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THE 83RD ANNUAL MEETING OF THE ASSOCIATION OF SOUTHEASTERN BIOLOGISTS

LITTLE ROCK

30 MARCH-2 APRIL 2022

T-shirt designed by Elisa Howansky
Lander University, Greenwood, SC

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The 2021-2022 Executive Committee.
Pictured from Left to Right: Chris Havran, Matt Heard, Kim Hays, Lyndsay Rhodes, Holly Boettger-Tong, Chris Brown, Chris Gissendanner, Charlie Horn, Heather Joesting, Hussein Mohamed, and Davy Giles. Not pictured: Veronica Segarra

FEATURED INSTITUTIONS

UNIVERSITY OF CENTRAL ARKANSAS™

UA LITTLE ROCK

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Lyndsay Rhodes, Florida Gulf Coast University, Fort Meyers, FL, lhrhodes@fgcu.edu
2025: Jennifer Mandel
NIcole Vanderhoff

Outgoing Executive Officers at the 2022 Little Rock Meeting

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

2023	Winston-Salem, NC (23-26 March*)	*Starts on Thursday
2024	Chattanooga	

The View from Here: A Message from the President

View From here 2022

2021-2022 was another remarkable year for ASB. After two meetings disrupted by the COVID-19 global pandemic, we were finally able to meet in person. Like most meetings, our meeting in Little Rock faced its obstacles. Meeting in Arkansas expanded our range further west than we have ever met before and for some of our regular attendees, this was quite a long trip, but we had a nice showing of members from Arkansas, West Tennessee, and Louisiana. We were still battling the lingering effects of the pandemic which dampened enthusiasm *and* funds for travel for many of us. Despite the reduced funds and further distance for some, we had a wonderful meeting with great presentations, great fun, and great friends!

We welcomed 544 registered attendees who gave nearly 400 presentations. We had a record number of field trips organized in part by the good folks at the Arkansas Natural Heritage Commission and the Southeastern Grassland Initiative. We had invigorating symposia and workshops, and a very active Exhibit Hall. Special thanks also to PULSE for their continued contributions to ASB's meeting and for hosting a symposium and workshop. We had a wonderfully entertaining and masterfully informative plenary speech by Dr. Marla Spivak from the University of Minnesota, who gave us practical tips to help save the bees. I know a few members have looked on their yards with new eyes and considered how to increase the flowers. And, although our Social was moved inside due to a chilly wind, we were happy to be together (and the students especially seemed to enjoy the dance floor).

During the year, members of the Executive Committee worked hard to update the Constitution and Bylaws. It had been some time since these important documents were officially edited, though more than a few needed changes had been accumulating. Following the latest versions of Robert's Rules of Order, we reworked the two documents into one that would be more direct and more practically fit with how the association has been run for several years. This more efficient 'Revision' document was approved by the membership in an online vote in February. We are now working on increasing the efficacy of our Leadership Guide, which lays out expectations of the executive officers and committees, as well as providing standards for all aspects of the association.

Dr. Chinyere Knight and Dr. Ted Zerucha continued to lead great movements within the Committee on Human Diversity (CHD) and the Publications Committee, respectfully. Members of the CHD looked closely at ASB's efforts to support diversity among biological scientists within and outside of our membership. As part of these efforts, three peer-reviewed articles were published with ASB representatives as authors.* Members also represented ASB at workshops aiming to help us improve diversity at our meetings and beyond. The Publications Committee has been working closely with Eagle Hill to support the editors and authors of our official journals *Southeastern Naturalist* and *eBio* as well as bring more benefits to our members. I know both committees have great plans for future projects and I cannot wait to share these with the membership as they develop.

I want to express my utmost gratitude to the members of the Executive Committee who work countless hours to make sure ASB carries out its mission to promote the biological sciences through the friendliest scientific meeting in the world. We look forward to bringing the meeting back to the middle of the Southeast next year and rest assured, the Executive Committee is already hard at work planning and preparing to put on the best meeting ever!

See you all in Winston-Salem!!!

Chris Brown

ASB President

*Peer reviewed articles representing ASB members and actions.

- Primus, C., A.N. Zimmerman, A.K. Terovolas, K.F. Block, C.G. Brown, M.D. Burton, A. Edwards, C.M. Etson, S.C. Flores, C. Fry, A.N. Guillory, S.L. Ingram, R. McGee, D.L. Neely-Fisher, S. Paxson, L. Phelan, K. Suggs, L.R. Vega, E. Vuong, J.L. Lujan, M. Ramirez-Alvarado and V.A. Segarra. 2022. Scientific societies fostering inclusivity in the life sciences through engagement of undergraduate scientists. *Frontiers* in Education. 7: Article 757816

- Hays, K.A., J.C. Havran, M.J. Heard, A.B. Morris, and L. Ovueraye. 2021. From Then to Now: Diversity, Equity, and Inclusion in the Association of Southeastern Biologists. *Frontiers in Sociology* 6: 755072.

- Segarra, V.A., C. Primus, G.A. Unquez, A. Edwards, C. Etson, S.C. Flores, C. Fry, A.N. Guillory, S.L. Ingram, M. Lawson, R. McGee, S. Paxson, L. Phelan, K. Suggs, L.R. Vega, E. Vuong, J.C. Havran, A. Leon, M.D. Burton, J.L. Lujan, and M. Ramirez-Alvarado. 2020. Scientific societies fostering inclusivity through speaker diversity in annual meeting programming: a call to action. *Molecular Biology of the Cell* 31: 2495-2501.

ASB 2022 R.H. Martin Plenary Session

Dr. Marla Spivak

Dr. Marla Spivak is a MacArthur Fellow and Distinguished McKnight Professor in Entomology at the University of Minnesota. Her research efforts focus on protecting and enhancing the health of honey bees, and on propagating floral rich landscapes to support all pollinators.

Spivak is interested in social insects in general, and honey bees specifically: social immunity, behaviors, breeding, and beekeeping on large and small scales. Her position is a 3-way split among research, teaching and extension, which allows breadth and freedom to explore basic mechanisms and/or real-world applications in our studies and educational endeavors.

