina. We counted the number of vultures at fifteen permanent roost sites once a month between November 2019-March 2020 and monitored the clutch size, number of predated young, and number of fledglings once a week between March-August 2020 at two black vulture rural nests and one black vulture urban nest. At each roosting or nesting site, we characterized local ground cover, vegetation height, canopy cover, and weather conditions, and measured landcover and road density in the surrounding landscape with radii of 0.4 to 20km. We assessed the effects of these variables on the number of roosting vultures using generalized linear models and multi-model inference. The best model of roost site selection included date, site, wind speed, utility corridor width, vegetation height, and amount of open water and developed landcover within 4km of sites. Of these variables, open water and developed landcover were both associated with higher numbers of vultures while wind speed, utility corridor width, and vegetation height were associated with lower numbers. The two rural black vulture nests each successfully fledged two young whereas the urban nest failed with no eggs hatched. Our study revealed that vulture roost numbers are associated with wind speed, utility corridor width, vegetation height, open water, and developed landcover, while successful vulture nests have decreased urban landcover.

P6 - Vertical layering of animals in forested ecosystems in northwest Tennessee

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Increases in vertical layering of vegetation in ecosystems tends correlate to higher diversity of animals due to increases in available niches. By placing feeders at different heights in the environment, our goal was to observe stratification of animals in forested ecosystems in northwest, Tennessee. We mounted 5 motion sensing cameras 1m above the ground and 5 cameras 3m above the ground. Directly in front of the cameras, we placed feeders baited with suet mixed with seeds, peanuts, and peanut butter. The cameras took a total of 31,190 photos and we were able to identify animals on 1,569 photos taken at 1m and 4,314 photos taken at 3m. We observed six species of mammals visiting 1m feeders and 5 species on 3m feeders. We observed 15 avian species visiting 1m feeders and 19 species using 3m feeders. While birds were observed feeding at both heights, they were photographed most frequently on the 3m feeders. The overall diversity of organisms observed was slightly higher on the 1m feeders. Overall, there was intermediate overlap in species composition between the two communities suggesting that some vertical layering is occurring within the forest. We also observed temporal layering since the majority of mammals visiting the feeders were nocturnal, whereas birds were more diurnal.

P7 - Consumptive and non-consumptive predatory effects of wood frog (*Lithobates sylvaticus*) tadpoles on aquatic invertebrate communities

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Consumptive effects of predation are those that involve a consumption of prey, and include limiting prey recruitment and initiating top-down trophic cascades. Non-consumptive effects of predation simply involve predator presence and associated cues of predation risk, which can alter foraging patterns of prey. Consumptive and non-consumptive effects of predation have been well-studied in fish and salamanders in freshwater ecosystems, but not in anuran tadpoles. Although tadpoles have been historically labelled as strict herbivores, recent research suggests they are opportunistic omnivores that feed on a variety of zooplankton, macroinvertebrates, and other amphibian larvae. However, the predatory effects of tadpoles on invertebrate communities are largely unexplored in ephemeral habitats in temperate climates. The goal of this study is to investigate the consumptive and non-consumptive predatory effects of wood frog (*Lithobates sylvaticus*) tadpoles on zooplankton and macroinvertebrate communities from ephemeral ponds in eastern Kentucky. To determine and compare proportions of herbivory, detritivory, and omnivory, I will

dissect tadpoles collected from ephemeral ponds in the Daniel Boone National Forest. I will then use mesocosms with separate free-swimming and caged tadpole groups along with a control with no tadpoles to separately quantify the consumptive and non-consumptive predatory effects of tadpoles on macroinvertebrate and zooplankton communities and primary productivity. I will also incorporate different levels of tadpole body size and habitat shading into this design to determine if these factors influence these effects. This study will provide ecologists a greater understanding of the potential consequences of anuran species loss on invertebrate communities in ephemeral, temperate habitats.

P8 - Overgrazing Effects on Desertification in Mexico

Austin Roberts

Thomas University, Thomasville, GA

Desertification is the transformation of fertile land into desert land over time. The main causes of Desertification include: >Drought>Deforestation>Inappropriate Agriculture >Overgrazing. This study focuses on the effects of Cattle overgrazing on Desertification in Mexico. Soil Degradation Severity has been chosen as the measure used in this research. Soil degradation severity is how much the soil quality has declined. If it is severe enough, this can lead to the growth of desert land over time. A Precipitation map is included to help illustrate the correlation of Cattle density and degradation.

P9 - Assessing human disturbance in Least Tern (*Sternula antillarum*) colonies in St. Augustine, Florida

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The Least Tern (*Sternula antillarum*) is a colonial nesting seabird that breeds along the coast in North, Central and South America as well as the Caribbean Islands. This species has suffered extensive habitat loss throughout much of its range and is designated as Threatened in the State of Florida. These birds are especially vulnerable during the breeding season due to nesting in frequently disturbed habitats such as beaches, sandbars, and shell rakes. Sign posts and ropes are frequently used to help protect nesting sites by warning the public of the presence of nesting birds and by establishing a buffer zone around the colony. In this study, we examined human disturbance in two Least Tern colonies located in St. Augustine, Florida: Anastasia State Park and Julia's Island. To achieve this, we used images recorded by remote digital trail cameras that were deployed in these colonies from April to July of 2020. The trail cameras, using a combination of motion-detecting and time-lapse triggers, allowed us to determine the type and frequency of disturbance, as well as the effects of these disturbances on the behavior of nesting terns. Preliminary analysis of the data shows that, despite the buffer zone established by the sign posts, humans are the most frequent disturbance to nesting terns and elicited the most responses in at least one of the two colonies we surveyed. When terns are disturbed, they can leave their nests for extended periods of time, leaving eggs and chicks exposed to the hot sun and to predators. When this occurs frequently, it may dramatically decrease nesting success. As this species is declining in most of its range, we suggest increasing conservation efforts around important nesting sites. These efforts could include increasing site supervision during weekends and holidays and expanding the buffer zone around the colony.

P10 - Differences in the number of birds flushed in response to calls given by bird eating and non-bird eating hawks at feeding stations in northwest Tennessee

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Recognizing potential threats can influence the energetic demands and therefore the survival of wintering birds. Reacting to sounds that are not a threat wastes time and energy that could be spent foraging. Our goal was to determine if wintering birds visiting feeding stations were more likely to flush upon playback of calls from a non-bird eating hawk (Red-tailed Hawk, *Buteo jamaicensis*) as compared to calls of a bird eating hawk (Cooper's Hawk, *Accipiter cooperii*). Observations were made at four feeding stations, each consisting of a blind with tube and platform feeders regularly baited with black oil sunflower seeds. We used a Bluetooth speaker paired with a smartphone to project calls using the Merlin Bird ID application. We allowed feeders to populate with birds before we played hawk calls. We counted the number of individuals of each species before and after playback. Overall, the mean number of birds was significantly lower after the playback of Cooper's Hawk calls as compared to before playback, but there was no difference in the mean number of birds present before and after playback of Red-tailed Hawk calls. This suggests that the birds at the feeding stations may be able to distinguish between the calls of bird eating and non-bird eating hawks. American Goldfinches (*Spinus tristis*) and Pine Siskins (*Spinus pinus*) reacted to Cooper's Hawk calls more strongly than Northern Cardinals (*Cardinalis cardinalis*) and White-throated Sparrows (*Zonotrichia albicollis*) suggesting that there may be species specific responses to particular threats.

P11 - The Invasive Pentastome Parasite, *Raillietiella orientalis*, Pervades Central Florida Habitats

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The establishment of *Python bivittatus* in southern Florida resulted in parasite spillover of the pentastome, *Raillietiella orientalis*, an endoparasitic crustacean that inhabits the respiratory systems of their definitive hosts (snakes). The species utilized by *R. orientalis* as intermediate hosts is currently unknown. Experimental infection studies (Palmisano et al., unpublished), suggest several species of Florida anurans and lizards can serve as intermediate hosts for *R. orientalis*; however, captive infection may

not accurately predict which species serve as hosts in the wild. To determine these natural intermediate hosts, we conducted field collections of lizards and frogs at Lake Woodruff National Wildlife Refuge and a residential area in central Florida. Our dissections indicate seven species of lizards and anurans harbored larval pentastomes. A significantly greater proportion of southern toads and Cuban treefrogs than brown anoles were infected. The intensity of infection varied greatly, ranging from 1-78 larvae in toads and from 1-10 larvae in brown anoles. In field collections of snakes, we found that eight different species were infected with *R. orientalis* including two novel definitive hosts (*Thamnophis sauritus* and *Micrurus fulvius*). Large proportions of the sampled pygmy rattlesnakes (20.2%) and black racers (66.7%) were pentastome-infected. This invasive parasite is now widespread in central Florida and infects a large number of native species in both natural and urbanized habitats. We predict a rapid expansion of the geographic range of *R. orientalis* given the species it utilizes as intermediate hosts, making it a major conservation issue for many snake species in the southeastern United States.

P12 - Quantifying Resource Partitioning among Insectivorous Bat Species; A Multimethod Approach

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Palmetto Bluff, South Carolina acts as a potential haven to 13 species of insectivorous bats. The Lower Coastal Plain has not reported a case of *Pseudogymnoascus destructans* (*Pd*) since the emergence of the fungal pathogen to the USA. The warmer weather of the coast reduces hibernacula time for bats which is when they are more susceptible to *Pd* infections. The various species of bats compete to fill the same niche, this leads bat biologist to question how various species succeed. One method of relieving competition is by partitioning resources needed to live. This study attempts to quantify resource partitioning by measuring activity time, prey availability, and dietary preferences. These data collected serve as a preliminary analysis to identify patterns in insect populations and activity time among bat species. Insect samples were collected using CO2 traps and UV light traps. These samples were then counted and sorted to the order level using a dichotomous key. Three SM3 Bat and one SM4 acoustic monitors (wildlifeacoustics.com) were deployed in the same sites as insect traps to monitor bat populations and to quantify activity time. DNA collected from bat guano from 22 individuals (6 species) captured at the same sites but at different times is currently being sequenced to profile diets. Using cytochrome oxidase I (COI) DNA sequences we can identify the species of insects found in the guano. The insect trap data shows a consistent decrease in Coleoptera and an increase in Lepidoptera, Hymenoptera, and Diptera. A regression shows a positive relationship between bat passes captured and gross weight of insects collected.

P13 - Feeder Cams and Photoperiods: Observing Feeder Bird Response to Sunrise and Sunset

Lauren Pharr, Caren Cooper, Bailey Rayfield, Isaac Carbajal, Holly Keepers, Kelsey Neilan, Leanna Jensen

North Carolina State University, Raleigh, NC

With expanding urbanization, anthropogenic noise and light pollution are having a drastic impact on species activity, communication, and physiology. Specifically, with avian species, circadian rhythms are just one of the many components affected. Thus, the timing of daily activity at bird feeders may vary across a rural or urban environment as well as with other environmental factors such as weather and photoperiod. We observed three bird feeders via webcams that were located in Recke, Germany, Ithaca, New York, and El Valle de Anton, Panama. At each feeder, we analyzed the frequency and daily timing of bird visits during periods surrounding sunrise and sunset.

By dividing the number of pre-sunrise or post-sunset visits by the total number of visits at dawn and dusk, respectively, we found that about 5.3-6.8% of birds were actively foraging prior to sunrise in all 3 sites while 7.3-12.3% of birds were actively foraging after sunset at all 3 sites. Birds in Germany continued to forage beyond 30-minutes after sunset while birds in New York and Panama stopped foraging within 15 minutes of sunset. During the sampling period, day lengths were longer (~16 hours) in the Northeastern United States and Germany whereas in Panama, day lengths were shorter (~11 hours). Also, during the sampling period, ambient temperatures were lower in the US and Germany (~7.8 degrees celsius and ~8.1 degrees celsius) than in Panama (~24.6 degrees celsius). Environmental conditions may have created different energetic constraints on birds at each site, yet the higher frequency of bird visits in Germany may be due to the lack of mammal competitors at that site.

P14 - Counting Bees: A Comparison of Survey Methods for Estimating Wild Bee Abundance

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Wild bees are essential pollinators in many natural and agricultural systems. However, wild bees and other pollinators are currently experiencing an unprecedented population decline. Researchers commonly rely on passive sampling methods such as pan traps to monitor pollinator populations, but the effectiveness of these methods has never been directly validated by absolute population estimates. To test the efficacy of pan traps, we conducted a mark-recapture study and deployed pan traps at three sites in the Butner-Falls of Neuse Game Lands near Raleigh, NC, in summer of 2020. We hypothesized that pan trap capture rates would not provide a valid proxy for bee population size. To estimate absolute population sizes of bees at three sites, we conducted mark-recapture surveys for four taxa: carpenter bees (*Xylocopa virginica*), green sweat bees (*Augochlorella* sp., *Augochlora pura*, and *Augochloropsis* sp.), longhorn bees (*Melissodes bimaculatus*), and leafcutter bees (*Megachile* sp.). We repeated the surveys for five total weeks, then compared the resulting population estimates to pan trap and aerial netting data collected at the same sites in alternate weeks by the NC Wildlife Resources Commission. Our results support our prediction that pan traps are highly biased and do not reflect absolute population sizes of the bees in this study. This study is the first to attempt a direct comparison of common pollinator monitoring

techniques with absolute population estimates generated from mark-recapture surveys at the community level. The results of this study indicate that more research is required to validate common monitoring protocols for these critically important but threatened pollinator species.

P15 - The effect of canopy openness on saproxylic Coleoptera diversity in the Wilson Creek Watershed

Sierra Croney, Henry Williams, Jane Dell

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Saproxylic insects are dependent on dead and decaying wood at some point in their lifecycle and are affected by forest management, including fire, which alters habitat characteristics. Canopy percent openness has resulted in a variation of insect diversity and abundance due to changes in habitat suitability. In the Wilson Creek watershed, located within the Grandfather Ranger District of the Pisgah National Forest, controlled burns were conducted creating canopies at different degrees of openness. Therefore, we assessed the effect of canopy openness on saproxylic beetle diversity. A total of 18 cross-directional flight intercept window traps were placed on nine plots within 3 canopy classes - open, gap, and closed. Collected specimens were sorted by order and assigned a morphospecies based on morphological characteristics, and diversity analyses run based on canopy class. Over 1,300 individual beetles from 140 morphospecies were collected. We found that both species richness and abundance were negatively correlated with canopy openness. Analyzing how the insect community responded to the stand's recovery, particularly within the order Coleoptera, allows for a better understanding of how the forest operates. Like many other insects, saproxylic beetles impact ecological processes such as nutrient cycling, essentially shaping how the system functions, and therefore, can inform management decisions that affect the amount of canopy openness.

P16 - Assessing insect assemblages at natural and constructed ridge-top wetlands in the Cumberland Ranger District of the Daniel Boone National Forest, KY

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Wetlands support high biodiversity and providing numerous ecosystem services to an expanded landscape, including habitat and source of forage for many organisms. In the Cumberland Ranger District of the Daniel Boone National Forest in Kentucky, more than 400 upland-embedded wetlands (UEWs) have been constructed to provide a permanent water source for bats and other game species. These constructed UEWs are not ephemeral and do not function hydrologically or ecologically as natural wetlands. Bat activity is currently being quantified at sites in the DBNF to compare natural and constructed wetlands. In order to better understand the importance of these wetlands in the context of foraging requirements for bats, we assessed insect activity at 2 natural and 2 constructed UEWs in the Cumberland Ranger District over the summer of 2019 using malaise and sticky traps. Collected insects were identified to the ordinal level, and abundance, richness, and diversity (H') were calculated in the context of wetland type (both trap types) and distance of traps from wetland (sticky traps only). For malaise traps, Kruskal-Wallis analyses indicated no differences between wetland types for abundance or richness ($P > 0.05$), but natural UEWs were less diverse than constructed UEWs ($P \leq 0.05$). Additionally, less insects were captured with sticky traps at natural UEWs versus constructed UEWs ($P \leq 0.05$). Finally, we did not find any evidence that distance from wetland influenced insect captures on sticky traps ($P > 0.05$). This study is important because it piloted methods to be used in continued research on wetlands in the DBNF and can inform future wetland restoration efforts.

P17 - The Effects of Habitat Edges and Ant Competition on the Distribution and Success of Carrion Beetles in Red Mountain Park

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We sought to determine whether carrion beetles and ants showed a varied distribution along an edge effect gradient in Red Mountain Park. Fire ants were expected to deter Silphid presence and be more common in the field and edge regions (Tschinkel 1988). The main hypotheses we investigated were whether precipitation and/or air temperature would influence ant activity and if this cascaded to Silphid activity. Additionally, we tested to see if there was a significant difference in species diversity among Silphid populations within and between the three regions we sampled: field, forest, and edge. Pitfall traps were baited with chicken left at room temperature for multiple days and placed along transects in the three different regions. We found that ant presence is inversely proportional to levels of rainfall (p-value of <0.05), as well as between sampling areas. We also found that with increased rainfall and therefore less ant presence, carrion beetles were trapped more often (p-value of <0.05). Our findings indicate that carrion beetle presence is heavily impacted by ants, which are themselves strongly affected by precipitation. Ultimately, the data supported both of our hypotheses as we were able to establish a close yet inverse correlation between carrion beetles and ants with respect to weather impact on their respective activities and interactions with one another.

P18 - Effects of Fire on Carabid Beetles (Coleoptera: Carabidae) in the National Ecological Observatory Network's (NEON) Southeast Domain (Domain 03)

Jason Brown

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Fire plays a critical role in shaping the ecology of the southeastern United States (U.S.) with many species reliant on a regular burn interval in order to thrive. However, fire was suppressed for much of the 20th century and has only recently been recognized as a necessary ecosystem process. Many land managers in the southeastern U.S. have now employed prescribed burns in order to reduce the risk of hazardous wildfires, suppress non-native or invasive species, and keep natural areas from becoming overgrown in order to maintain a healthy ecosystem. The land managers at the three terrestrial sites located in NEON's Southeast Domain—the Disney Wilderness Preserve (DSNY), the Jones Center at Ichauway (JERC), and the Ordway-Swisher Biological Station (OSBS)—utilize prescribed fire and the plots where ground beetles are collected using pitfall traps are affected. Because carabid beetles were previously found to be sensitive to environmental changes, the effects of fire on ground beetles collected at these sites were investigated by comparing abundance, richness, and diversity between unburned and burned plots from 2014-2019. The metrics compared were variable between plots and between sites with no clear trend emerging. The species composition between burned and unburned plots was also inconsistent. The results indicated that fire is likely to have effects on the biodiversity of carabids in the southeastern U.S., but further investigation is needed in order to determine other drivers. Furthermore, the results demonstrated that carabids are great responders to environmental changes, such as land management, and should continue to be studied.

P19 - A potential new species of planaria (*Phagocata sp.*) localized to Blount Springs, Blount County, AL based on nuclear and mitochondrial DNA sequences

Sarah G. Thomas, David A. Johnson

Samford University, Birmingham, AL

Earlier our lab identified a novel planarian found approximately 30 m downstream from a sulfur springhead at Blount Springs, Blount County, AL (33.930, -86.793) as a member of the genus *Phagocata* based on the partial sequence of the mitochondrial gene *cytochrome c oxidase I (COI)*. Here we report that further analysis indicates that this *COI* sequence is nearly identical to that of a previous published *Phagocata* for which there is no known locality. We also report here the sequences of this worm's nuclear rRNA genes. This report serves as the first site locality for this yet-to-be described species of *Phagocata* and adds nuclear sequence data for this planarian.

P20 - Differences in baiting methods and ground arthropod communities in two old field habitats

Casey James, Wayne Rossiter, Wayne Rossiter

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Arthropods represent an important part of tall grass and old field prairies, potentially influencing plant abundance and quality (particularly among forbs), as well as the trophic structure of communities. However, significant differences in arthropod diversity and abundance can result from different collection techniques. In this study, we compared multiple collection methods (plot-transect sampling, sweep netting, and pitfall traps with three different bait types) in two well-developed old fields separated by 0.6 km located in Gallia County (OH). Overall, 57 taxa-species were identified, and abundance ranged from 0-508 arthropods per sample, but was greatly right-skewed ($\bar{x} = 31.15 \pm 75.26$). Based on Bray-Curtis (BC) dissimilarity indices, arthropod community diversity was quite similar between sites (BC = 0.28). In contrast, collection methods were strongly biased, and targeted different taxa (average BC pair-wise difference = 0.76 ± 0.27). Mean per-sample species richness was higher in plot-transect and sweep net collections ($\bar{x} = 7.83$ and 7.00 respectively) compared to pitfall traps ($\bar{x} = 3.53$). However, baited pitfall traps attracted a greater abundance of arthropods ($\bar{x} = 34.93 \pm 82.92$ compared to $\bar{x} = 14.3 \pm 6.11$). Methods involving visual targeting were more likely to collect larger arthropods that climb and fly, while pitfall traps successfully captured ground-dwelling arthropods. We conclude that multiple sampling methods should be implemented when assessing arthropod community structure in prairie ecosystems, and the combination of the methods utilized here are sufficient to account for most species in these systems.

P21 - The Spatial Sensitivity of the Proboscis in *Manduca sexta*

Emily Hudgins, Joaquin Goyret

The University of Tennessee at Martin, Martin, TN

Manduca sexta are crepuscular-nocturnal hawkmoths that use olfactory and visual stimuli to locate floral nectar. They forage by hovering in front of flowers and probing the surface of the flower with their proboscis, providing them with tactile information from floral features, such as the grooves in the corolla. The moth will then follow a groove while flying back-and-forth to obtain the nectar. By utilizing surrogate flowers with varying groove widths (1 mm, 0.1 mm, 0.5 mm, and 0 mm i.e. a smooth surface), the spatial sensitivity of the proboscis was able to be determined. Results showed that *Manduca sexta* are able to discern grooves as small as 0.1 mm upon the surrogate flower's surface. In our poster we discuss these results, future directions, and an ongoing control for the possible influence of visual detection of grooves.

P22 - mTORC inhibition in the development and lifespan on *Vanessa cardui*

Cheyenne Mills, Lynn Kee

Stetson University, Deland, FL

The mechanistic target of rapamycin (mTOR) is a kinase that is conserved from yeast to mice to humans. mTOR functions in integrating signals to control cell and organismal growth, metabolism and ageing. Rapamycin, an inhibitor of mTOR extends the lifespan of many organisms, including worms, flies and mice. In this study, we investigated the effect of rapamycin on the development of *Vanessa cardui*, commonly known

as painted lady butterflies. We observed that *V. cardui* caterpillars that have been fed rapamycin have a decreased growth rate and larval size. We also report that rapamycin fed caterpillars take a longer time to form chrysalis and do not hatch out of the chrysalis. These findings suggest that the butterflies cannot hatch due to impaired or delayed wing development. Future studies will investigate the effect of rapamycin treatment on mTOR target proteins.

P23 - Recent northward range expansion of the invasive ant *Pheidole obscurithorax*

Juan Jeronimo Rangel, Joshua Gibson, Alan Harvey

Georgia Southern University, Statesboro, GA

Invasive species can vary markedly in the timing and rate of range expansion following their establishment in a new location. *Pheidole obscurithorax*, a large, distinctive ant native to South America, was first recorded in North America from Mobile, AL in 1949. By 2015, it had spread along the Gulf Coast east to central Florida and west to eastern Texas. Despite its native range spanning 27.5° of latitude, its invasive range has been notably restricted to just the 3.5° of latitude south of 31.5°N. In the intervening time there have been no reports of this ant outside of this latitudinal range in either the scientific literature or on tools utilized by citizen scientists (e.g. inaturalist, bugguide, etc.) In October, 2020, we first noticed this ant on the Statesboro campus of Georgia Southern University. Within a month we located over 80 nests on campus, as well as additional nests elsewhere in Bulloch County, representing an over 100-km northward expansion. The widespread appearance of *P. obscurithorax* in Bulloch County is unexpected and somewhat puzzling given the large size and distinctive morphology of this species, as well as its prior invasion history (i.e., extensive east-west but limited northward range expansion). One possibility is that this apparent sudden, disjunct range expansion is an artifact of incomplete sampling; thus, we plan to conduct more systematic surveys to determine its current distribution in Georgia. We also plan to conduct genetic analyses to address the possibility that this population represents a secondary introduction, potentially from a South American population more cold-tolerant than the original Argentinian source population.

P24 - Assessing Intraspecific Relationships: A Phylogeographic Analysis of Genetic Variation in the Three-lined Salamander (*Eurycea guttolineata*)

Sarah Roy, David Beamer

Nash Community College, Rocky Mount, NC

The ability to accurately delimit species is of vital importance, particularly when dealing with taxa whose speciation is not immediately apparent. Phylogeographical analysis has emerged as a method that allows us to link micro and macroevolutionary processes in order to better understand speciation and divergence of sister taxa. Until recently, the Three-lined salamander (*Eurycea guttolineata*) was considered to be a subspecies of the Long-tailed Salamander (*Eurycea longicauda*). The most recent taxonomic analysis used both morphology and allozyme data to support the status of *E. guttolineata* as its own species. Our study aimed to produce a phylogenetic reconstruction of intraspecific variation across the range of *E. guttolineata*, with the intention of providing reliable data for future comparison studies of *E. guttolineata* and *E. longicauda*. Using mtDNA analyses of the cytochrome b (Cyt b) gene and Bayesian inference models, we produced a phylogenetic reconstruction of *E. guttolineata*. Additionally, we were able to compare cyt b haplotypes of *E. guttolineata*, and *E. longicauda*. Our analysis of *E. guttolineata* was characterized by a surprisingly low level of genetic diversity. This could potentially be due to a recent range expansion, or a large amount of gene flow between subpopulations throughout their range. Of utmost interest in our findings, was the identification of cyt b haplotypes characteristic of *E. guttolineata* in southern populations of *E. longicauda* (within the species contact zone). Further investigation of the species contact zone is needed, and hybridization frequencies in this zone may provide insights on determining parapatric speciation between these two species.

P25 - Seining for stream salamanders: Season and site matters but not time of day

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Sampling for salamanders in streams can be challenging as different techniques can lead to biased estimates of populations. One type of stream sampling that has been underutilized for assessing salamander abundance is kick-seine sampling. Currently it is unknown if kick seining is a viable method for estimating salamander abundance and salamander body condition. Therefore, we conducted a study to investigate how stream salamander abundance and body condition changed across seasons and during the time of sampling (day versus night) using kick seining. We sampled six streams in western North Carolina every three months over a 12-month period in 2019-2020. Each stream had a 10-m stretch that was sampled during diurnal and nocturnal sessions on the same day. We found that salamander abundance significantly differed by site but not by time of day and season. Salamander body condition varied also by site and season but not time of day. Our study indicates that kick-seine sampling is a viable technique to estimate stream salamander abundance. It also suggests that kick-seining sampling yields similar abundance estimates regardless of the time of day but that seasonal variation does exist. Overall, future work should consider comparisons of kick seining to other stream salamander sampling techniques.

P26 - Testing Species Limits in Mud and Red Salamanders (*Pseudotriton*)

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Pseudotriton is a genus of salamanders currently consisting of two species, *P. montanus* and *P. ruber*. Both species of *Pseudotriton* are endemic to a large portion of the southeastern United States. Recent research has demonstrated that *P. ruber* has been shown to be largely homogeneous throughout its range, and that the *P. ruber* subspecies do not reflect phylogenetic relationships. *Pseudotriton montanus* has been studied far less, its secretive nature, as a typically fossorial species makes it difficult to study throughout its relatively large range. There are four currently accepted subspecies of *P. montanus*. These subspecies include *P.m. montanus*, *P.m. diasticus*, *P.m. flavissimus*, and *P.m. floridanus*. The goal of this study is to survey the variability of *P. montanus* individuals sampled across their geographic range, and test whether the currently recognized subspecies represent independent evolutionary lineages. Here we present a phylogenetic reconstruction of the mtDNA gene, ND2, from populations sampled throughout the range of *P. montanus*. This data shows that *P. montanus* is far more divergent than *P. ruber* and suggests that *P. montanus* may consist of multiple species.

P27 - Investigation of a salamander community and potential spotted salamander (*Ambystoma maculatum*) extirpation from an ephemeral wetland preserve in the Charlotte, NC urban area

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Salamander populations are highly dependent on the quality of both the aquatic and terrestrial environment. Ephemeral wetlands are ideal breeding locations due to a lack of fish predators, but these habitats have been degraded in many parts of the SE United States. Whitehall Nature Preserve in Charlotte NC is an ephemeral wetland preserved by the non-profit Catawba Lands Conservancy. Historically, both spotted salamanders (*Ambystoma maculatum*) and marbled salamanders (*Ambystoma opacum*) had populations at this site. However, sporadic research projects over the years have anecdotally observed only marbled salamanders and spotted salamanders have not been observed since 2007. Our objective was to perform a monitoring study of the salamander community at Whitehall to determine if the spotted salamander is extirpated or simply rare. We set out 18 cover boards placed along 4 transects within (and adjacent to) the ephemeral wetlands within the preserve. We also checked cover boards that were previously installed (in 2015, n = 8) that occur on the transition zone between the wetland and upland (when full). The cover boards were observed every 2 weeks for over one year with a gap during the summer months of 2020. Spotted salamanders were never observed under any cover boards when visiting the wetland. Marbled salamanders were seen frequently during common migration periods (late fall through late winter). Observations over the first 6 months found that very few marbled salamanders used the new cover boards and preferred the older cover boards. However, by fall 2020, marbled salamanders were using the new cover boards extensively. Our data are preliminary (and not exhaustive) but seem to support the potential extirpation of spotted salamanders from Whitehall Nature Preserve. Monitoring will continue with the use of Wild ID software to track individual salamanders using color pattern and visual identification.

P28 - Preliminary Analysis of Morphometric Data for an Ongoing Autecological Study of the Northern Watersnake, *Nerodia sipedon sipedon*, in a West Virginia Stream

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The northern watersnake, *Nerodia sipedon*, is a natricid ubiquitous across aquatic habitats of the eastern United States and is often found in high abundance. The prevalence of *N. sipedon* has garnered extensive research, much of which concerns its reproduction. However, thorough, long-term studies on the biology and ecology of *N. sipedon* within stream ecosystems, as well as Appalachia, are lacking. The purpose of this study is to analyze autecological data from ongoing research on a *N. sipedon sipedon* population within Short Creek, a rural stream in the northern panhandle of West Virginia. Morphometric, dietary, thermal, habitat and movement data were recorded for each capture. This analysis primarily focuses on morphometric data in an attempt identify any potential variation from data collected in past studies concerning different habitats. Future research will use neonate morphometrics as baseline data for growth estimations, employ mark-recapture data to estimate a population size, and build upon the established data set.

P29 - Investigating the Distribution and Taxonomic Status of *Eurycea wilderae*.

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Scientists have been investigating the distribution and taxonomic status of *Eurycea bislineata* and have been applying molecular biology techniques since the 1980s. The three traditionally recognized subspecies are *E. b. bislineata*, *E. b. cirrigera*, and *E. b. wilderae*. Recent molecular research suggests that the current taxonomy of two line salamanders under represents the evolutionary diversity. However it is unclear which existing binomials should be applied to which populations of *Eurycea*. Here we focus on the taxonomic and distributional status of *Eurycea wilderae* by comparing topotypic material with populations collected throughout the range of *E. b. cirrigera* and *E. b. wilderae*. Our results suggest that the distribution of *E. b. wilderae* is vastly different from published range maps. Furthermore, our molecular phylogenetic reconstruction and statistical analysis of linear morphological measurements demonstrates unequivocally that most populations currently referred to as *Eurycea wilderae* are in fact other species.

P30 - Coverboard size preference of reptiles and amphibians on a suburban campus

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Coverboards provide a long-term, but low maintenance way to assess herpetofaunal diversity in a landscape. Here, we provide preliminary results of an ongoing study of reptile and amphibian diversity in a temperate forest on a Metro-Atlanta college campus. In May 2019, we established two transects of 10 arrays of coverboards in a wooded area north of Georgia Gwinnett College, in Lawrenceville, GA. Each array consisted of three plywood coverboards of different sizes: small (30.5cm x 30.5cm), medium (61cm x 61cm), and large (61cm x 122cm). Each transect ran from a powerline cut downhill through a hardwood forest to the floodplain of the Yellow River. Each array was approximately 20m apart. Coverboards were checked once a month since their establishment. Thus far, we have found four snake species, two lizard species, four anuran species, and three salamander species. Animals have been seen utilizing all sizes of coverboards, but snakes, lizards, and amphibians are less likely to be found under the small coverboards. There is little difference in preference between the medium and large coverboards. We see a temporal change in species presence over time, with snakes using coverboards in the spring, summer, and fall months, while salamanders, mostly red-back salamanders (*Plethodon serratus*), are found in the winter months. Lizards were more likely to be found away from the floodplain, while snakes and amphibians were found throughout the site. We will continue to monitor this site and hope to mark individuals to assess movement and repeated use of coverboards.

P31 - A preliminary comparison of Eastern Hellbender (*Cryptobranchus alleganiensis*) habitat across the Ridge and Valley province of southwest Virginia

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The Eastern Hellbender (*Cryptobranchus alleganiensis*) is a secretive amphibian preferring clean, clear, fast-flowing streams across the Appalachian Mountain region. Increasing hellbender declines and associated conservation concern have led to the development of stream restoration initiatives aimed at restoring hellbender habitat in degraded streams. However, little is known about the specific habitat requirements of hellbenders in understudied parts of their range, a factor that inhibits the design of restoration projects. We performed habitat and environmental DNA (eDNA) surveys for hellbenders across 11 watersheds in the Ridge and Valley province of southwest Virginia, with the goal of comparing habitat characteristics (catchment-scale land use, water quality, fine sediment intrusion, substrate size/type, and channel morphology) across sites with and without known hellbender populations. We found no significant difference in habitat structure across streams with and without historic hellbender records. However, we did uncover that streams within this region fall into two general, statistically-distinct habitat types: high-gradient streams characterized by step-pool morphology and larger boulder cover and valley streams characterized by riffle-run-pool-glide morphology and higher amounts of bedrock slab substrate. Hellbenders are known from both stream types in our study region, suggesting that there is not a single, "one size fits all" habitat type preferred by hellbenders across southwest Virginia's Ridge and Valley province. These results indicate that regional conservation programs targeted towards the restoration of hellbender habitat will likely need to account for these higher-order differences in stream structure.