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 and Sponsors

Martin Microscope.com

PULSE

Southeast Regional Network

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

2022 Affiliate Organizations

NABT
National Association of Biology Teachers

Southern Appalachian Botanical Society
Publishing Castanea since 1936

Botanical Society Of America
Southeast section

Society of Herbarium Curators
Southeast chapter

ECOLOGICAL SOCIETY OF AMERICA
esa
Southeast chapter

Districts I and II

2022 Exhibitors

Arkansas Native Plant Society
ANPS

Western Carolina University

CMS
Capital Microscope Services

University of Louisiana Monroe
ULM
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University of Central Arkansas™

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Winthrop University

UA Little Rock

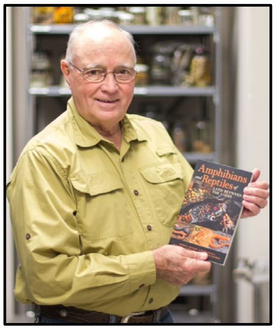
East Carolina University

JSU Biology

Florida Gulf Coast University

Southern Appalachian Botanical Society
Publishing Castanea since 1936

A Tribute to Dr. Floyd Scott
(1944-2021)



Dr. Arthur Floyd Scott, age 77 passed away Sunday, April 25, 2021 from a sudden illness. Floyd and his twin brother Lloyd were born on January 10, 1944 in Dickson County, TN. Floyd earned his B.S. and M.Ed. degrees from Austin Peay State University in Clarksville, TN and his PhD in Zoology from Auburn University. His PhD research was on the Ecology of the musk turtle (Sternotherus minor). Before coming back to Austin Peay as an Assistant Professor in 1978, he held positions at University of South Alabama and Union College.

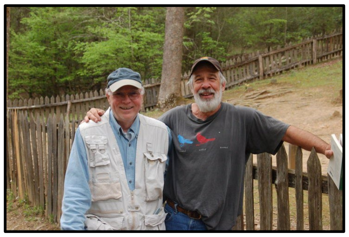
Dr. Scott became a member of the Association of Southeastern Biologists in 1968, and for over 50 years he brought students to the meetings and also served as a Member-at-Large, and Vice President of the society. In fact he also met one of his best friends, Dr. Eugene Wofford at that first ASB meeting he attended. Floyd loved to dance and was always out on the dance floor at the Thursday night social. He was also a longtime leader for the Spring Wildflower Pilgrimage in the Great Smoky Mountains National Park. His Salamander walks along with John Byrd were always a favorite among pilgrims and other leaders alike.

Dr. Scott's wife, Malinda, asked if I could arrange something in Floyd's honor at ASB. I was able to obtain funds from several donors and implement two student awards in Herpetology at ASB. The Dr. Floyd Scott student oral presentation award and poster award in Herpetology. This year at the annual ASB meeting in Little Rock, both awards were presented: Nelle Jenkins of the University of Louisiana at Monroe was awarded $300 for her oral presentation on "Investigation of a shell-rot disease affecting freshwater turtles in a northeast Louisiana bayou," and Ryan Davenport of Georgia Gwinnett College was awarded $300 for his poster entitled "Froggy goes to school: Hylid frogs on a suburban college." Hopefully both of these awards will be given in Floyd's honor for many years to come.

One of Floyd's friends and co-author of several publications, Dr. Bill Redmond, wrote the following tribute to Floyd that is better than anything I could contribute.

Dr. A. Floyd Scott's Legacy
By William H. Redmond Jr (September 3, 2021)

For future generations of biologists and nature enthusiasts, especially in Tennessee, Dr. Scott's legacy includes many achievements. In addition to the many students guided and influenced, perhaps his most enduring legacy was the development and implementation of two Austin Peay State University (APSU) websites, Atlas of Amphibians in Tennessee and Atlas of Reptiles of Tennessee. Currently, APSU Biology Department's website lists Dr. Scott as coauthor and website manager of these two atlases. Dr. Scott was much more than manager of these two websites. The title "website-master" seems more appropriate.



Soon after the 1996 Atlas of Amphibians in Tennessee was printed, Dr. Scott proposed that it be developed into a website resource. His goals were to make a widely available web tool that would be easy to use, stimulate interest in the distribution of amphibian species in Tennessee, and promote amphibian conservation. This website went online in 1999. In 1998, he initiated and led efforts to develop a complimentary website for reptiles that was launched online in 2008. In total, these two websites have been operating and achieving Dr. Scott's original goals for over 20 years. Both have proven to be valuable reference and learning tools for biologists and the general public. Both have stimulated significant advances in understanding distributions of amphibian and reptilian species in Tennessee.

Dr. Scott was the primary force behind implementation and subsequent long-term success of both websites. At his insistence, both websites were refreshed quarterly to add new data, make needed taxonomic changes, and correct errors. He was the scientific gatekeeper and spent an enormous amount of time learning the software intricacies of website management. He was truly website-master of both sites. At the time of his death, he was in the initial stages of developing a strategy to transfer these responsibilities. Hopefully, this legacy will continue and be improved as new technology becomes available.

If you would like to contribute to the Dr. Floyd Scott Herpetology Award, please send your donation to the ASB treasurer.

By
Patricia B. Cox PhD
ASB Past-President
10 April 2022

ASB PRESTIGIOUS AWARDS PRESENTED AT THE 2022 ASB MEETING IN LITTLE ROCK, AR

CAREER AWARDS

ASB JOHN HERR LIFETIME ACHIEVEMENT AWARD **None awarded**

ASB MERITORIOUS TEACHING AWARD **Dr. Riccardo Fiorillo**
Professor of Biology
Georgia Gwinnett College

ASB LUCRECIA HERR OUTSTANDING BIOLOGY TEACHER AWARD The Lucrecia 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.

No recipient this year

ASB SUPPORT AWARDS

THE LAFAYETTE FREDERICK UNDERREPRESENTED MINORITIES SCHOLARSHIP **Candace Swepson,** Catawba College

SUPPORT AWARDS FOR FIRST-GENERATION UNDERGRADUATE STUDENT MEMBERS OF ASB
Ellen Goza, Georgia Southern University
Arilyn Lynch, Catawba College
Kasey Moore, Northwestern State University of Louisiana
Everette Rhymer, Catawba College
Heather Sempsrott, Georgia Southern University

SUPPORT AWARD FOR GRADUATE STUDENT MEMBERS OF ASB
Henson Leigha, Appalachian State University
Hope Hebert, University of Louisiana Monroe
Claire Martin, Appalachian State University
Sushil Dahal, Mississippi State University
Nicholas Engle-Wry, Mississippi State University

Ashley Hull, Appalachian State University
Nelle Jenkins, University of Louisiana Monroe
Alexander Gregory, Georgia Southern University
Thomas Hennessey, Western Carolina University
Shannon Gillen, James Madison University
Justin Hinson, Georgia Southern University
Avery Young, University of Tennessee Chattanooga
Garrett Billings, University of Tennessee Chattanooga
Brandon Wheeler, Western Carolina University

ASB RESEARCH AWARDS

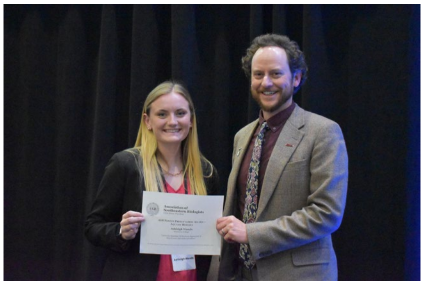
ASB STUDENT RESEARCH AWARD – **Erika R. Moore**, University of Memphis
"Reevaluating genetic diversity and structure of *Helianthus verticillatus* (Asteraceae) after the discovery of new populations"

ASB RESEARCH AWARD None Awarded

ASB PRESENTATION AWARDS

ASB STUDENT POSTER PRESENTATION AWARD – ANIMAL BIOLOGY **Paige Brewer**, Arkansas State University
"Diversity and abundance of ectoparasites on birds in Northeastern Arkansas"

ASB STUDENT POSTER PRESENTATION AWARD – AQUATIC BIOLOGY **Ashleigh Woods**, Wesleyan College
"Lavender Essential Oil Reduces Aggression in Male Crown-tail *Betta splendens*"



ASB STUDENT POSTER PRESENTATION AWARD – CELL AND MOLECULAR BIOLOGY

Nazneen Begum, University of Arkansas at Little Rock
"Up-regulation of *Osh6* targets an anti-aging membrane trafficking pathway"

ASB STUDENT POSTER PRESENTATION AWARD – MICROBIOLOGY

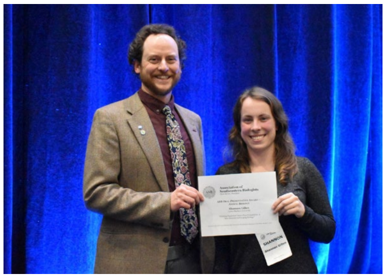
Hannah Walsh, Campbell University
"Characterization of Entomopathogenic Fungi Metabolites Isolated from North Carolina Soil"

ASB DR. FLOYD SCOTT AWARD FOR THE BEST POSTER PRESENTATION AWARD IN HERPETOLOGY

Ryan Davenport, Georgia Gwinnett College
"Froggy Goes To School: Hylid Frogs on a Suburban Campus"

ASB STUDENT ORAL PRESENTATION AWARD – ANIMAL BIOLOGY

Shannon Gillen, James Madison University
"Pilfering Passerines? Inter-Class Competition: A New Direction in Foraging Ecology"



ASB STUDENT ORAL PRESENTATION AWARD – AQUATIC BIOLOGY

Jessica Lenz, University of North Alabama
"Antipredator Behavior of *Elimia paupercula*, Sooty elimia, in response to *Faxonius yanahlindus*, the Spinywrist crayfish"

ASB STUDENT ORAL PRESENTATION AWARD – CELL AND MOLECULAR BIOLOGY

Jonathan Jansma, High Point University
"Fenbendazole exerts antiproliferative effects on cervical cancer cells by inhibiting mTOR signaling pathway"

ASB STUDENT ORAL PRESENTATION AWARD – MICROBIOLOGY

Amber Richards, University of Georgia
"Epidemiological analysis of two *Salmonella serovar* Kentucky lineages in food animal production and human illness"

ASB DR. FLOYD SCOTT AWARD FOR THE BEST ORAL PRESENTATION AWARD IN HERPETOLOGY

Nelle Jenkins, University of Louisiana Monroe
"Investigation of a shell-rot disease affecting freshwater turtles in a northeast Louisiana bayou"

AFFILIATE AWARDS PRESENTED AT THE 2021 VIRTUAL MEETING

NORTH CAROLINA BOTANICAL GARDEN AWARD

Ben Brewer, Appalachian State University
"Assessing the Health of Gray's Lily *(Lilium grayi*) with Demographic Monitoring"

SOUTHEAST CHAPTER OF THE ECOLOGICAL SOCIETY OF AMERICA – TRAVEL AWARDS

Cassie Bacon, Marshall University
Paurava Thakore, University of Louisiana Monroe
Bibek Kandel, University of Louisiana Monroe

SOUTHEAST CHAPTER OF THE ECOLOGICAL SOCIETY OF AMERICA – EUGENE P. ODUM

Paurava Thakore, University of Louisiana at Monroe
"Loss of relict oak forests along coastal Louisiana: A multiyear analyses using Google Earth Engine"

SOUTHEAST CHAPTER OF THE ECOLOGICAL SOCIETY OF AMERICA – ELSIE QUARTERMAN-CATHERINE KEEVER AWARD

Mattie Harris, Georgia Southern University
“Sex and Starvation Influences Latrotoxin Expression in the Brown Widow Spider"

SOUTHERN APPALACHIAN BOTANICAL SOCIETY – CONFERENCE SUPPORT AWARD

Alana Hicks, University of Tennessee at Chattanooga
Ashley Hull, Appalachian State University
Brandon Wheeler, Western Carolina University

Claire Martin, Appalachian State University
Connor Purvis, Francis Marion University
Erika R. Moore, University of Memphis
Leigha Henson, Appalachian State University
Thomas Hennessey, Western Carolina University

SOUTHERN APPALACHIAN BOTANICAL SOCIETY – RICHARD AND MINNIE WINDLER AWARD IN ECOLOGY

Erika Moore (and Jennifer Mandel), University of Memphis
Moore et al. 86(2)196-213: Reevaluating genetic diversity and structure of *Helianthus verticillatus* (Asteraceae) after the discovery of new populations.

SOUTHERN APPALACHIAN BOTANICAL SOCIETY – RICHARD AND MINNIE WINDLER AWARD IN SYSTEMATICS

Nicole M. Fama, Brandon T. Sinn and Craig F. Barrett, West Virginia University
Fama N.M. B. T Sinn and C. F. Barrett . 86(1): 1-21. Integrating genetics, morphology, and host specificity in conservation studies of a vulnerable, selfing, mycoheterotrophic orchid.

SOUTHERN APPALACHIAN BOTANICAL SOCIETY – EARL CORE STUDENT RESEARCH AWARD

Leigha Henson, Appalachian State University
“Warming and precipitation effects on several common moss species of the southern Appalachian mountains.”