P32 - Habitat Heterogeneity and Fish Communities Relative to Debris Dams in East Fork Indian Creek, Menifee County, KY

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Large woody debris influences many physical and biological aspects of stream ecosystems. One way woody debris can be arranged in a stream is as a debris dam. While studies have shown that debris dams can retain large amounts of particulate matter and support more abundant and diverse invertebrate communities, few studies have assessed their influence on fish. In this study we assessed how woody debris dams alter habitat heterogeneity, fish diversity, fish biomass, and fish communities upstream and downstream of dams in East Fork Indian Creek at the Red River Gorge in Menifee County, KY. Overall, debris dams did not significantly alter any response variable ($p > 0.05$). This may likely be because East Fork Indian Creek is a high gradient stream with large boulder substrate. Previous studies have found that the influences of large woody debris are largely hindered in these types of environments because large boulders already provide habitat heterogeneity for diverse communities. These results suggest that debris dams may act in a similar manner. The findings of this study can aid ongoing restoration efforts at East Fork Indian Creek.

P33 - Analysis of stream restoration efforts in an agriculturally impaired sub-watershed of the Chesapeake Bay

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The Chesapeake Bay watershed spans several states, supports diverse ecosystems, and is economically crucial to local communities. However, many agricultural practices in this region are detrimental to stream health. The Smith Creek watershed, in northwestern Virginia, was designated a showcase watershed by the United States Department of Agriculture in 2010. It has undergone widespread restoration efforts conducted over the

past decade, such as improving in-stream habitat and establishing riparian buffers, but has had minimal biotic evaluation. This study will undertake a comprehensive analysis of restoration progress in the watershed by sampling three reaches in each of ten to fifteen farms representing different methods of restoration and varying times since restoration occurred. At each site, aquatic macroinvertebrates will be collected from riffle microhabitats. Organisms will be identified to family and used to calculate diversity, abundance, the Virginia Stream Condition Index, and the Chessie B-IBI. These indices will be linked to substrate size, aquatic vegetation, land use within 10 m, elevation, distance to roads, duration since restoration, and restoration method using ordinal linear models. Restoration method, agriculture within 10 m, and substrate size are predicted to significantly influence stream health, and stream health is predicted to improve with time post-restoration. We anticipate that this study will identify important variables for predicting the success of various restoration methods, and thus benefit restoration efforts throughout the Chesapeake Bay watershed.

P34 - Morphological and molecular identification of the Saddle Crayfish: *Faxonius durelli* (Decapoda: Cambaridae) along streams throughout Giles County, Tennessee.

Rainey Tyler, Samantha Kilian, Stephanie Gutierrez, Stanton Belford

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Crayfish in North America undergo continued threats, such as habitat fragmentation, degrading water quality, and addition of invasive species to their local habitats. Research to track crayfish populations and maintain accurate taxonomy is necessary. This study used morphological and molecular analyses to identify the saddle back crayfish species, *Faxonius durelli* (Decapoda: Cambaridae). We determined size and morphology at streams in Giles County, southern Tennessee during spring and fall over a 3-year period. Hand-held seines were used to collect crayfish, then morphological data were recorded, such as carapace length (CL), total length (TL), and weight. We used hand-held tweezers to collect 30-50 mg of crayfish tissue, which were stored in 0.5 ml vials containing 95% ethanol. Crayfish were photographed in situ, for later comparison after genetic sequencing. Specimen DNA were extracted using an E.Z.N.A tissue kit, followed by PCR, then enzymatic cleanup, before sequencing at the COI gene. Results showed that crayfish TL and weight differed significantly among sites during collection times: Spring and Fall, over a 3-year period (ANOVA, $p < 0.05$), and total length ranged between 21-40 mm. Molecular and phylogenetic analysis were done by sequencing the cytochrome oxidase subunit I (COI) gene, which identified the crayfish species as *Faxonius durelli*. Although annual surveys are important to track crayfish population size and frequencies, time periods during spring and fall may also be necessary to collect data, as these time periods can track juveniles and adult frequencies. Accurate crayfish identification is necessary to determine potential conservation efforts for endangered crayfish species, and morphological data can be used to compare the ecological habitat in relation to potential threats.

P35 - Comparing basil production in two aquaponics systems with different solid removal methods, biofilter media, and grow bed effluent output

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Aquaponics is a form of crop and fish production that combines conventional aquaculture and hydroponics to create a closed-loop, recirculating growth system that uses 95% less water than traditional aquaculture and agriculture practices. However, some challenges remain in the development of a sustainable and profitable aquaponics industry, primarily due to the energy demand for system operation. To overcome these challenges, technologies that reduce energy input and/or increase crop/fish production must be developed. The aim of this research was to compare basil production in hydroponic grow beds for two aquaponics systems that differ in the method of solid removal (backwash settling chamber vs. sock filter), biofilter media (biobeads vs. Kaldnes media), and effluent input into the grow bed (single input vs. multiple inputs). Specifically, basil growth and productivity were measured in three separate locations within the grow beds of both system designs over an 8 week period. Results showed significantly greater final plant height, mean weekly growth rate, aboveground and belowground biomass, and total biomass in the system using sock filtration, Kaldnes media, and multiple effluent inputs into plant grow beds. Furthermore, there was no significant difference in final plant height and mean weekly growth rate in the three locations within the grow beds for this system design, suggesting that nutrients were efficiently circulated within the grow bed. Overall, the results suggest that an aquaponic system using sock filtration, Kaldnes media, and multiple effluent outlets into grow beds efficiently circulates nutrients, resulting in increased basil growth and productivity. The increased plant production resulting from this aquaponic system design has the potential to contribute to increasing the viability, productivity, and profitability of the aquaponics industry.

P36 - Patterns of infection by *Posthodiplostomum minimum* in centrarchid fishes from southern Ohio

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Title: Patterns of infection by *Posthodiplostomum minimum* in centrarchid fishes from southern Ohio
University of Rio Grande, Wildlife Conservation Program

Posthodiplostomum minimum is one of the most ubiquitous and pervasive trematode parasites of freshwater centrarchid fishes. While numerous subspecies exist in the complex, this trematode is found in more than 100 species of fishes (2nd intermediate host), often parasitizing every host individual in a given system. This parasite exhibits a classic complex (heteroxenous) life cycle, actively transmitting from pulmonated snails (1st intermediate) to fish 2nd intermediate hosts, before being trophically transmitted to wading birds and other vertebrate predators. Previous studies (e.g. Davidson and Rossiter, 2018) observed host mass, species, and ecosystem attributes to be strong predictors of *P. minimum* intensity. Here, we explore the infection patterns (prevalence and intensity) of *P. minimum* in five lakes and ponds in southern Ohio, ranging in size from

0.73-98.0 hectares in area. As previously observed, Generalized Linear Models (GLM) demonstrated host size and species to be useful predictors of infection intensity ($p = 0.0003$ and 0.006 respectively). Bluegill (*Lepomis macrochirus*) and hybrid sunfishes exhibited the highest mass-specific infection loads. We did not observe the parasite in rockbass (*Ambloplites rupestris*), but did find it in the warmouth sunfish (*L. gulosus*). However, contra previous work in the region, we failed to detect any relationship between system (lake/pond) size and infection intensity. We speculate that this may be a consequence of distance and isolation of lake/pond systems, and lower visitation rates by definitive host predators.

P37 - Exotic fish biomass exceeded native fish biomass in a central Florida spring.

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In Florida, the problem of exotic species introduction into freshwaters is particularly acute. The USGS Nonindigenous Aquatic Species database includes 245 entries for exotic or hybrid fish that have been found in Florida waters, most from tropical or subtropical Central or South America, Africa, or southeast Asia. Volusia Blue Spring, a first magnitude spring in central Florida, supports varying densities of at least six species: blue tilapia (*Oreochromis aurea*), two armored catfish (*Pterygoplichthys disjunctivus* and *Hoplosternum littorale*), grass carp (*Ctenopharyngodon idella*), pirapitinga (*Piaractus brachipomus*), and chanchita (*Cichlasoma dimerus*). To evaluate the contribution of exotic species to the fish biomass of the spring, we counted and measured native and exotic fish in fall 2020 at two locations, one near the headspring and one near the confluence of the St. Johns River. For small species, we seined three locations at each site and measured all of the individuals captured. For larger species, we snorkeled the entire site, counted the fish that we observed, and photographed representative fish with a GoPro outfitted with two underwater lasers mounted with parallel beams 7 cm apart. We measured the fish on the photographs and calculated their length using the 7 cm reference points on the side of each fish photographed. We converted these lengths into biomasses using published length-weight relationships and summed the biomasses of all native and exotic species separately. Then we calculated the percent difference between native and exotic biomass. In eight of the ten samples, the exotic species biomass exceeded that of native species (exotic species biomass = 17% lower to 2,154% higher than native biomass). Although the native species outnumbered the exotic species, these data suggest that the exotic species may have a greater effect on spring ecosystem function than their densities would suggest.

P38 - The effects of detritivores on leaf litter breakdown in experimental ponds

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Caddisfly larvae and crayfish can play a major role in stream food webs by having strong negative effects on leaf litter breakdown. However, less is known about their role in pond food webs and subsequent impacts on ecosystem function. To evaluate the effects of two common species inhabiting ponds in the NC mountains (the caddisfly *Platycentropus* spp. and the crayfish, *Cambarus bartonii*), we conducted a mesocosm experiment. We deployed four different food webs (1 large crayfish, 2 small crayfish, 11-15 caddisflies, or no detritivores) to determine the effects of these detritivores on a common leaf litter type (Oak) over 6 weeks. To standardize detritivore biomass, treatments had different densities. We found a marginally significant effect of detritivore treatment on leaf litter decomposition relative to leaf litter controls. Leaf litter biomass did decline through time but was dependent on detritivore identity. Specifically, the effects of two small crayfish caused the greatest decline by the conclusion of the experiment. Our results indicate that detritivores can have effects on pond leaf litter but that this effect may be limited based on species and body size. Future studies should expand and explore the greater range of conditions (detritivore densities, top predator presence, resource availability) that could explain the role of caddisflies and crayfish in pond food webs.

P39 - Assessing the Presence and Concentrations of Microplastics in the Gizzards of Virginia Waterfowl

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Microplastics are defined as plastic fragments smaller than 5mm which originate from sources such as manufactured pellets, personal care products, and the breakdown of larger plastic items. They have become a ubiquitous water pollutant in recent years, and while a substantial amount of research on their impacts on marine ecosystems has been conducted, the presence of microplastics in freshwater systems and organisms remains less understood. In this study, we assessed the presence and concentrations of microplastic particles in the gizzards of the Canada Goose (*Branta canadensis*) hunted in the Piedmont and Coastal Plain of Virginia. Gizzards were bisected, then their contents were removed for analysis. Internal gizzard contents were digested in 30% hydrogen peroxide with an iron catalyst, then were density separated in a saline solution order to isolate microplastics. Samples were then visually inspected under a dissecting microscope. Preliminary results show that one out of six gizzards contained microplastic fibers at a concentration of 0.07 fibers/gram. Though this project is currently ongoing, we have provided some preliminary evidence suggesting that waterfowl not only ingest microplastics, but retain them in their digestive systems. As we continue this study, we will assess several more individual geese as well as various species of duck, such as Ring-necked Duck (*Aythya collaris*), Long-tailed Duck (*Clangula hyemalis*), and Bufflehead (*Bucephala albeola*). We also plan to use fluorescence microscopy with Nile Red to further identify microplastics in these samples. This work will help to provide an increased understand of the threat microplastics pose to aquatic waterfowl.

P40 - Landscape genetics of a *Fundulus* spp. hybrid zone in Northeastern Florida

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Hybridization, the interbreeding of diagnostically distinct populations, is relatively common in both animal and plant taxa whenever reproductive isolation is not complete. Studies of hybridization are essential for understanding processes related to speciation, the regulation of species ranges, and the role of ecology in each of these processes. Two closely related killifish species (*F. heteroclitus* and *F. grandis*), overlap in range and form a narrow hybrid zone along part of Northeastern Florida. Little is currently known about the extent of hybridization between these two species and whether their respective ranges are associated with any environmental parameter. Therefore, a study was conducted to assess the spatial genetic patterns of the hybrid zone in an attempt to determine: 1) the current edges of the hybrid zone, 2) whether the hybrid zone is environmentally determined or not, and 3) if any environmental patterns correlate with the genetic patterns. Samples of fishes were collected from 10 locations spanning the putative range of the hybrid zone (~40 km) at regular intervals. Each fish was genotyped at four highly differentiated loci (3 nuclear and 1 mitochondrial). Patterns of genetic differentiation among sites were determined utilizing STRUCTURE and environmental parameters of predominant vegetation (mangrove and salt marsh grasses), temperature and salinity were tested for correlations with observed genetic patterns. Strong evidence for a mosaic hybrid zone was found suggesting an environmental component to the spatial patterns of the hybrid zone, however, none of the environmental parameters tested correlated strongly with the genetic patterns.

P41 - CRISPR-Cas9 Assisted Genetic Knockout of *twist1b* and *twist2* in Zebrafish

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First discovered in *Drosophila*, the *Twist* gene family has been discovered to play a crucial role in early development during dorso-ventral patterning, mesodermal specification, and cranial neural crest formation (vertebrates only). Over time, the gene has duplicated into orthologs and paralogs that can be compared among species. The two most researched being orthologs *Twist1* and *Twist2* in mice and humans. Zebrafish have further duplicated the original *Twist* genes into the paralogs *twist1a*, *twist1b* (corresponding to mammalian *Twist1*), *homolog twist2*, and the novel *twist3*. Our research is focused on *twist1b* and *twist2*. We want to better understand their role in the formation and differentiation of the sclerotome, a subcompartment of the embryonic somite, into the connective tissues that make up the axial skeleton by creating a full length *twist1b* knockout as well as a *twist2* knockout. Our research has indicated a role for both *twist1b* and *twist2* during sclerotome differentiation, specifically for axial skeleton cell fates. This coupled with the orthologous *Twist* gene makes the zebrafish a good model organism to further study *Twist*'s role in sclerotome development among organisms. Our current genetic mutant zebrafish lines for *twist1b* and *twist2* show genetic compensation, thus masking any obvious phenotype. For this reason, we are targeting the entire coding region of these two *Twist* genes using the CRISPR-Cas9 system. Our results will provide information that can be applied to developmental disorders related to the sclerotome as well as future treatments of injuries to the connective tissues of the axial skeleton.

P42 - The effect of a biological scaffold in combination with basic fibroblast growth factor on wound healing activity of mouse fibroblasts

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Dermal tissue wounds can be slow to heal and are vulnerable to infection, which can lead to a long, painful recovery. These wounds can have significant physical, psychological, and financial consequences for patients. Biological scaffolds, which are artificial extracellular matrices that support a healing wound, show promise in accelerating the healing process of tissue wounds, preventing infection, and reducing scarring. Scaffolds can give a healing wound structure and strength, protect wounds from infection, keep wounds moist, increase oxygen supply, and may even attract cells involved in wound healing when ECM proteins are used. In this study, the effect of the combination of the PureCol® EZ Gel (Advanced BioMatrix, 2020) and basic fibroblast growth factor on NIH-3T3 mouse fibroblast wound healing capabilities was investigated. The PureCol® scaffold is a collagen-based hydrogel. A scratch assay was used to investigate the effect of the treatment on cell migration and proliferation, and RT-PCR was used to investigate the effect of the treatment on collagen type 1 alpha 1, matrix metalloproteinase-2, and interleukin-1 beta expression, all of which are genes highly involved in wound healing. The combination of PureCol® and bFGF is expected to increase the wound healing ability of the fibroblasts as compared to the control, and is expected to upregulate the expression of all genes. Characterizing the effects of the PureCol® scaffold and bFGF on wound healing processes may indicate the effectiveness of collagen scaffolds as treatments for tissue wounds.

P43 - Observing effects of WIN55,212-2 activation of the endocannabinoid system in zebrafish development

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Cannabinoids are a commonly used drug worldwide and their use has been reported during pregnancy. This is despite the fact that not very much is known about their effects on the developing fetus. The endocannabinoid system in humans plays a role in homeostasis and things such as mood, memory, and reproductive and fertility, among others. In our current study, we administered the endocannabinoid agonist, WIN55,212-2, during early stages of zebrafish development. Our results show that activation of the endocannabinoid system with WIN55,212-2 disrupts normal development, causing a shortened anterior-posterior axis in the embryo. We examined zebrafish embryos that were treated with this agonist and

looked at expression of genes of interest *in situ* hybridization and compared results to untreated fish. Specifically, we looked at expression of endocannabinoid receptors Cnr1 and Cnr2 within these groups. This study will help to reveal potential defects during development that are due to cannabinoid exposure.

P44 - Identifying Freshwater Sponges Along with Creating a New Database

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Freshwater sponges are widely distributed throughout the world. Freshwater sponges are sessile invertebrates, living in rivers, lakes, or slow streams. They filter water flow through their bodies to obtain nutrients. In a 1969 study, Dr. Michael Poirrier at Louisiana State University conducted a freshwater sponge survey in Louisiana and identified the species strictly on morphological characteristics. Due to the limitations at the time, no molecular work was conducted in the original study.

In the current survey being conducted in Dr. Miller's lab, the same morphological techniques from Poirrier's study are being used with the addition of molecular data for identification. The purpose of this study is to identify freshwater sponges using a new molecular database developed using Louisiana freshwater sponges.

Since June 2019, over 125 sites have been surveyed and over 160 sponge samples have been collected. DNA was extracted, and a portion of the cytochrome oxidase gene was sequenced. Sequences were checked and edited for ambiguities using the MEGA X (Molecular Evolutionary Genetics Analysis) software. Maximum-likelihood phylogenetic trees were then constructed using Muscle alignments within the MEGA X software. NCBI (National Center for Biotechnology Information) BLAST was then used to further confirm the species on the molecular level. Throughout the study over 150 Louisiana freshwater sponges were identified. The development of this database has been tested to be used as an identification tool for freshwater sponges in Louisiana. It will be used by future student interns and by students who are conducting freshwater sponge research as part of their course work.

P45 - The Effect of 17 alpha-hydroxyprogesterone caproate on Breast Cancer Cell Activity

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The effects of progesterone on breast cancer is under researched, despite its role in healthy breast development and function. 17 alpha-hydroxyprogesterone caproate (17-OHPC) is a synthetic progesterone commonly used to prevent preterm labor. Despite being approved under the brand name Makena by the FDA in 2011 there is still no research on the effect, short or long term, that this treatment may have on breast cancer or any other female hormone related cancers. In this study, the effects of 17-OHPC on breast cancer cell mobility and invasion are investigated via scratch assay, using T-47D cells. Cells were exposed to treatment conditions of 10, 20, 40, 80, and 160 nM. Expression of PTK2 and PAR1 genes are evaluated via RT-PCR. Concentrations between 10nM and 40 nM are expected to show a significant increase in cell movement into the scratch area, increasing at higher dosage. The highest concentration, 160 nM, is expected to show no further increase in motility as compared to the 80 nM concentration. PTK2 and PAR1 expression is expected to be upregulated at all 17-OHPC concentrations. Assessing the risk that this treatment may have on breast cancer is crucial for understanding 17-OHPC as well as to progress our understanding of progestins and breast cancer as a whole.

P46 - Investigation of medicinal properties of *Crassocephalum crepidoides*

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The Vietnamese Montagnard community of Greensboro, North Carolina has been ingesting *Crassocephalum crepidoides* due to its resemblance to a medicinal plant native to Vietnam. The plant contains alkaloids which might benefit learning and memory function in older adults. This research investigated the biochemical and behavioral effects of *Crassocephalum crepidoides* to further understand its potential function and the strength of its impact. Plants were grown from seed in Elon's greenhouse and the leaves were air-dried. Upon performing the Ellman enzyme activity assay, it was found that an aqueous decoction of dried leaves significantly inhibited the enzyme acetylcholinesterase when compared to solvent control. Acetylcholinesterase helps maintain the homeostatic state of acetylcholine in the body, which is a compound involved in neuron connection and memory function. If the enzyme is inhibited, levels of acetylcholine increase and this has been hypothesized to compensate for lower levels in older adults. Older zebrafish were exposed to various concentrations of the extract in their tank water for one week and then trained for three days using negative reinforcement until they swam to the chosen arm of a T-maze. After 24 hours, the learning ability of the fish was tested by observing if they chose the correct arm without use of reinforcement. Memory was assessed by testing the fish every 48 hours until they no longer chose correctly. Preliminary results suggest exposure to extract increases both learning and memory when compared to control fish. These results, if they hold up to further analysis, may open up possible avenues for drug development for treatment or prevention of cognitive decline in the elderly.

P47 - Analyzing the FMN binding site in the mitochondrial outer membrane protein mitoNEET using FMN analogs

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MitoNEET is a [2Fe-2S] cluster protein located in the mitochondrial outer membrane and an essential regulator of energy metabolism in human cells. In previous studies, we have illustrated that the redox-active [2Fe-2S] clusters in the C terminal domain of mitoNEET can be reduced and oxidized by reduced flavin mononucleotide (FMNH₂) and oxygen/ubiquinone-2, respectively, hinting that mitoNEET may be a novel redox enzyme catalyzing the transfer of electrons between FMNH₂ to oxygen/ubiquinone. Here, we studied the FMN binding site in MitoNEET utilizing FMN analogs: Lumichrome and Lumiflavin. Lumiflavin has shown the same ability as FMN in mediating the redox reaction of the mitoNEET [2Fe-2S] clusters at a nanomolar concentration in the presence of flavin reductase and NADH under aerobic condition. Moreover, electron paramagnetic resonance (EPR) experiments reveal that both lumiflavin and FMN can change the EPR spectrum of the reduced mitoNEET [2Fe-2S] clusters and generate a covalently bound complex with mitoNEET under blue light exposure suggesting specific interactions of FMN/lumiflavin with the [2Fe-2S] clusters in mitoNEET. Conversely, lumichrome fails to mediate the redox reaction under the same experimental condition and does not change the EPR spectrum of reduced mitoNEET [2Fe-2S] clusters on blue light; instead, it inhibits FMNH₂ mediated electron transfer via mitoNEET. Above results indicate that lumichrome may act as a potential inhibitor to block the electron transfer activity of mitoNEET.

P48 - Investigating how a single point mutation in *FUS1* alters yeast cell fusion

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Cell fusion is an important process in a wide range of living organisms. However, limited information is known about this mechanical process. One mechanism that involves cell fusion is mating of the yeast *Saccharomyces cerevisiae* by having two haploid yeast cells fuse to become one diploid cell. The cell walls of the two opposing yeast cells come into contact and slowly start degrading at the specific contact area so that the two plasma membranes can fuse. If the cell wall starts to degrade in an improper area, it can cause significant harm to the cells, but without any degradation, the cells will never fuse. Cell fusion is therefore regulated by genes that promote fusion properly to avoid causing harm to the cell. One gene that has a direct impact on yeast cell fusion is *FUS1*. Fus1 is a transmembrane protein that regulates cell fusion by degrading the cell walls between mating pairs. Fus1 is thought to localize mating-specific vesicles that contain hydrolases to break down the cell wall. Thus, a complete deletion of *FUS1* blocks fusion before cell wall degradation. There are two known protein domains in Fus1, a transmembrane domain and a SH3 domain. SH3 domains are known to mediate protein-protein interactions, however how this domain specifically functions in Fus1 is unknown. I therefore created a single point mutation using site-directed mutagenesis in a highly conserved residue of the SH3 domain in Fus1. This single point mutation changes residue 469, a Histidine, into an Alanine. Using a Quantitative mating assay, I found that fusion in cells containing *fus1-H469A* was significantly blocked, shown by a lack of plasma membrane fusion between mating pairs. Preliminary data visualizing Fus1 protein localization in mating-induced haploid cells hints that the H469A mutation may affect the efficiency and location of Fus1 during fusion.

P49 - Synergistic combination of nanoparticles and anti-parasitic/protozoan agents on human pancreatic cancer viability

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Pancreatic cancer has become one of the deadliest forms of cancers due to the low survival rate upon diagnosis. Chemotherapy is necessary but has harsh side effects. Traditional chemotherapy treatment leaves the patient immunocompromised and prone to infections. The purpose of this study is to identify a new method of pancreatic cancer therapy that can potentially prevent opportunistic infections. Nanoparticles is shown to be promising in treating cancers. Our lab shows that nanoparticles have antibacterial/anti-virulent properties. In this study, three types of synthesized nanoparticles were tested for anti-cancer properties against pancreatic (PANC) cancer. The synergistic impact of combining nanoparticles with ivermectin (anti-parasitic) or metronidazole (anti-bacterial and anti-protozoal) on pancreatic cancer cell viability were investigated. It was hypothesized that synthesized nanoparticles (along with the ivermectin and metronidazole) could decrease the viability of pancreatic cancer cells. To test this hypothesis, we synthesize 1) silver nanoparticles capped with glutathione (AgNP-glut), 2) silver nanoparticles citrated (AgNP-cit), and 3) silver-gold bimetallic nanoparticles capped with glutathione (AuAgNP-glut). Ivermectin and metronidazole compound solutions were prepared. PANC cancer cells and Human Umbilical Vein Endothelial Cells (HUVEC-non-cancerous primary cells) were grown and plated in 6-well plates and then incubated with the nanoparticles (in the presence or absence of ivermectin or metronidazole). Cell morphology was monitored over 2-hour increments using the FLOid cell imager and the cell viability was tested using the AlamarBlue reagent (resazurin). Results show that AgNP-glut and AuAgNP-glut can reduce cell viability in pancreatic cancer cells. In combination with ivermectin, all three nanoparticles with ivermectin are shown to be most effective at decreasing the cell viability of PANC cells. No visible impacts were observed on the normal primary HUVEC cells. In conclusion, our findings support our hypothesis. Findings of this research may be used to create a potentially safer cancer treatment for those with pancreatic cancer.

P50 - Blocking Buffers and their effects on Mammalian Histone and Cytochrome C

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Mammalian histones are highly alkaline proteins found in the nuclei that organize DNA into chromosomes and regulate transcription. Cytochrome c is a heme protein that is found between the inner and outer mitochondrial membranes and functions to transfer electrons of the respiratory chain. We are investigating the interactions between histones and mitochondria and cytochrome C and mitochondria by using cell fractionation and Western Blotting to identify the histones and cytochrome C. The blocking step in the process coats the membrane with proteins or other molecules to reduce non-specific binding of the antibodies. Although 5% nonfat dry milk is widely used as a blocking buffer, we are testing different blocking buffers, as different blocking buffers yield different results, enhancing the signal or reducing it, depending on the specific antibodies used, and the optimal blocking buffer for a given antibody must be determined by experimentation. We use 5% nonfat dry milk (BLOTTO) as a control for all experiments, it is essential to use this variation of milk because it reduces background noise and helps produce good, clear bands. Since antibodies to histone H3 and cytochrome C are low-affinity and give a weak signal, we are therefore testing different blocking buffers, such as milk concentrations ranging from 1 to 5%, BSA ranging from 1 to 5%, and hemoglobin ranging from 1 to 5%, as well as gelatin at 3%, and PVP or PEG individually ranging from 1 to 4% and different combinations of the aforementioned blocking buffers to determine which blocking buffer gives the best detection signal to the histone and cytochrome C. Our preliminary results indicated that PVP/PEG combinations provided the strongest signal for both histone and cytochrome C, while gelatin tends to strip the proteins completely off of the blot and reduce the signal.

P51 - Establishment of a Transient CRISPR-Cas9 System for Promoter Recombination in *C. neoformans*.

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Cryptococcus neoformans is an opportunistic pathogen renowned for inducing cryptococcal meningoencephalitis in immunocompromised individuals. This basidiomycetous, obligate-aerobe yeast is also a robust model organism for studying fungal genetics. Despite prior research, therapeutics selective against *C. neoformans* are marked by limited options and risk of severe complications. Alternative drug designs are desirable, and molecular biological techniques are being used to spearhead research into novel drug targets. One such potential drug target is a mitochondrial protein – DNA Polymerase Gamma (PolG). To probe the necessity of the cryptococcal PolG ortholog (*CnMIP1*), I have established a transient CRISPR-Cas9 system capable of inducing gene recombination via Homology Directed Repair (HDR) in a *C. neoformans* serotype D strain.

Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-Cas9 is a gene editing technique that uses an RNA guide to induce precise DNA damage. Conventional gene editing and chromosomal integration in *C. neoformans* has relied upon biolistic techniques; CRISPR poses to be a more precise and cost effective method allowing for easier gene manipulation *in vivo*. Accordingly, a transient CRISPR system with guide RNAs targeting exon2 of cryptococcal *URA5* was developed to test for recombination with a geneticin resistance (*NEO^R*) gene in an easily screenable target gene. Trials have yielded preliminary evidence for site-specific recombination and gene disruption, resulting in dual *NEO^R* and *ura5Δ* phenotypes.

This system is being tailored to target the *CnMIP1* promoter for recombination with a gene cassette containing a *NEO^R* gene, a copper-regulatable *CTR4* promoter, and a *GFP* expression marker. To accomplish this, a multi-fragment ligation technique was used to rapidly assemble the cassette in a small vector. This will be used as an HDR template for CRISPR-induced replacement of the *CnMIP1* endogenous promoter, so that gene expression may be conditionally regulated such that *CnMIP1* necessity can be genetically ascertained.

P52 - Expression of *Col2a1a* and *Col1a2* genes during Sclerotome Differentiation into Axial Skeleton in the Zebrafish

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Zebrafish have a long-standing reputation in molecular biology for being an outstanding model to view vertebrate organisms' development. The zebrafish's structural development is relatively rapid compared to higher vertebrates, yet their development is just as complex. During the zebrafish gastrula period (5.25-10 h), during embryogenesis, cell movement and tissue expansion occur, creating the three primary germ layers: ectoderm, mesoderm, and endoderm. Within the endoderm and mesoderm, Collagen, type II, alpha 1a (*col2a1a*) is expressed in several structures such as the fin, floor plate, head, and skeletal system. A subset of mesodermal cells, known as the sclerotome, gives rise to the axial skeleton, consisting of cartilage, bone, and associated connective tissues. This study aims to understand how different cell fates in the developing axial skeleton are formed. Two genes expressed within the sclerotome, *twist1b* and *twist2*, were knocked down via morpholino injection at the single-cell stage to disrupt sclerotome development. Using *in situ* hybridization, we studied the expression of the *col2a1a* gene and found it is involved in forming the bone, tendon, and cartilaginous structures within the axial skeleton. Specifically, we found that *twist1b* and *twist2* genes are required for proper *col2a1a* expression within these developing tissues. To follow-up on these findings, further investigation on the BMP pathway related to osteogenic differentiation will provide more data on the bone and tendon differentiation pathway.

P53 - The Role of HD5 on Mediated Cell Death

Erin Lisk, Amanda Williams

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Inflammatory Bowel Disease (IBD), consists of both Crohn's colitis and Ulcerative colitis. IBD includes chronic inflammation and damage of the gastrointestinal tract. Crohn's colitis is specifically isolated to the large bowel and sometimes penetrates through all bowel layers. Ulcerative colitis, while also located in the large bowel, it is isolated to the epithelial layer of the intestines. Alpha Defensin 5 (HD5) is highly expressed in Crohn's colitis compared to Ulcerative colitis patients. HD5 is secreted by Paneth Cells to protect crypts from pathogenic bacteria by binding to

the plasma membrane and lysing the cells. However, HD5 should not be found in the large intestine. Therefore, we hypothesize that HD5 is causing host cell death within the large intestine through a caspase-mediated pathway, contributing to symptoms of IBD. If HD5 is causing apoptosis through activating a caspase, then we should see a reduction in apoptosis when the cells are treated with HD5 and those caspases are blocked. If ZVAD, a broad caspase inhibitor, is added to cells prior to the addition of HD5, there should be a decrease in apoptosis. We measured the apoptosis using Annexin V and flow cytometry. If the HD5 is activating an apoptotic pathway, then by adding the ZVAD, there should be a decrease in apoptosis versus when there is no ZVAD added to the cells. This experiment will provide more of an understanding of how HD5 may be impacting disease progression within the colons of people with Crohn's colitis.

P54 - Roles of Scleraxis and Dystrophin During the Development of Zebrafish Tendons

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Zebrafish are a well-known model organism used to study events during embryonic development, specifically in vertebrate organisms. Somitogenesis is a key process that occurs during embryonic development that allows for patterning of the vertebrate axial skeleton. Somites are blocks of mesoderm that form along the anterior to posterior axis of the embryo. The somite later compartmentalizes to include the sclerotome, which goes on to give rise to the various components of the axial skeleton, including bone, cartilage, and tendons. The fate of these sclerotome cells depends on gene expression within this compartment of the somite. In our current study, we examined the expression of the tendon genes *scleraxis (scxa)* and *dystrophin (dmd)*, which are required for proper tendon formation. To gain a better understanding of this developmental process, we knocked down two genes expressed within the sclerotome, *twist1b* and *twist2*, to determine how sclerotome cells make the decision to commit to the tendon fate. Our results show that both *twist1b* and *twist2* genes were necessary for the expression of *scxa* and *dystrophin* genes within the tendon progenitors. By studying this developmental process, we are able to better understand the role of *twist1b* and *twist2* during tendon differentiation during development of the axial skeleton.

P55 - Expression of Sox5 gene during Sclerotome Development

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During early development of vertebrate embryos, a process called somitogenesis occurs in the embryonic mesoderm tissue that produces somites. Somites are segmented blocks of paraxial mesoderm that are positioned on either side of the neural tube in a developing vertebrate embryo. Shortly after somitogenesis, the somite begins to compartmentalize into distinct regions: the dermatome, the myotome, and the sclerotome. The sclerotome is known to give rise to the axial skeleton, including structures such as bone, cartilage, and tendons. The early sclerotome is characterized by expression of genes *pax1* and *pax9*. Previous research in our lab shows that development of the axial skeletal vertebrae elements are impacted by differential gene expression within the sclerotome. *twist1b* and *twist2* are genes that are expressed in the sclerotome during axial skeletal development. The gene *sox5* encodes a transcription factor involved in the regulation of chondrogenesis during formation of the vertebral body in zebrafish. In this study, we examined the expression of *sox5* when *twist1b* and *twist2* were knocked down using injection of morpholinos in the single cell stage. Our results demonstrate that *twist1b* and *twist2* knockdown affect expression of *sox5* within the developing axial skeleton. By studying gene expression within the sclerotome of zebrafish embryos, we are able to understand the role that sclerotomal genes play during vertebral development. Identifying these important genes can be useful in developing potential therapeutic targets for disorders of axial skeleton tissues.