Tara Hall, Western Carolina University
“A study of morphological, cytological, and molecular variation in the eastern North American flowering plant, *Micranthes virginiensis* (Saxifragaceae)”

Merry Conlin, North Carolina State University
“The inconspicuous *Ludwigia*: quantitative habitat characterization of critically imperiled *Ludwigia ravenii* (Onagraceae)”

SOUTHERN APPALACHIAN BOTANICAL SOCIETY – OUTSTANDING STUDENT ORAL PRESENTATION AWARD

Rachel Jessup, North Carolina State University
"Status and habitat surveys for the critically imperiled Tall Barbara’s Buttons (*Marshallia legrandii*)"

Erika R. Moore, University of Memphis
“Reevaluating genetic diversity and structure of *Helianthus verticillatus* (Asteraceae) after the

discovery of new populations"

SOUTHERN APPALACHIAN BOTANICAL SOCIETY – OUTSTANDING STUDENT POSTER PRESENTATION AWARD

Skyler Fox, Furman University
"What is a population? Assessing genetic structure of federally endangered *Dalea foliosa* in Middle Tennessee"

SOUTHERN APPALACHIAN BOTANICAL SOCIETY – ELIZABETH ANN BARTHOLOMEW AWARD

Ronald Lance, Chimney Rock Park in North Carolina

SOUTHEASTERN SECTION OF THE BOTANICAL SOCIETY OF AMERICA – OUTSTANDING STUDENT PAPER AWARD IN PLANT SCIENCE

Rachel Jessup, North Carolina State University
"Status and habitat surveys for the critically imperiled Tall Barbara's Buttons (*Marshallia legrandii*)"

SOUTHEASTERN SECTION OF THE BOTANICAL SOCIETY OF AMERICA – OUTSTANDING STUDENT POSTER AWARD IN PLANT SCIENCE

Ryan Long, Jacksonville State University
"Revealing cryptic species in the Japanese Nezasa bamboos (*Pleioblastus* section *Nezasa*, Poaceae) using AFLP markers"

ASB Presentations

1 - First report of meiofauna biodiversity from the Tennessee River

Francesca Leasi, Jessica Cline, Noura Elsaeed, Luke Qualey

University of Tennessee at Chattanooga, Chattanooga, TN

Small-sized (< 2mm) invertebrates, commonly known as meiofauna, are abundant and ubiquitous in all aquatic ecosystems, performing key functions such as nutrient cycling and sediment stability. Yet, their unexplored diversity and response to disturbances limit our capacity to understand, mitigate, and remediate the consequences of pollution and environmental changes. The biodiversity of meiofauna is largely overlooked especially in freshwater habitats. For example, the Tennessee River hosts more aquatic species than any other region in North America and contains one of the most diverse aquatic ecosystems in the world, however, to our knowledge, nothing is known about the meiofauna diversity from the Tennessee River. To overcome this knowledge gap, we have investigated the biodiversity of meiofauna along the Tennessee River in Hamilton County (Chattanooga area). Samples were collected from sites that are characterized by specific environmental variables (e.g., pH, temperature, dissolved oxygen, etc.) and degrees of urbanization. From each site, we have investigated both aquatic and benthic meiofauna using a metagenomic approach. Results reveal that the Tennessee River is a hotspot of biodiversity also for meiofauna, besides bigger species. In a range of just a few miles, we have discovered the presence of over 10 animal phyla and thousands of species co-existing locally. We also analyzed potential correlations with the measured environmental variables and suggest that meiofauna may be a useful tool for biomonitoring freshwater ecosystems.

2 - Understanding sensory modality utilization on the crepuscular-nocturnal hawkmoth Manduca sexta

Emily Hudgins

The University of Tennessee at Martin, Martin, TN

Sphingids (hawkmoths) are known to share a diurnal lepidopteran ancestor. Nevertheless, most hawkmoths are nocturnal. It has been shown that many nocturnal hawkmoths are more reliant on (and learn better) olfactory than visual signals during the night. On the other hand, *Macroglossum stellatarum,* a hawkmoth species that reverted to diurnal activity, are known to more readily rely and learn visual (colors) than olfactory stimuli when foraging on flowers during the daytime. These differences suggest an evolutionary divergence within sphingids, which is supported by neuroanatomical allometric differences between nocturnal (larger olfactory bulb) and diurnal moths (larger visual neuropils). *Manduca sexta* are large, crepuscular-nocturnal hawkmoths that forage during times of twilight illumination and during the night. Here, we are investigating whether they are “hard-wired” to weight more olfactory stimuli regardless of the illumination conditions, or if they are behaviorally flexible, and olfactory signals are weighted more than visual signals during the nocturnal activity, and vice-versa during crepuscular activity. *Manduca sexta* are trained to learn between a yellow, honeysuckle-scented, rewarded feeder and a blue, bergamot-scented, unrewarded feeder. After training, we are testing their ability to learn and if there is a sensory modality with more salience than the other. Trials have been completed under diurnal conditions, and we are now performing the experiment under nocturnal illumination. The comparison of diurnal to nocturnal illuminations on the same species, will help us understand whether the preponderance of the use of olfactory stimuli during foraging is affected by the illumination conditions, showing behavioral flexibility, or if olfaction is more salient regardless of illumination conditions, showing phylogenetic constraints.

3 - Trematode Diversity in Molluscan Hosts in Northwest Louisiana (BBB)

Kasey Moore, Sarah Sargent, Joshua Shelton, Cynthia Doffitt

Northwestern State University, Natchitoches, LA

Trematodes are parasitic flatworms with specific and complex life cycles, involving a molluscan host and one or two vertebrates, commonly a piscine host and an avian or mammalian host. The obligate nature of these parasites, and the ease of sampling from intermediate molluscan hosts, makes larval trematodes a promising bioindicator of vertebrate host species diversity within an ecosystem. Ultimately, this research aims to identify trematodes that infect local mollusk populations and examine their potential as vertebrate biodiversity indicators. In September and October 2021, 458 aquatic snails were collected from the Natchitoches National Fish Hatchery (Natchitoches, LA) production ponds containing either Ictalurus punctatus (channel catfish) or Esox niger (pickerel). Snails were subdivided into pools of approximately 10 individuals and housed in enclosures containing sterilized spring water. Snails were observed for 14 days to detect infected individuals, indicated by the release of cercariae (juvenile trematodes) into the surrounding water. Overall, 3.06% (14/458) of snails were found to be infected. These infected snails were housed individually in 10-mL sterilized spring water. Average daily cercariae counts were estimated by sampling 1-mL of the water in 0.1-mL aliquots from each enclosure each day over a total of seven days. Average cercariae released from each snail ranged from 244.6 to 5715 cercariae/mL/day. Subsamples of these cercariae were preserved for genetic sequencing and morphological identification. Of the cercariae collected, three morphologically distinct types were observed. Identification of larval trematode species is ongoing. This study will lead to further investigations involving infection studies, and/or vertebrate host surveys. (BBB)