P56 - N-acetyl-cysteine (NAC) treatment results in gene expression changes in an induced OCD mouse model

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Obsessive Compulsive Disorder (OCD) is characterized by spontaneous, repetitive behaviors for which there is no reliable pharmacologic treatment. N-acetyl-cysteine (NAC) is an over-the-counter-supplement that has shown some promise in OCD patients. OCD can be induced in mice by injecting a pharmacologic agonist of the 5-HT1b receptor, resulting in OCD-like behaviors. When OCD-induced mice are given NAC supplementation in their water 3 weeks prior to 5-HT1b agonist injection, the OCD-like behaviors are improved. NAC supplementation in the water 1 week prior to OCD-induction, however, did not ameliorate OCD-like behaviors. To determine what might be happening at a molecular level with respect to NAC supplementation in OCD-induced mice, the goal of the current study was to determine if gene expression was altered due to both OCD-induction and/or NAC supplementation. Mice were treated with either 1 week of NAC supplementation, 3 weeks of NAC supplementation, or water prior to OCD-induction. Mice not induced with OCD were also included as controls. Mice were sacrificed 3 hours after pharmacologic-OCD induction, and their brains were homogenized with a 22g syringe prior to RNA extraction (Qiagen RNeasy Kit). qPCR was then performed to determine if changes in gene expression had occurred. Two reference genes were used during the qPCR analysis (*YWHAZ* and *PPIA*). Expression of *KCNJ3*, *KCNJ5*, *KCNJ6*, and *KCNJ9* remained unchanged in all experimental and control groups. Expression of *ADCY10* and *CREB* increased in the OCD-induced mice who had been supplemented with NAC 3 weeks prior to OCD-induction, whereas the expression of *HTR1B* decreased in these 3-week NAC treated, OCD-induced mice. These findings suggest that there is a molecular change in gene expression that occurs in NAC-treated mice that is correlated with amelioration of OCD-induced behaviors.

P57 - Biological features of SARS-CoV-2 virus suitable to be used by RT-PCR technique

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During COVID-19 Pandemic, RT-PCR is widely used for detection of SARS-CoV-2. 'RT' in RT-PCR has two definition, one is 'Reversed Transcription', and the other is 'Real-Time' which means amount of replicated genes corresponding timeline indicated as intensity of fluorescent light. The two definition represents main mechanism of RT-PCR. My research objective is figuring out which biological features of SARS-CoV-2 make it detectable by RT-PCR technique, and how RT-PCR works corresponding the features of SARS-CoV-2. My research helps clinical researchers understand clearly the mechanism of SARS-CoV-2 RT-PCR test, and it increases accuracy of examination procedure. Also, it helps understanding more about features of SARS-CoV-2. The data of SARS-CoV-2 from my research is useful in development of vaccine, or action plan towards the pandemic.

RNA from COVID-19 patients' nasal swab samples was extracted. Master-mix (MMLV RTase, dNTPs, DNA polymerase, primer/probe sets for SARS-CoV-2 and phage control) was added to RNA. Subsequently, RT-PCR examination was conducted.

After reversed transcription and spectrofluorimetry process in RT-PCR, light from fluorophores on probes of viral genes was detected.

SARS-CoV-2 virus is retrovirus, doing reversed transcription from RNA to cDNA. It uses RNA dependent DNA polymerase. Instead of natural enzyme, MMLV was used in RT-PCR, and it worked successfully in reversed transcription of SARS-CoV-2. The first definition of 'RT', 'Reversed Transcription', matches the feature of retrovirus doing reversed transcription.

Probe with quencher and fluorophore attaches to single strand DNA, and degrades by DNA polymerase. Near each other, quencher absorbs light from fluorophore. After degradation, quencher separates from fluorophore, and light is detected. In RT-PCR, cDNA replication was done successfully by polymerase, and light from fluorophore on probes of viral gene was detected. Therefore, 'Real Time' the second definition of 'RT' which means light detected corresponding timeline after replication, matches the feature of SARS-CoV-2 virus doing replication of cDNA.

P58 - Connection of alpha defensin 5 and apoptosis of colon cells in Crohn's colitis patients.

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As of 2018, 1.6 to 3.1 million Americans suffer from inflammatory bowel diseases (IBD). IBD affects various parts of the GI track through inflammation, damaging the tissue and interfering with nutrient uptake. The inflammation and tissue damage causes several symptoms such as abdominal pain, rectal bleeding, joint pain and diarrhea. These symptoms will come and go in flares, decreasing the quality of life of those inflicted. IBD can be broken down into two subtypes: Ulcerative colitis and Crohn's colitis. While ulcerative colitis will stay in the epithelial layer of the gut, Crohn's colitis could penetrate all layers of the colon. It is still unknown what causes IBD, however the body's immune system is known to play a role in its progression. In patients with IBD, their immune systems either do not respond properly or over react, causing unchecked chronic inflammation.

A study done by Williams, et al. found that alpha defensin 5 expression is increased in the colon of Crohn's patients compared to their ulcerative colitis counterparts. In normal circumstances, HD5 works to protect against pathogenic bacteria in the small intestine. It does so by binding to their plasma membrane and causing cell lysis. However, with the presence of HD5 in the large intestine in Crohn's patients, we hypothesize that it is interacting with the membrane of our gut cells in a similar fashion as it does with bacteria in the small intestine, contributing to the apoptotic cell death we see in Crohn's patients mucosal layer.

To test this hypothesis, NCM 460 colonocytes were treated with HD5 for 8 and 12 hours, respectively. Protein was extracted, and caspase levels will be measured by western blot. The information gathered will help us to better understand the role of HD5 in the pathogenesis of Crohn's Disease.

P59 - Amyloid- β -Induced chemotaxis behavior and neuronal morphology in transgenic *Caenorhabditis elegans*

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Amyloid- β accumulation and toxicity is a hallmark of neuronal degeneration in Alzheimer's disease. Transgenic *Caenorhabditis elegans* expressing human Amyloid- β in muscles and neurons serves as a model system to study the effect of Amyloid- β in developing organisms. In this study, we used the transgenic Amyloid- β *C. elegans* strains to investigate the effect of muscle and neuronal expressed Amyloid- β on chemotaxis behavior and structure of amphid and phasmid chemosensory neurons. We report that expression of Amyloid- β in muscles and neurons reduces chemotaxis of *C. elegans* to diacetyl. We also show that Amyloid- β expression in neurons inhibit amphid and phasmid neuronal uptake of fluorescent lipophilic dye in adult *C. elegans*, suggesting the structure of neurons are negatively affected in adult worms. Future studies will investigate whether ciliated endings of the sensory neurons have formed, and whether signaling molecules can localize to the sensory neurons in Amyloid- β expressing neurons.

P60 - Progesterone Receptor Dynamics: Effects of Immunomodulation on Receptor Expression in HeLa Cells

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In these experiments HeLa cells were maintained in culture in MEM + 10% FCS. For experimental trials, HeLa cells were seeded in 96 well plates at a density of 30×10^3 cells/well and stimulated with varying concentrations of progesterone. To determine calcium dynamics, a Fluo-4 NW calcium assay kit (Molecular Probes) was utilized. Briefly, 100 ml of the dye loading solution was added to each well and allowed to incubate at 37°C for 30 min followed by room temperature for an additional 30 min. Fluorescence was then measured on a flow cytometer using instrument settings appropriate for excitation at 494 nm and emission at 516 nm. Results indicated a 40% increase in calcium mobilization at all concentrations of progesterone. These results are encouraging for further studies into the mechanisms of calcium dynamics in mammalian cells.

P61 - Exploring Anandamide's Role In Embryonic Zebrafish Development

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An explosion in research on the endocannabinoid system has yielded many important discoveries of how this system acts on the central and peripheral nervous system and other organs. The endocannabinoid system is comprised of endogenous cannabinoids like anandamide, which bind to two receptors, CB1 and CB2. Anandamide is an endogenous fatty acid neurotransmitter and is known to affect various physiological processes, including appetite regulation, reproduction, and lipid metabolism. The presence of Cnr1 and Cnr2 (present in zebrafish and homologous to CB1 and CB2) receptors eleven hours post-fertilization also suggest anandamide's involvement with embryonic development (Carnevali and Migliarini 2009). For this study, zebrafish embryos were given anandamide drug treatments to examine this agonist's effects on the developing embryo. Previous research from our lab had demonstrated cardiac defects when zebrafish embryos were exposed to exogenous anandamide. Using in situ hybridization, we examined the expression of Cnr1 and Cnr2 receptors to see what effects anandamide had on the development of the endocannabinoid system. This research can help us better understand the importance of the endocannabinoid system on embryological development. With the legalization of marijuana in many states in the U.S, this research will contribute to what effects modulating the endocannabinoid system has on embryonic development.

P62 - The Role of At5g61470 in Arabidopsis Development

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The seed of *Arabidopsis thaliana* is made of zygotic endosperm and embryo, and an outer layer of maternal seed coat. Immediately after fertilization, endosperm nuclei divide rapidly without cellularization, while absorbing nutrients from maternal tissues. After endosperm cellularization, growth of endosperm slows while embryo growth accelerates as it absorbs nutrients from endosperm. Endosperm is composed of micropylar, chalazal and peripheral endosperm. Being in proximity to the embryo, micropylar endosperm may play a role in regulating the growth and morphogenesis of the embryo. At5G61470, a C2H2 like transcription factor, has been previously identified as a gene expressed in uncellularized micropylar endosperm. Our goal is to understand the role of At5G61470 during endosperm development and how that may affect the interaction between endosperm and the embryo. To confirm expression of At5G61470 in uncellularized micropylar endosperm, its promoter was cloned in front of a GFP reporter gene. The resulting promoter-GFP construct was used to transform Arabidopsis through agrobacterium-mediated floral dip. The analysis of GFP expression pattern in transgenic plants confirmed At5G61470 promoter activity in micropylar endosperm before cellularization. To study the function of At5G61470, a gain-of function approach was used because a loss-of-function mutant (SALK_022934) showed no discernable seed phenotype. The coding region of At5G61470 was cloned downstream of either a double 35S promoter or RGP3 promoter. The resulting constructs will be used to transform Arabidopsis. The double 35S promoter was used to overexpress At5G61470 throughout many plant tissues, while the RGP3 promoter was used to overexpress At5G61470 in cellularized micropylar endosperm. If At5G61470 controls a developmental program specific to uncellularized micropylar endosperm, overexpression of At5G61470 is expected to activate this program ectopically and lead to abnormal phenotype in other tissues, such as leaves and cellularized micropylar endosperm. Over-expression transgenic plants will also allow us to identify downstream target genes controlled by At5G61470.

P63 - Flora of Alligator Creek Wildlife Management Area, Wheeler County, Georgia

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Recently acquired by Georgia Department of Natural Resources, Alligator Creek WMA comprises about 1,255 hectares of sandhills and associated habitats located at the confluence of Little Ocmulgee River and Alligator Creek in the upper coastal plain of southeastern Georgia. Our field efforts since 2016 have resulted in vouchering of 733 vascular plant species, including one species previously not recorded for Georgia, the discovery, description, and mapping of populations of 11 rare taxa, and the description and mapping of more than 15 community types. Rare or otherwise noteworthy plants documented for the area include *Agalinis tenella*, *Elliotia racemosa*, *Litsea aestivalis*, *Marshallia ramosa*, *Penstemon dissectus*, and *Rhynchospora harperi*. Community types include various phases of Xeric Sandhill Forest (from early to relatively intact late successional), Darlington Oak-Mixed Hardwood Upland Forest, Loblolly Pine-Darlington Oak Woodland, Sandhill Swamp Tupelo Hillside Seepage Forest, Loblolly Bay Swamp Forest, Pond Cypress Depression Forest, Maidencane Pond, Slash Pine and Early Successional Flatwoods, Wet Slash Pine-Pond Pine Flatwoods, Early Successional Seepage Swamp, Blackwater Bottomland Hardwood-Pine Forest, and Blackwater Ogeechee Tupelo Floodplain Forest.

P64 - Developing an Understanding of Elon University Forest's Carbon Budget through Analysis of Soil Carbon

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Climate change and other environmental stressors have been shown to alter the amount of carbon that is either emitted or stored in various components of forest ecosystems. Changes in soil organic carbon (SOC) and total cation exchange capacity (CEC) that are evident after forest regeneration can be studied to understand everchanging carbon budgets. This study was conducted to study the successional changes of the soil composition, using the Elon University Forest (EUF) that contains many plots of various ages and past land use practices as a space-for-time substitution for the greater Piedmont region of North Carolina. While the EUF has been studied extensively for species demographics, the understanding of its soil chemistry is not as developed. To achieve this, soil was extracted from plots identified and characterized by species and age using previous studies. Soil was dried, prepared, and sent out for a physiochemical analysis. Statistical analysis when grouping the plots by similar age group yielded results showing that forest age has a significant effect on the CEC, with 48.8% of variance between groups being an effect of age. Plots that were pine dominant and hardwood dominant were grouped and compared to the other plots, revealing that dominant tree species have a statistically significant effect on the CEC of the forest, with 9.57% of variance between groups resulting as an effect of dominant tree species. There was also a statistical difference when comparing the plot that has a land-use history of being an orchard to the other plots with similar past land use. It was concluded that increasing age and changing species composition could result in a concerning, low carbon budget of the Piedmont forest ecosystem.

P65 - A Half-Century of Forest Composition Change: Examining an Old-Growth Mesophytic Forest in Eastern Kentucky

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Lilley Cornett Woods (LCW), located in eastern Kentucky in the Cumberland Plateau ecoregion of Appalachia, is the site of an ongoing long-term study of its 102 hectare old growth forest. The study was started in 1971 by Dr. Bill Martin with the establishment of 135 permanent 0.08 hectare plots that have been subsequently resampled approximately every 10 years. The objective of this research is to evaluate changes in overstory tree species composition over the past 50 years by comparing data from 2020 to data from the five previous surveys. During each census of these plots, including the one in 2020, every living tree with a diameter-at-breast-height (dbh) of at least 2.5 centimeters was measured and identified to the species level. Trees with a dbh of 12.5cm or greater were classified as overstory trees. Importance values were then calculated by summing the relative values of density and basal area for comparison across all sampling efforts. Preliminary results reflect trends seen elsewhere as oak (*Quercus*) species have declined while maple (*Acer*) species have continued to increase in dominance. Although past trends at LCW reflected the importance of eastern hemlock (*Tsuga canadensis*) and ash (*Fraxinus*) species in eastern Kentucky, their subsequent population crashes from the hemlock woolly adelgid (*Adelges tsugae*) and emerald ash borer (*Agrilus planipennis*), respectively, are reflected in the 2020 data. This data is valuable as a null comparison for secondary-growth mesophytic forests in southern Appalachia, as LCW is protected from obtrusive anthropogenic activities such as logging and mining.

P66 - Investigation of an indirect defense mechanism of *Chapmannia floridana* (Florida alicia) in Florida scrub

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Plants have many direct defenses, such as thorns and toxins, which increase their survival and reproduction. Some plants have indirect defenses as well, such as glandular trichomes (i.e., sticky hairs) that entrap carrion, which attract predators that consume the carrion. Predators deter herbivores from harming the plant, leading to an increase in the survival and/or reproduction of the plant. Flowering stems of *Chapmannia floridana* (Florida alicia), a perennial plant that is endemic to Florida, are covered in sticky hairs, which may act as an indirect defense. We assessed 84 flowering *C. floridana* stems across six habitats in the Florida scrub ecosystem. We measured the total flowering stem height and the height where trichomes started, counted the number of fruits, flowers, and buds present, and documented any damage to reproductive structures. We also counted the number of carrion, herbivores, and predators on *C. floridana* flowering stems. There was no difference in the length of the trichome-covered portion of flowering stems among habitats. We found a positive correlation between the length of the trichome-covered portion of *C. floridana* flowering stems and the number of carrion trapped. Only 10% of fruits, 15% of flowers, and 19% of flower buds we counted on flowering stems were damaged. We found predators (i.e., spiders) on 6% of flowering stems and herbivores (e.g., grasshoppers, leafhoppers, caterpillars) on 37% of flowering stems. We found no association between habitat and damage (for scrubby flatwoods and firelane habitats only) and no association between carrion presence and damage. However, the probability of damage to reproductive structures decreased as the number of trapped carrion increased. Overall, our results suggest that herbivory of *C. floridana* reproductive structures is relatively low and glandular trichomes on *C. floridana* may be acting as an indirect defense.

P67 - Patterns of shared airspace: bat foraging strategies

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Most species of bats in the eastern United States forage using echolocation calls that consist of different frequencies and different patterns of sound production. Bats using calls with similar frequencies can cause interference in echo patterns, that in turn, may affect the ability of individuals to hunt insect prey. Therefore, two individuals of different bat species with call frequencies that are similar may avoid using the same

airspace at the same time. Our study examined whether several bat species in west Tennessee with similar call frequencies tended to forage in the same airspace at the same time. We hypothesized that most bats would not forage in the same airspace at the same time. We predicted that most recordings would not contain more than one bat in the immediate airspace. Furthermore, we predicted that when bats did share the same airspace, they would be less likely to be species that both used the same frequency range. We collected data at five locations in west Tennessee from Fall 2020 through Spring 2021 using Wildlife Acoustics SM4BAT detectors. We initially analyzed bat passes using SonoBat v.4.2.2 North America with the West KY/TN classifier followed by manual vetting. Activity varied by time, species, and location at the five study sites.

P68 - Current Plant Community Composition at the Sheffield Wildlife Management Area.

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The Sheffield Wildlife Management Area (WMA), located within the Piedmont ecoregion, was established to provide important wildlife habitat and ensure the protection of the Raccoon Creek watershed. It is currently a mosaic of forests that have experienced relatively light management. However, due to long-term fire suppression, the rare montane longleaf pine ecosystem that used to be present in some areas has been greatly diminished. The goal of this study is to provide baseline data on plant community structure across the Sheffield WMA (and eventually also the adjoining Paulding WMA) to aid in planning and monitoring current and future restoration efforts, as well as help determine the success of those efforts.

Thirty-six plots were set up near the top of ridge lines on either north or south facing slopes. Plots were located in areas where longleaf pine was historically dominant as determined by the presence of old stumps. Each plot was composed of three adjacent 10m x 10m squares parallel to the fall line within which each tree was identified to species and its DBH recorded. Cover of herbaceous species and seedlings/saplings was estimated in six 2m x 2m plots within each larger plot. From this data we calculated relative density, dominance, frequency, and average percent cover. Diameter size class frequencies of longleaf pine will be presented and compared to those of other longleaf pine forests with various management histories. We compared the communities on the two slope aspects and will present the beginning of a comprehensive species list for the whole Sheffield WMA. Results indicate a lack of longleaf pine in the smaller diameter size classes, along with clear differences in the frequency and dominance of various tree species between the two slope aspects. Biodiversity as measured by the Shannon Index was greater on the south slopes.

P69 - Monitoring Changes in the Composition and Structure of Vegetation in Elon University Forest over 10 years

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Elon University Forest (EUF) is a 56-acre teaching and research forest that contains a patchwork of forest ages ranging from about 45 years to a never clear-cut woodlot with trees exceeding 250 years. The varying ages across EUF, caused by 18th and 19th century farming practices, make it an ideal location for forest successional studies. During the last 10 years, the majority of the forest composition research on EUF has involved sampling permanent 20 x 50 meter plots, a standard way of measuring forest succession. Although the permanent plots are located in different forest types characterized by dominant vegetation and apparent successional stage, they do not necessarily accurately represent the entirety of vegetation on EUF. The present study uses prism cruising, a non-permanent sampling technique that was utilized on EUF in 2010 to cover a greater area more quickly. The results from the present study were compared with data from the baseline 2010 cruise and with successional changes documented in permanent plots from 2010 and 2018. This provided a more thorough picture of the changes to EUF through time and space. Using the non-permanent sampling method, we found greater *Pinus virginiana* (Virginia pine) and *Pinus echinata* (shortleaf pine) dominance that was not represented by the permanent plots. This pine dominance was expected for an early-successional forest like EUF and supports the prediction that prism sampling provides a different structural understanding of EUF. Additionally, gradual successional changes in EUF from 2010 to 2020 were evidenced in the non-permanent sampling method as shortleaf pine dominance decreased and *Liquidambar styraciflua* (sweetgum), *Quercus stellata* (post oak), and *Quercus alba* (white oak) dominance increased. Transitions in the dominant species at each time period indicated by both sampling methods suggest that forest composition in EUF is in a continual state of change, especially its younger forests.

P70 - A comparison of bat activity and species richness in suburban and rural west Tennessee ponds.

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An important aspect of species conservation is an understanding of habitat use of organisms. A greater proportion of natural habitats are being converted to suburban and urban environments, potentially affecting the species that use those regions due loss of critical microhabitat features within those environments. Several bat species in Tennessee use ponds to forage and wooded areas to roost. Our study examined whether there was a difference in bat activity and species richness between suburban ponds and rural ponds located in west Tennessee. Wildlife Acoustics SM4BAT detectors were used to collect data at 5 ponds in west Tennessee: 2 located in suburban areas and 3 located in rural areas. Bat activity and species richness were determined using analysis with SonoBat v. 4.2.2 North America West KY/TN classifier and by manual vetting of bat passes. Bat activity varied by pond and by pond type. Species richness did not vary by pond type but did vary between ponds.

P71 - Conservation of fruit-frugivore networks in human dominated landscapes in the Neotropics may rely upon specialized interactions.

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The alarming rate of ecosystem deterioration due to anthropogenic influences has bolstered the study of mutualistic interactions due to their strong influence on ecosystem function. Seed-dispersal mutualisms ensure the local persistence and gene flow of plants in any community but are especially critical in tropical regions. Neotropical ecosystems host numerous species of birds and a large proportion of the bird community consumes fruits either obligatorily or opportunistically. Available bird habitat in these systems has diminished due to deforestation and loss of habitat is a primary driver for decline in populations of neotropical bird species. Given the importance of the ecosystem services provided by birds, determining methods to protect their remaining habitats is important. We aimed to identify priority plant species that provide resources for birds in diverse, biodiversity-friendly agroforests. Fruit-frugivore foraging observations were recorded in 2008 in six coffee farms in the San Luis Valley, Puntarenas, Costa Rica. We constructed a weighted bipartite network and used quantitative modularity analysis to determine the topological roles of all observed plant species. The full network comprised 21 trees, 56 birds, with a total of 1296 interactions. The network was found to be significantly modular, indicating that subsets of more specialist interactions dominated the network, and consisted of 6 modules. All plant species were identified as peripherals except *Ficus laterisycy*, which was a connector. Network connectors are expected to play core roles in the network, linking species and enhancing stability. Therefore, *Ficus laterisycy* will be beneficial to conservation of fruit-frugivore interactions. Though our modularity analysis only identified one connector, the network is nested and highly modular with a high robustness index suggesting it can withstand loss of species, altogether suggesting that the high degree of specialization may be stabilizing the network.

P72 - Temporal and spatial overlap of margays (*Leopardus wiedii*) and their potential prey

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The margay (*Leopardus wiedii*) is a small, near threatened neotropical cat. Its diet consists of small mammals, birds, amphibians and lizards. We compared the temporal and spatial activity of margays and their potential mammalian and avian prey via camera traps deployed in Wildsumaco Wildlife Sanctuary, Ecuador. Potential prey species captured include numerous bird species, small rodents, squirrels and opossums. The margays were largely nocturnal and had the largest spatial overlap with squirrels, followed by small rodents and birds. The species with the greatest temporal overlap with the margay are rodents who also display nocturnal behavior.

P73 - Predictive niche modeling for the identification of crop pests and pathogens of greatest concern in the US

Christopher Randle, Laura Bianchi, Jesus Castillo, Nicholas Reger, Justin Williams

Sam Houston State University, Huntsville, TX

Cotton, small grains such as wheat and rice, and grapes are significant commodities in US agriculture. These crops experience continual threats from invasive pests and pathogens; predicting the spread of these pathogens into croplands may provide guidance for preventive measures against yield loss. Ecological niche models allow prediction of habitats suitable for pest and pathogen persistence given occurrence and bioclimatic data from their native range. In this study, ecological niche models will be used to project areas of the US in which habitats are suitable for colonization by non-native pests and pathogens of cotton, small grains, and grapes for the purpose of 1) identifying global hotspots from which pests and pathogens are most likely to be transported to US croplands, 2) ranking pests and pathogens from greatest to least concern for persistence in both croplands and natural habitats, and 3) identifying areas of The US most likely to serve as suitable habitat to dangerous pests and pathogens. Worldwide occurrence data was obtained from the Cooperative Agricultural Pest Survey, and 19 environmental correlates the WorldClim database. These were used to develop niche models against arthropod and plant pests listed as priority pests by USDA-APHIS Cooperative Agricultural Pest Survey, using maximum entropy, boosted regression trees, and model averaging. The models were then used to identify areas of highest habitat suitability both in the US and from potential source habitat.

P74 - A multi-century fire history from the Potomac Highlands of West Virginia

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Tree-ring reconstructions of past fire activity provide context for forest management and restoration objectives. Our primary objective in this study was to develop a new fire history in the Potomac Highlands of West Virginia where published reconstructions are particularly sparse, but efforts to develop prescribed fire plans are on the rise. We produced a 273-year (1739-2011) fire-scar record from 57 yellow pine (*P. pungens*, *P. rigida*, and *P. virginiana*) trees spread across five topographically diverse sites on Short Mountain in Hampshire County. Fire occurred every 7-15 years on average at individual sites, while a landscape-scale analysis indicates that fire frequency did not change over nearly 160 years (1855-2011). Fires, however, were significantly less extensive during the “exclusion era” (post-1930). No conclusive relationships between drought and fire were identified, although the most extensive fire year (1930) was uniquely dry. These findings complement nearby fire-scar and sediment charcoal records and provide new context for the application of prescribed fire in the Potomac Highlands.

P75 - Banking on the future of rock outcrops: analysis and comparison of soil seedbank and extant aboveground vegetation of two high-elevation rock outcrop communities

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The Southern Appalachian Mountains are an ancient region that supports an assortment of high-elevation communities. Rock outcrops support a rich biodiversity of rare/endemic species and alpine relicts representative of the Pleistocene. Rock outcrop communities can be classified into different types, but the two addressed in this study are montane red-cedar (MRC, defined by the presence of *Juniperus virginiana*), and non red-cedar (NMRC, lacking *Juniperus virginiana*). These precariously balanced communities are strongly threatened by habitat destruction, air pollution, and global warming; increased knowledge of the biodiversity and biogeography of flora will aid in conservation and management efforts. Understanding the soil seedbank and its similarity to the aboveground vegetation is imperative to evaluating the differences in species diversity, processes (environmental filtering), and seed dispersal/recruitment between outcrop types. Soil core samples were taken Spring 2020 from 3 MRC and 3 NMRC sites and utilized in a seedling emergence experiment to analyze species abundance/diversity within the soil seedbank. Herbaceous flora on the same sites were inventoried over two summer months to determine similarity between the soil seedbank and the extant aboveground vegetation on MRC and NMRC sites. Overall, both MRC and NMRC sites displayed high soil seedbank and aboveground vegetation species diversity. The results indicate wide variation in the soil seedbank composition of both MRC and NMRC sites. The species compositions of the aboveground vegetation of MRC and NMRC sites were significantly different with strong clustering by site type, while the seedbank compositions were not significantly different. Further, separation between the soil seedbank composition and extant vegetation of both MRC and NMRC sites was demonstrated. These results indicate that MRC and NMRC sites are similarly affected by seed dispersal/recruitment. However, ecosystem processes (environmental filtering) may influence the germination and establishment of seedlings and perpetuate differences in species composition of MRC and NMRC rock outcrop communities.

P76 - Geomorphic Morphometric Differences between Populations of *Speyeria diana* (Lepidoptera: Nymphalidae)

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Wing shape in butterflies can be used as a character to measure individual and population-level differences in adult forms. We conducted a geometric morphometric analysis of wing shape for *Speyeria diana* (Lepidoptera: Nymphalidae), a species currently threatened across portions of its range. We digitized 243 pinned *S. diana* specimens from natural history museums in North America and Europe to compare wing shape and size across the historical and current distribution. We used principal components analysis (PCA) to compare variation in forewings and hind wings. We used the PC scores in a MANOVA to test for differences, and interactions, between male and female specimens, eastern and western specimens, low and high elevation specimens, and specimens collected before and after 1950. We found significant differences between wing shape in male and female specimens, with male forewings being narrower and more elongated, making them well suited for patrolling behavior. Female forewings were rounded and wider, reflecting their life history, because much of their life is spent on the forest floor in search of oviposition sites. We found significant regional differences in male forewing shape, reflecting the long-term geographic and genetic separation between these groups. We also found significant differences in female forewing shape between low and high elevation sites. *Speyeria diana* female forewings from high elevation populations were narrower than low elevation populations, indicating that these females may be more mobile than those from low elevations with wider forewings. The wing shape of western populations of *S. diana* appears to be adapted for low dispersal, supporting other recent findings that also indicate western populations of *S. diana* are both spatially and genetically isolated. The future of *S. diana* will require the thoughtful preservation of well-connected high elevation habitats, especially in the western distribution where dispersal is more limited than in the east.

P77 - Confirmation of the occurrence of the Locally Endangered Variety, *Lactuca hirsuta* var. *sanguinea*

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We report a new record of *Lactuca hirsuta* var. *sanguinea* (Bigelow) Fernald (Asteraceae), growing in several locations in Nantucket, MA, documenting the first collections in over fifty years within the state of Massachusetts. The taxon is commonly known as hairy wild lettuce and is primarily found in the eastern United States. A review of the literature found disagreements among sources on the status of *L. hirsuta* var. *sanguinea* as a variety. We have observed morphological differences in coloration that support the varietal distinction. Specifically, plants of *L. hirsuta* var. *sanguinea* have purplish-maroon involucre bracts, ligule tips, stems, and leaf veins and edges. Observations of herbarium specimens reveal that these striking color differences are lost when the plant material is dried, which we believe has influenced whether certain sources have recognized *L. hirsuta* var. *sanguinea* as a variety. We therefore support the conclusion made by Bigelow that *Lactuca hirsuta* var. *sanguinea* should be recognized as a distinct variety. We plan to combine these morphological data with molecular phylogenetic analyses of *L. hirsuta* and *L. hirsuta* var. *sanguinea* from additional sampling locations.

P78 - Influences of eutrophication on reproduction and development in Cope's Gray Treefrog (*Hyla chrysoscelis*): A proposal

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Eutrophication in aquatic systems results in algal blooms and subsequent oxygen depletion that leads to mass mortality events and alterations in aquatic community structure and function. However, many sublethal effects of eutrophication, such as behavioral changes in the absence of mortality, are poorly understood. Cope's Gray Treefrogs (*Hyla chrysoscelis*) minimize risk by selecting reproductive sites that exhibit reduced hydroperiods and predation risk, but eutrophication can present complex indicators of site quality. Although oxygen depletion often results from eutrophication, habitats with reduced oxygen are likely less to be colonized by aquatic predators. Additionally, moderately increased primary productivity due to eutrophication may benefit growth, as larval *H. chrysoscelis* are largely herbivorous, but such production may attract predators. To address these potentially conflicting cues of site quality, I propose to characterize patterns of adult amphibian habitat selection and subsequent larval success in response to eutrophication of simulated wetland habitats using a mesocosm design. First, we will determine if males and females show equal patterns of reproductive site selection between: a) experimentally enhanced mesocosms characterized by increased N and P treatments; and b) unmodified controls by observing male calling behavior and female oviposition behavior. Second, we will determine if the observed patterns of selection in adults are adaptive by rearing larvae in similarly enhanced treatment and unmodified control tanks and observing larval growth rates and size at/time to metamorphosis. The results of this thesis research will provide a more comprehensive view of the sublethal effects of anthropogenic eutrophication in wetlands habitats.

P79 - Response of Chestnut Hybrids to Forest Management Strategies in West Virginia

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The American Chestnut (*Castanea dentata*) was once a co-dominant canopy species in Eastern forests of the United States. A pathogenic fungus (*Cryphonectria parasitica*) decimated this tree species to functional extinction over sixty years ago. Our research attempts to identify forest management strategies for increasing the success of hybrid chestnut (BC₃F₃ generation) plantings in forested ecosystems. We manipulated factors that may facilitate seedling survival and growth in an Appalachian cove forested ecosystem in West Virginia. We created canopy gaps of different sizes (40% vs 60% canopy openness) to manipulate light with the prediction that seedlings would perform best in larger gaps. Within these gaps, we added landscape fabric on every other row to decrease vegetative competition. We placed 12" tree shelters around half of the seedlings planted within the gaps to protect them from rodent predation. All gaps were surrounded by deer fences. After five years, seedlings had significantly greater diameter and height relative growth rates with landscape fabric ($p < 0.05$). The interaction between landscape fabric and gap size was significant for both variables ($p < 0.05$). Tree shelters had a significant positive effect on seedling height (but not diameter) regardless of gap size ($p = 0.001$). Survival was significantly greater in small gaps (73%) compared to large gaps (42%). *Rubus* spp. physically crushed the seedlings and reduced light levels in higher light conditions. In conclusion, we recommend planting chestnut seedlings in small gaps without landscape fabric, or a large gap with herbaceous management. Planted chestnut seedlings compete best under these conditions in an Appalachian cove ecosystem.

Keywords: *Castanea dentata*; *Cryphonectria parasitica*; Height and Diameter; Survival; Southern Appalachian Cove; Gap Size; Tree Shelter; Landscape Fabric

P80 - The Effectiveness of Stream Restoration on Benthic Macroinvertebrate Communities and Water Quality

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The Shenandoah Valley encompasses some of the highest agricultural producing regions in Virginia, many of which are major contributors of nutrients and sediment to receiving waterways. To help reduce this pollution, the Conservation Reserve Enhancement Program (CREP) assists landowners in the installation of riparian restoration projects in which cattle are fenced out or a riparian buffer is planted. We examined the temporal effects of riparian restoration and the impact of upstream land use on water quality for eleven farms participating in the CREP program for various times (from 1 to 14 years). We hypothesized that the length of time that the CREP program has been established would have a positive effect on the water quality of a stream. Water quality was quantified by measuring benthic macroinvertebrate assemblages using the Hilsenhoff Biotic Index (HBI), Virginia Stream Condition Index (VA-SCI), and the Shannon Diversity Index. GIS analysis was also employed to calculate upstream land use and stream channel characteristics: land use, canopy cover, slope, impervious surface, relief, road density, and watershed area were assessed for the watersheds and 100-meter stream buffers at each sampling site. Single variable and multiple linear regressions were performed separately within the watershed and buffer zones. The time since restoration showed a significant positive relationship with VA-SCI ($R^2 = 0.441$, $p = 0.007$) and a significant negative relationship with HBI ($R^2 = 0.267$, $p = 0.049$). When upstream land use variables were included in multiple regressions, the relationships were stronger: time since restoration, the percentage of upstream agricultural land use and impervious surfaces predicted VA-SCI values (adj $R^2 = 0.579$, $p = 0.005$) and HBI values (adj $R^2 = 0.452$, $p = 0.011$). These data show that CREP efforts are having a positive effect on water quality, and that upstream land use is also an important factor.