4 - Microculture of sea urchin larvae from *Lytechinus variegatus*

Victoria Gibbs, Hannah Lafiosca, Amy Wright

Birmingham-Southern College, Birmingham, AL

Sea urchins are valuable models for understanding genetic control of early deuterostome development, and they can be useful for understanding the interactions between genotype and phenotype. Elucidating such interactions requires genetic tools such as CRISPR-Cas9 and RNAi applied to the genome. Genetically modified (GM) embryos are typically produced in relatively small numbers, ranging from dozens to a few hundred. Standardized larval culture techniques designed to rear small numbers of embryos through the larval and settlement stages will be key for tracking genes through adulthood and creating GM breeding lines of sea urchins. Whereas, embryos and larvae of cold-water species of sea urchins have been used in past years, a warm-water species may be more amenable to GM work. *Lytechinus variegatus* is a temperate-tropical species of sea urchin that inhabits the nearshore seagrass communities of the Gulf of Mexico. The embryos and larvae of *L. variegatus* can be reared at room temperature (approximately 22°C), and larvae begin settlement within three weeks of fertilization, which is much faster than many cold-water species. In this study, we investigated housing and feeding strategies for rearing 10 larvae through settlement in 20 mL glass test tubes. Sea urchin larvae (full siblings) were housed in 20 mL test tubes containing 15 mL of synthetic seawater (Instant Ocean). Tubes were divided equally between one of two devices to simulate oceanic waves: a rotator or an orbital shaker (n=10 tubes per device). We also investigated the role of a native food source derived from sea grass (n=5 tubes per device). Larval survival and growth were monitored for three weeks and settlement rates recorded. There were no significant differences in measured metrics among the groups; however, trends indicated slightly improved growth and settlement rates for larvae housed in the rotator and fed algae supplemented with seagrass detritus.

5 - Get to know your new neighbor: biology of the introduced brown widow spider

J. Scott Harrison

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Introduced species often generate ecological and economic costs. These species can also serve as interesting natural experiments as they are often exposed to new ecological conditions, undergo dramatic fluctuations in population size, and produce offspring that are interpopulation hybrids. The brown widow spider (*Latrodectus geometricus)* is thought to be native to South America or Southern Africa, but its distribution has expanded to most continents by human introduction. In the continental USA, *L. geometricus* was first documented in south Florida in the 1930s, but since the early 2000s has become abundant in northern Florida, Georgia, South Carolina, Alabama, Mississippi, Louisiana, Texas, and southern California. This species is commonly found around urban structures including shopping centers, homes, parks, and landscaping areas. In this talk, I will summarize research on the evolutionary ecology and population dynamics of brown widows in the context of its propensity to establish introduced populations. Results indicate that the distribution of genetic variation in the southeastern US consistent with multiple introductions. In addition, inbreeding depression is significant when mating occurs between related individuals, indicating that significant inbreeding has been avoided during the introduction of this species and that local dispersal mechanisms may allow for the avoidance inbreeding. Finally, bacterial endosymbionts are common but seem to only have minor impacts on the reproductive biology and ecology of this species.

6 - Brood provision composition in alfalfa leaf-cutting bees (Megachile rotundata)

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Alfalfa is the third most valuable crop grown in the US, with an estimated value of 10 billion dollars. It is primarily grown for hay to feed livestock, especially dairy cows, though it is also used to feed sheep and honeybees for the production of honey. Alfalfa leaf-cutting bees (ALCB, *Megachile rotundata*) are solitary bees accidentally introduced to North America in the late 1930's and are currently the most managed solitary bee in the US. They are preferred as alfalfa pollinators over the generalist honeybee since ALCB is more effective at pollinating these plants, significantly increasing seed production. With the continuous decline of honeybee colonies due to parasites and diseases, there is renewed interest in ALCB, not only to pollinate alfalfa, but other crops as well such as blueberries and cranberries. Unfortunately, the diversity of plants visited by these bees has been little studied, so a first step in trying to widen the use of ALCB for pollination services is to understand what other plants they visit. In this study, we examine the pollen composition of 83 brood provisions collected from 20 nests of *Megachile rotundata* using rbcL to determine the origin of the pollen. Our results show that even when the bees are released in an alfalfa field, 35% of the pollen they collect for brood provision is not alfalfa. Female ALCB construct a sequence of brood cells, between 8-12 per nest. Our study also shows there is a significant difference between the composition of the older and the more recent cells constructed.

7 - Evolutionary history of a globally distributed group of ectoparasitic lice from doves

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Parasites are the most diverse group of organisms on earth, yet we know relatively little about the factors that drive this diversity. The diversification of obligate parasites can be particularly shaped by the evolutionary history of their hosts. Over long periods of time, this can result

in patterns of host-parasite evolution that mirror one another. However, other factors, such as parasite dispersal, can drive parasite diversification independent of the host. Here, we assess the macroevolutionary patterns of a globally distributed group of ectoparasitic body lice from doves. These insects are closely associated with their hosts, but do have some ability to disperse between hosts, which could result in host switching. We used whole genome sequence data of lice to reconstruct the phylogeny of 58 species of body lice from 51 species of doves, including representatives from every continent except Antarctica. We then compared the louse phylogeny to an existing dove phylogeny to test for codiversification (host-driven diversification) versus host switching (parasite dispersal). From the genomic data set, we estimated a well-resolved and highly supported phylogenetic tree of the body lice. Cophylogenetic comparisons with an existing host phylogeny indicated high amounts of codiversification between doves and their lice, but also some instances of host-switching. These patterns suggest that dove diversification played a significant role in the diversification of lice, but host evolution was not the only factor driving parasite diversity. Host ecology, habitat, and/or biogeographic history could have played roles in promoting dispersal and host switching of the parasites. Our study highlights that parasite evolution is often driven by complex interactions among different factors that can have varying effects over long periods of time.

8 - 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.

9 - Identifying metrics for predicting successful stream restoration in an agriculturally impaired Chesapeake Bay watershed

Julia Portmann, Bruce Wiggins

James Madison University, Harrisonburg, VA

The Chesapeake Bay watershed spans several states, supports diverse ecosystems, and is crucial to local economies. However, agricultural practices in this region impair water quality. The Smith Creek watershed, within the Shenandoah Valley, was designated a showcase watershed in 2010 by the United States Department of Agriculture to demonstrate the efficacy of implementing restoration projects. We sampled fifteen farms ranging from unrestored to thirty-six years since restoration. At each site, we conducted a kick-net survey, measured canopy cover, algal density, substrate size, and bank height and angle. We identified macroinvertebrates to family and calculated the Virginia Stream Condition Index (VSCI), the Chessie B-IBI, diversity, and the percent dominant families. We also calculated the percent pasture, cropland, and forest within 30 meters (m) of the stream. Using single and multiple linear regressions, we identified several metrics that predicted healthy macroinvertebrate communities. We found that the Chessie B-IBI was positively correlated with time since restoration (p=0.03, R2=0.333), as was diversity with D90 substrate size (p=0.02, R2=0.383). The VSCI was significantly predicted by time since restoration, and percent pasture and forest within 30 m (p=0.02, R2=0.475). The Chessie B-IBI was best predicted by time since restoration, bank height, bank angle, and D90 together (p=0.01, R2=0.660). Diversity was best predicted by time since restoration, D90, and pasture within 30 m together (p=0.02, R2=0.499). Lastly, percent dominant was significantly predicted by time since restoration, canopy cover, and D90 (p=0.002, R2=0.701). Allowing streams time to recover after restoration implementation was the most important factor for improving water quality. However, since time is not always available, improving in-stream habitat can also increase the likelihood of a successful restoration project. By taking these measures when restoring streams, we can more effectively improve water quality throughout the watershed and thus improve the health of the Chesapeake Bay.