P81 - Evaluating the use of non-invasive hair snares and DNA barcoding to assess mesocarnivore abundance and diversity

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Mesocarnivores, whose diets consist of roughly 50% meat, tend to be a difficult group of mammals to study as many species are nocturnal and extremely secretive. Although their importance tends to be overlooked, they cause significant cascades at the community level through their dietary habits. Hair snare sampling is a non-invasive way to obtain genetic samples from target animals. In this project, we used hair snares containing sardine lures to obtain hair follicles of mesocarnivores. The aim of this project is to evaluate the abundance and diversity of mesocarnivores located within the Warren Wilson College forest in Swannanoa, NC. We used hair snares in combination with DNA barcoding to identify species that are visiting these traps. Game cameras were also used to confirm individual visitors to research sites. To begin this process, twelve hair snares targeting small mesocarnivores were built using PVC pipes, glue strips and other materials. They were randomly deployed over a six week period in four separate sections of forest, each with slightly different habitat types. Twenty-five hair samples were obtained and DNA extraction protocols for mammalian hair follicles were optimized. PCR will be used to isolate cytochrome oxidase I (*COI*), and after sequencing, the Basic Local Alignment Search Tool (BLAST) will be used to identify species. The long-term goal of this project is to establish methods to identify populations of lesser-known mesocarnivores, such as the Appalachian eastern spotted skunk and mustelids found in western North Carolina. We will present a methodology for hair snare construction, as well as discuss the importance of their location, and their potential for obtaining mesocarnivore samples to be used to identify the species of visitors in order to assess species diversity.

P82 - Correlation Between Kemp's Ridley Sea Turtles (*Lepidochelys kempii*) and Black Coral Reef (Order: Antipatharia)

Megan Phillips

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In this study, Kemps Ridley Sea Turtles and Black Coral Reefs were studied to see if there was a direct relationship between the two species Both species were analyzed through secondary databases. In past studies, it was indicated that sea turtles and coral reefs had a direct relationship with one another. There appears to be a direct geographic correlation between Kemps Ridley and Black Corals. Four maps were created to study Kemps Ridley Sea Turtles and Black Coral Reefs. Both Kemps Ridley and Black Corals have decreased over the years due to pollution from human activity, poaching, and lighting near the shores of beaches. Kemps Ridley and Black Corals are beautiful creatures that have a purpose in this world. To keep these amazing creatures alive, it is important to educate the general public on how to protect them.

P83 - The Oak Conservation Alliance: Forming an interdisciplinary network of allies to help prevent and monitor pathogens in the oak family (Fagaceae)

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The oak family (Fagaceae) represents many ecologically, ethnobotanically, and economically important species, including the oaks, chestnuts, and beech. However, multiple pathogenic diseases—such as sudden oak death, oak wilt, and beech bark disease—are threatening their long-term health and conservation. Synergistic, interdisciplinary, and cross-agency collaborations will be required to effectively monitor and plan for these threats. To this end, we have organized the Oak Conservation Alliance and have made (and are seeking more) allies from research and academic institutions, state agencies, non-governmental organizations, tribal organizations, private sectors, community scientists, and other groups to help carry out our goals. Forming this alliance is helping to provide a stronger framework for dynamic collaboration, educational outreach, and funding opportunities. Community forum discussions have been held, representing stakeholders from various backgrounds that have provided valuable insights to address concerns. Monitoring and educational methods include the use of mapping technologies, remote sensing, tissue sampling, community scientist applications, and various online platforms, merged with various approaches from the humanities. One methodological approach utilizes a delineated project nested within the iNaturalist social networking service where anyone—using their iNaturalist smartphone app—can take georeferenced and annotated photos of suspected symptomatic plants, which will then be stored in a database for plant pathologists to view, organize, and follow up with on-site if the symptoms appear diagnostic. The resulting data will be funneled into databases for use in future research, including spatial analyses, risk assessments, and ecological impact studies to help understand and preserve our valuable ecosystems and heritage in eastern North America.

P84 - Coastal biodiversity and phylogeny on coral reef communities along the north-eastern coast of Trinidad: A race to share scientific knowledge in the wake of ecological risks associated with benthic destruction resulting from a proposed port development

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Caribbean coral reef communities continue to follow the global trend of facing demise due to current ecological crisis. Each year records hotter months, higher coral mortality, and increased anthropogenic stressors continue to aggressively counteract coral growth. Coupled with development and pollution, we continue to see imminent threats to Caribbean reefs. Intricate relationships between local marine species in comparison to other Caribbean islands can assist in marine conservation efforts. Annual biodiversity monitoring from 2005-2020 using line and point transect, video, and quadrat techniques were used to collect benthic data for reef communities located along the northeastern coast of Trinidad. Molecular techniques and phylogenetic analysis were used to identify conspecific species, which can be problematic in this region. For approximately 15 years, research conducted at sites along the northeastern coast of Trinidad, has improved local benthic community knowledge for a mixture of undefined patch reefs and fringing reef. Over 257 species have been identified thus far, with average cnidarian coverage between 30-45% at sites. Invertebrate species, such as the rock-boring sea urchin (*Echinometra lucunter*) showed high population densities and size

distributions in low wave energy, compared to high wave energy environments. Both black and red color morphs are genetically identical to *E. lucunter*, and are samples from the southern-most part of the Caribbean Sea. Numerous zoanthid color morphotypes were identified as *Palythoa caribaeorum*, *Zoanthus aff. pulchellus*, and *Zoanthus aff. sociatus*. *Symbiodiniaceae* genera were identified as *Cladocopium* and *Symbiodinium* *Palythoa* and *Zoanthus spp.* respectively. Current records for cnidarian species phylogeny continue to show this region to be a unique area, however momentum to develop a proposed local port in the area threatens to completely halt research, and a 100% loss of benthic reef communities is imminent. This ecological crisis can be averted with data presentation and identification of species in marine environments.

P85 - Identification and Comparison of Arbuscular Mycorrhizal Fungi and Soil Microbiomes Between American Chestnuts and Surrounding Hardwoods

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The American chestnut (*Castanea dentata*) has lived on the brink of extinction ever since chestnut blight was introduced at the start of the 1900s. The goal of this study is to investigate the potential association between arbuscular mycorrhizal fungi and American chestnut plants. Although the symbiotic association between plant roots and arbuscular mycorrhizal fungi (AMF) has been shown to benefit plants primarily through facilitating an increase in nutrient uptake (primarily phosphorous), AMF may also function in the enhanced protection of plants from root fungal pathogens. While there have been studies on the relationship between mycorrhizae and the American chestnut tree; *Castanea dentata*'s diminutive population size and mycorrhizae's mutualistic behavior make it difficult to draw significant correlations between the two, and most of these studies have focused solely on ectomycorrhiza and not AMF.

In this study, we will be researching how AMF species that associate with American chestnut trees differ from their surrounding tree species in north Georgia by sampling in each cardinal direction in a ten-meter radius from individual chestnuts. In addition, through the use of next gen DNA techniques we will examine the microbiome community of chestnut roots and compare them to the surrounding soil and select hardwood plants in the vicinity. In the lab, DNA extraction using a Soil Extraction Kit for both soil and root samples will be performed followed by DNA amplification and replication to identify AMF, plant roots, and soil microbiome communities. All DNA samples will be sent off for analysis. We expect to see similarities in fungal colonization between individual American chestnut trees of different stands and to observe differences between American chestnuts and the surrounding hardwoods. Our hope is that our findings can provide information that will help contribute towards the future mechanisms of revival of American Chestnut populations.

P86 - Reproductive Effort and Output Within and Between Two Species of Pitcher Plant (*Sarracenia*)

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Sarracenia jonesii (Jones' pitcher plant), a federally threatened species, is sometimes outplanted into sites where its congener *Sarracenia purpurea* var. *montana* (mountain purple pitcher plant), a federal species of concern, grows. However, anecdotal evidence, and grey literature from breeders, suggests that species distinctions within this genus are maintained primarily through allopatry, and that plants in sympatry hybridize readily. Observations of phenotypic hybrids at sites where these species co-occur, and genetic confirmation of hybrid parentage, led us to ask about the potential for, and realization of, interspecific breeding. In summer 2019, we monitored *S. jonesii* and *S. purpurea* var. *montana* at two sympatric western North Carolina field sites. Parental species and their phenotypic hybrids were visited weekly during the flowering season to assess plant phenological stages and to collect anthers for pollen viability analysis; ovaries were collected after floral senescence to analyze seed production, seed viability, and seed germinability. Seed collections were repeated in summer 2020. Results revealed significant overlap in flower production and receptivity, and showed that pollen from both species maintained high viability even after anthers were shed. Parental species and their hybrids all produced large numbers of seeds; viability of these seeds is being assessed. These data demonstrate the potential for hybridization between two species of conservation concern under field conditions, and suggest that interventions such as floral bagging should be undertaken to restrict gene flow across these permeable species boundaries. Future investigations will compare parental species' seed production in sympatry vs. allopatry, and will discern parental versus hybrid status of the seed generation.

P87 - Measuring bat activity and species richness at ponds versus recently restored wetlands

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A large proportion of Tennessee's wetlands have been lost due to human activities such as agriculture, channelization and sedimentation. The loss of wetlands has led to economic and environmental consequences including the deterioration of erosion control, increased flood damage, increased water pollution and decreased species diversity. The restoration of Tennessee's wetlands is critical to the wellbeing of the environment. Many restoration projects involve monitoring ecologic indicators such as changes in plant, invertebrate, avian or amphibian species diversity. However, monitoring changes in bat activity and bat species diversity could also effectively serve as a mammalian indicator of wetland function due their use of the wetlands and the ease of acoustic monitoring. We compared both bat species presence and bat activity at well-established permanent ponds in west Tennessee to that found at nearby restored wetlands in various stages of restoration. Regardless of size, bat activity was greatest at ponds followed by older aged restored wetlands, then younger aged restored wetlands. Bat species richness was not correlated with habitat type nor restoration age or permanence of the water impoundment. Therefore, bat activity as a suitable indicator of wetland function warrants further investigation.

P88 - Factors Contributing to Reproductive Patterns in the Federally Threatened Shrub, Virginia Spiraea (*Spiraea virginiana*)

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Virginia spiraea (*Spiraea virginiana*) is a perennial shrub with both sexual and asexual modes of reproduction, found in riparian habitats throughout the Appalachian Mountains. The species was listed as federally threatened in 1990 due to hydrologic disturbance, and populations might suffer from inbreeding depression. In this series of experiments, we examined factors that could challenge the species' survival. We compared reproductive effort and output among populations, manipulated breeding systems to see their effects on seed production, identified insect visitors to ascertain potential pollinators, used physiological measurements in experimental gardens to determine whether the species is shade-tolerant, and tested the potential for hybridization with Japanese spiraea (*Spiraea japonica*), an invasive congener. Results showed variation in reproductive effort and seed production among genetic individuals and populations, and analyses of breeding systems are ongoing. Guilds of insect visitors varied widely in their potential pollination roles; because Virginia spiraea pollen loads on ants and flies were negligible, it is likely that other groups (beetles, bees, wasps) are the plant's major pollinators. Virginia spiraea's photosynthetic rate did not saturate until full light, and unshaded plants produced more corymbs, suggesting that removal of woody species could increase the species' performance under field conditions. Finally, although reproductive effort was high in Japanese spiraea, cross-pollinations between native and invasive spiraea produced no seeds. This work will inform efforts to restore and augment populations of Virginia spiraea throughout its range, and will ensure the continued persistence of existing clones.

P89 - Inadvertent Damage to Non-Target Trees Due to Timber Removal and Equipment Transport

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Damage to trees by logging equipment along the travel route (within the park) to the timber-harvesting site was observed at San Felasco Hammock State Preserve Park. This was a 200-acre salvage harvest operation in response to the presence of southern pine beetles (*Dendroctonus frontalis*) in loblolly pine (*Pinus taeda*) within the park boundaries in the summer of 2018. One of the purposes of the harvest was to remove trees that are infected with southern pine beetles, with the goal of preventing them from moving into the upland pine community dominated by long-leaf pine (*Pinus palustris*) trees within the park. Along the logging vehicle travel route (1.9 miles), sixty trees were damaged, 37 were hardwoods and the remainder pine. The damage were assigned values of 1-4, one being the least amount of damage, rubbing of bark, four was the highest level of damage, broken limbs and or deep cuts into tree. Some trees had multiple injuries but at different levels. Level 2 was assigned to trees that had bark removed and the phloem or cambium were visibly exposed. Overall, the majority of injuries (two-thirds) was classified at a level two. Of the *Pinus* species that were injured on this route, 22.7 % were infected with black turpentine beetles (*Dendroctonus terebrans*). This species of beetle is often found in stressed or injured trees but it is not likely to kill the tree. This amount of damage in such a short travel distance has significant management implications. In 2019, the trees on this route area were removed for a long-term restoration plan.

P90 - Buzz-Worthy Relations: Floral Visitation in Two High-Elevation Rock Outcrop Communities

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In the southern Appalachian Mountains, sparsely distributed rock outcrops harbor a significant number of rare and endemic plants. To assess plant-pollinator relationships in rock outcrop communities, I evaluated floral resources and floral visitation between April and October, 2020, on three mafic (Montane Redcedar) rock outcrop communities and three felsic (Non-Montane Redcedar) rock outcrop communities on the Highlands-Cashiers Plateau in North Carolina. Data are being analyzed to compare the diversity of floral visitors in mafic and felsic rock outcrop plant communities, to assess potential seasonal shifts in floral visitor communities, and to evaluate diversity and visitation rates between flowering species. Preliminary findings indicate primarily generalist interactions with comparable diversity of floral visitors in Montane Redcedar and Non-Montane Redcedar communities, though floral visitor diversity and visitation rates on Montane Redcedar sites were higher in early spring than on Non-Montane Redcedar sites. The results of this research provide new insight to the phenology and diversity of plant-pollinator relationships on rock outcrops, aiding future land management and conservation efforts in these unique communities.

P91 - Dendroecology and carbon storage potential of a mature oak-hickory stand in the southern Appalachians

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Disturbance events such as fire and drought play a significant role in forest growth, composition, and structure. Understanding the long term effects of ecological disturbances is increasingly important as climate change continues to exacerbate natural disasters and droughts. Our study seeks to understand the disturbance history and growth rates of a mature oak-hickory stand in Pisgah National Forest, NC. We harvested cross sectional samples from the stumps of 236 recently felled mature trees. Each sample captured the tree's growth rings from pith to bark. By counting and measuring each growth ring, we gain insight into the growth patterns, release events, and ages of each sample tree. The species within the study site were divided into two functional groups based on pore size and water potential; diffuse porous (*Acer* and *Liriodendron*) and

ring porous (*Quercus* and *Carya*). We hypothesize that the diffuse porous species will be more sensitive to past disturbance events compared to ring porous species. In addition, we are interested in understanding the carbon storage potential for the site. Private landowners as well as industrial timber organizations have a growing interest in a forest's ability to sequester and store carbon. However, the effect climate change will have on carbon storage remains unclear. The objectives of this study are to 1) establish a growth and disturbance history of the stand via dendrochronology and tree ring analysis and 2) quantify the carbon storage potential for each species. We hope to better understand how past disturbances, especially drought, have impacted growth and carbon storage of species prominent throughout the southern Appalachians.

P92 - Evaluating mammal diversity across habitats fragmented by a power line cut

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Georgia Gwinnett College, Lawrenceville, GA

The constant transformation and expansion of cities due to population growth and urbanization negatively impacts the habitat of native mammal species. Habitat loss and habitat fragmentation can affect population size, movement, species richness, and genetic diversity. Georgia Gwinnett College is located in Gwinnett County, one of the fastest growing regions of the Atlanta metro area. This study was conducted to evaluate the diversity and movement of mid-sized to large mammals living in a wooded area on the Georgia Gwinnett College campus but which is split by a human-made corridor created by a power line cut. Diversity was measured using motion-detecting trail cameras. Time spent in an area was approximated by the number of pictures taken of each species. Cameras were placed in three different locations: (1) in a small patch of woods closer to campus and which contains a moderately used trail, (2) in the power line cut, and (3) in a larger wooded area distal to campus and the power line cut and further from human disturbance. Our results indicate there is more diversity of mid- to large-sized mammals in the wooded areas on either side of the power line cut compared to within the power line cut. Mammals also spent more time in the larger wooded area away from human disturbance than in the wooded area closer to campus and much less in the power line cut.

P93 - The Effects of Hi-Yield Super Concentrate Killzall™ II on *Hexastylis* Leaf Growth, Color, and Wilting

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Hexastylis naniflora (Heartleaf Ginger) is a small, heart-shaped evergreen plant native to Southeastern North America and is currently federally threatened. In this study, we partnered with the Catawba Land Conservancy (CLC), a non-profit organization that aims to conserve the lands of the Southern Piedmont region of North Carolina, to research how the pesticide Killzall can be used to eliminate invasive plant species like Kudzu and Japanese Privet while conserving the non-target species *Hexastylis*. The active ingredient in Killzall, glyphosate, is used in weed control but has been found to produce negative effects on non-target plants due to residue left in the environment after application.

Over the course of 5 weeks, 23 *Hexastylis minor* plants were treated and observed in a lab. The control group consisted of 4 plants and the remaining 19 were divided into four groups, receiving varying doses of the glyphosate mixture, ranging from the highest application rate to 0.25x the highest application rate. Each week the plant length, leaf length, and leaf color were recorded using predetermined scales. Lack of change in physical characteristics influenced us to administer a second dose to each plant. Even after the second dose was added, little change occurred in color and growth.

Since the *Hexastylis* in our study showed little to no physical changes in response to the herbicide, we concluded that the plant has a high resistance to glyphosate and that the herbicide poses little risk of nontarget contamination to the plant. Past literature suggests that this unexpected resistance could be due to a hormesis effect or reduced translocation of the herbicide. Other reasons could include water pulling residue away from the plant or slow plant growth. However, more research is needed to determine assumptions of high plant resistance in this experiment.

P94 - Effects of Grassy Bald Management on Plant Community Composition within the Roan Mountain Massif

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Grassy balds are important and rare ecosystems present within high-elevation areas of the Roan Mountain massif in the southern Appalachian Mountains. These areas are dominated by native grasses and sedges, but contain many endemic, endangered, and rare species. Threats include encroachment by surrounding herbaceous and woody species. Restoration and management efforts have been conducted on these balds for approximately 30 years by the Forest Service and Southern Appalachian Highlands Conservancy. In 1987-1988 Hamel and Somers conducted vegetation analyses on these balds to characterize the plant communities found there before intensive management began. In summer 2020, we resurveyed the vegetative community on Round, Jane, and part of Grassy Ridge Balds to compare current plant community composition to that before intensive management began. Using similar methodology to Hamel and Somers, a similar density of transects and 1 m² vegetative sampling plots were established across the balds. At each plot we recorded percent coverage of plant species or genus, percent slope, aspect, and average soil depth. Management records were compiled to determine management history (e.g. the number of times mowed, etc.) of every individual plot. Vegetative community patterns were assessed with multivariate analysis, and these were compared to management history. Preliminary PCA analysis revealed plots separating on an axis along a gradient from high *Rubus* to high grass cover. The effects of 30 years of active management will be assessed by comparing plant community composition from the surveys in the 1980s to data collected in this study.

P95 - Decadal leaf-fall input to a headwater stream: What affects annual leaf production by riparian zone trees?

Clay Runck

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Seasonal input of leaf-fall from riparian vegetation comprises the bulk of the coarse particulate organic matter (CPOM) base for secondary production in small headwater streams in deciduous forests. Thus, secondary production of aquatic consumers in these systems is highly dependent on energy and nutrients contained in CPOM derived from terrestrial primary production. This study reports 11 years (2009-2020, no data for 2012) of leaf-fall input to a first-order headwater stream in a deciduous forest watershed on the campus of Georgia Gwinnett College. Annual leaf-fall biomass input directly into the stream averaged 422 grams dry-mass/m² (g DM/m²), which translated into a cumulative total that averaged 63.2 kg DM each season (October-January) into the 150-m segment of stream monitored in this study. Lateral input of leaf biomass was not measured. There were significant differences in annual leaf-fall biomass over the 11 years of measurement. Annual means varied by a factor of 2.5, from a low of 222 g DM/m² (2011) to 562 g DM/m² (2019). However, no significant relationships were detected between leaf-fall biomass input and climate variables (e.g., precipitation, temperature, degree days, growing days, etc.; however, soil moisture and depth to water table were not measured in this study). Leaf production by mature, well-established riparian zone trees in the vicinity of this groundwater-fed stream are likely not limited by availability of water even during drought years.

P96 - Understanding cryptic diversity in the poorly understood Dinoflagellate species, *Cryptothecodinium cohnii*John Ramsby

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The fundamental biological question “what is a species” has concerned biologists for centuries. There exist multiple concepts used to identify species, however they often disagree with one another as the ideal applicability of each concept often only applies to certain organisms. This results in different species being identified by each concept. This “Species Problem” pertains to eukaryotes, which are a major domain of life. Most eukaryotic organisms, including dinoflagellates which we study, are microscopic and can be found in every ecosystem. They exert profound effects on all lifeforms as well as the planet itself. Thus, an understanding of microbial diversity is highly sought after, both as it relates to evolution and to ecological stability.

Cryptothecodinium cohnii is an enigmatic Dinoflagellate with obscure ancestral origins and unclear species boundaries. It is suspected that the extensive collection of *C. cohnii* isolates are *Cryptothecodinium*-like Dinoflagellates and do not represent a single species, instead representing a cryptic species complex composed of several species, which are superficially similar. Previous results from our lab including phylogenetic analysis of multiple *C. cohnii* strains, have demonstrated their close relationship to one another, however with significant genetic difference. Differences, which are potentially equivalent to species level divergence.

In order to understand the potential hidden diversity in the species group we propose a method to determine the presence of cryptic *C. cohnii* species. This will involve building on previously acquired DNA marker sequences as well as analyzing the rDNA sequences for differences which are indicative of species level divergence.

This research is significant because it directly addresses the fundamental question “what is a species” in a novel, empirical fashion by applying model systems biology to test current paradigms of species boundaries while increasing the general understanding of how different species concept correlate with one another.

P97 - Geometric morphometric analysis of candidate species within *Desmognathus fuscus*.Perla Morales¹, Kathryn Davis², David Beamer²¹Nash Community College, Wilson, NC, ²Nash Community College, Rocky Mount, NC

Recent work in our lab has uncovered multiple candidate species within the widely-distributed complex of the Northern Dusky salamander, *Desmognathus fuscus*. Evidence for genetic divergence includes both mitochondrial and nuclear sequence data. However, little is currently known about morphological differences among these newly-found lineages of *D. fuscus*. We conducted geometric morphometric analyses to check for variation. We assembled photographs of *D. fuscus* specimens, representing eight different mitochondrial clades, in tps file format and plotted twelve homologous landmarks on each image using the program tpsDig. We then produced a series of dorsal and ventral measurements using Morphue software. In order to control for size, we converted the raw measurements into ratios, which we statistically analyzed in R software through independent sample t-tests comparing different lineages. Our analysis suggests that there are statistically significant examples of morphological deviation between some of these clades.

P98 - Characterization of Differential Expression Patterns throughout Development of the Trembler-J Mouse Model for Charcot-Marie-Tooth Syndrome

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Mutation and abnormal expression of the peripheral myelin protein 22 (PMP22) is causative of one the most common inherited peripheral neuropathies in humans, Charcot-Marie-Tooth 1A (CMT1A) disease. The heterozygous Trembler-J (*Tr*^{+/+}) mouse is a model for PMP22-associated peripheral neuropathy characteristic of CMT1A. Although its function is not completely understood, *PMP22* is differentially expressed in neural and non-neural tissues, where it is thought to be involved in proper myelination of peripheral nerves and control of normal cell growth and differentiation, respectively. As a means of understanding the role of *Pmp22* in non-neural tissues, temporal patterns of gene

expression were evaluated in non-neural tissues throughout embryonic and post-natal development of the Trembler-J mouse. In this study we used mRNA Differential Display to profile the *Tr^{1/+}* transcriptome in non-neural tissues throughout embryonic (E9.5-E17.5) and postnatal (D1-D42) development. At each developmental time point, differentially expressed sequences were cloned and sequenced to identify genes of potential importance to normal tissue development. Using the technique of mRNA Differential Display, we have identified 85 differentially expressed genes, 25 of which were validated by quantitative reverse transcription PCR (qRT-PCR). Ontological classification revealed dysregulation of genes primarily involved in cell communication and signal transduction (21%), regulation of nucleic acid metabolism (20%), protein metabolism (14%) and cell growth and/or maintenance (13%). Sequence analysis of the upstream region suggests that transcription factors in the EGR family may be common regulators of this set of genes. Our analysis shows that several genes are differentially expressed relative to the copy number of non-mutated *pmp22* alleles. We predict that the collective interaction of these genes may be important to cellular processes central to the development of tissues, in which *pmp22* may be functioning as a *Gas* gene.

P99 - Microsatellite marker transferability and characterization for *Xyris torta* (Xyridaceae)

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By performing congeneric comparisons of genetic diversity, phylogenetic context can be provided and better elucidate evolutionary or environmental factors that affect genetic diversity levels. *Xyris torta* is a wetland plant widespread throughout the central and eastern United States. The extensive geographic range of this species contrasts with its congener *Xyris tennesseensis*, a federally endangered plant with extremely low levels of genetic diversity found in only a few populations in three southeastern states. To contextualize these results, a primer survey was completed to identify microsatellite markers that could eventually be used to gauge the genetic variability in *Xyris torta*. In the initial part of the survey, 14 previously published microsatellite primers for *X. tennesseensis* were tested for transferability to *X. torta*, utilizing a total of 20 individuals from five populations across the species' geographic range. Twelve of these loci were resolved for *X. torta*, with all being polymorphic. To fortify the number of resolved loci for both species, 30 previously untested microsatellite primers were examined for amplification in both *Xyris* species, using the same populations and number of individuals for *X. torta*, plus 16 individuals from four *X. tennesseensis* populations. Seven of these primers were resolved for both species, with four being polymorphic for *X. tennesseensis* and all seven being polymorphic for *X. torta*. Overall, 19 polymorphic loci were resolved for *X. torta*, with a range of 2-7 alleles each, and averaging 3.37 alleles per polymorphic locus. Despite limited sample sizes, *X. torta* displayed higher allelic diversity at the species level than was previously reported for *X. tennesseensis*; however, allelic diversity was low at the population level as most populations had only a single allele at each locus. Additional sampling will more accurately determine the genetic diversity levels in *X. torta* and allow for valuable comparisons with *X. tennesseensis*.

P100 - Genetic and evolutionary conservation analysis in *C. elegans* to examine the functional conservation of human genes and decipher variants of uncertain significance

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Impressive technological advances in genome sequencing have surpassed our capability to interpret the clinical implications of the genetic variation we discover. The majority of genetic variants identified in patients are currently clinically classified as “variant of unknown significance,” (VUS) where their causation of disease or association with disease risk are unclear. Explorations of VUS in genetically tractable model organisms, such as *Caenorhabditis elegans*, are integral studies for assessing the functional conservation of human genes and understanding the functional consequences of disease-associated variants. VUS tend to be missense variants that are particularly challenging for interpretation. We examined missense VUS identified in patients with a wide range of diseases with *C. elegans* orthologous genes, including attention deficit hyperactivity disorder, type 2 diabetes mellitus, cystinuria, and supravalvular aortic stenosis. We identified conserved missense VUS in the following human genes and orthologous *C. elegans* genes: *DRD5* and *dop-2*; *INSR* and *daf-2*; *PEPD* and *K12C11.1*; *SLC3A1* and *atgp-2*; *ELN* and *ssq-1*. Preliminary genetic, evolutionary conservation, and protein modeling analyses suggest structural and functional impact for some of these VUS, warranting further *in vivo* investigation. We are working to optimize polymerase chain reaction-based genotyping assays and phenotyping assays to generate and assess CRISPR-Cas9-engineered *C. elegans* models containing each VUS. These findings fuel our research pipeline that facilitates assessment of the functional conservation of human genes and structure-function analysis of disease-associated variants through CRISPR-Cas9-engineered *C. elegans* models with *in vivo* functional assays to decipher variants of uncertain significance.

P101 - Utilization of CRISPR technology in characterization of the molecular defect of 9p deletion syndrome

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9p deletion syndrome is a genetic disorder in which patients inherited a faulty chromosome 9 with a missing piece of chromosomal DNA from one of the parents. These patients have triangular shaped head (called trigonocephaly), severe mental disability, heart defect and autistic-like behavior. Trigonocephaly is a key feature of 9p deletion syndrome and is seen in 83% of patients with 9p deletion. A broader term for the distorted skull is craniosynostosis. Scientists have identified several genes which cause craniosynostosis when they are mutated. However, none of these genes are located on human chromosome 9, thus are unlikely the cause of the trigonocephaly seen in 9p deletion patients. The cause of the trigonocephaly in 9p deletion syndrome remains to be elucidated. Cerberus 1 (CER1) gene is a candidate gene for trigonocephaly, located in 9p23, and plays an important role in the correct formation of the anterior-posterior axis in vertebrates. To investigate the potential role of CER1

gene in causing trigonocephaly, we used CRISPR technology to precisely remove a regulatory element, enhancer 5008, near CER1 gene. CRISPR is a new and powerful tool in genome editing. CRISPR stands for clustered regularly interspaced short palindromic repeats. We used CRISPR and Cas9 to make double stranded DNA cuts in the pre-selected DNA sequences on human chromosome 9p. The human cells used include a fibrosarcoma cell line, an embryonic kidney cell line, a mesenchymal progenitor cell line and a lymphoblastoid cell line. We precisely deleted the enhancer 5008 located ~1 Mb to CER1 gene using CRISPR in all cell lines mentioned above, except the lymphoblastoid cell line, which was due to a very low transfection rate. We are currently investigating the effect of the enhancer on the CER1 gene activity in the human fibrosarcoma and mesenchymal progenitor cells.

P102 - Genetic structure of black bass in northern Georgia lakes

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Species identification aids in fishery management's efforts to maintain biodiversity within water systems. Spotted bass (*Micropterus punctulatus*) and Alabama bass (*Micropterus henshalli*) have similar morphological characteristics despite no close genetic relatedness, and the Georgia Wildlife Resources Division classifies both species as "spotted" bass. In the southeast United States, spotted bass populations are distributed across the Tennessee River basin, while native Alabama bass populations are found in the Coosa River Basin. Both are known to have been introduced to the Chattahoochee River Basin, and Alabama bass are suspected to have been introduced into lakes in the Tennessee River drainage. Populations classified as "spotted" bass have expanded in the Chattahoochee and Savannah River drainage, to the detriment of other black bass populations, namely the Smallmouth bass. This project employs the use of microsatellite markers and the universal barcoding mitochondrial gene COI to achieve species identification within and among populations containing black bass with similar morphological characteristics. From three sampling sites in north Georgia, Lake Blue Ridge, Lake Chatuge, and Lake Nottely, fin clippings from 288 fish were obtained for mitochondrial DNA analysis and forty-eight black bass samples from each lake were used to investigate population genetic structure employing 15 microsatellite loci. These analyses indicate that all three lakes contained genetically similar populations, with no detection of spotted bass individuals in the population sampled.

P103 - The Role of *FIS2* and *AGL62* in regulating the expression of *InvINH1* and *InvINH2* in *Arabidopsis thaliana*

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Angiosperm seeds are embryonic plants enclosed in seed coats. During double fertilization, the egg cell and the central cell are fertilized by two sperm cells, which give rise to the embryo and the endosperm, respectively. In plants with nuclear endosperm, such as *Arabidopsis*, the endosperm enters a syncytial phase after fertilization, when the endosperm nuclei undergo mitosis without cytokinesis. After endosperm cellularization, the endosperm experiences cell death and is eventually absorbed by the embryo. Our lab had discovered that two invertase inhibitors (*InvINH1* and *InvINH2*) produced in the embryo-surrounding region of the endosperm are capable of suppressing embryo growth during the syncytial phase. In this study, we investigated whether *InvINHs* expression are regulated by two known regulators of syncytial endosperm development, *FIS2* and *AGL62*. *InvINH1* and *InvINH2* promoter-GFP fusions were first introduced into *fis2* or *agl62* mutant background. GFP expression was then analyzed in mutant plants that were homozygous for the promoter-GFP transgene. Our data indicated that both *InvINH1* and *InvINH2* promoter-GFP fusions were up-regulated in *fis2* mutant, and down-regulated in *agl62* mutant, suggesting that *FIS2* and *AGL62* are the repressor and the activator of *InvINHs* expression, respectively. Since *FIS2* is known to suppress *AGL62* expression, we have identified a linear pathway that activates *InvINHs* expression after fertilization and represses *InvINHs* expression after endosperm cellularization. This precise timing of *InvINHs* expression in the syncytial endosperm is likely required for the proper coordination of embryo and endosperm growth during early stage of seed development.

P104 - Determining Cause and Heredity of the Expression of Duchenne Muscular Dystrophy in a Female Carrier

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This study examined the genetic basis and heredity of a proband that is a symptomatic female carrier of Duchenne Muscular Dystrophy with a deletion involving exon 45. The proband's family includes an unaffected father and older brother, while the mother and identical twin sister have the deletion but remain fully asymptomatic. As a recessive X-linked disease, the rarity of a symptomatic female for DMD cannot be understated. This study explored the method of inheritance in this family through various techniques. Creatine-Kinase levels were first examined in the proband and the twin sister to confirm that only one was truly symptomatic. X-inactivation testing led to a need to perform PCR of a large section of the X chromosome throughout the family to examine the possibility of recombination in the mother through further analysis of the amplified DNA. After determining the true mode of inheritance, RNA isolation from fibroblast cell lines, reverse transcriptase, and RT-PCR were performed to analyze expression levels in an attempt to discover the cause for the varied phenotypes between the twin daughters. With the findings of homologous recombination and highly skewed x-inactivation, this study gained further insight into a rare case with great implications for other x-linked illnesses and a further understanding of Duchenne Muscular Dystrophy.

P105 - Investigating Propagation of Brewer's Yeast and Possible Biofilm-related Spoilage at a Local Microbrewery

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The recent rise in microbrewery businesses has resulted in a demand for procedures that optimize efficient maintenance and cultivation of yeast starter cultures. This research was initially mounted as a collaboration with a local craft brewery in order to determine generation times, appropriate storage and growth conditions for their yeast strains. The brewery also experiments with new flavors by adding fresh fruit to some of their brews. Occasionally this has led to spoilage of the beer. Biofilm production due to microbial contamination was thought to be associated with the loss of a quality product. To investigate this phenomenon, the presence of biofilm build-up connected with fruit addition was planned *in situ*. However, the impact of the COVID-19 pandemic and the related lockdown guidelines resulted in the shift to an *in vitro* approach. The yeast strains provided by the brewery were grown in two types of media and stored at two different temperatures. Growth curves were formulated, following up to 4 months of storage, to assess the viability of the cultures. Initial findings suggest that storage temperature showed no noteworthy difference in growth or viability, and only one strain showed differences associated with the type of growth media. Biofilm assessment was achieved by inoculation of a broth base with either the yeast provided by the microbrewery and/or the microbiome naturally colonizing the fruit skins. The biofilms were stained and observed via fluorescent microscopy, followed by measurement of optical density. Though the cultures inoculated with yeast were frequently observed to secrete biofilms, the cultures inoculated with fruit did not present any additional biofilm production. Further analysis will determine whether the trends we observed have any significant associations with the storage and growth conditions investigated, as well as whether the presence of fruit impacts the production of biofilm in our model.

P106 - The Isolation of Pyrene Degrading Indigenous Bacterial Species

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Polycyclic aromatic hydrocarbons (PAHs) are hydrophobic micropollutants and are resistant to environmental degradation. They pose adverse health concerns to people and the environment due to their toxic, mutagenic, and carcinogenic effects. In particular, the PAH pyrene, is a dangerous pollutant (according to the EPA), that is toxic to mammals, particularly in their kidneys. It has a ubiquitous presence in ecosystems as pyrene forms due to incomplete combustion of organic compounds. The purpose of this study is to investigate the microbial bioremediation of pyrene in soil. This was achieved by isolating competent pyrene-degrading microbes near a community grilling site on the grounds of Wingate University, Wingate, North Carolina. Soil samples were collected from the site and spiked with pyrene in concentrations of 0.3, 1.5, 3, 6 mg/g, and a control group which was not spiked was also included. Soil samples were incubated for 1 week and 0.5g of soil was used to create culture enrichments by supplementing minimal media (MM) broths with pyrene to a final dilution of 100mg/L. After a 4-week shaking incubation (100rpm) at room temperature, in the dark, serial dilutions (10^{-6}) were plated on MM agar plates supplemented with pyrene (100mg/L). Representative colonies were isolated and purified and are currently in the process of phylogenetic identification and biochemical characterization. Presumed pyrene degrading bacterial isolates were present in the soil at an average of 1.71×10^6 CFUs/g of spiked soil; control soils had comparable bacterial population sizes indicating that lithotrophs were also present in the soil samples. Confirmed pyrene degrading bacterial isolates will be further investigated for their potential for bioremediation practices.

P107 - Identification and characterization of oil degrading bacteria.

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We live in a world where oil is used extensively in daily activities. Crude oil is made into petroleum products which are used from automobiles, gasoline, produce heat and electricity, and its by-products make plastics, polyurethane, and solvents. By identifying microorganisms that naturally metabolize and break-down hydrocarbons, the pollution created from use of crude oil can be minimized through bioremediation. In a samples of oil saturated soil, various bacteria were isolated and determined its morphology and Gram reaction. Colony PCR was performed using 16S ribosomal RNA to identify its genus and species. Two methods were used to measure their capacity for growth under a single hydrocarbon source in Bushnell Haas Broth. A time course experiment with plate counts were executed to measure quantitative data with a conventional engine oil and use of redox dye 2,6-Dichlorophenolindophenol (DCPIP) was used for qualitative data with n-Hexadecane. It is expected that if the bacteria were able to survive in the oil saturated soil and is able to thrive in a media with hydrocarbon as its sole carbon source, it will be able to degrade oil and can further explore its mechanism in the process of degradation.

P108 - The characterization of the microbiome for the Northern two-lined salamander (*Eurycea bislineata*) and its ecological interactions with the pathogen *Batrachochytrium dendrobatidis*

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Fungal pathogens are a major threat to amphibians worldwide, but the most prevalent fungal pathogen is *Batrachochytrium dendrobatidis* (Bd). Bd is a chytrid fungus that is highly virulent and has been linked to population decline in numerous amphibian populations across the world due to the development of chytridiomycosis. Bd infects the amphibian's skin by rooting their spherical thalli into the amphibian's keratinized epidermal layer of their skin, disrupting the exchange of many vital molecules such as oxygen, carbon dioxide, and ions. The focus of this project was to characterize the skin microbiome of the Northern two-lined salamander. The resident microbiome of an individual is intricately linked to

its survival and overall health due to its role in metabolism, the immune system, and in defense. It has been demonstrated that the microbiome plays a vital role in pathogen-host interactions, so it is vital to better understand the role that the microbiome plays when it comes to preventing pathogens, such as Bd. This project focused on describing the microbiome of the Northern two-lined salamander by collecting swabs from individuals caught along the Blue Ridge Parkway. All bacterial samples were isolated on R2A media and the 16S rRNA gene was extracted using a freeze-thaw technique. Once the DNA was extracted, a PCR was run, and samples were sent off for sequencing. We are currently, using sequences to identify each unique morphotype that was cultured on R2A. The hope is that this project is to act as springboard for future work when bacterial isolates can be used in a challenge assay against Bd in hopes of finding bacterial strains that inhibit the fungal pathogen.

P109 - Modulatory role of silver nanoparticles and cinnamaldehyde on virulence factor and chaperone expression of *Streptococcus mutans*, *Staphylococcus aureus*, and *Streptococcus pneumoniae*

Christyn Byrd, Tanisha Etienne, Emmanuel Williams, Crispo Richardson, Christa Horton, Roland Williams, Cassy Louis, Lianna Taffe, Lydia Tesfaye, Matthew Dye, Zerahiah Joseph, Jordan Seal, Elaine Vanterpool

Oakwood University, Huntsville, AL

Microbial pathogens possess mechanisms to ensure survival, colonization and evasion of the host. Such mechanisms include the regulation of virulence factor and chaperone expression. These strategies ensure that pathogens could successfully establish an infection. It is important that we evaluate ways of regulating the survival and virulent strategies of these bacterial pathogens. In this study, we hypothesize that silver nanoparticles (AgNP) and cinnamaldehyde (Cn) could disrupt the expression of bacterial virulence factors and chaperones of *Streptococcus mutans*, *Staphylococcus aureus* and *Streptococcus pneumoniae*. To test this hypothesis, we incubated the bacterial pathogens with sub-inhibitory concentrations of AgNP or Cn and specific target protein expression (sortase A, ScpA, TSST-1, enterotoxin, DnaK and HtrA) were quantified using ELISA. A t-test was performed to determine significance. Results show that AgNP and Cn modulate the protein expression of virulence factors and chaperone of these pathogens. For virulence factor expression, *S. mutans* sortase A is upregulated by 14% (with AgNP) and downregulated by 51% in the presence of Cn. A decrease in DnaK expression in *S. mutans* up to 30% and a 15% downregulation in HtrA is observed. In *S. aureus*, TSST-1 expression is downregulated up to 33% and ScpA expression downregulated up to 32%. Expression of enterotoxin A in *S. aureus* is upregulated 25%. The DnaK expression in *S. aureus* is downregulated up to 28% by and HtrA downregulated by up to 35%. DnaK chaperone expression of *S. pneumoniae* was downregulated up to 18% with HtrA showing a 23% upregulation. These findings support our hypothesis that AgNP and Cn can modulate the survival and virulent strategies of bacterial pathogens. Findings from this study can be used to further investigate the microbial pathogenic mechanisms leading to prevention of microbial-induced complications.

P110 - Inhibition of *Escherichia coli*, *Streptococcus pyogenes*, and *Staphylococcus aureus* biofilm by silver nanoparticles and cuminaldehyde

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Non-complicated microbial infections are easily treatable with common antibiotics. However, microbial pathogens can create a microenvironment conducive to evasion of host defenses and antimicrobial therapeutics. An example of such include the bacterial biofilms. The cemented biofilm protects the bacteria by resisting external stressors, including antibiotics, which could potentially result in more serious outcomes and complications. It is important to identify ways of reducing microbial biofilm formation. The objective of this study was to evaluate whether silver nanoparticles (AgNP) and/or natural compound cuminaldehyde (CA) could inhibit the formation of microbial biofilm of pathogens, including *Escherichia coli*, *Streptococcus pyogenes* and *Staphylococcus aureus*. We hypothesize that AgNP and CA could decrease the biofilm formation of microbial pathogens. To test the hypothesis, AgNP and CA were incubated with microbial pathogens and assessed for biofilm formation using a biofilm assay. Data were analyzed in comparison to the untreated controls. Results show that CA can decrease biofilm formation in *E. coli* up to 65%, *S. pyogenes* up to 97%, and *S. aureus* by up to 96%. AgNPs, however, decrease complete biofilm formation in *S. pyogenes* by up to 98%, but increases biofilm formation of *S. aureus* and *E. coli* up to 191.7%. The information found in this study can be used to find more natural compounds that inhibit biofilm formation as well as a delivery method for these compounds into the infected host.

P111 - Bacterial Community Structure and Diversity in Different Levels of Lead (Pb) Contaminated Soils

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Soil lead (Pb) contamination is a recognized global health problem that has been shown to have adverse effects on human health. The structure of microbial communities is an important index of soil quality. We did a preliminary assessment of the effects of Pb contamination on the microbiome of three sites in Georgia, USA. Soils with different levels of Pb-contamination were collected from Decatur (20 ppm Pb), KSU Field Station (90 ppm Pb); Cedartown (3800 ppm Pb). Two sub-samples were collected from each location. The taxonomic classification levels of phylum and class were used because it best exemplifies subjective dissimilarity whilst limiting phylogenetic complexity. We hypothesized that, as Pb levels increased in the soil: (1) diversity of soil microbes would decline, (2) diversity among samples would increase. The results showed that Cedartown has a distinct distribution of some phylogenetic taxa while Decatur and KSU Field Station have similar abundance profiles. The Shannon diversity index was greatest in Cedartown samples and is statistically different at the phylum level but not the class level.

P112 - Gram-Positive Bacterial Species may be more susceptible to Curcumin Extract than Gram-Negative bacteria

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Abraham Baldwin Agricultural College, Tifton, GA

The chemical structure of curcumin is said to be the reason for its anti-inflammatory and antimicrobial properties that protects plants from pathogens and ultraviolet radiation. Curcumin is a yellowish curcuminoid compound found in the rhizome of Turmeric plants. Turmeric has been used in a several Asian and Caribbean dishes to add color and flavor to meals. Curcumin was found to have anti-inflammatory properties within the body as it inhibits the NF- κ B pathway to decrease the production of cytokines to support immune response. The medical use for curcumin has not been verified or confirmed because of its minimal bioavailability and instability as a chemical. Curcumin may possess antimicrobial properties against certain strains of bacteria that cause infections in humans. Some of the more common bacterial infections are caused from the overgrowth and colonization in various parts of the human anatomy.

In this study the antimicrobial capability of curcumin was tested against non-infectious gram-negative and gram-positive bacteria including, *E. coli*, *Shigella*, *Bacillus subtilis*, *Shigella flexneri* and *Staphylococcus aureus*. Soxhlet extractor was utilized to extract curcumin from turmeric and the Kirby-Bauer sensitivity test was employed to verify the sensitivity of the afore-mentioned bacteria in various concentrations. Our results indicated that all concentration used in Kirby-Bauer sensitivity test have demonstrated clear zones of inhibition (between 7-13 mm), showing numerically larger zones against gram-positive bacteria.

P113 - The Identification of Potential Antibiotic Producing Bacteria from Soil at Campbell University

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Soil microbes live in a highly competitive environment and have evolved adaptations to enhance their chances for survival, such as the production of antibiotics. While antibiotics have transformed medicine, bacteria are becoming less susceptible to them. The rate of bacteria obtaining resistance is much higher than the rate of discovering new antibiotics to treat the diseases these bacteria cause. There is an especially important need for new antibiotics to treat infections in our youngest population, neonates. In this study, soil samples were collected from two different sites in Buies Creek, NC and bacteria from the soil was cultured on Potato Dextrose Agar (PDA) and Tryptic Soy Agar (TSA). Pure colonies were obtained of isolates that showed potential antibiotic production against *Enterococcus raffinosus*. Polymerase Chain Reaction (PCR) was performed to amplify the 16S rRNA gene and successful PCRs were purified and sequenced. The putative identification was found for 12 soil isolates.

P114 - Defending The Immune System: The Immunoprotective Effects of Nanoparticles and Natural Compounds

Jorden Seal, Audrey Alfred, Chrystal Gouling, Jayde Frederick, Danielle Malivert, Chelsea Thomas, Crystal Ware, Jordan Jones, Chidinma Wilson, Jasmine Thornhill, Caleb McIver, Elaine Vanterpool

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Staphylococcus aureus, *Streptococcus pneumoniae*, and *Escherichia coli* are microbial pathogens that can evade their host's immune mechanisms, causing infections such as toxic shock syndrome, pneumonia, and neonatal meningitis. These microbial pathogens can colonize the host and disseminate throughout its system by degrading and inhibiting immune defense proteins such as immunoglobulin A (IgA) and complement component 3 (C3). Previous studies have found that silver nanoparticles (AgNPs) can act as antimicrobial agents and as a virulence regulator. With this knowledge, this study seeks to evaluate the efficacy of AgNPs, as well as natural compounds cuminaldehyde (CA) and sabinene (Sb) in preserving the structural integrity of IgA and C3. We hypothesize that AgNP, CA, and Sb can protect immune factors IgA and C3 from microbial degradation. To test this hypothesis, we incubated the pathogens with either phosphate-buffered saline (PBS), AgNPs, or the natural compounds, followed by experimentation utilizing SDS-page and Western Blot. Our results found that AgNPs and CA preserved the integrity of *S. aureus*-treated IgA but not *E. coli*-treated IgA. In addition, we found that Sb and AgNPs protected C3 from degradation by *S. pneumoniae*. Our findings suggest that AgNPs and natural compounds may be viable virulence regulating agents against *S. aureus* and *S. pneumoniae*.

P115 - Tracking Carbon Utilization in the *Microcystis* Phycosphere

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Aquatic ecosystems are threatened by harmful algal blooms (HABs) globally. In the past few decades, blooms have occurred with increasing frequency, with this trend expected to continue as global temperatures rise and nutrient loading increases. *Microcystis spp.* are cyanobacteria that cause destructive HABs worldwide, including in Lake Erie in North America and Lake Tai (Taihu) in China. *Microcystis spp.* exude a carbon-rich extracellular polymeric substance (EPS) around their cells that heterotrophic bacteria are found embedded in. These heterotrophic bacteria are thought to benefit from the close association with *Microcystis* as a source of carbon. The mechanisms of carbon exchange between *Microcystis* and associated heterotrophic bacteria are not well known. The goals of this project were to build a synthetic consortium of 36 bacteria isolated from a *Microcystis* bloom in Taihu in 2018 and to trace carbon exchange between the bacterial consortium and *Microcystis* using stable-isotope probing metatranscriptomics (RNA-SIP). Incubation of axenic *Microcystis aeruginosa* NIES 843 with this bacterial consortium caused a significant increase in the growth rate of the cyanobacterium during the exponential phase of growth. To understand the molecular mechanisms that underlie bacterial utilization of *Microcystis*-derived carbon, the Taihu bacterial consortium was incubated with *Microcystis* isotopically labeled with ^{13}C -bicarbonate. Members of the consortium that were able to utilize *Microcystis*-derived carbon incorporated the

isotope into their RNA, providing a direct measure of metabolic function that was paired with metatranscriptomes. The isotopically labeled RNA was separated from the unlabeled RNA using a CsCl density gradient and ultracentrifugation. Comparison of metatranscriptomes from the labeled and unlabeled populations provide new insight into the mechanism of carbon utilization capabilities of bacterial cHAB partners in the *Microcystis* phycosphere.

P116 - Nanoparticles prevent *Staphylococcus aureus*-induced apoptosis in human endothelial cells

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Staphylococcus aureus can cause serious infections and complications in its host. *S. aureus* produces virulence factors, like toxins and hydrolytic enzymes, that can cause cellular damage. It is imperative that we find ways of reducing the virulent, damaging hydrolytic enzymes of *S. aureus* and other microbial pathogens. The purpose of this study is to evaluate if nanoparticles could serve as potential protease inhibitors leading to protection of human cells against protease-induced apoptosis. It is our hypothesis that silver (AgNP) and silver-gold nanoparticles (AuAgNP) could prevent *S. aureus*-induced apoptosis in Human Umbilical Vein Endothelial Cells (HUVEC) by reducing *S. aureus* hydrolytic enzyme function. To test the hypothesis, *S. aureus* secreted, and cell associated enzymes were incubated in the presence or absence of synthesized NPs and tested for protease and collagenase activities, NP-treated and untreated microbial fractions were incubated with HUVEC cells, morphology of the HUVEC (by the FLoid Cell Imager) were determined and the levels of the apoptosis indicator, cleaved PARP, were evaluated using a Cleaved PARP ELISA Kit. The toxicity of the nanoparticles on HUVEC were also evaluated. All data were compared to the untreated controls. Results show that nanoparticles can reduce *S. aureus* enzymatic activities up to 42% and collagenase activities up to 40%. In the absence of nanoparticles, *S. aureus* extracellular proteins induces apoptosis in HUVEC cells resulting in an increase in PARP cleavage by 30-40%. In the presence of monometallic AgNP or bimetallic AuAgNP nanoparticles, *S. aureus* extracellular proteins prevents the induction of apoptosis in HUVECs. NPs are not shown to be toxic to the HUVECs. The results support the hypothesis that nanoparticles can prevent *S. aureus*-induced apoptosis in HUVEC. In conclusion, data from this study can be used to help find new ways of preventing human cell damage caused by *S. aureus* virulence factors.

P117 - Evaluation of Microbial Load in a Broiler Facility: Comparison of Soybean Hull to Rice Hull Litter

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A trial was conducted to compare the microbial profiles of soybean hull litter versus rice hull litter in a broiler facility. Using standard culture methods, total aerobic bacterial counts and total gram-negative bacterial counts (lactose fermenting and non-fermenting) were determined at weekly intervals during a single grow out cycle. Samples were also evaluated for the presence of *Salmonella* species. Total aerobic counts were significantly higher in rice hull litter compared to soybean hull litter. Lactose fermenting gram-negative counts were also higher. These data indicate that soybean hulls may be a preferred to rice hulls for pathogen reduction in broiler facilities.

P118 - Bacterial colonization of the environment of veterinary rehabilitation clinics

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The presence of potentially pathogenic bacteria on surfaces in veterinary clinics is problematic for people and animals. In this study we collected samples from five veterinary rehabilitation clinics to study viable bacterial colonization at sites throughout the clinics. Sampling involved using double transport swabs (Fisherbrand, with Stuart's liquid medium) and water samples, collecting approximately 30 swabs from each clinic. After collection the swabs were placed on ice and transported to a microbiology lab on the UTC campus for processing. One of the two swabs was used to inoculate Hardy's Cdiff Banana broth (for *Clostridium difficile* [Cdiff]). The second swab was used to inoculate (line inoculation) five different types of media, including Hardy CHROM MRSA agar (methicillin resistant *Staphylococcus aureus* [MRSA], and *S. intermedius* [SIM]), Mannitol Salt Agar (*S. aureus*), Eosin Methylene Blue agar (enterics [ENT]), Pseudomonas Isolation Agar (*Pseudomonas* sp.), and Tryptic Soy Agar [TSA] (non-specific). Water samples were diluted and spread directly onto media. The most prominent species we saw throughout the clinics was Cdiff (on nearly 50% of all swabs collected). Enterics were the next most encountered bacteria at 18% of swabs. We found both MRSA and SIM on 9% of swabs collected. Of the clinic sites sampled, the largest number of positive swabs were found on harnesses/life jackets used in the underwater treadmill (33% positive swabs). For water samples collected from the underwater treadmills, total bacterial counts ranged from 1.6 to 2.7 e3 cfu/ml, with the predominant cell types being enteric. For many of the animals using these clinics, Cdiff and MRSA pose few risks. However, SIM tends to be more pathogenic for dogs, and we found notable levels of this *Staphylococcus* species throughout the clinics sampled. Targeted cleaning/disinfecting in these clinics could help reduce risks of infection for both animals and humans utilizing these clinics.

P119 - Database Analysis of Novel, Lead Compounds that Inhibit Biofilm Production in *Bacillus subtilis*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and *Streptococcus mutans*.

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Bacterial resistance to antibiotics has become a serious threat to modern medicine. Traditional antimicrobials work by killing bacteria or inhibiting bacterial growth, and due to bacterial rapid reproductive rates and overuse of traditional antibiotics, resistant bacteria are quickly selected. Therefore, alternative treatments must be explored. A potential target is bacterial communication pathways that lead to biofilm formation. Biofilms are extracellular matrices that provide a protective environment for the bacteria, including avoidance of the host immune system. Gene expression for biofilm formation is controlled by a communication system that utilizes quorum sensing: bacteria recognize a threshold level of signaling molecules called autoinducers and then a response ensues. By synthesizing small compounds which resemble autoinducers, we hope to competitively inhibit the pathways responsible for the formation of biofilm in order to decrease the selection of antibiotic-resistant bacterial strains.

Carboxylic acid derivatives were coupled to amino acids through a dehydration synthesis to produce families of novel lead compounds. Biofilm inhibition was measured via a traditional crystal violet assay. The results collected were compiled into a comprehensive database organized by species and compound families. To date, over 300 compounds have been tested for biofilm inhibiting capability. Of those 300 compounds, 28 have been confirmed to inhibit biofilm formation without utilizing bactericidal or bacteriostatic properties. Compounds containing variations of halogenated functionality centered around aromatic rings, in addition to trans-cinnamic acid derivatives, have been found to possess anti-biofilm properties in *Bacillus subtilis*, *Staphylococcus aureus* and *Streptococcus mutans*. Over 100 additional compounds will be analyzed and added to the database to confirm the trends. In addition to being useful for designing new novel lead compounds, the database in combination with genetic analyses may allow the connection of compound structures to a specific pathway in biofilm formation: the signal transduction cascade or the construction of biofilm.

P120 - Allium can decrease the function of bacterial cytotoxins and proteases and serve as a synergistic enhancer for cancer therapeutics

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Streptococcus pyogenes and *Staphylococcus aureus* produce toxins and enzymes that can damage their host. *S. pyogenes* streptolysin O and *S. aureus* α -hemolysin, can bind and lyse human red blood cells and other cells. It is important to find ways of blocking these cytolytic proteins and proteases. The allium family have strong antioxidant properties and compounds like allicin that has strong medicinal properties. The purpose of this study is to evaluate if allium could inhibit streptococcal and staphylococcal cytotoxic/cytolytic and protease activities. To achieve this, allium extracts were prepared (garlic, purple, yellow, and white onion). *S. aureus* protease activities were analyzed by incubating garlic extracts with extracellular secreted proteins of *S. aureus* and evaluating using the EnzChek protease assay kit. Controls included *S. aureus* samples without any extract. Streptolysin O and α -hemolysin (in the presence or absence of allium extracts) were incubated with RBCs. Intact RBCs were separated and the cell-free liquid fractions were analyzed using a spectrophotometer (OD 600). To evaluate the ability of streptolysin O to damage non-RBC cells, streptolysin O was incubated with pancreatic cancer cells (PANC) and primary Human Umbilical Vein Endothelial Cells (HUVECs) in the absence or presence of the allium extracts. Results show that garlic can reduce *S. aureus* protease activities by up to 85%. All the allium tested show to be able to reduce streptolysin O cytolytic function against RBCs by 45-61% but not able to inhibit *S. aureus* α -hemolysin function. Interestingly, streptolysin O incubated with HUVEC and PANC cells did not show to cause any visible changes, but when streptolysin O is incubated along with purple onion extract, streptolysin O is capable of inducing change in PANC morphology. Also, the garlic extract causes PANC cells to detach from the T-flask. In conclusion, allium can inhibit selected bacterial cytotoxins and enzymes.

P121 - Anthocyanins elevate flower temperature in 10 plant taxa

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Anthocyanins absorb strongly in green and UV-B wavebands, which may induce warming of pigmented plant organs. Yet, studies attempting to measure thermal effects of anthocyanins in flowers have yielded mixed results. However, often these studies fail to control for factors known to affect plant temperatures, e.g. wind, evapotranspiration, and angle/amount of incident sunlight. Furthermore, no studies have differentiated between warming effects of green versus UV-B wavebands by anthocyanins. In the current study, we used horticultural varieties of flowering plants exhibiting low, medium, and high anthocyanin, to test for possible warming effects of anthocyanins under sunlight including (Aclar) and excluding (Courtguard) UV wavebands. The study took place in the Mariana Qubein Botanical Garden on the campus of High Point University in High Point, North Carolina. Ten plant taxa representing ten families were sampled. Evaporative cooling was minimized by using excised flowers, which induced stomatal closure. Wind was minimized by conducting experiments in an outdoor, walled enclosure that was open to the sky, and inserting flowers into a white cardboard piece so that flower petals were flush with the larger surface. All flowers were angled perpendicularly towards the sun. The temperature of individual sets of conspecific flowers were simultaneously measured using a Fluke infrared imaging camera, following 1 min exposure to full sunlight. Six replicates were used per species. Anthocyanin content positively correlated with petal temperature in all nine species. Warming effects ranged from 1°C to 8.2°C (relative to white flowers). The warmest flowers were those with high anthocyanin content paired with dermal papillae and a large, flat morphology (e.g. pansy, impatiens). A significant UV effect was observed in one species (*Begonia x semperflorens-cultorum*), which is known to possess acylated anthocyanins. These results suggest that anthocyanin have a significant, concentration-dependent warming effect on flowers owing primarily to their absorbance of green wavelengths.

P122 - Gas Exchange Characteristics from Differently Colored Leaves of *Croton petra*

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Croton petra is an ornamental shrub native to Indonesia, Malaysia, Australia, the Western Pacific Ocean islands and India which displays yellow, red, green, and purple on its leaves. These non-green pigments are made of a combination of anthocyanin (red to purple) and carotenoids (yellow to orange). The ecophysiological implications of color variegation in the leaves of *Croton petra* have not been well studied, but seem to suggest that leaf pigments might act to protect them from high light stress. Photosynthesis was measured at various saturating light in leaves of varying colors using the Li-6800 gas exchange system. Rates of photosynthesis were lower in leaves with higher concentration of anthocyanin pigment (purple and red leaves), and increased proportionally with chlorophyll pigment (light and dark green leaves). Rates of stomatal conductance paralleled those for photosynthesis. Light curves were conducted by varying light levels from 0 to 1500 $\mu\text{mol m}^{-2}\text{s}^{-2}$ on green and non-green patches from the same leaf, or from adjacent leaves of near the same age. To determine how light intensity may affect pigment production, plants were grown under varying light conditions of full sun, and 60% shade. Rates of photosynthesis and pigment levels were determined for plants in each of these light treatments.

P123 - Longleaf pine seedling physiology: a tale of two soils

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Longleaf pine (*Pinus palustris* Mill.) exhibits a unique form as a seedling delaying stem growth for up to 10 or more years. In this so called “grass-stage” the seedling grows a taproot sometimes up to a meter long. Keeping its meristem at soil level offers protection from the frequent fires that occur in the system while the taproot allows for water access and starch storage for re-flushing of needles post-fire. With renewed interest in reforestation across its former range, understanding seedling-level physiology will be crucial in successful restoration efforts. Under our changing climate, it is important to record current variation in physiological adjustments the seedlings make under different environmental conditions to predict what might happen in the future. This study aims to understand adjustments that grass-stage longleaf seedlings make on different soil types.

Gas exchange and leaf water potentials were measured during the summer of 2019 on seedlings on two soil types of different drainage classes (sandy and loamy sand). Differences between sites were expected based on the water-holding capacities of these two soils and were reflected in the differences in mid-day water potentials at each site. During a drought in mid-September, pre-dawn water potentials were much lower on the sandy site. Gas exchange varied slightly between sites especially time of day when maximum stomatal conductance was reached. Seedlings from each site were excavated and the following measurements taken on the whole seedling: bulk leaf xylem water flow, stem flow and root flow. Partitioning these data helps us understand the where the hydraulic resistors might be in the path water takes from the roots to the atmosphere through the seedlings. In knowing the plant’s water status along the continuum, we can better monitor regeneration conditions and make informed decisions as we continue to restore this tree across its range.

P124 - Impacts of Polyploidy on the Ecophysiology of *Solidago altissima*

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The evolutionary importance of polyploidy in plants is still a subject of much research. Polyploidy could be an evolutionary dead end or it could lead to reproductive isolation and creation of new species. Goldenrod (*Solidago altissima*) is a North American herbaceous perennial with diploid, tetraploid, and hexaploid populations: diploids (MWD) and tetraploids are restricted to the midwest while hexaploids occur in both the midwest (MWH) and east (EH). Polyploids generally have larger cells, which can affect stomatal densities, sizes, plant morphology, gas exchange, and plant hydraulics. In a common garden at Appalachian State University, EH had larger and more horizontally oriented leaves than MWD and MWH, but MWH were taller. EH plants had the lowest total chlorophyll amounts. MWD leafed out and flowered earliest, followed by MWH, while EH was the latest. A drought experiment was performed on greenhouse grown plants using a split-pot design. Gas exchange measurements were made using a Li-6800 and water potentials with a Scholander Pressure Chamber. Prior to imposition of drought, photosynthetic rates (*A*) were higher in MWH and MWD, and lowest in EH. As the experiment persisted through June and July, *A* and stomatal conductance (*g_s*) declined in both treatments, but droughted plant rates dropped steeply 7 days after cessation of watering and were significantly lower than those for watered plants. By the end of the experiment, cytotypic differences for *A* and water potential were absent in both treatments. However, *g_s* remained higher in MWH for watered plants, which also had the lowest water use efficiency among all cytotypes. Light response curves were conducted on well-watered plants and aside from higher light saturated *A* for MWH plants, no other light response parameters differed among cytotypes. Why diploids do not occur in the east and why MWH and EH differ are currently being investigated.

P125 - Analysis of Acetylcholinesterase (AChE) Enzyme Inhibitors in *Huperzia lucidula* Endophytic Fungi

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The objective of this research is to isolate endophytic fungi found in *Huperzia lucidula* and identify their Acetylcholinesterase enzyme inhibiting abilities. Endophytes are bacteria or fungi that live symbiotically near or within healthy plant tissue. In contrast to pathogens, the presence of

endophytes is harmless or even beneficial to the plant. Endophytes are capable of producing secondary metabolites that are of special interest to medicinal research. For example, the alkaloid Huperzine A acts as an inhibitor to the enzyme Acetylcholinesterase (AChE), which has been found to be effective in the treatment of Alzheimer's disease.

Huperzine A is traditionally isolated from the southeast Asian "toothed clubmoss", *Huperzia serrata*, a clubmoss in the Huperziaceae family. The use of *H. serrata* for Alzheimer's treatment has resulted in a decline in *H. serrata* populations from unsustainable poaching practices, prompting the need for research on supplementary sources of Huperzine A. In recent years, Huperzine A-producing endophytes have been isolated from *H. serrata*, which provide new avenues to isolate the alkaloid from cultures. Existing studies indicate that the North American "shining clubmoss", *Huperzia lucidula*, also produces Huperzine A, making it a candidate for Alzheimer's disease treatment. Although Huperzine A has been found in *H. lucidula*, no research has been published identifying which of its endophytes, if any, produce the sought-out enzyme inhibitor. In this project endophytes within *H. lucidula* will be analyzed for their biological activity by an enzyme inhibitor assay. Several endophyte strains have been isolated already and are available for analysis. Endophytes that have the AChE inhibitor will be tested by HPLC for the presence of Hup-A and identified by DNA sequence. The results from this project can be used in future research to indicate target endophytes that can be considered for isolation and extraction of Huperzine A.

P126 - Analysis of Pecan Tree Tissue Grown in Copper Contaminated Soils by ICP-OES

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Metal contaminants in soil can have far-reaching consequences including adverse effects on human, animal, and plant health. Metal contamination can be defined as an 'abnormally high concentration introduced by an anthropogenic source'. The goal of our study is to analyze contamination in rural areas as previous studies have focused on urban/suburban locations. In an initial study of a pecan orchard in Peach County, analysis revealed elevated levels of copper present in the soil. Concentrations of copper decreased with the distance from the trees which is consistent with observed patterns when copper is found in pesticides or fertilizers. Analysis of soil pH indicated that copper could potentially be mobilized into plant tissues.

The goal of this study is to determine if elevated copper levels in the soil are taken up into the various tissues of the pecan trees. We are investigating this question by analyzing the concentration of copper in various tree tissues to study translocation and placement. The focus of our analysis is the pecan fruits because they are intended for human consumption. However, analysis of other tissues could yield information potentially relevant to other crops. Elemental analysis is needed as copper toxicity can result in significant decreases in plant growth but does not present obvious symptoms as is common with other metals. The samples were prepared using acid digestion and will be analyzed using Inductive Coupled Plasma-Optical Emission Spectrometry (ICP-OES).

P127 - Helping Conservationists Easily Identify *Sarracenia purpurea* var. *montana*, *S. jonesii*, and Their Hybrids in the Field.

Todd Brasseur

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Hybridization of rare species poses complicated issues for species managers. For example, hybridization and introgression blur the boundaries between species and poses challenges for maintaining species identity. However, gene flow into populations of rare or endangered species can increase genetic diversity, may facilitate adaptation to changing environments, and may facilitate the persistence of threatened populations. Regardless of whether managers want to prevent or facilitate hybridization, it is important for them to recognize the hybrids of the pitcher plants observed in this study. The goal of this project was to identify a quick method that managers could use to identify hybrid pitcher plants in the field. We compared the morphology of *Sarracenia purpurea* var. *montana* (mountain purple pitcher plant), *S. jonesii* (Jones' pitcher plant), and their putative hybrids at two sites in Western North Carolina. We conducted principal components analysis on eight pitcher measurements. The plants formed two major clusters that differed significantly in PC1. One cluster was distinguished by tall, narrow pitchers with hoods angled tightly over pitcher apertures, whereas the other cluster was distinguished by shorter, broader pitchers with hoods angled away from the pitcher aperture. These clusters mostly, but not entirely, corresponded to our *a priori* identification of individual *S. purpurea* var. *montana* and *S. jonesii* plants. Two plants we identified as putative hybrids were intermediate in PC1 score. Although the genetic identity of these plants remains to be confirmed, our morphological measurements provide a promising method of identifying hybrids.