10 - Variation in Stream Chemistry and Abundance of Suspended Microbes Along an Elevation Gradient in Northwestern South Carolina

Krista Just, Greg Lewis, Sonali Patel

Furman University, Greenville, SC

Environmental conditions and the abundance of organisms may vary along elevation gradients. Many studies have examined such gradients in terrestrial ecosystems, but fewer have examined how elevation gradients may influence aquatic ecosystems. The goal of our study was to determine if the water chemistry and abundance of suspended microbes in small forest streams varied along an elevation gradient in the Piedmont and Blue Ridge provinces in northwestern South Carolina. We hypothesized that streams at lower elevations would have higher concentrations of suspended bacteria and fungi due in part to higher water temperatures than would be found in higher elevation streams. During June-August

2021, we collected environmental data and water samples from 22 first to third order streams draining watersheds with >78% forest cover and <1% impervious surface cover. Elevations at the sample locations varied from 87 m to 590 m. Each stream was sampled once under baseflow conditions. In the field, we measured instantaneous discharge, pH, water temperature, conductivity, and dissolved oxygen. In the lab, water samples were analyzed for turbidity, dissolved organic carbon, major ions, ammonium, dissolved iron, dissolved silicon, total heterotrophic bacteria, total coliform bacteria, *Escherichia coli*, enterococci, and fungi (yeasts and molds). Discharge tended to increase with increasing elevation. By contrast, solute concentrations, turbidity, pH, and water temperature were highest at lower elevations and decreased with increasing elevation. As predicted, concentrations of bacteria and fungi also were inversely related to elevation, and they were positively correlated with water temperature. However, concentrations of microbes generally were more strongly correlated with dissolved iron concentrations and turbidity than with water temperature. Additional research is needed to better understand which environmental factors exert the greatest influence on microbial abundance along the elevation gradient in this region.

11 - Paleback Darter Seasonal Occupancy in Main Channel and Off-channel areas of Lick Creek in the Ouachita Mountain Ecoregion in west-central Arkansas

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Paleback Darter *Etheostoma pallididorsum* is endemic to the Ouachita Mountains in west-central Arkansas. Limited information is known regarding characteristics of off-channel habitat used by Paleback Darter and how use of off-channel habitats changes seasonally. Our objective was to quantify habitat characteristics associated with seasonal occupancy of off-channel areas by Paleback Darter. We used a multi-season occupancy model to quantify habitat characteristics associated with seasonal occupancy of Paleback Darter. We georeferenced off-channel habitats along the entire length of Lick Creek in Norman, Arkansas. We used stratified random sampling to select main-channel sites and off-channel sites. We used 30 off-channel sites and 30 main-channel sites to assess changes in seasonal occupancy along the length of Lick Creek. We sampled these sites two times during the summer season (July - September 2021) and two times during the winter season (January - February 2022). Naïve occupancy estimates suggested changes in seasonal use of off-channel and main channel sites by Paleback Darter. Habitat characteristics of off-channel and main-channel sites may influence the distribution of Paleback Darter along the longitudinal and lateral gradients of streams.

12 - Abundance of Suspended Bacteria and Fungi in Urban and Rural Streams in Northwestern South Carolina

Sonali Patel, Greg Lewis, Krista Just

Furman University, Greenville, SC

Streams in urban areas can receive elevated inputs of nutrients, other dissolved substances, and microbes from a variety of sources, including impervious surfaces, underground infrastructure, and lawns. Given that urban land cover has expanded dramatically in the southeastern United States over the past several decades, it is important to understand the resulting influences on stream ecosystems and implications for human health. In contrast to studies of bacteria in urban streams, relatively few studies have tested whether fungal abundance differs between urban and rural streams. The major goal of our study was to compare the abundance of suspended bacteria (including fecal-indicator bacteria) and fungi in urban and rural streams in the South Carolina Piedmont and Blue Ridge physiographic provinces. During June-August 2021, we sampled 9 urban and 9 rural streams under baseflow conditions. For all streams, watershed areas ranged from 1.2 km² to 9.4 km², and all sample sites occurred at elevations between 196 m and 315 m. Impervious surface cover was 21-55% in urban watersheds and <1.2% in rural watersheds. At each sample site, we measured pH, conductivity, water temperature, dissolved oxygen, and instantaneous discharge, and we collected water samples for quantification of turbidity, solute concentrations, and concentrations of total heterotrophic bacteria, total coliform bacteria, *Escherichia coli,* enterococci, and fungi (yeasts plus molds). Consistent with previous studies, we found that urban streams had significantly higher specific conductance, concentrations of most measured solutes (including dissolved organic carbon, bicarbonate, calcium, and nitrate), and concentrations of total heterotrophic bacteria and total coliforms. However, we found no significant differences in discharge, water temperature, pH, turbidity, or concentrations of dissolved oxygen, dissolved silicon, magnesium, *E. coli*, enterococci, or fungi between urban and rural streams. Additional research is needed to determine whether the abundance of fungi attached to substrates differs between urban and rural streams.

13 - Dietary and Morphological Changes in Luxilus pilsbryi in Response to Stream Drying

Jessica Rath, Rebeka Bradford, Sahara Morgan, Chance Garrett, Ginny Adams, Reid Adams

University of Central Arkansas, Conway, AR

Intermittent streams, characterized by cessation of flow over lengthy periods of time, play an essential role in maintaining biotic diversity and integrity of perennial streams. Adaptations of some fishes inhabiting intermittent steams include increased diet breadth and, in one study, increased gut length when food quality and quantity decreased. *Luxilus pilsbryi*, the Duskystripe Shiner, is endemic to intermittent and perennial streams of the Ozarks, and has a diet consisting primarily of macroinvertebrates and some vegetation. Individuals were collected from Rockhouse Creek, an intermittent tributary of the Kings River, during the wet season (winter and spring) and dry season (summer and fall). We found that

gut length (adjusted for standard length) varied significantly across seasons, with the longest gut lengths found during spring (ANCOVA, $p<0.01$). Gut contents were identified to the lowest possible taxon, enumerated, and weighed. Fish collected during spring consumed more total food (by mass) relative to all other seasons. Winter and spring stomachs contained mostly aquatic macroinvertebrates while the stream was flowing, but summer and fall stomachs mostly contained amorphous material—consisting of plant, detrital, and algal materials- during periods of intermittency, characterized by pool isolation. The seasonal shift to a more herbivorous diet did not correspond with increased gut length, suggesting *L. pilsbryi*, in contrast to previously studied species, cannot compensate for low/poor food periods with morphological adjustments of gut length and may reflect their facultative association with intermittent headwater streams.

14 - Antipredator Behavior of Elimia paupercula, Sooty elimia, in response to Faxonius yanahlindus, the Spinywrist crayfish

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Sooty elimia, Elimia paupercula, is an endemic freshwater gastropod located in north Alabama. These snails coexist with several snail predators including the Spinywrist crayfish, Faxionus yanahlindus. However, little is known about antipredator behavioral responses of Sooty elimia, especially avoidance behaviors to crayfish predators. To examine antipredator behaviors in Sooty elimia, we recorded the average distance snails spent from a source of various predation cues. The cues included chemical cues from the Spinywrist crayfish alone, alarm cues from crushed conspecifics, or a combination of both crayfish and alarm cues. Each alarm cue treatment was compared to a control which contained no cues from predators or conspecifics. Experiments were conducted in the laboratory using 38-L aquaria with three replicates for each of the four treatments. Each experiment was repeated 3 times. Snails were observed and distance recorded relative to the treatment stimulus every hour for 24-hours. A mixed-effects model was used to compare treatments. Distance was used as the response variable and treatment as the explanatory variable. Individual snails, replicate number, and trial period were used as random variables. We concluded that there was a significant effect of treatment stimulus on the snail's average distance. Snails that were exposed to the combined cues of crayfish and crushed snails were on average further away from the stimulus than snails in other treatments. While Sooty elimia displayed predator avoidance behaviors in a laboratory setting, it is still unknown how strong these behaviors would be in natural settings. When snails are exposed to predation cues in a natural stream setting other factors such as stream flow may influence detectability and response to cues by the snails, and as a result the snails' antipredator behaviors.

15 - Predictive Species Distribution Modeling of Molluscan Agricultural Pests to Assess the Probability of Future Invasions in the United States

Kayla Hankins, Austin Brenek, Laura Bianchi, Nicholas Reger, Ashley Morgan-Olvera, Justin Williams, Christopher Randle

Sam Houston State University, Huntsville, TX

As a result of the rapidly increasing globalization of the world's economy, travel, and trade, the introduction of non-native invasive species, made either intentionally or accidentally, is a well-documented phenomenon. Industries such as the horticulture, pet, and live-food trades are a major culprit in the dispersal of non-native alien species around the globe. Invasive terrestrial gastropods pose a significant and understudied threat to US agriculture, native biodiversity, and public health. Thus, the objective of this research is to use publicly available occurrence data sourced from the Global Biodiversity Information Facility (GBIF) to generate a suite of predictive species distribution models, including the General Additive Model (GAM), Maximum Entropy (Maxent), Boosted Regression Trees (BRT), and a comprehensive ensemble model to better identify areas of potentially suitable habitat for high-risk invasive terrestrial mollusk species in the US. All models were evaluated using a variety of statistical metrics, including Area Under the Receiving Operating Characteristic curve (AUC-ROC), Pearson's Correlation Coefficient (COR), Kappa, and the True Skill Statistic (TSS). The results generated from this study will be used to better inform quarantine measures, future threat assessments, long-term pest monitoring projects, and pest-management strategies should any of these species manage to successfully establish in any suitable areas located throughout the US.

16 - The effects of fire frequency on species richness and composition of the herbaceous layer in mixed-oak forests over 25 years

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In fire-adapted plant communities, frequent fire promotes biodiversity through multiple mechanisms. Prescribed fire is now widely used throughout the eastern United States (U.S) to increase herbaceous biodiversity and enhance oak and pine regeneration, following widespread fire suppression policies of the 20th century. Our goal was to quantify the effects of fire frequency on herbaceous layer species richness and composition over a 25-year period in southern Ohio, U.S., and determine whether plant community responses to fire differed in xeric and mesic sites. In 2019, we re-sampled 45 mixed-oak forest plots established in 1995 that were part of a fire experiment with three fire frequency treatments: control (unburned), periodic fire, and annual fire. In each plot, all vascular plant species were recorded within each of 16 2 m2 quadrats. We calculated changes in species richness through time and related changes in richness to fire regime characteristics and soil moisture using linear mixed effects models. To characterize changes in species composition through time in relation to fire history, we used non-metric multidimensional scaling and PERMANOVA. Changes in species richness from 1995 to 2019 were significantly positively related to fire frequency ($p < 0.01$, pseudo $R^2 = 0.34$). The median change in species richness for control plots (no fire) was approximately 0, while species

richness increased through time on all periodically burned (range = 2 to 33) and annually burned plots (range = 4 to 22). Increases in species richness were driven primarily by recruitment of perennial grasses and forbs, and resulted in large directional shifts in species composition. Changes in species richness did not significantly differ across soil moisture categories. These results suggest that fire can be an effective management tool for maintaining and increasing plant biodiversity in the herbaceous layer of mixed-oak forests within the Southern Alleghany Plateau.

17 - Pilfering Passerines? Inter-Class Competition: A New Direction in Foraging Ecology

Shannon Gillen

James Madison University, Harrisonburg, VA

Life below the leaves often goes unexplored. Shrews have lived in this space for millions of years, carving out an existence in harsh habitats around the world. Two species of shrew live in the Shenandoah Valley of Virginia: The least shrew (Cryptotis parva) and the southern short-tailed shrew (Blarina carolinensis). Shrews make trails in the ground substrate while they continually forage for food, caches being a way to save this food for later. Foraging trails and caches for these species are found, mapped, and marked for both species, and for the first time in the case of the least shrew. In addition, the Animal Monitoring Data Station (AMDS), patented at the start of this study, is used to obtain non-invasive data on these mammals. Of further interest is how the caches of shrews fare when they are stored along their foraging trails. Both birds and small mammals cache food and in turn, pilfer the caches of other members of their own taxa. What has not been explored, is if songbirds pilfer the caches of small mammals. This possibility may heavily impact the ability of shrews to survive considering their high metabolic rates. Using the AMDS, shrews' weight over time, along with coat condition, is used to ID to individual and species. In addition, image data is used to observe what bird species are visiting and where they are seen foraging. Treatment sites are those with a feeding platform to attract birds to the area. Birds that are ground feeders and cachers are the most prolific visitors and are the species most often seen near foraging trails and caches, treatment sites having more instances in all cases than control sites. The information presented here opens doors to future studies focused on foraging interactions between taxa.