P128 - Reassessment of Species Boundaries and Phylogenetic Relationships in the *Desmodium ciliare* complex (Fabaceae) Using Morphological and DNA Data

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Desmodium (Beggars ticks/lice, Tick-trefoils) is a genus of approximately 280 to 300 species within Fabaceae (Subfamily Papilionoideae, Tribe Desmodieae). A largely weedy group in temperate North America, beggars ticks hold true to their name by epizoochorous dispersal via hooked hairs on the segmented loments that attach to vertebrate fur and human clothing. Within the Southeastern United States, the *Desmodium ciliare* group is one of two *Desmodium* species complexes that have been historically difficult, with much argument about the limits of species and the role of hybridization. There are three commonly recognized species within the *D. ciliare* group, *D. ciliare* (Muhl. ex Willd.) DC., *Desmodium marilandicum* (L.) DC., and *D. obtusum* (Muhl. ex Willd.) DC., with two supposed hybrids in addition to the three main species: *D. ciliare* × *Desmodium strictum* (Pursh) DC. and *D. ciliare* × *Desmodium paniculatum* (L.) DC. The three putative species in this complex differ morphologically by terminal leaflet length:width ratio, amount of pubescence on stems (and leaves), whether uncinately pubescent (with hooked

hairs), pilose (sometimes with uncinat pubescence), or glabrate, and petiole length. To test the species boundaries, focused principally on material collected in Mississippi where all of the three putative species occur, principal component analysis (PCA) of morphological characteristics and analyses of both plastid and nuclear DNA were utilized. DNA data currently includes nuclear ITS and plastid trnL-F, with analysis by both parsimony and Bayesian methodologies, but other regions are being investigated for variation. This study aims to test the species boundaries in the *Desmodium ciliare* complex, to resolve the relationships between the species, and to resolve the relationships of the *D. ciliare* complex among other *Desmodium* found in Mississippi.

P129 - Mississippi's Native Dyes

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Dyeing with plants is an old process. For many centuries people depended on natural dyes to achieve desired colors. It was well known that specific plant organs (fruits, stems, leaves, roots, blossoms, bark) can yield dyes. Today, synthetic aniline dyes are readily available at any major retailer and have cast a shadow on the utility of natural dyes. In this study, natural dyes were made from plants that grow and are abundant in the Mississippi Delta. Flowers of goldenrod (*Solidago*), foliage from blackberry (*Rubus pensilvanicus*), fruit from pokeberry (*Phytolacca americana*) and American holly (*Ilex opaca*), female cones and foliage of bald cypress (*Taxodium distichum*), roots from madder (*Rubia tinctorum*), leaves of sassafras (*Sassafras albidum*), galls from oaks (*Quercus*), and more were collected in Fall 2020. Glass containers were used in preparing the dyes. Three-inch squares from 100% cotton sheets were simmered on a stove with a borax solution for an hour the night before the dyeing process to cleanse the fabric of additives. The time for dyes to bind to the fabric ranged from a few minutes to several hours. An alum mordant was added to some dye baths to brighten the color; coppera (Iron (II) Sulfate) was added to other dye baths to dull the color. For example, goldenrod flowers produced a cream color without a mordant but intensified to a bright yellow with a mordant. Mordants also strengthened the red color produced by madder root. Tannins, associated with oak galls, caused the dye to easily adhere to the fabric without a mordant. Pokeberry fruit and American holly produced brightly colored dye baths, but their color did not bind with the fabric despite the use of an alum mordant. Future work will explore other dye colors generated by Mississippi plants as well as how they bind to fabrics.

P130 - Quantifying the Effects of Drought on Longleaf Pine Plant Communities

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Climate change is increasing the frequency and severity of drought in the southeastern US with important implications for plant communities including: loss of biodiversity, declines in primary productivity, and shifts in species composition. However, drought impacts may differ depending on existing soil moisture and species physiological tolerances to drought. We characterized the impacts of drought on longleaf pine (*Pinus palustris* Mill.) plant communities over three decades by re-sampling permanent vegetation plots with increases in drought since 1993. In summer 2019, 10 1000m² vegetation plots were resampled in South Carolina and Georgia, which represented xeric, intermediate, and mesic sites. In each plot, we identified all plant species, and identified and measured the diameter at breast height of each woody plant. We quantified changes in species richness and composition, tree basal area and density, along with changes in community-level mean traits across time to relation to drought. Sites had increases in cumulative drought severity index and decreases in standardized precipitation evapotranspiration index (mean decrease = -0.18) since the 1990s. Sites with the largest increases in species richness were intermediate or mesic, while the two sites that lost species through time were located in xeric settings. Xeric plots also had decreases in tree density, suggesting these sites are losing young trees. Changes in species richness were positively related to changes in tree density and negatively related to changes in basal area, indicating sites with larger reductions in basal area also had larger increases in species richness. Species composition (as measured by Bray-Curtis dissimilarity) exhibited greater shifts in xeric sites. Community-level leaf nitrogen decreased, while C:N ratios increased in most sites, suggesting a shift toward more drought-tolerant strategies. Collectively our results suggest that xeric longleaf pine plant communities may be more vulnerable to the effects of climate change than intermediate or mesic sites.

P131 - Rice (*Oryza sativa*) – an important crop in the Mississippi Delta

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Rice (*Oryza sativa*) is considered one of the world's most important crops; it is a dietary staple for over 3 billion people. Major production of rice originated in China 9000-12,000 years ago. This species spread into Europe in the 15th century and later into South America and western Africa. Rice is currently a major commercial agricultural crop in six U.S. states: Arkansas, California, Louisiana, Missouri, Mississippi, and Texas. Paddy rice, where rice is grown in an irrigated or flooded field, is the main type of rice cultivation in the Mississippi Delta. Many varieties of rice are grown, milled, processed, and sold in the Mississippi Delta: long grain, medium grain, short grain, brown, U.S. jasmine, black japonica, white, parboiled, and more. Differences in these rice varieties pertain to a combination of factors including texture, nutrients, processing, color, and flavor. For example, white rice is formed from brown rice during the milling process. White rice is preferred in many recipes, but contains a lower daily value of manganese, magnesium, niacin, thiamin, and selenium, compared to brown rice. To help combat these deficiencies, white rice is enriched in iron, niacin, and thiamin to help restore some of the lost nutrients and energy potential that occur during processing. Brown rice possessing a higher nutritional content is associated with better health, reducing the risks of heart attacks and stroke. Milled rice also is significantly lower in minerals including calcium, phosphorus, zinc, iron, and copper and vitamins such as niacin and riboflavin compared to rough rice. Parboiled rice undergoes a steam-pressure process prior to milling and helps to combat disease such as beriberi. To help reduce

malnutrition, hunger, and undernourishment throughout the world, genetic engineering is being used to enhance rice varieties to increase nutritional value, shorten life cycle, and resist pests.

P132 - The Effects of Experimental Wind Disturbance Severity on Herbaceous Species Diversity, Richness, and Species Composition in a Georgia Piedmont Forest

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Herbaceous species are often the most diverse component of forests, yet are far less understood than woody plant communities. Disturbances may contribute to richness in the herbaceous layer by allowing numerous species to establish that typically are excluded from intact forest. Based on the intermediate disturbance hypothesis, we hypothesize that wind disturbance events of intermediate severity will facilitate the greatest diversity and richness of herbaceous species when compared to severe disturbances or undisturbed forest. We also predict that species composition will diverge depending on disturbance severity level. To test this, we created an experimental wind disturbance of two levels - 50% damage severity (severity based on percent basal area felled) and 100% damage severity - using chainsaws near Watkinsville, GA in 2018. In 2019 we visited the disturbance, measuring percent cover of herbaceous species within randomly placed 1m circles in the 100% severity treatment (n = 47), 50% severity treatment (n = 47), and undisturbed forest (n = 49). We found, contrary to our hypothesis, that average Shannon diversity values for the treatments increased with disturbance severity; herb diversity was lowest in undisturbed forest at 0.20+/-0.25 and highest in 100% damage severity treatment at 1.21+/-0.48. Mean species richness was 1.20+/-1.00 in undisturbed forest, 2.09+/-1.54 in 50% severity plot, and 5.19+/-2.68 in 100% severity plot. Results from NMDS show broad overlap in species composition based on percent cover between the severity treatments. These results support the growing body of literature that suggests greater disturbance severity is key in leading to high herbaceous species diversity. However, there is a need for ongoing studies of the herb layer to better understand the lasting changes of different severity wind disturbances.

P133 - A preliminary assessment of chloroplast sequences in *Coccoloba uvifera* (Polygonaceae) for use in phylogeographic analyses

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Coccoloba uvifera L. (sea grape) is a tropical member of the Polygonaceae family and a significant component of coastal habitats along the Atlantic, Caribbean, and Pacific coasts of the neotropics. We analyzed chloroplast DNA collected from *C. uvifera* leaves from North America (Florida), Central America (Belize) and six island sources (Aruba, Antigua, Bahamas, Jamaica, Trinidad, and Tobago) across the neotropics. Five plastid DNA sequences (four intergenic regions and ndhA intron) were concatenated for each of 42 individuals, yielding sequences approximately 4717 base-pairs in length and 36 potentially informative sites. Thirteen insertions/deletions (INDELS) were assessed by the simple gap coding method. Network analysis identified 26 haplotypes with five haplotypes shared among individuals and 21 unique. Genetic relationships among haplotypes were complex, although plants from Florida, Belize and the Bahamas were generally distinct from Aruba, Antigua, Jamaica, Trinidad and Tobago plants. Most of the genetic variation was partitioned between populations (63.8%) and less among (36.2%). Bayesian Phylogeographic Coalescent Analysis indicates two broad groups (Bahamas, North and Central America; the Lesser Antilles and Aruba) separated approximately 1.2 mybp (million years before present), with significant island/source spatial structure within the last 50,000 to 100,000 ybp.

P134 - Paleoenvironmental and Taphonomic Implications of Palynological Samples from the Forest Hill Formation

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The early Oligocene Forest Hill Formation (Vicksburg Group) in Mississippi is a nearshore terrestrial unit consisting of laminated sands, and dark carbonaceous clays with lignite beds. In 2020, two palynological samples were collected by coauthors: one from Smith County and the other from Yazoo County, near Sartartia. Both samples contain an abundance of well-preserved and diverse palynomorphs of pollen, spores, and algal cysts indicative of a warm temperate environment. The Smith County sample is associated with a rich and diverse assemblage of well-preserved plant macrofossils, including palm fronds along the fissile bedding planes of fresh exposures. Palynomorphs from this site are representative of an oak-hickory-willow coastal forest bordering freshwater riverbanks and a storm surge zone flanking the eastern side of the Mississippi Embayment. In a 300-point count, angiosperms comprised 59%, conifers 11.4%, pteridophyte trilete spores 19%, monolete spores 1.5%, freshwater algal forms 9% and dinoflagellates cysts and acritarchs 1.5% of the assemblage. The Yazoo County sample was collected at the most northern and up-dip limit exposure of the formation along the axis of the Mississippi Embayment. This sample indicated a backwater, enclosed bay setting based on the higher quantity of *Anemia* (22%) and *Cyathidites* (7%) spores. In this 300-point count, angiosperms comprised 48%, conifers 3%, spores 40%, and freshwater algal forms 9% of the assemblage. Common pollen types include Aquifoliaceae, Arecaceae, Betulaceae, Chenopodiaceae, Cornaceae, Fabaceae, Fagaceae, Juglandaceae, Malvaceae, Oleaceae, Platanaceae, Salicaceae, Ulmaceae, and the form genera *Liliacidites* and *Tetracolporites*. Conifers include Cupressaceae and Pinaceae. Spores include *Anemia*, *Dictyophyllidites*, Lycopodioidae, Ophioglossaceae, Osmundaceae, Polypodiaceae, *Sphagnum*, among others. A few unidentified dinoflagellates and freshwater algal cysts of Zygnemataceae were also noted. The pristine preservation of the palynomorphs suggests that they are primarily of local origin.

P135 - A dazzling array of phenotypic diversity in the monophyllic wintergreen orchid, *Tipularia discolor*

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The terrestrial, wintergreen orchid *Tipularia discolor* produces only a single leaf per year, which may exhibit a broad range of leaf color patterns and textures. Current hypotheses to explain this diversity focus on herbivory deterrence and/or camouflage, since single leaves post a concentrated risk, and experimental defoliation has been shown to directly impact reproductive output for many years. The purpose of this study was to document the natural foliar diversity that occurs in natural populations of crane fly orchid in the piedmont of North Carolina, as a preliminary step towards determining their patterns of inheritance via traditional crosses. Distinct leaf color patterns observed on adaxial (upper) surfaces included: solid green epidermis, solid purple epidermis, silver spots beneath the upper epidermis (associated with loose mesophyll packing), purple epidermal spots of various sizes, yellow streaks, and textural “warts” of various sizes. More often than not, leaves expressed combinations of two or more of these features simultaneously, and purple spots were often paired with silver spots and warts; solid purple surfaces were commonly associated with warts. Abaxial surfaces also differed between individuals, either appearing solid purple, solid green (absence of purple), or an intermediate hue. We have observed all of these phenotypes return on the same plant year after year, even when light, fertilizer, and water are controlled for in a greenhouse setting. Next steps will include crossing individuals with each color variation with solid green individuals to look for Mendelian inheritance patterns in subsequent generations.

P136 - The Extended Specimen: A case study in salvaging a historic herbarium collection.

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The Extended Specimen concept recognizes that there is a constellation of data types associated with the physical specimens of natural history objects, that these diverse datasets accumulate over time, and that their integration can lead to surprising (cross-) disciplinary discoveries. However, such associated data types often become disassociated from their natural history specimens and become unverifiable over time. The challenge set forth by the Extended Specimen concept is to develop curatorial practices and data integration techniques that can bridge this ever-widening gap. Here we report an ongoing collaboration between the Ted R. Bradley Herbarium (GMUF) and the Fenwick Library Digital Scholarship Center (DiSC) to operationalize the Extended Specimen concept in the salvage, digitization and curation of the Lord Fairfax Community College herbarium (LFCC). LFCC comprises ca. 20,000 herbarium specimens and over 4000 pages of collection notes that record textual and illustrative metadata about the specimens beyond that reported on the herbarium labels themselves. LFCC represents the life’s work of Professor Robert Simpson and has significant historical and scientific value for understanding the flora of north-western Virginia and its exploration in the late 20th century. In order to link LFCC herbarium specimens with their collection notes efficiently and effectively, we trialed integrating the SERNEC Symbiota platform with Omeka S, a next-generation web publishing platform that is designed to interpret digital cultural heritage collections and link to other online resources. We include our workflows for processing, annotating, and digitizing LFCC during its salvage, linking each specimen record in Symbiota to its digitized notebook page, and building search queries to interrogate the notebooks via their Omeka S site. We also report our initial discoveries about this collection – at the intersection of regional floristics and the history of science - that were uncovered as a consequence using this new tool.

P137 - West Virginia University Herbarium Digitization Update

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This poster summarizes three digitization projects at the WVU Herbarium. The NSF “Keys to the Cabinet” digitizing and georeferencing grant, targeting botanical specimens from across the southeastern U.S., concluded at the WVU Herbarium in June 2019. Nearly 92,000 plant collections in 223 families, 1314 genera and 4639 species from the 12-state region were imaged and uploaded to the SERNEC portal. Label data from all West Virginia material has also been transcribed.

A multi-year U.S. Forest Service contract was funded to support student labor for invasive plant research. Initially, this project compiled label information from WVU Herbarium records worldwide for seven species. Subsequent studies narrowed the focus to four non-native plants: *Arthraxon hispidus*, *Glechoma hederacea*, *Persicaria longiseta*, and *Stellaria media*. Ongoing work is adding data for these species from national and regional herbarium portals.

The final project is a 3-year NSF Pteridophyte Collections Consortium grant. The award is distributed among nine research centers to digitize fern herbarium specimens and fossils. The WVU Herbarium is participating through the research hub at University of North Carolina, Chapel Hill. More than 8900 WVU Herbarium fern collections have been imaged and will be linked to specimen label information at the online portal. These three projects demonstrate a sample of digitization foci in taxonomy, floristics, and ecology.

P138 - Floristic Checklist of Shenandoah River State Park (SHSP) Warren Co., Virginia

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Shenandoah River State Park (SHSP), created in 1999, encompasses 1619 acres in the northern Shenandoah Valley in Warren County, Virginia. SHSP lies in the Ridge and Valley physiographic province and borders the eastern shore of the South Fork of the Shenandoah River, which is ca. eight km west of Shenandoah National Park. The region has a long history of modification by humans, as recorded by the presence of multiple Native American tribes including the Iroquois and Shawnee nations and European farmers prior to the American Revolution. SHSP encompasses eight ecological community types, as designated by the Virginia Natural Heritage Program that span upland forests (277 masl), including G2/S2 ranked shale barrens and S1 ranked inland wetlands. However, SHSP lacks an exhaustive checklist of its plant species that could be used to manage its natural resources. A SERNEC portal search revealed that Warren County ranks 50th of 95 Virginia counties of total plant collections (n = 2063) and last among the five northern Shenandoah Valley counties. The diversity of plant communities within SHSP, combined with the relatively sparse collection history of Warren County, indicates that a floristic checklist will likely uncover county records as well as rare species in need of conservation. Ongoing specimen collection at SHSP will continue through 2021 and 2022 and will be documented in iNaturalist to connect with the larger community and augment herbarium records. We estimate that this project will document 550 – 650 plant taxa, whose data will be shared through the SERNEC Symbiota portal, and will deposit ca. 1200 herbarium specimens in GMUF and UNC. We anticipate that checklist will not only be useful to the many stakeholders of SHSP – and engage the community of users on iNaturalist - but will make substantive contributions to our understanding of the flora of Virginia.

P139 - Herbarium and Field Studies on Metal-Hyperaccumulating Plants from Ultramafic Soils of Guatemala

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The recent discovery of nickel-hyperaccumulator plants in the Neotropics prompted further exploration of the nickel-rich ultramafic areas of this region. The most extensive serpentine and nickel-laterite deposits in Central America occur in eastern Guatemala. Recent developments in X-ray fluorescence analysis technology allow rapid, nondestructive measurement of specimens in the field and in herbaria. A survey of herbarium specimens collected in the Izabal Department of Guatemala, targeting genera known to hyperaccumulate metals elsewhere, revealed several new hyperaccumulators, as well as their general distribution of hyperaccumulation. Recent studies in Mexico have reported nickel hyperaccumulation in *Orthion* spp. (Violaceae). In Guatemala, *O. subsessile* was found to hyperaccumulate nickel and occasionally cobalt, and *O. montanum* is newly reported to hyperaccumulate nickel, with concentrations exceeding 5000 µg/g. *Chionanthus panamensis* (Oleaceae) is a newly discovered facultative hyperaccumulator with an extensive geographic range stretching from southern Mexico to Panama and displaying nickel concentrations approaching 5000 µg/g. *Arachnothryx linguiformis* (Rubiaceae) is a new obligate nickel hyperaccumulator, and the first species in its genus (previously included in *Rondeletia*) known to hyperaccumulate any metal. This species is endemic to areas around Lake Izabal, Guatemala, and seems to live exclusively on ultramafic substrates. Subsequent plant collection and corresponding soil sampling at several field sites in Guatemala revealed relatively consistent foliar nickel concentrations across populations of *A. linguiformis*, with no significant correlation between soil and plant nickel concentrations. The maximum nickel concentration observed in *A. linguiformis* was >10,000 µg/g (1% of dry weight), with a mean of approximately 3800 µg/g. Discovery of new hyperaccumulators may be important for the development of biotechnology for environmental remediation (phytoremediation) and metal recovery (agromining), and presents interesting cases for conservation and research in plant ecology and physiology.

P140 - Seed Bank Densities and Composition of Forest Edge and Understory Sites

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Soil seed banks from a forest understory and a forest edge at the Wingate University Campus Lake at Wingate University in Wingate, North Carolina, were investigated to compare species composition and seed density. This came about due to earlier observations which showed that no herbaceous plants were found in the forest understory whereas several herbaceous plants were present along the forest edge. Soils were randomly collected in November 2019 after seed rain had occurred along a forest edge and corresponding understory in the same tree stand. Five 0.5 m² plots were randomly selected along the forest edge as well as in the forest understory. Five soil cores (28.3 cm² each) were collected from each plot to a depth of 5 cm, one taken at each corner of the plot and one taken from the center. Soils were stored in polyethylene containers with lids at 5°C in a Percival incubator and were exposed to 24-hour dark. Soils were sieved to determine seed presence using five mesh sizes. Soil in each sieve was reviewed using a dissecting scope at 7.5x magnification to aid in identification. The average seed density of the forest edge was determined to be 18,115 seeds/m². The average seed density of the forest understory was determined to be 6,408 seeds/m². A single species comprised 81.8% of the forest edge seed density and 77.9% of the forest understory seed density and was the only species found in every soil core from both the edge and understory core samples. Twenty-three species were found in the edge and thirteen species were found in the understory with ten species overlapping. These data suggest that absence of plants in the understory may be due to a smaller seed bank and lower species diversity when compared to the forest edge.

P141 - Characterizing phenology and fecundity of *Spartina alterniflora* in Georgia coastal salt marshes

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Spartina alterniflora is the dominant plant species in salt marshes along the East and Gulf coasts of the US, playing a critical role in salt marsh growth and maintenance and contributing to the high net primary productivity characteristic of these habitats. The purpose of this research was to characterize the phenology (fruiting/flowering status and seed count) and fecundity (seed viability and germination success) of *S. alterniflora* across three salt marsh sites in Chatham County, Georgia, of varying marine influence. Mature spikelets were collected from random individuals in Fall 2019 and 2020, seeds per spikelet were counted, and seeds were placed in cold, wet storage for three months. After this cold stratification period, seeds were tested for viability using the Tetrazolium test. Additionally, seeds collected in Fall 2019 were continually monitored for germination rate and survival for 1 year. Preliminary results show a significant effect of marsh site on the number of seeds per spikelet for the Fall 2019 collection, with significantly more seeds in the marsh furthest from the ocean. However, seed viability for the Fall 2019 collection was significantly greatest at the marsh site nearest to the ocean. Data on germination success of Fall 2019 and phenology and fecundity of the Fall 2020 collection are currently being analyzed and will be compared to Fall 2019 results and published studies on the fecundity and phenology of *S. alterniflora* for other regions.

P142 - Course-embedded Undergraduate Research Experiences: CUREs for closing the performance gap in under-prepared and under-represented groups in STEM fields

Clay Runck, Judy Awong-Taylor, Allison D'Costa, Tirza Leader, Cindy Achat-Mendes, Chantelle Anfuso, David Pursell

Georgia Gwinnett College, Lawrenceville, GA

The School of Science and Technology at Georgia Gwinnet College has incorporated Course-embedded Undergraduate Research Experiences (CUREs) for the past 8 years as part of a comprehensive systems approach model to transform STEM learning, student engagement, and inclusivity for our student population. Central to our model is the growing body of evidence that shows a link between student research and lasting learning, and that research experiences increase students' interest in careers in STEM. Incorporating multiple CUREs throughout all four years of matriculation for all STEM majors provides a mechanism for successfully engaging large numbers of students in undergraduate research and provide them with the skills and confidence to seek out independent, faculty-mentored research or alternative summer research opportunities. Results from an on-going, in-depth study that currently includes 2 years (4 semesters) of quantitative and qualitative assessment data on the impact of CUREs on student success and engagement, including impact on ethnicity, gender, course grades, and student attitudes show: (1) CUREs have led to a more positive belief in self-efficacy for all questions pertaining to communication, experimental design, career choices, and critical thinking/problem solving; (2) an emerging trend for course grades to be higher in CURE sections versus controls in biology and chemistry but not math and Information technology; and (3) no significant effect of CUREs on mean course grade for any race except for African Americans. Taken together, our current data suggest that CUREs, a High Impact Practice, may be helping to close the performance gap in under-prepared and under-represented groups in STEM fields. Successes and challenges of implementing our CURE model at Georgia Gwinnett College, an open access institution with a highly diverse population of students, including many from groups traditionally underrepresented in STEM education, will also be presented.

P143 - Using Assessment Data to Improve Student Learning in an Undergraduate Biology Program

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Recently, the faculty of Longwood University's Biology program revised their curriculum to better align with the American Association for the Advancement of Science's 2011 call to action, "Vision and Change in Undergraduate Biology Education." With the twin goals of assessing the new curriculum and continually improving student learning outcomes, the faculty implemented James Madison University's LID (Learning Improvement by Design) program. Our three-year study focused on improving student performance on scientific research papers, review papers, and general audience papers. Randomly selected student writing samples were evaluated using detailed rubrics. Our initial assessment found that students only met the assessment target for approximately half (51%) of the pre-established criteria. Following teaching modifications based on the initial assessment, there was dramatic learning improvement. By the last year of the study, students met the assessment target for 86% of the criteria. Here we describe how, using the LID method, the Biology program faculty collaborated with university stakeholders to begin the assessment process, collected student data, analyzed it to identify areas for improvement in the biology program, and made targeted suggestions to refine teaching in core courses. Finally, we discuss future directions for assessing and improving other student learning outcomes in our program, and we share a framework model and keys for success that other programs might adopt.

P144 - Increasing Student Learning and Motivation: Implementation of Specifications Grading in a Sophomore Level Undergraduate Cell Biology Classroom

Shoshana Katzman, Jennell Talley, Alessandra Barrera, Elisabeth Javazon, Jennifer Hurst-Kennedy, Mary Diaz, Mary Beth Anzovino

Georgia Gwinnett College, Lawrenceville, GA

Specifications (specs) grading is a grading system developed by Dr. Linda Nilson in which mastery of specific educational outcomes is the basis for the final grade that a student earns in the course. Implementation of the types of assessments used for specs grading has shown to be beneficial for student learning and motivation compared to traditional grading systems. We designed a specs grading strategy in a sophomore-level Cell Biology course, creating 20 individual learning outcomes (LOs). The grade earned in lecture depended on the number of LOs that the student

mastered. If students were unable to master the content on their initial attempt, they could earn re-takes for each LO assessment by completing an assignment associated with the information covered in that LO. Here, we present how specifications grading was implemented in Cell Biology, student performance related to course content, and assessment of student attitudes towards the use of this grading strategy.

P145 - Does active learning have long-term effects? Tracking the persistence and success of at-risk students through the curriculum

Emily Prince, Lisa McDonald

Lander University, Greenwood, SC

In order to address the gap in achievement in biology classes and persistence in the biology program between underrepresented minorities (URM), first-generation college students, low socio-economic status students, and other students, we redesigned Lander University's introductory biology course (BIOL 111) in 2017. The content taught in one semester was divided into two semesters, and the course was restructured to include more formative assessments and focus on active learning. To assess the results of the change, we compared students enrolled in the "old" BIOL 111 from 2015 - 2016 to those enrolled in the "new" BIOL 111 from 2017 - 2018. We assigned students a risk-assessment (RA) score based on their number of risk factors for failure (i.e., URM, first-generation, and low socio-economic status), and tracked students through the program. The change in course structure had a dramatic effect on the success of students in BIOL 111, increasing success rates (i.e., students earning a "C" or higher) from 52% to 70%. The success rate of students with the highest RA score increased from 19% to 51%, indicating a narrowing achievement gap. The percentage of students enrolling in a biology course during the second semester of the freshman year increased dramatically, but the increase did not translate to increased retention in the biology program or Lander University at the sophomore or junior-level. Differences in achievement reappeared in the junior-level Genetics course. While the success rate of students who had taken the old BIOL 111 was only 59%, the success of students who took the new BIOL 111 was 91%, with the most dramatic difference in students with the highest RA scores. We will continue to track students as they progress through the program, focusing on success in upper-level courses and graduation rates.

P146 - Assessment of a fluorescence microscopy and mammalian cell culture CURE with an underrepresented STEM student population

Jennifer Hurst-Kennedy, Michael Saum, Cindy Achat-Mendes, Allison D'Costa, Elisabeth Javazon, Shoshana Katzman, Ernest Ricks, Jr., Alessandra Barrera

Georgia Gwinnett College, Lawrenceville, GA

Georgia Gwinnett College (GGC) is an access institution with a diverse student body, located in metro Atlanta. To strengthen research skills, teach employer-valued cell biology laboratory techniques, and increase student engagement, a semester-long, inquiry-based CURE was developed and implemented in Cell Biology with Laboratory (BIOL3400K), a sophomore-level course, which serves as a "gateway" to all upper-level Biology courses. This CURE centers on the investigation of a student-chosen experimental factor on the viability of cultured, mammalian cells. Through participation in this CURE, students gain experience in cell culture, fluorescence microscopy, and viability assays, and strengthen important research skills, such as literature searches, graphing, and data analyses. The impact of this CURE on student learning gains and attitudes was assessed using a pre-/post- content exams and the Colorado Learning Attitudes about Science Survey (CLASS). Our data show that all students made significant content gains. Female students made larger learning gains than male students. Additionally, minority students performed better than majority students in some content areas. Student attitudes did not change, or in some cases were slightly more negative after the CURE. Overall, this CURE had a positive impact on students by engaging them in an inquiry-based laboratory experience.

P147 - Virtual Fruit Fly Simulation for Teaching Mendelian and Non-Mendelian Modes of Inheritance in Genetics Courses

Sierra Holton, William Baglivio, Joseph Graham, Derek Cotton, Amy Wiles

Mercer University, Macon, GA

Teaching complex biological concepts in a manner that allows students to fully understand and retain material poses a problem for even the most experienced educators. With the advancement of technology, biology labs that could only be completed in-person can now be taught virtually. The purpose of this project is to allow upper-level Genetics students to perform crosses with *Drosophila melanogaster* in a comprehensible online format. The authors developed a computer program so that results from crosses could be generated quickly. While using the virtual fly program, students can strengthen their understanding of Mendelian and Non-Mendelian modes of inheritance. Seventy-one students in Genetics at Mercer University during Fall 2020 were given a set of virtual stock strains to conduct these crosses. The stock strains included single, double, and triple mutant strains that encompassed a total of 25 genes, with three of these genes containing more than two alleles. Once students created their desired crosses, the professor and TAs manually ran these crosses through the program to generate resulting offspring. Over the semester, students were expected to utilize the results of these crosses to determine the mechanisms of inheritance for each mutant strain. Students used multiple generations of flies in their analyses. Additionally, students were required to use the results to find the map distance between double and triple mutant strains, find the presence of lethal genes, conduct complementation testing to discover three unknown genes, and determine if genes were autosomal or sex-linked. An accessible web interface is being created from a Python script that will generate results from crosses almost instantaneously. Student groups will have their own accounts to be able to track their crosses, while the instructor will have the ability to view each group's work.

P148 - How do pandemic-related instructional changes affect the achievement gap in a freshman biology course?

Emily Prince, Kerry Hansknecht, Lisa McDonald

Lander University, Greenwood, SC

The COVID-19 pandemic has altered content delivery in higher education, with unknown implications. In 2016, our department redesigned our introductory biology course (BIOL 111) to focus on formative assessments and active learning. The course met face-to-face three days per week until fall 2020, when we transitioned to a hybrid model. Students then attended in person one day each week, with a second day being optional (a few students attended entirely online). Online videos provided lecture material, and students used the limited class time to work on practice assignments and ask questions. Social distancing made group work difficult, and concerns about viral spread required a permissive attendance policy. We hypothesized the course structure changes would decrease student success, disproportionately affecting at-risk students. To test our hypothesis, we assigned students a risk-assessment (RA) score by summing their risk factors for failure (i.e., underrepresented minority, first-generation, low socio-economic status, and female). We compared course success (i.e., final grades of C or higher) between students in the face-to-face course from 2017-2019 and students in the hybrid/online course in 2020. The success rate of students with an RA score of 1 or 0 was largely unchanged, moving from 79.3% in the face-to-face course to 81.4% in the hybrid course ($p = 0.8569$). In contrast, the success rate of students with an RA score ≥ 2 decreased dramatically, from 62.1% in the face-to-face course to 46.6% in the hybrid course ($p = 0.0179$). The primary difference between the two modes of instruction was that the withdrawal rate of RA ≥ 2 students tripled from 7.6% in the face-to-face course to 23.3% in the hybrid course. Our results suggest that the educational effects of the COVID-19 pandemic are not felt equally by all students and may undermine efforts to close the achievement gap in STEM fields.

P149 - Implementation of No-Cost, Open Educational Resources (OER) for Cell Biology at Georgia Gwinnett College

Breen Riley, Jennell Talley, Rebecca Higgins, Jennifer Hurst-Kennedy, Alessandra Barrera, Shoshana Katzman

Georgia Gwinnett College, Lawrenceville, GA

To reduce the cost of educational materials needed by a large number of STEM majors attending Georgia Gwinnett College (GGC), we generated a no-cost, open educational resources (OER) textbook for Cell Biology (BIOL 3400K). At GGC, Cell Biology is a sophomore-level course that is a required pre-requisite course for a variety of STEM tracks within the School of Science and Technology. In addition to cost reduction, we unified the content of the textbook with the learning outcomes to ensure that students have a clear understanding of what is expected in their learning. Surveys were administered to assess student perception of OER materials and their experience related to learning outcomes, comparing those with access to a traditional textbook to those with access to OER. Data showed positive student attitudes about learning, accessibility, and cost of the provided OER.

P150 - Teaching biodiversity and spatial scale concepts using open-access vegetation datasets from the National Ecological Observatory Network (NEON)

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Biodiversity is a complex, yet essential concept for undergraduate students in ecology and other natural sciences to grasp. As beginner scientists, students must learn to recognize, describe, and interpret patterns of biodiversity across various spatial scales and understand their relationships to ecological processes and human influences. It is also increasingly important for undergraduate programs in ecology and related disciplines to provide students with experiences working with large ecological datasets to develop students' data science skills and their ability to consider how ecological processes that operate at broader spatial scales (macroscale) affect local ecosystems. To support the goals of improving student understanding of macroscale ecology and biodiversity at multiple spatial scales, we formed an interdisciplinary team that included grant personnel, scientists, and faculty from ecology and spatial sciences to design a flexible learning activity to teach macroscale biodiversity concepts using large datasets from the National Ecological Observatory Network (NEON). We piloted this learning activity in six courses enrolling a total of 109 students, ranging from mid-level ecology and GIS/remote sensing courses, to upper-level conservation biology. Using our classroom experiences and a pre/post assessment framework, we evaluated if our learning activity resulted in increased student understanding of macroscale ecology and biodiversity concepts and increased familiarity with analysis techniques, software programs, and large spatio-ecological datasets. Overall, results suggest that our learning activity improved student understanding of biological diversity, biodiversity metrics, and patterns of biodiversity across several spatial scales. Participating faculty reflected on what went well and what would benefit from changes, and we offer suggestions for implementation of the learning activity based on this feedback. This learning activity introduced students to macroscale ecology and built student skills in working with big data (i.e., large datasets) and performing basic quantitative analyses, skills that are essential for the next generation of ecologists.

P151 - Does course structure matter? Transferring first-year performance gains to upper-level courses

Lisa McDonald, Emily Prince

Lander University, Greenwood, SC

In the fall of 2017, we redesigned the biology curriculum at Lander University. Our goals were to increase retention in our program and to increase flexibility within the major. We were particularly interested in addressing the achievement gap between higher risk students (underrepresented minorities (URM), students with low socio-economic status, first-generation college students) and other students. We found that changing the structure of the first biology course in our program from lecture-based to active-learning with increased course structure (more frequent, lower impact assessments) had important, positive outcomes for students with a higher number of risk factors in that introductory course. To investigate whether increased course structure has a similar impact on students in their upper-level courses, we assigned each student a risk-assessment (RA) score (students with more risk factors have a higher score), and we determined whether each upper-level course had a lower-level of structure (at least 70% of course points from exams and quizzes) or a higher-level of structure (<70% of course points from exams and quizzes). We found that students entering the program under the redesigned curriculum had significantly higher final exam scores and significantly higher course grades in their upper level courses than students who began the program in the two years prior to this implementation. The largest gains were observed for students with higher RA scores. This increase in performance was largely independent of course structure; student achievement improved in courses with both higher and lower structure. Our findings demonstrate that students are gaining skills necessary for long-term success in our upper-level courses as a result of the new biology curriculum. Not only are students showing improvement in courses similar to the new first-semester course, but also in more memorization-heavy, lecture-based courses across our program.

P152 - A CURE for Biotechnology Labs to Identify Genetically Modified Foods

Ernest Ricks, Jr., Cindy Achat-Mendes, Jennifer Hurst-Kennedy, Robert Haining

Georgia Gwinnett College, Lawrenceville, GA

This CURE provides students the opportunity to learn and use leading techniques in biotechnology, while strengthening their understanding of the central dogma of biology, and facilitating an authentic research experience. In one module, students can use PCR to detect the presence of common genes found in genetically modified (GM) foods. In a second module, students can isolate messenger RNA, synthesize cDNA, and employ real-time quantitative PCR to investigate the expression of GMO genes. The last module utilizes Enzyme-Linked Immunosorbent Assay (ELISA) to detect the presence of GM proteins. Students receive training in lab research/STEM skills including troubleshooting equipment, experimental design, maintaining a lab notebook, writing manuscript-style lab reports, and oral presentation of research findings. Students are required to know the purpose of reagents and procedures rather than follow cookie-cutter recipes. They learn the theory and application of PCR, real-time PCR, and ELISA to investigate the relationship between genes, RNA and proteins, respectively, in GM foods. This CURE resulted in over 20 campus and regional conference student presentations over the past 3 years. The effectiveness of this project was assessed by evaluating gains in *student learning and student attitudes* towards research and STEM careers. Assessment tools included: *a) pre- and post- content surveys* (multiple choice questions that are linked to course learning objectives), *b) 4-year URE student survey*, and *c) Lab report rubric designed by the Biology Faculty*. The attitudinal survey data suggest that following participation in the GM foods lab design students: 1) Became more knowledgeable about the testing of genetically modified foods and central dogma; 2) Appreciated designing and taking ownership of their own research project; 3) Expressed better understanding of research in the biotechnology field. Significant outcomes of this new lab curriculum include student-initiated hypothesis-driven authentic research projects, troubleshooting and critical thinking as students worked through technical challenges.

P153 - Preliminary Assessment of a Bioinformatics CURE in an Introductory Genetics Course about SARS-CoV-2

Jennell Talley, James Nolan, Adrienne Cottrell-Yongye, Elisabeth Javazon, Jill Penn

Georgia Gwinnett College, Lawrenceville, GA

The Department of Biology at Georgia Gwinnett College incorporates Course-based Undergraduate Research Experiences (CURE) in most of our biology lab courses. We created a multi-week, SARS-CoV-2 themed research project for students in an Introductory Genetics course. Students learn the history and biology of the SARS-CoV-2 virus, develop hypotheses, and design their own experiment to analyze and compare various aspects of the SARS-CoV-2 virus. Students also present their findings in either oral or written form. Experiments ranged from students analyzing how the virus spread to a specific geographical area to investigations of various mutations in the viral genome and possible implications of the mutations. During their investigations, students actively engage with collaborative databases, such as NCBI and GISAID. GISAID is internationally recognized as one of the leading consortium experts use to investigate the novel coronavirus. Here we present preliminary data exploring if this CURE impacts students' long-term retention of basic techniques used in bioinformatics by assessing students the semester after being exposed to the CURE and comparing their knowledge to those who did not have the CURE. We will also present our current effort in determining how this CURE impacts students' perceptions regarding their ability in science. To learn more about the design and implementation of this CURE we have an oral presentation in the symposium: A CURE for your Curriculum.

P154 - Supporting Underrepresented Students in STEM through Peer Supplemental Instruction

Chantelle Anfuso, Cindy Achat-Mendes, Judy Awong-Taylor, Cynthia Johnson, Tirza Leader, Katherine Pinzon, Jamye Curry Savage, Benjamin Shepler

Georgia Gwinnett College, Lawrenceville, GA

According to recent statistics, Black/African American and Hispanic/Latino individuals comprised 13.4% and 18.5% of the U.S. population (2019 U.S. Census Bureau), but attained only 8.2% and 13.0% of awarded STEM degrees and comprise only 5.6% and 7.5% of the STEM workforce, respectively (2019 *Women, Minorities, and Persons with Disabilities in Science and Engineering Report*, NSF). Even when these students do choose STEM majors, they struggle in STEM programs, and are more likely to change majors or leave college. Therefore, it is important to improve educational outcomes for students belonging to these underrepresented minority (URM) groups.

Georgia Gwinnett College (GGC) is an open access institution with over 50% of STEM students belonging to URM groups. Here, we investigate the impact of a direct academic support program called Peer Supplemental Instruction (PSI) on different student populations. As Black/African American students enter GGC with lower average HS GPAs, exhibit higher DFW rates, and graduate at lower rates compared to their peers, we are particularly interested in PSI's effect on these students. We present final course grade data aggregated over five semesters and nine gateway STEM courses, and examined as a function of PSI attendance, incoming HS GPA (used here to indicate college preparedness), and racial/ethnic demographics. Detailed analysis shows that all three factors have a significant effect on final course GPA. Frequent PSI attendance has the greatest impact for the least prepared students and shows no significant effect for well-prepared students. Black/African American students make up a disproportionate percentage of underprepared students and thus see the largest average benefit of frequent PSI attendance, with an average final course GPA increase of 1.02 when attending 10+ vs. 1 – 2 sessions. This work indicates that PSI is a promising method to assist underprepared students from URM groups.

Beta Beta Beta National Biological Honor Society District I and District II Meetings

BBB Oral Presentations

BBB Talk 1 - *Daphnia pulex* Reproduction In Response to BPA and BPA Derivatives

Abigail Walters

Catawba College, Salisbury, NC

Bisphenol A (BPA) is an industrial chemical used in the formation of polycarbonate plastics and epoxy resins, which are used in the manufacturing of food packaging and water bottles. BPA has been shown to mimic the hormone estrogen, allowing it to react with estrogen receptors and affect their function. Previous research has shown that exposure to BPA through food and beverage packaging can increase the risk of adverse health effects on the brain, prostate gland, mammary glands, behavior, and reproduction. Thus, BPA was banned from the manufacturing of everyday plastics, but was promptly replaced with BPA derivatives, like BPAF and BPS, which were thought to be more stable than BPA. However, these BPA replacements may have more potent consequences on human health. This research project aims to investigate the reproductive effects of BPA and BPA derivatives on *Daphnia pulex*. *D. pulex* are freshwater crustaceans that are used in research for their easy reproducibility and sensitivity to toxins. Previous studies have not examined the reproductive effects of BPA and BPA derivatives in *D. pulex*. Thus, we will examine the effects of BPA, BPAF, and BPS in varying concentrations on the reproduction rates and age of sexual maturity. Due to the estrogenic effects of BPA and BPA derivatives, we expect that reproduction rates will increase and *D. pulex* will reach sexual maturity earlier when exposed to BPA and BPA derivatives. The results of our findings could indicate possible impacts on *D. pulex* populations, freshwater ecosystems, and human health.

BBB Talk 2 - Determining the potential of gene flow between baldcypress and pondcypress

Joshua Sprouse

Bridgewater College, Bridgewater, VA

I surveyed seedlings grown from seeds extracted from the cones of baldcypress (*Taxodium distichum*) and pondcypress (*Taxodium ascendens*) trees to determine the potential for cross-pollination. Two parent trees were sampled from populations that are less than 1.5 miles apart near Walterboro, SC. A PCR-RFLP analysis was conducted of a single nucleotide polymorphism in the trnC-ycf6 intergenic spacer region of the chloroplast that was identified by Lickey (unpubl.) as a putative diagnostic character separating baldcypress and pondcypress. The haplotypes of 175 seedlings originating from the two baldcypress parents and 92 seedlings originating from the two pondcypress parents were compared to the haplotypes of each parent. Preliminary data confirms that chloroplasts are inherited through the pollen in *Taxodium*, and that baldcypress haplotypes can be found in some pondcypress seedlings and vice versa.

BBB Talk 3 - The Monilophyte and Lycophyte Flora of Three Natural Areas in Spartanburg, South Carolina

Damaris Vega, Moriah Gomez

Converse College, Spartanburg, SC

Spartanburg County, in the upper piedmont of South Carolina, consists of mostly secondary succession pine and oak-hickory forests that were previously used as farmlands. Three natural areas near the geographic center of Spartanburg County were studied to determine and compare their lycophyte and monilophyte floras. Because these natural areas are geographically close to each other and because they have similar histories and forest types, we expected their floras to be similar. However, we expected some differences between one area which is closer to the residential part of the city. We made collections in Peter's Creek Heritage Preserve and the Pacolet River Heritage Preserve three times over the summer months of 2020. We made collections at the wilderness area of the Duncan Park neighborhood twice over the same time period. Thirty seven specimens of ferns and lycophytes were collected from these areas. These collections were identified and mounted at Converse College, and they are housed in the Converse College Herbarium (CONV). Overall, we found 17 species in the area. Of these species, two were common to all three areas. Six taxa, *Woodsia obtusa* ssp. *obtusa*, *Woodwardia areolata*, *Dryopteris intermedia*, *D. erythrosora*, *Pleopeltis polypodioides* ssp. *michauxiana*, and *Osmunda spectabilis*, were each found in only one area. We compared the floras of these areas using Sorrenson's coefficients, which ranged from 0.33 to 0.63, indicating that these areas are not floristically different from each other.

BBB Talk 4 - Removal of Palladium Ions from Polluted Water

Caleb Guerra, Nicholas Spader

Abraham Baldwin Agricultural College, Tifton, GA

Heavy metal pollution has become an increasing problem around the world due to industrialization and modernization. Humans are migrating into cities where more factories are being built to compensate for the demands of the increasing population. Factories use and produce heavy metals, which are non-biodegradable materials that lead to the pollution of local water sources when disposed of improperly. One of those heavy metals is Palladium and it is known for being extremely toxic and carcinogenic to humans. This heavy metal has been exceedingly prevalent in car factories, where it is used as a catalytic converter, and in pharmaceutical labs. Our research is focused on the removal of Palladium ions using Diatomaceous Earth (DE) silica from Palladium containing water samples. Previous findings from other research have shown that silica nanoparticles are effective in the removal of Palladium ions from water. We chose DE as a filtering material because of its porous nature, polar functional (silanol) group on the surface, and high surface area. Silanol binds strongly with Palladium ions by ion-dipole interaction, which facilitates in removing the ions from water. To determine the concentration of the Palladium ions in the water samples, we used Inductively Coupled Plasma-Optical Emission Spectroscopy (ICP-OES) before and after filtration. In our preliminary results, we found that DE can remove Palladium ions up to 171 ppm (mg of Pd²⁺/L). However, we expect the DE filtration system to exhibit greater adsorption capacity beyond the upper limit that we have tested so far. In the future, we also plan to compare the filtration ability of the DE system with a hybrid filtration system of DE and activated charcoal for the filtration of Palladium ions from water.

BBB Talk 5 - Improved Filter Design for Removal of Cadmium and Palladium Ions from Water

Nicholas Spader, Caleb Guerra, Caleigh Eberhardt

Abraham Baldwin Agricultural College, Tifton, GA

Heavy metal pollution has become an increasing problem around the globe due to industrialization. The electronic industry, mining, and agricultural products produce a high volume of heavy metals waste that goes to landfills, to running water, and eventually to drinking water supplies if they are not disposed of properly. Heavy metals such as mercury, lead, cadmium, cobalt, and palladium are known to be toxic. In this study, we are designing a filtration system made from diatomaceous earth (DE) and activated charcoal to remove cadmium and palladium ions from water samples. We choose DE particles because of their uniform microscopic porous structure, and high surface area with a polar functional group that can have strong interaction with heavy metal ions. In our preliminary research, we tested the adsorption of the cadmium (Cd²⁺) and palladium (Pd²⁺) ions over time on activated Carbon and DE, separately. We found that adsorption of Cd²⁺ and Pd²⁺ on Carbon was independent of time on the scale we used (1 to 60 minutes), while adsorption of Cd²⁺ and Pd²⁺ on DE Silica was dependent on time with a maximum adsorption at 60 minutes. Carbon was a better adsorbent as compared to DE Silica-based on the solutions we used (1000ppm and 2000ppm). We plan to expand the study using a mixture of Activated Carbon and DE particles for the removal of Cd²⁺ and Pd²⁺ ions from water samples to see if the adsorption capacity of the filter is altered.

BBB Talk 6 - Comparison of histological techniques to determine intersex prevalence and severity in testes of Largemouth Bass (*Micropterus salmoides*) and Spotted Bass (*Micropterus punctulatus*) from the Chattahoochee River, Georgia, U.S.A.

Abigail Abernathy, Elizabeth Klar, Cherish Jordan, Meenal Joshi, Michael Newbrey

Columbus State University, Columbus, GA

Feminization of male fish, also known as a type of intersex, has been found to be present in many species of fish around the world. Intersex is characterized by the presence of one or more oocytes in the gonads of male fish. Previous studies have not adequately quantified or compared the severity of intersex between cross and longitudinal sections of testes. Traditionally, intersex severity was assessed using cross sections, and ranked on a scale of 0-4. Our goal was to compare the severity of intersex between two sectioning techniques in Largemouth Bass and Spotted Bass, and compare the traditional scoring system to a new method of scoring based on the density of oocytes per mm² of tissue. Finally, we compared the severity of intersex between the two species. Largemouth Bass (*Micropterus salmoides*) (n=41) and Spotted Bass (*M. punctulatus*) (n=23) were collected from Lake Oliver, a reservoir of the Chattahoochee River, Columbus, GA. Testes from each fish were prepared histologically with one testis cut into three cross sections, while the other was cut longitudinally. After staining with hematoxylin and eosin, the two sectioning techniques showed different intersex severity values. Longitudinal sections in Largemouth Bass revealed an average severity index of 1.67, while cross sectioning yielded an average severity index of only 0.87. In Spotted Bass, the longitudinal sections had a severity index of 1.36, while the cross sections only found an average severity of 1.00. Density of oocytes per mm² of tissue could potentially improve intersex severity determination between specimens by using the total number of oocytes present in the testicular tissue.

BBB Talk 7 - Determining Optimal Root Conditions for Successful Culturing of Turtle Grass (*Thalassia testudinum*)

Amber Rhodes

Union University, Jackson, TN

Turtle grass, *Thalassia testudinum*, is one of the most dominant species of sea grass in the tropical Atlantic. Seagrass communities are being negatively affected by humans, with decreases being documented across many areas. *Thalassia testudinum* provides sediment stabilization for the ocean floor, critical habitat for marine life, and a food source for many species. Additionally, it serves as a highly effective carbon sink. The roots of *T. testudinum* are connected via rhizomes to other shoot structures, enabling it to share resources and support.

This is a lab study which aims to investigate effective growth strategies of *T. testudinum* in culture with the goal of utilizing these cultures in future reintroduction strategies, or future lab studies. Specifically, the study investigated the best root structure and environment for the survival

and growth of cultured seagrass. Lab experiments were conducted in 9 controlled tanks with 3 different root structures (single shoot bare root, single shoot grow bag, and multiple bare root shoots (3) attached via rhizome) over the course of 3 weeks. The shoots were marked before the experiment began and any growth was measured at the end of the 3 weeks. Three iterations of the experiment were conducted. An ANOVA was conducted to determine if significant differences existed in growth for the different root conditions. No significant differences were noted between the treatments. Future studies could be directed at ways to ensure long term survival of *T. testudinum* in culture.

BBB Talk 8 - DNA barcoding of corticolous lichens to determine species richness and abundance in relation to proximity of traffic in Nashville, Tennessee

Bethany Wood, Taylor Ruscitti, Gerald Archer

Belmont University, Nashville, TN

Lichens, a symbiotic relationship between fungi and algae, are often used as bioindicators of air quality. Lichens absorb water and nutrients from the air causing them to be affected by air pollution levels. We predicted an increase in lichen richness and abundance in urban areas as distance from high-traffic areas increased. Corticolous lichen samples were collected from three locations in Nashville, Tennessee with varying proximity to high-traffic streets. Bark was taken from each sample tree to compare its pH with the abundance of lichen found on each tree. Given the challenges of field identifying lichens, DNA isolation and amplification was used to sequence and identify lichen species using Bold Systems and BLAST. Of our three locations, we saw differences in coverage, abundance, and richness of lichens. Factors such as use of chemicals, pollution levels, bark pH and tree species may also affect lichen diversity. Collected lichen samples were preserved and documented to establish the beginnings of a lichen library at Belmont University. This library was also used to compare phenotypes across species found to be genetically similar. This study provides a baseline data set for future analysis of air quality and land use within Nashville, Tennessee.

BBB Talk 9 - Molecular Phylogenetics of the Cricket Assassin Wasps (Hymenoptera: Rhopalosomatidae)

Christopher Johnson, Bailey Krebs

Union University, Jackson, TN

The ectoparasitoid wasps of Family Rhopalosomatidae (Hymenoptera: Vespoidea) develop as larvae on the outside of their cricket hosts. Rhopalosomatidae includes 72 species in only four extant genera but due to their rarity in collections, rhopalosomatids are notoriously understudied among wasps. Within Rhopalosomatidae, two morphological forms exist—macropterous forms with fully developed wings, including the genera *Rhopalosoma* (Cresson), *Paniscomima* (Enderlein), and *Liosphex* (Townes), and a brachypterous form with vestigial wings (*Olixon* (Cameron)). Morphological analyses indicate that the brachypterous *Olixon* could represent a basal lineage of Rhopalosomatidae and that the genera *Rhopalosoma* + *Paniscomima* share a close relationship. However, no molecular phylogeny exists to support these hypotheses. Here, we present the first family-level molecular phylogeny of Rhopalosomatidae using the barcoding gene *cytochrome oxidase I*. Phylogenies were reconstructed using Neighbor Joining, Maximum Likelihood, and Bayesian analyses. Each method revealed a phylogeny that supports *Olixon* as sister to the rest of Rhopalosomatidae, but recovers *Paniscomima* nested within a clade of *Rhopalosoma*, indicating that these genera may need to be synonymized. Including additional genes in future studies is necessary to confirm these hypotheses.

BBB Talk 10 - Background levels of intersex in Largemouth Bass (*Micropterus salmoides*) revealed through histological evaluation of gonadal tissue from three interconnected water bodies

Meenal Joshi, Elizabeth Klar, Abigail Abernathy, Amy Sibley, Jeremy Belt, Michael Newbrey

Columbus State University, Columbus, GA

Intersex, the presence of oocytes in male gonadal tissue, has been studied as an abnormal phenomenon in gonochoristic species. Previously published studies do not explicitly identify the background levels of intersex in male Largemouth Bass (*Micropterus salmoides*), and this lack of knowledge limits our ability to interpret the species-specific severity of intersex. Perturbations to fecundity are considered to be minimal if a population exhibits a hypothetical value of 65% intersex when compared to a natural background level of 60% intersex. In contrast, the effect of intersex on fecundity is interpreted to be much greater if the hypothetical background level was 0% intersex. We hypothesized the occurrence and prevalence of intersex should be the same among the Chattahoochee River and two of its tributaries, Columbus, GA, USA. Largemouth Bass were collected using backpack and boat electrofishing techniques from Lindsey and Heiferhorn creeks, and Lake Oliver of the Chattahoochee River. Gonads from all fish were prepared histologically and stained using hematoxylin and eosin. In Largemouth Bass from Lake Oliver (n=41 males), the occurrence of intersex was 78%. However, in Lindsey and Heiferhorn creeks (n=22 males), the occurrence of intersex is 16.7%. This evaluation demonstrates that low levels of intersex can be expected in Largemouth Bass and also showcases the extremes in intersex among connected waterbodies within the same drainage.

BBB Talk 11 - Novel Microglial NF-κB Animal Model Characterization

Ryan Frerichs

Augusta University, Augusta, GA

Glioblastoma (GBM) is the most common form of brain cancer in adults, and is often fatal within one year of diagnosis, even with treatment. The tumor microenvironment in GBM is thought to be one of the main contributors to its resistance to treatment. The tumor microenvironment is

composed of a high percentage of resident microglia as well as macrophages which migrate from the periphery. Signaling between GBM cells and microglia via the NF- κ B signaling pathway can alter the phenotype of the microglia, changing them from phagocytic cells (M1) to tumor promoting cells (M2). Microglia in the M2 state help the GBM grow and spread instead of destroying the tumor. Deleting the NF- κ B pathway could prevent the microglia from changing phenotype and make the tumor less resistant to treatment. The Bradford lab created a conditional p65 knockout mouse model by crossing p65^{fl/fl} mice with CX3CR1^{creER/+} mice. As p65 is a major transcription factor needed for the canonical NF- κ B pathway, this model should have greatly reduced NF- κ B signaling in microglia upon tamoxifen administration. Currently, the model is being tested to ensure that p65 is being deleted appropriately, which has proven difficult as NF- κ B levels in non-diseased brain are normally extremely low. To combat this, mice were implanted with syngeneic GBM tumor cells, to raise p65 levels and a western blot was performed to determine p65 levels in the mice brains. The western blot showed a significant increase in p65 levels for the brains that had GBM cells implanted. This experiment will help us moving forward with model characterization.

BBB Talk 12 - The Attempted Isolation of *G. rubripertincta* Bacteriophage and Annotation of *G. terrae* Phage “YungMoney”

Irene Kuriakose, Jennifer Easterwood

Queens University of Charlotte, Charlotte, NC

In the Spring of 2020, attempts were made to isolate bacteriophage using the bacterial host *Gordonia rubripertincta*. This project was a part of the SEA-PHAGES program, in which students work to discover and characterize new bacteriophage, viruses with the ability to infect bacteria and the potential to fight bacterial infections. Over the course of eight weeks, five sets of soil samples were collected and tested for signs of phage, using enriched isolation methods. Various changes were made to the methods to reduce suspected contamination. These changes included extra filtration, different incubation temperatures, and an off-soil method where soil samples were incubated, centrifuged, and filtered before adding *G. rubripertincta*. Though these changes helped resolve contamination, phage was not isolated, and protocols could not be continued due to the COVID-19 pandemic and quarantine orders. Possible reasons for the lack of phage isolation from the host *G. rubripertincta* include reduced host recognition and soil sample location. In the Fall of 2020, the *Gordonia terrae* phage “YungMoney”, sequenced at the Pittsburgh Bacteriophage Institute, was adopted for genome annotation. The bioinformatics software DNA Master and resources HHPred, NCBI Blast, Starterator, and Phamerator were used to annotate the genome by analyzing the coding regions, starts, and functions of individual genes. “YungMoney” is of the Siphoviridae morphotype and has small, turbid plaques with a circularly permuted genome. After isolation, this phage was registered in the Actinobacteriophage Database, a phage database open to the public, and is currently one of twenty-one sequenced phages in the DC1 subcluster. “YungMoney” has 60,495 base pairs, 95 open reading frames, and a 67.3% Guanine-Cytosine (GC) content. With the isolation and annotation of “YungMoney”, a new phage with the potential to infect the pathogenic host *G. terrae* has been found.

BBB Talk 13 - The Effect of Invasive Plants on Soil Bacterial Communities

Solomon Turner

Brevard College, Brevard, NC

Exotic plants threaten the stability of native ecosystems through the development of positive feedback loops which facilitate invader success. Soil microbial communities in invaded soils respond to positive feedback loops through increased decomposition rates and nutrient pools. The objective of the present study was to determine if the invasive monocrops of Bamboo (*Phyllostachys* sp.), Ivy (*Hedra* sp.), and Grass (*Fescue* sp.) on the campus of Brevard College, NC, cause changes in the bacterial diversity of their invaded soils compared to native *Rhododendron* (*Rhododendron* sp.). Three methods were used to obtain a representation of the soil's biological and chemical profiles in response to changes in the plant taxa. Bacterial enumeration was employed to determine if culturable bacteria were present in soil samples. Soil nutrient tests were used to analyze the growing conditions beneath each plant and assess the potential for microbial activity. BIOLOG EcoPlate assays were used to obtain Community Level Physiological Profiles (CLPPs) of the metabolic diversity for each plant for a comparison of functional diversity. Each soil sample produced culturable bacteria on nutrient agar plates. *Rhododendron* sp. had the most acidic soil pH and *Phyllostachys* sp. had the highest cation exchange capacity; soil nutrient concentration was generally below target levels for each sample. There was no significant difference in Shannon Diversity among the four soil bacterial communities. We suggest that there was no significant difference between native and non-native soil samples because of the sampling regime; it is well documented that invasive plants alter the chemical and biological profile of soil communities.

BBB Posters

BBB Poster 1 - The Effects of Cannabidiol and Hu331 on Embryonic Neural Development in *Danio rerio*

Morgan Meador

Lipscomb University, Nashville, TN

With a growing popularity of prescription and recreational use of marijuana, there has been increasing interest on the effects of this drug on early neurological development. Cannabidiol (CBD), the major non-psychoactive component of marijuana, has been approved by the FDA for use as a therapeutic agent for children two years and older². Even so, there is limited research on its effect of CBD on early development. CBD oxidizes into Hu331, a chemical inhibitor of topoisomerase-II beta (TOP2B) and potential anti-cancer therapy. TOP2B relieves DNA supercoils during replication and transcription and is also required for proper neural development. Previous studies in our lab have shown that early Hu331 exposure results in reflex deficits and axon guidance defects. In 2019, our lab started to investigate the effect of CBD exposure on early development. Our data suggests that CBD exposure causes neuro-development defects similar to those induced by with HU331 exposure. Our findings have shown that axon guidance is impacted by both Hu331 and CBD exposure. This study further explores the impact of CBD and Hu331 on axon guidance, neural differentiation and cell death.

BBB Poster 2 - Monitoring of Bacterial Pathogens in Mobile and Bon Secour Bays

Jahnavi Raval, Joong-Wook Park

Troy University, Troy, AL

In summer 2019, sediment samples were collected from five sites along the Mobile and Bon Secour Bays in the Gulf of Mexico. The characteristics of collected sediments (pH, temperature, salinity, conductivity, and TDS) were measured and PCR-based detection has been used to target fifteen genera of waterborne pathogenic bacteria in the samples. Currently, from about one third of the target pathogens tested, some pathogens have been detected in several samples. We expect our data to show the types and locations of pathogens in the Mobile and Bon Secour bay areas, which will help to predict the risk of waterborne pathogens under different salinity levels.

BBB Poster 3 - Determining the HD5 binding affinity to NCM colon cells

Elizabeth Fisher

Lipscomb University, Nashville, TN

Inflammatory Bowel Disease (IBD) causes chronic inflammation of the gastrointestinal tract. IBD is diagnosed early in life of males and females and is considered a lifelong disease. The prevalence of IBD has significantly increased and is now considered one of the most common gastrointestinal diseases. In the US, approximately 1.6 million people have IBD, with 70,000 more people diagnosed each year. IBD that is present in the colon has two disease subtypes, Ulcerative Colitis (UC) and Crohn's Colitis (CC). Our lab has previously published that Human alpha-Defensin 5 (HD5) was found to be overexpressed in the large bowel of CC patients but showed normal expressions in the colon of UC patients. HD5 is an innate immune peptide that is commonly found in the small intestine. This peptide is encoded by the DEFA5 gene and is produced by crypt Paneth cells that line the small intestine. HD5 is antimicrobial and non-specifically kills bacteria, viruses, and fungi by compromising the microbial membrane. In the small intestine, HD5 keeps the environment sterile by opsonizing and destroying foreign pathogens. We are interested in determining the effects of overexpression of HD5 in the pathogenesis of CC. Our lab found that when Normal-Derived Colon Mucosa (NCM) cells were exposed to HD5 (unpublished data), there was increased cell death and decreased wound healing in cell culture. Therefore, we hypothesized that HD5 has at least one binding partner on colonic epithelial cells. In order to test our hypothesis, we have performed binding assays of HD5 to NCM membrane and cytosolic protein fractions and we will perform co-immunoprecipitations followed by amino acid sequencing to determine what HD5 is binding to on NCM cells. This information will allow us to better understand HD5's role in the pathogenesis of CC and how it contributes to the severity of the disease phenotype.

BBB Poster 4 - Towards an Understanding of Phylogenetic Relationships in *Seymeria* (Orobanchaceae)

Caroline Shaw, Sharon Spiess

Abraham Baldwin Agricultural College, Tifton, GA

Seymeria is a relatively small genus of root hemiparasites in Orobanchaceae. Root hemiparasites retain the ability to photosynthesize while also establishing a xylem-to-xylem connection via the roots of host plants. The distribution area of *Seymeria* includes the eastern United States to Mexico. Pennell described 22 species and one subspecies in his 1922 revision of the genus and used this information to construct a rudimentary cladogram, primarily based on anther dehiscence. Turner confirmed 12 species, described three new species in 1982, and added another three new species 13 years later. His revision and new discoveries were focused on the species distributed throughout Mexico only. The most recent taxonomic work on the genus has been the addition of a new species in 2017. Phylogenetically, few *Seymeria* specimens have been included in studies focusing on the origins of parasitism and holoparasitism. This project seeks to use molecular techniques in addition to morphological characteristics to elucidate the evolutionary relationships within *Seymeria*.

BBB Poster 5 - Examining the Genotoxic Effects of BPA and its Derivatives in *Daphnia pulex*

Kasey McLamb

Catawba College, Salisbury, NC

Bisphenol A (BPA) is a synthetic compound used to manufacture food containers and plastic bottles. BPA has been found to seep into the food and drink contained in the packaging, creating the potential for adverse human health effects. Although BPA has been banned in the manufacturing of everyday plastics, its derivatives (BPAF and BPS) are now being used as replacements and also have the potential for negative health consequences in humans, including DNA damage. The accumulation of BPA and its derivatives have the potential to produce single and double strand DNA breaks, as well as cause DNA methylation. Thus, our research project investigated the DNA damaging effects of BPA and its derivatives on *Daphnia pulex*, a species of freshwater crustaceans. *D. pulex* are commonly used in toxicological studies due to their sensitivity to various toxins and high reproductive rate. In this research project, *D. pulex* were exposed to BPA, BPAF, and BPS at various concentrations and I tested multiple markers of DNA damage. Data from these experiments provide insight into the potential DNA damage that humans could encounter as a result of BPA (and derivatives) consumption.

BBB Poster 6 - Genetic Analysis of Biofilm Production Pathways in *Streptococcus mutans* Inhibited by Novel Lead Compounds.

Vy Nguyen, Gabriella Longway

Biology Department, Mercer University, Macon, GA

Bacterial virulence is associated with biofilm formation. Biofilms are extracellular matrices that protect bacteria from the host immune system. The formation of biofilm is a cellular response initiated by quorum sensing, the communication system utilized by bacteria. We are interested in understanding the genetic pathways that control biofilm production and have synthesized and tested several biofilm inhibiting drugs that can help us deduce these pathways. We have previously disrupted the process of biofilm formation with novel lead compounds that resemble autoinducers, the chemical signaling molecules used in quorum sensing, that potentially act as competitive inhibitors. Genetic screens on modified Congo Red plates were used to isolate strains that produce less biofilm than wild type *Streptococcus mutans*. The isolates' diminished biofilm formation are then confirmed with a crystal violet assay, and doubling-times are measured to ensure that a change in growth rate is not the source of a reduction in biofilm. We have isolated several mutants in *Streptococcus mutans* that display decreased biofilm formation and no longer respond to biofilm inhibiting compounds alanine 4-Chloro-3-nitrobenzoic acid and valine 2-Fluoro-5-nitrobenzoic. The mutated pathway is therefore the same pathway acted on by these previously successful compounds. Analyses of the genomic sequences from the isolates will allow us to identify the genes involved in these specific biofilm producing pathways.

BBB Poster 7 - Journey to the gut: Exploring the viability of probiotic microbial migrants following gastric exposure

Justin Leonard

Catawba College, Rockwell, NC

The intestinal microbiota is important for nutrient metabolism, maintaining the gut immune system, and preventing gut permeability. Recent reports have even linked imbalances in gut microbiota to defective neurodevelopment and declining neural function. Given the critical roles the gut microbiota plays in human health, the maintenance of these bacterial populations is critically important. In recent years, the usage of consumer-grade probiotic supplements has increased, yet the ability for these probiotic strains to effectively colonize the gut remains a matter of debate. Non-specific host defenses, including stomach acid and digestive enzymes, help protect against pathogens and may also impair the successful migration of probiotic strains to the gut. We aim to test the viability of probiotic strains in response to physiological conditions simulating the gastric compartment. Because most probiotic products are not regulated by the Federal Food and Drug Administration, we first confirmed the viable bacterial content of Activia probiotic yogurt through culturing and will identify bacterial species using 16S ribosomal RNA (rRNA) gene sequencing. Then, we will assess the *in vitro* viability of probiotic bacteria after exposure to experimental conditions mimicking those of the gastric compartment. We also plan to repeat 16S rRNA gene sequencing to survey the diversity of surviving strains. We predict that we will observe an overall decline in probiotic viability, as well as a reduction in diversity after simulated gastric exposure.

BBB Poster 8 - *Candida* spp. Detection by Innate Immune Cells is Promoted by β (1-3)-Glucan Unmasking

Parneeta Mohapatra, Sonny Patel, Arthi Shankar

Mercer University, Macon, GA

Growing resistance, toxicity, and side effects to current classes of antifungal agents have generated a strong need for further therapeutic developments. *Candida* spp. are the most common causes of human fungal infections, and they include painful, oral, and vaginal mucosal infections, as well as lethal, invasive bloodstream infections. A key factor for recognizing *Candida* species by innate immune cells (Dectin-1) is the detection of β (1-3)-glucan found in the inner cell wall. However, the fungus decreases the efficiency of immune detection by covering β (1-3)-glucan with a layer of mannosylated glycoproteins, which is referred to as masking. This study aims to find the gene(s) that enhance the exposure of β (1-3)-glucan, leading to increased recognition of *Candida* species by macrophages. We screened several cell wall mutants for unmasking by staining each cell with β (1-3)-glucan antibody and showing the increased chitin level by staining with calcofluor white. We also used atomic force microscopy to visualize the cell surface topography and estimate the elastic properties of the cell wall. Overall our data

demonstrated primary evidence suggesting that mutants *mn10Δ/Δ*, *orf19.5412Δ/Δ*, *mn9Δ/Δ*, *orf19.3869Δ/Δ* in *Candida albicans* and clinical strains 1099, 1100, and 1101 in *Candida auris* showed unmasking in the presence of sublethal caspofungin concentration, which promotes the detection by innate immune cells. These genes could serve as potential drug targets that can be used to address resistant strains and rapid clearance of the pathogen inside the host.

BBB Poster 9 - Evaluation of the influence of thermal variation on mating behavior of Madagascar Hissing Cockroaches (*Gromphadorhina portentosa*)

Rebecca Boesen, Sheala Brown

Thomas University, Thomasville, GA

Madagascar hissing cockroaches *Gromphadorhina portentosa* are best known for their large size and hissing demeanor. However, they are also unique in the fact that they are ovoviviparous, or contain their fertilized eggs until live birth occurs, approximately 60 days after fertilization. These mid-latitude, exothermic species prefer a temperature range of 80-90 degrees. The aim of this experiment is to alter the temperature range of the cockroach in order to evaluate the influence of thermal variance in mating behavior. This research question is of interest due to the increase of temperatures when heating homes in the winter months, and therefore the probable increase in cockroach offspring. In this experiment, the male and female cockroaches are separated into tanks based on three temperature setting 75, 85, and 95 degrees. Three females and one male will be evaluated individually for each temperature setting in order to ensure accuracy in our measurements. Mating behavior is evaluated through attachment of the genitalia and hissing.

BBB Poster 10 - Investigating the Effects of JUUL Pod Extracts on Human Oral Microbiota-Associated Species

Brooke Freeman, Sydney Goertzen

Catawba College, Salisbury, NC

Although JUUL technology was recently released to the public (September 2017), it has gained rapid popularity, often with young adults. Only two years later, several lung-related health issues and deaths have been tied to frequent JUUL use. The purpose of this study is to determine the effects of JUUL pod 'juice' on microbes associated with the human oral mucosa. The direct inhibitory effects of JUUL extract were evaluated using a zone of inhibition analysis on two common mucosal bacterial species, *Corynebacterium xerosis* and *Neisseria subflava*. Such bacterial species are of interest due to their proximity to the mucosal layer and their direct association with a healthy human-microbial environment. Disruption of colonization by these species plays a key role in the development of human-microbial imbalances such as inflammatory bowel disease (IBD). Further testing was conducted by taking a buccal swab sample from human subjects both who JUUL and do not JUUL. The bacteria samples were grown in a petri dish with nutrient agar over several days (48 to 72 hours) in a 37 °C incubator. Unfortunately, the COVID-19 pandemic caused this research project to end prematurely. We intend to begin collecting samples and analyzing results again in August 2020 to prioritize the safety of the participants and researchers involved. Based on the results from the preliminary studies, we expect to find those who have a high JUUL usage frequency will have detection of *Fusobacterium nucleatum* and *Porphyromonas gingivalis*, species that are often correlated with poor oral health.

BBB Poster 11 - The changing composition of a green ash (*Fraxinus pennsylvanica*) dominated piedmont swamp forest in North Carolina due to the arrival of the emerald ash borer (*Agrilus planipennis*)

Jay Bolin, Madison Kluge, Arilyn Lynch, Matthew Rodriguez

Catawba College, Salisbury, NC

The Emerald Ash Borer (EAB) is a relatively new invasive species to the central piedmont of North Carolina. Our goal is to measure the decline and patterns of change in a Green Ash dominated swamp forest in the Catawba College Fred Stanback Jr. Ecological Preserve (FSJEP). In fall 2019 we established six, 200 m² plots using a nested plot design to measure changes in canopy, sapling, and herbaceous vegetation. We resampled the plots in fall 2020. Our canopy data indicated a relatively low diversity in the tree canopy, trees importance values in descending order (of the top 6), green ash (*Fraxinus pennsylvanica*), sweet gum (*Liquidambar styraciflua*), red maple (*Acer rubrum*), black willow (*Salix nigra*), American elm (*Ulmus americana*), and the American Sycamore (*Platanus occidentalis*). The canopy was dominated by green ash, accounting for 68% of trees greater than 10 cm dbh. In fall 2019 and fall 2020, 20% and 54%, respectively, of green ash trees were visibly infected with signs of EAB infection ("D" shaped EAB exit holes in the bark, larval galleries under the bark, and/or copious adventitious bark sprouts). 12% of the green ash trees in fall of 2020 were dead. The importance value of green ash declined from 1.6 in 2019 to 1.5 in 2020.

BBB Poster 12 - The Effects of Climate Change on Phenology of Hemiparasite, *Seymeria cassioides* (Orobanchaceae)

Sharon Spiess, Caroline Shaw

Abraham Baldwin Agricultural College, Tifton, GA

Seymeria cassioides (Orobanchaceae) is a root hemiparasite that has a distribution range that covers the Southeastern US Coastal Plain. Hemiparasites are characterized by being photosynthetic and partially parasitic on the roots or shoots of a host plant. Flowering and fruiting times are determined by environmental factors, such as temperature and precipitation. These factors set the biological clock of the plant, and environmental changes could cause flowering and fruiting times to adapt in response. Studies have shown that alterations in temperature and

precipitation due to climate change is affecting phenology times of flowering plants causing them to experience a phenology shift. For spring flowering plants, this usually means an earlier flowering time. The National Centers for Environmental Information: National Oceanic and Atmospheric Administration shows a 1.67°C increase in the average temperature of the US Southern Plains and Gulf Coast from June through December 1895 to 2020. The goal of this project is to determine if *Seymeria cassioides*, a fall flowering hemiparasite, has experienced a phenological shift due to climate change. For this project, over 450 digital herbarium species were observed, databased, and assigned a number correlating to their phenophase. Phenophases were defined by pre-flowering or vegetative (0), <50% flower buds open (1), >50% flower buds open (2), <50% fruit present (3), >50% fruit present (4), 100% fruit present (5), and buds, flowers, fruit present (6). Preliminary analysis indicates that over the collection period, populations of *Seymeria cassioides* exhibit a phenological shift where flowering is taking place earlier and fruit development is taking place later. This shows that climate change has the potential to affect fall flowering hemiparasitic plants, such as *Seymeria cassioides*.

BBB Poster 13 - Eggshell organizing factor 1 protein in *Psorophora ferox* mosquitoes

Austin Snide

Catawba College, Salisbury, NC

Mosquitoes may serve as vectors for infective agents that cause human pathologies such as West Nile, Zika, and Malaria; and therefore controlling mosquito vector populations is an important step towards protecting human health. In a recent study by Isoe et al. (2019), researchers found that mutation of the Eggshell Organizing Factor 1 (EOF1) protein in *Aedes*, *Culex* and *Anopheles* mosquito genera resulted in 'defective' eggs that were discolored and failed to reach maturity to larvae. One genera that has not been evaluated for the EOF1 protein is *Psorophora*. The purpose of this study is to determine if the EOF1 protein is present in the species *Psorophora ferox*. This is an ideal species to study because they can be potential vectors for a variety of pathogens, they belong to the Aedini taxonomic group shared with the *Aedes* genera which possesses EOF1, and they are highly abundant in the late summer in our ecological preserve. Using published primer sequences, we tested primer combinations known to amplify EOF1 from *Anopheles*, *Aedes* and *Culex* genera on *Psorophora* extracts. A putative EOF1 gene was shown to be amplified using primer sequence EOF1-36304, and after further sequencing analysis the amplified gene was shown to be identical across each *Ps. ferox* (99.9 %) sampled thus far. Here we discuss our continued research into the putative *Ps. ferox* EOF1 gene by further sampling of local *Psorophora* species, identification of homologous genes in the published nucleotide database, and determination of open reading frames (ORF) of this putative gene as a way to connect this novel *Ps. ferox* gene to the published EOF1 gene.

BBB Poster 14 - Efficacy Testing of Sodium Chloride, Calcium Chloride, and Magnesium Chloride on *Streptococcus mutans* Biofilm Production

Gautham Mudireddy, Armith Eechampati

Mercer University Department of Biology, Macon, GA

Antibiotic resistance is a global issue resulting from the misdirection and over-use of antibiotic drugs. Potential mechanisms of curbing antibiotic-resistant and subsequent virulence are thus, beneficial to the medical community. An avenue in which bacteria confer virulence and avoid immunity is through an extracellular matrix called biofilm, which facilitates bacterial adherence to various structures, such as teeth. One bacterium, *Streptococcus mutans*, secretes biofilm, which increases its ability to cause dental caries. Biofilms result from cell-to-cell communication in which bacteria that reach a certain density initiate a signal transduction pathway that forms the extracellular matrix. This process is known as quorum sensing. The synthesis of novel lead compounds that mimic the molecules of the signal transduction pathway could disrupt the quorum sensing between bacterial cells and inhibit the formation of the biofilm matrix. Previously tested novel lead compounds have exhibited success in biofilm inhibition in *Streptococcus mutans*; however, the amount of bacterial growth in the overnight was insufficient. Several replicates of testing biofilm production with varying overnight culture incubation times with additional NaCl concentrations demonstrated a significant increase in biofilm growth for testing in the crystal violet assay. However, maximal biofilm growth presented as inconsistent at varying concentrations. Sporadic growth of *Streptococcus mutans* biofilm in NaCl points to efficacy testing of other salts as a potential avenue for consistent growth. As such, maximal biofilm growth resulting from CaCl₂ and MgCl₂ will be juxtaposed with NaCl at constant molarities. The patterns of biofilm growth for each salt will be shared. Production of a greater amount of biofilm should maximize our testing ability of novel lead compounds in the future.

BBB Poster 15 - Determining the storage method that best preserves acorn fat content of *Quercus palustris* and *Q. alba*

Cheyenne Villarosa¹, Sydney McTigue¹, Sabrina Volponi²

¹*Bridgewater College, Bridgewater, VA*, ²*Bridgewater College, Penn Laird, VA*

Quercus palustris and *Quercus alba* acorns are a primary component in many wild animal diets, particularly during preparation for winter. The high amounts of carbohydrates and fat found in acorns account for their elevated nutritional value, making them an ideal food for surviving the winter months. Although wildlife rehabilitators may want to feed their patients natural diets, collection and storage of acorns is space and time limited. Our research examined the best method of preparation and storage of acorns that limits mold growth and nutritional deterioration. After the acorns were collected from two sites in Bridgewater, VA, USA, we processed and stored them in the following combinations: air dried, oven dried, or not dried, and in air storage, the refrigerator or the freezer. After one month (both species) and six months (*Q. alba* only), we freeze dried subsamples from each tree for fat extraction. Preliminary results show wide variability between trees in white oaks. We expect a similar result for pin oaks. In all instances, refrigeration caused the most mold growth. Our findings will provide rehabilitators with practical recommendations for acorn storage allowing for more natural diets in rehabilitation.

BBB Poster 16 - STEM Obstacles in the Collegiate Setting

Morgan Smith

Thomas University, Thomasville, GA

The STEM field produces innovative individuals who drive economic growth and scientific development. STEM also has one of the largest job fields, providing competitive salaries and opportunities for advancement. Despite the potential of STEM careers, enrollment in STEM majors is low and attrition at the collegiate level is high. This warrants an analysis of the major selection process and identification of factors that affect STEM students in the academic setting. In this study, STEM and non-STEM majors will complete an online, anonymous survey about their education experience and the process of major selection. The survey will be emailed to all undergraduate students at Thomas University and participation is voluntary. Survey responses will be analyzed for significant trends within their respective groups to provide insight into these key areas. This data will allow educators to develop strategies to encourage STEM enrollment at the high school and college levels, and improve the STEM college education experience.

BBB Poster 17 - Evaluation of the headwaters of the Chattahoochee River watershed for human consumption and habitat suitability for *Percina crypta* and *Bothrioplana semperi*

Megan Phillips

Thomas University, Thomasville, GA

White County, GA lies in the Piedmont and Blue Ridge ecoregions of Northeastern, GA. This region is unique due to its formation of the headwaters of the Chattahoochee River, and the northernmost origin of the formation of the Chattahoochee River watershed as the river flows through the Chattahoochee National Forest. The region also serves to provide 70% of the drinking water for the Metropolitan Atlanta area. The region is home to the southernmost natural population of rainbow, brook, and brown trout in the state of Georgia, and is a critical habitat for the federally endangered *Percina crypta* (Halloween Darter), as well as many other federally listed residents. This study evaluates the correlation between low levels of dissolved oxygen, fecal coliform bacteria and *Bothrioplana semperi* (parasitic flatworm). It also assesses the quality of the watershed for drinking water and habitat suitability for *Percina crypta* and *Bothrioplana semperi*.

BBB Poster 18 - *Iva* (Asteraceae) genome size estimates with an emphasis on *Iva annua* a forgotten native American food plant

E. Malachi Gray, Zachary Gray

Catawba College, Salisbury, NC

The genus *Iva* contains 9 species of semi-woody shrubs and herbs. This genus is centered in North America and the West Indies. We collected and used DNA flow cytometry to generate C-values for three *Iva* species. The C-value is a measure of the amount of DNA in an organism's nuclear genome. We used the C-values to compare the genome sizes for each of the *Iva* species included in the study, which we hope to relate to ploidy level variation to explore speciation and evolution in the genus. Baseline C-value data in this genus is required to explore genome evolution in a lost domesticated crop, sumpweed (*Iva annua*). The seeds of *Iva annua*, sumpweed, have been posited as a pre-maize food crop of indigenous Americans in the mid-western and eastern regions of the USA. The genome variation if detected in extant populations of *Iva annua* may represent vestiges of phenotypes related to historical domestication.

BBB Poster 19 - Unearthing Novel Antibiotic Compounds from Soil-dwelling Bacteria

Jacob Hiatt

Catawba College, Salisbury, NC

In the microscopic world, bacteria have long been in fierce competition for resources. As a result, many bacterial species have evolved the ability to produce molecular "weapons" that negatively impact the physiological processes of their competitors. Some of these compounds have since been adapted for use as antimicrobial therapies and are commonly known as antibiotics. Unfortunately, pathogenic bacteria are continually evolving resistance to one or more of these therapeutics, resulting in increased incidences of antibiotic-resistant, or multi-drug resistant, infection. Alarming, the research and development of novel antimicrobial therapeutics has slowed to a snail's pace, due largely to the idea that antimicrobial development is not a lucrative financial opportunity. As the antibiotic resistance crisis continues to grow, it is imperative that new and effective antimicrobial metabolites are identified. One way of doing this is to isolate bacteria from the environment and screen them for their ability to exert an antimicrobial effect when co-cultured with other bacterial species. Many known antibiotic-producers are actually soil-dwelling bacteria; therefore, the collection and screening of bacterial isolates from soil samples is one major approach to antibiotic discovery. This project, which is part of a global, student-led research initiative known as Tiny Earth, will involve the collection and isolation of soil-dwelling bacteria from soil samples. These isolates will be screened for antibiotic production through co-cultures with laboratory-grade resistant bacterial strains known as ESKAPE-safe relatives. Identification of antibiotic-producing species will be followed by genetic analysis and metabolic testing for genus-level identification. Finally, antimicrobial metabolites will be extracted and used in follow-up experiments to confirm antimicrobial action.

BBB Poster 20 - Investigating the Prevalence of *Dirofilaria immitis* in Mosquito Vectors from Salisbury, Rowan County, North Carolina

Candace Swepson

Catawba College, Salisbury, NC

The prevalence of heartworm infection in canines, especially in the southeastern United States, has increased greatly in the past few years (Drake 2018). According to the Companion Animal Parasite Council (CAPC), in 2019, 1 out of every 46 dogs in Rowan County, North Carolina, tested positive for canine *Dirofilaria immitis*, more commonly known as heartworm. This devastating disease is due to the transmission of *Dirofilaria immitis* microfilariae via the bite of a mosquito vector. At Catawba College we have a healthy ecological preserve that is surrounded by not only the campus and but neighborhoods, and has many recreational uses for not only the Catawba community, but the surrounding residents. Importantly, our preserve contains 54% of the mosquito species diversity described in the state of North Carolina, all within a mere 68 Ha (Hartwig, 2018). Several of these established species are proposed vectors for *D. immitis* transmission. Therefore, we sought to identify the prevalence of *D. immitis* in known mosquito vectors within our ecological preserve and in surrounding localities of Salisbury, North Carolina. There have been no published studies like this proposed study to our knowledge in North Carolina since the 1980s. Here we discuss the results thus far of vector-status for mosquito populations from the Catawba College Ecological Preserve using a PCR-based detection method described previously (Ferreira et al., 2015), and the long-term implications for owner education and prevention therapies.

BBB Poster 21 - Soil sleuthing: Student-sourcing the antibiotics discovery pipeline

Jasmine Wiitala, Oryan Malul

Catawba College, Salisbury, NC

In the microscopic world, bacteria have long been waging war against each other. In their competition for resources, many bacteria have evolved the ability to use chemical weapons that target the physiological processes of competing bacteria. Today, we know these weapons as antibiotics and regularly use them to treat bacterial infections in humans. However, overuse of these drugs has created new strains of antibiotic-resistant “super-bugs”, some of which are impervious to many of the antibiotics that are currently approved for therapeutic use. As resistant strains continue to emerge, it is imperative that we develop effective alternatives. In the past, *Acinetobacter*, a group of bacteria commonly found in the soil, have been an excellent source of novel antibiotic compounds. However, it is estimated that less than 1% of Actinobacteria species have actually been identified, suggesting the possibility that new sources of antibiotics are living in the ground beneath our feet. Our project aims evaluate antibiotic production in bacteria isolated from locally-obtained soil samples. Antibiotic-producers will be established in pure culture for further identification by 16s rRNA gene sequencing, and metabolic testing. Antibiotic compounds will then be extracted for further confirmatory testing and results will be logged in an international database curated by Tiny Earth, a research program based at the University of Wisconsin-Madison.

ASB Special Events

Panels

Panel: Publish with ASB

Joerg-Henner Lotze
Director Eagle Hill Institute

Karl Miller
FWC Fish & Wildlife Research Institute
Moderator

Ted Zerucha
Appalachian State University

The Editor and Publisher of the peer-reviewed journals *Southeastern Naturalist* (SENA) and *eBio* hosted a panel session to provide an overview and answer questions about publishing in these official journals of the ASB.

The *Southeastern Naturalist* (Print ISSN #1528-7092 and Online ISSN # 1938-5412) is a peer-reviewed journal that publishes original articles focused on natural history research related to all aspects of the biology and ecology of terrestrial, freshwater, and marine organisms and the environments of the southeastern portion of North America.

eBio (ISSN 2165-6657) is a peer-reviewed journal that publishes original articles and notes focused on the biology of organisms as it relates to the structure, function, and development of their internal systems, and as it pertains to their use in medical and other applications not directly related to the ecology and conservation of species or their habitats. Subject areas include, but are not limited to, biochemistry, biotechnology, cell biology, genetics and genomics, immunology, microbiology, molecular biology, neurobiology, physiology, parasitology, and toxicology.

Panel: Diversity, Equity, and Inclusion

Veronica Segarra
Interim Chair and Assistant Professor of Biology, High Point University

Selwyn A. Williams
Associate Professor, Biological Sciences B.S. Program
Coordinator, Miami Dade College

Edward Moreira Bahnon
Assistant Professor at the Dept. of Surgery and the Center for Nanotechnology in Drug Delivery at UNC Chapel Hill.
Moderator

Loretta Ovueraye
Vice Provost for Workforce Programs & Professional Learning at Miami Dade College

The Diversity committee luncheon panelists spoke on their experiences as a minority in the biology and the natural sciences discipline and provide strategies for faculty to provide comfortable learning environment for students as well as sharing coping and success skills to students.

Panel: Spring Wildflower Pilgrimage

Joey Shaw, University of Tennessee at Chattanooga

The Spring Wildflower Pilgrimage began in 1951 and has been held annually in the Great Smoky Mountains National Park in April. It is a non-profit event that brings expert field biologists, conservationists, naturalists, and land managers together with the interested public to enjoy nature and educate on natural history, biology, ecology, conservation of natural resources, and land management. Although named the “Spring Wildflower Pilgrimage” from its inception, there have been many interdisciplinary programs. For example, during the second SWFP in 1952, there were 11 total programs and these included two birding and one photography program. The number of interdisciplinary programs has increased substantially to include: fungi, lichens, birds, mammals, insects, reptiles, nocturnal organisms, bones, parasites, ecology, fire ecology, biomes, woody plants, herbaceous plants, medicinal plants, mosses and liverworts, photography, herbarium museum tours, citizen science, astronomy, biological illustration, nature journaling, and more. Over the last 70 years, the GSMNP has endured ecological hardships from invasive insect outbreaks to fires and specialty programs have been variously integrated. In recent times, the Pilgrimage has had approximately 200 separate programs, or educational events, and brought nearly 1000 members of the public from 35 states and three to four countries into contact with ~120 experts in nature’s greatest classroom. Funds raised offset travel expenses of the leaders and support reduced or free admission for students and children. To maintain the continuity of the event, it was held virtually through iNaturalist in 2020 and once again fulfilled its mission – bringing the public into contact with experts in science and conservation. In 2018, ASB became a partner to the Pilgrimage and the outreach potential of this event greatly expanded. I will present the history and successes of this event, from notable people and places to setbacks and struggles, and ultimately present a vision for its long-term future.

Panel: Funding Your Research

Mona Behl
Director of NOAA's Sea Grant Program at the University of Georgia

Roland Roberts
Program Director of the National Ecological Observatory Network (NEON)

Linda Musumeci
Director of Grants and Fellowships at the American Philosophical Society

Join representatives from the National Science Foundation, Georgia Sea Grant and American Philosophical Society as they discuss funding opportunities and best practices in grant proposal preparation.

Workshops

WORKSHOP: How to use digital escape rooms to supplement online lab practicals and help promote student active learning

Joni Criswell, Anderson University, Anderson, SC

Have you been frustrated by the digital resources available for online lab learning especially for labs covering anatomy based topics? Do you find that there is either too much/too little information in these digital resources or student frustration when trying to use these resources? This workshop will focus on how to use free software to create custom digital escape rooms to help supplement online lab practicals and/or promote student active learning via online meetings (i.e. Zoom). This session will also include how to incorporate the digital escape rooms into either Google forms and/or an course platform (i.e. Canvas).

WORKSHOP: Virtual Research: Using public data portals for undergraduate research

Lyndsay V. Rhodes, Florida Gulf Coast University, Fort Myers, FL

The current pandemic environment has made bench research more difficult, particularly in the undergraduate setting. However, there are a wide variety of published data sets that hold a wealth of information and can be used to answer many more questions - if you know where to find it and how to use it. Using this data doesn't have to require a degree in bioinformatics! This workshop will explore the types of information that are available, where to find useful data sets, and how to use that information to answer scientific questions. Further, participants will learn how to develop questions that could form the basis of future student projects. We will be using cancer data as an example to walk through the process.

Field Trips

FIELD TRIP: Georgia: In the Hands of Private Landowners

Miranda Gulsby, Quail Forever, Albany, GA

Approximately 93% of the land in Georgia is owned by private landowners. Private lands across the US also provide habitats for nearly 2/3 of all federally listed wildlife species and an unknown number of habitats for state protected species. With those numbers in mind, when we talk about conservation of wildlife and their habitats, we cannot forget how valuable private landowners are in the equation. The Working Lands for Wildlife, supported through NRCS and countless partner organizations, aims to provide these landowners the technical and financial assistance they need to restore and improve wildlife habitats on their land. This program is voluntary for landowners so we work to discover what they value most about their land and build relationships in the hope that leads to conservation minded landowners. As biologists, we must remember that "perfect is the enemy of good". This virtual field will be hosted by Miranda Gulsby, Wildlife Biologist with Quail Forever based in Carrollton, GA. On this virtual field trip, we will discuss how the Working Lands for Wildlife program operates in the real world and we will be visiting a few of these properties involved in this program in Georgia. For those out there interested in wildlife biology as a career, we will also discuss some of the skills and experiences that have led myself and others to private lands conservation.

FIELD TRIP: Longleaf Pine Savannah, Lake Thoreau Environmental Center, Hattiesburg, Mississippi.

Mac Alford, The University of Southern Mississippi, Hattiesburg, MS

Approximately 93% of the land in Georgia is owned by private landowners. Private lands across the US also provide habitats for nearly 2/3 of all federally listed wildlife species and an unknown number of habitats for state protected species. With those numbers in mind, when we talk about conservation of wildlife and their habitats, we cannot forget how valuable private landowners are in the equation. The Working Lands for Wildlife, supported through NRCS and countless partner organizations, aims to provide these landowners the technical and financial assistance they need to restore and improve wildlife habitats on their land. This program is voluntary for landowners so we work to discover what they value most about their land and build relationships in the hope that leads to conservation minded landowners. As biologists, we must remember that "perfect is the enemy of good". This virtual field will be hosted by Miranda Gulsby, Wildlife Biologist with Quail Forever based in Carrollton, GA. On this virtual field trip, we will discuss how the Working Lands for Wildlife program operates in the real world and we will be visiting a

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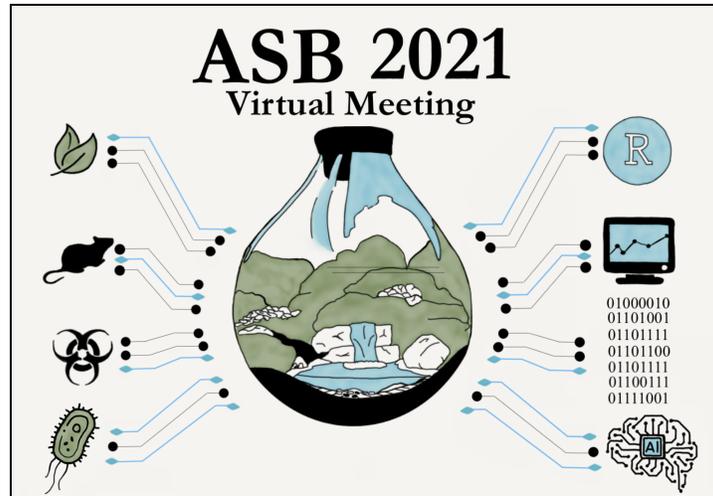
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THE 82ND ANNUAL MEETING OF THE ASSOCIATION OF SOUTHEASTERN BIOLOGISTS

VIRTUAL

24-26 MARCH 2021



T-shirt designed by Sara Schoen entitled
"Exploring biology through screens and machines"

ASB Affiliate Organizations



SE SECTION



SE CHAPTER



SE CHAPTER



TRIBETA DISTRICTS I & II

Association of Southeastern Biologists 2021

Meeting-At-A-Glance

Wednesday March 24 –

Friday March 26 2021

Virtual

All events listed as EST

Monday, March 22

| Time | Event | Location |
|------|--|--------------|
| Open | Meeting website and presentation videos open | Meeting page |

Wednesday, March 24

| Time | Event | Location |
|-------------------|---|----------------|
| 1:00 PM - 4:00 PM | ASB Executive Committee Meeting | ASB Zoom Link |
| 1:00 PM - 4:00 PM | SABS Executive Council Meeting | SABS Zoom Link |
| 4:00PM – 6:00 PM | Welcome and lenary: Including Diversity in STEM Panel Speakers: Kelly M. Mack, Ph.D Edward Moreira Bahnson, Ph.D Verónica A. Segarra, Ph.D Selwyn A. Williams, Ph.D | Live event |

Thursday, March 25

| Time | Event | Location |
|-------------------|---|-----------------------------------|
| 7:00 AM - 4:00 PM | Help and Collaboration Room Feel free to use this space to ask for help or to meet up with a colleague and network. | Live event |
| 7:00 AM – 5:30 PM | ASB Poster Sessions | ePosters with accompanying videos |
| 8:00 AM – 9:00 AM | ASB Paper Presentations Animals: Entomology Animals: Herpetology Community Ecology Microbiology | Prerecorded video presentations |

| | | |
|---------------------|---|---|
| 8:00 AM – 10:00 AM | Plant Anatomy and Physiology Symposium 1- Integrating Virtual Mentoring and Professional Development Experiences with Field-Based Summer Undergraduate Research | Live event |
| 9:00 AM – 10:00 AM | Q&A for oral presentation sessions Animals: Entomology Animals: Herpetology Community Ecology Microbiology Plant Anatomy and Physiology | Live event |
| 10:00 AM – 11:00 AM | ASB Paper Presentations Animals: Entomology Animals: Herpetology Community Ecology Microbiology Plant Diversity and Evolution | Prerecorded video presentations |
| 10:00 AM – 11:00 AM | Publish with ASB Panel (Southeastern Naturalist session) | Live event |
| 11:00 AM – 12:00 PM | Q&A for oral presentation sessions Animals: Entomology Animals: Herpetology Community Ecology Microbiology Plant Diversity and Evolution | Live event |
| 12:00 PM – 1:00 PM | Lunch Diversity, Equity, and Inclusion Panel hosted by ASB Human Diversity, ESA and Education Committee SHC SE Chapter Luncheon/Business Meeting | Live event Live event |
| 1:00 PM - 2:00 PM | ASB Diversity Committee Business Meeting | Live event |
| 1:00 PM - 2:00 PM | ASB Education Committee Business Meeting | Live event |
| 2:00 PM – 3:00 PM | ASB Paper Presentations Animal Ecology Conservation Ecosystem Ecology Microbiology Plant Diversity and Evolution Workshop 1 - How to Use Digital Escape Rooms to Supplement Online Lab Practicals and Help Promote Student Active Learning | Prerecorded video presentations Live event |
| 3:00 PM – 4:00 PM | Q&A for oral presentation sessions Animal Ecology Conservation Ecosystem Ecology Microbiology Plant Diversity and Evolution | Live event |

| | | |
|-------------------|--|--------------------------------------|
| 4:00 PM – 5:00 PM | ASB Business Meeting (all members welcome) | Live event |
| 4:45 PM – 5:30 PM | SABS/BSA Student Reception | Live event |
| 5:30 PM - 6:30 PM | Thursday Night ASB Social Walsh Trivia | Live event - Trivia Hosted Zoom Link |

Friday, March 26

| Time | Event | Location |
|-------------------|--|-----------------------------------|
| 7:00 AM - 4:00 PM | Help and Collaboration Room Feel free to use this space to ask for help or to meet up with a colleague and network. | Live event |
| 7:00 AM – 4:00 PM | ASB Poster Sessions | ePosters with accompanying videos |
| 8:00 AM – 9:00 AM | SABS/BSA Business Meeting | Live event |
| 8:00 AM – 6:00 PM | β β β Officers & Judges Room | β β β Zoom Link |
| 8:00 AM – 8:30 AM | β β β Welcome and Business Meeting (all delegates MUST attend) | Live event |

| | | |
|--------------------|--|---------------------------------|
| 8:00 AM – 9:00 AM | ASB Paper Presentations Animal Ecology Conservation Ecosystem Ecology Cell and Molecular Biology Plant Diversity and Evolution | Prerecorded video presentations |
| 8:00 AM – 9:00 AM | | |
| 9:00 AM – 2:30 PM | Workshop 2 - Using Public Data for Undergraduate Research | Live event |
| | Symposium 2 - A CURE for your Curriculum: Implementing Course-embedded Undergraduate Research (CUREs) into your Curriculum | Live event |
| 8:30 AM – 9:00 AM | β β β Paper Presentations - District II | Prerecorded video presentations |
| 9:00 AM - 10:00 AM | β β β Q&A for oral presentation sessions - District II | Live event |
| 9:00 AM – 10:00 AM | Q&A for oral presentation sessions Animal Ecology Conservation Ecosystem Ecology Cell and Molecular Biology Plant Diversity and Evolution | Live event |

| | | |
|---------------------|---|--|
| 10:00 AM – 11:00 AM | ASB Paper Presentations Animal Ecology Conservation Aquatic Ecology Cell and Molecular Biology Plant Floristics and Systematics Publish with ASB Panel (eBIO session) Spring Wildflower Pilgrimage Panel | Prerecorded video presentations Live event Live event |
| 8:30 AM – 9:00 AM | β β β Paper Presentations - District II | Prerecorded video presentations |
| 9:00 AM - 10:00 AM | β β β Q&A for oral presentation sessions - District II | Live event |
| 11:00 AM – 12:00 PM | Q&A for oral presentation sessions Animal Ecology Conservation Aquatic Ecology Cell and Molecular Biology Plant Floristics and Systematics | Live event |
| 12:00 PM - 1:00 PM | Past Presidents Meeting | ASB Zoom Link |
| 12:00 PM - 1:00 PM | ESA Business Meeting | Live event |
| 2:00 PM – 3:00 PM | Funding Your Research | Live event |
| 2:00 PM – 3:00 PM | ASB Paper Presentations Population Ecology Conservation Aquatic Ecology Scholarship of Teaching and Learning | Prerecorded video presentations |
| 2:00 PM - 3:00 PM | β β β Paper Presentations - District I | Prerecorded video presentations |
| 3:00 PM - 3:30 PM | β β β Q&A for oral presentation sessions - District I | Live event |
| 3:00 PM – 4:00 PM | Q&A for oral presentation sessions Population Ecology Conservation Aquatic Ecology Scholarship of Teaching and Learning | Live event |
| 3:30 PM – 4:00 PM | β β β District I & II meeting | Live event |
| 4:00 PM – 5:00 PM | ASB Awards Ceremony | Live event |
| 5:00 PM - 6:00 PM | β β β Awards | Live event |

On Demand Field Trips

| | | |
|-------------|--|--------------------------------|
| Field Trips | <p>Field Trip: Longleaf Pine Savannah, Lake Thoreau Environmental Center, Hattiesburg, Mississippi</p> <p>Contact mac.alford@usm.edu for general information about the station.</p> <p>The Lake Thoreau Environmental Center consists of two adjacent compartments, one given to the University of Southern Mississippi over 100 years ago by a railroad company following timber harvest of the virgin longleaf pine and the other given to the University by a retired professor who valued nature. The two parts were joined together, the biology faculty were tasked to manage the property, and a building was constructed for education and to house the herbarium and ichthyological collection. Our tour will cover the second-growth longleaf pine savannah, which has been restored with regular fire and for which a flora was recently published.</p> | Prerecorded video presentation |
| | <p>Field Trip: Quail Forever</p> <p>Quail Forever is dedicated to the conservation of quail, pheasants and other wildlife through habitat improvements, public awareness, education, and land management policies and programs.</p> <p>Miranda Gulsby</p> | Prerecorded video presentation |

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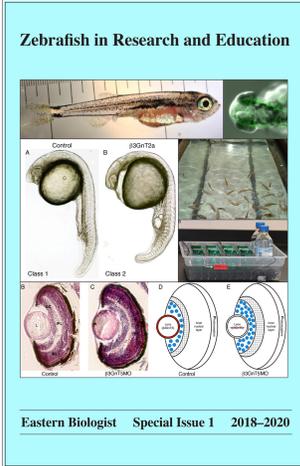


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