18 - What kinds of islands host redundant versus unique bird communities? An analysis of the Chesapeake Bay's avian metacommunity structure

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Island metacommunities are not only great models for understanding metacommunity dynamics as a whole but are also of great interest to conservationists in their own right. One important aspect of metacommunity structure is the degree of nestedness—whether or not less speciose communities are perfect (redundant) subsets of more speciose communities. Another important metric is modularity—the degree to which communities belong to clusters of similar communities whose members do not overlap. Environmental gradients have received little attention as predictors of such patterns. I examined bird communities on islands within Chesapeake Bay, USA. Many small islands within the bay make ideal natural laboratories for avian metacommunity dynamics. These islands represent a gradient of sizes, degrees of isolation, and habitat types; begging the question of which of these variables best predicts patterns of nestedness and modularity. Presence-absence data were collected from thirteen islands from the southern end of the Bay from June to August of 2021. Three matrices were developed (ranked by size, isolation, and habitat type, respectively) and evaluated for both nestedness and modularity. Island size produced the greatest degree of nestedness, even when accounting for variation in species richness across islands. None of the island characteristics exhibited strong patterns of modularity. These results suggest that, on a broad scale, avian island metacommunities can be accurately represented by the few largest islands.

19 - Modeling the sequential behaviors of simultaneous predator and prey patch use

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Models investigating predator-prey games often fix one player's behavior while allowing the other to make patch use choices. Here, we use adaptive dynamics to model changes in behavioral rates of a predator and prey, while explicitly allowing both to make decisions simultaneously. Our model focuses on a two-patch situation. The prey can move between an open patch, allowing for energy intake but also predation risk, and a refuge with no possibility of energy intake or predation risk. The predator can move between that patch, where it can attack prey, and an alternative patch that provides a fixed rate of energy intake, and consequently imposes a missed opportunity cost (MOC) of using the focal patch. The model predicts how the rates of movement by the players are influenced by specific parameters, including the predator's lethality and MOC, as well as the information available to the players. For example, our model predicts that the time a prey takes to emerge from its refuge and the time a predator waits for the prey to emerge depend on the sequence of events leading to the prey entering the refuge. For instance, the predator would leave the patch more quickly and the prey would emerge from the refuge more quickly if the prey entered the refuge after a failed attack rather than as part of its time allocation.

20 - Sums, limits, and video tapes: why Dr. Neufeld's calculation on the importance of math in biology just doesn't add up

Patrick Cain

Georgia Gwinnett College, Lawrenceville, GA

At the 82nd ASB Annual Meeting, Dr. Neufeld made the argument that calculus should not be a requirement in the curriculum of an undergraduate degree in biology. His main points were 1) the math problems faced in a typical calculus class are not relevant to biology majors, 2) many professions do not require competency in calculus, be it physicians or conservation biologists 3) scientific journal articles broadly lack the use calculus, and 4) calculus discourages promising students from completing degrees. Dr. Neufeld advocates that students take a flexible curriculum of calculus in highly applied contexts. Ultimately, biology students should be exposed to calculus, learn to do simple problems, and learn its utility in biology. Here, I offer a counterpoint to Dr. Neufeld's arguments.

21 - Investigating conserved pollinator attractants as a driver of hybridization in Heuchera.

Nicholas Engle-Wrye, Ryan Folk

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Little is known about environmental drivers of hybridization, but its phylogenetic distribution across plants is heterogeneous, suggesting that plant traits may play a role in its frequency. Conservatism of biotic niche could explain why some plants are prone to hybridization, as conserved pollination strategies would lead to a lack of pollinator assemblage divergence and therefore opportunities for gene flow, although this hypothesis has yet to be tested. The taxonomic tribe Heuchereae (Saxifragaceae) is a well-characterized system for pollinator interactions and particularly for floral scent, the primary pollinator attractant in the group. Floral volatile organic compounds (VOCs) in this clade, characterized to date in *Asimitellaria* and *Lithophragma,* are hypervariable at the population level and are responsible for selectivity of specialized pollinator assemblages including parasitic *Greya* moths, bees, fungus gnats, syrphids, and other insects. High levels of interspecific divergence may be responsible for the relatively low levels of hybridization observed in these groups. *Heuchera* flowers, by contrast, attract a generalist pollinator assemblage, including pollinators shared with other genera. While floral volatiles have yet to be characterized for this genus, they will offer insight into whether the diversity of prezygotic isolation mechanisms across a recent radiation are predictive of hybridization rate.

Given that pollinator-mediated gene flow primarily hinges on floral volatile compounds in the relatives of *Heuchera*, I here investigate whether the particularly high rates of hybridization observed in *Heuchera* may be associated with low interspecific divergence of these pollinator attractants, using as a system the hybrid zone between *H. americana* and *H. richardsonii* in the midwestern US. Preliminary data, from ~90 *Heuchera* representing 21 populations suggests that shared classes of VOCs and to some extent individual compounds occur within the hybrid complex while other *Heuchera* that do not hybridize with these species have distinct species-specific compounds.

22 - Population genomics and biogeography of Symphyotrichum in Mexico and the eastern U.S

Sushil Dahal, Ryan Folk, Carolina Siniscalchi

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Biotic disjunctions, the occurrences of related organisms in disconnected areas of the Earth, have attracted scientific attention for the past 200 years. The eastern North American (ENA) – eastern Asian (EA) disjunction is the classic and best studied pattern of disjunct distribution. Large numbers of species and genera show a secondary eastern North American (ENA) - Mexican (M) disjunction, but despite being represented in many familiar plants (bald cypress, flowering dogwood, sweetgum, partridgeberry, etc.) this is poorly understood. In this project, we use Symphyotrichum subgenus Virgulus to investigate the origin and timing of biogeographic connections across Mexico and the eastern US. Symphyotrichum, comprising most species traditionally treated as asters in the New World, is one of the most diverse genera in the eastern US. Its broad presence across major biomes also makes it an excellent system for investigating phylogeographic breaks across eastern North America and Mexico. We performed a sequence capture on DNA libraries obtained entirely from herbarium specimens using the Angiosperms353 baitset. We used HybPiper to assemble the sequence data and used standard methods: concatenation in RAxML-NG and coalescence in ASTRAL-III to perform phylogenetic analysis. We performed divergence time estimation using BEAST and treePL. We then used the R package BioGeoBEARS to infer ancestral regions and biogeographic transitions between North America and Mexico. Our molecular data suggest a recent radiation of Symphyotrichum of about 5 million years ago (late Miocene), with early connections to Mexico in ancestral lineages that closed off shortly after, contrary to the Quaternary date traditionally favored. Overall, vicariance was recovered as the primary mechanism connecting these regions. A complete lack of movement between these regions after 3.5 mya suggests that the aridification of the interior of North America was directly implicated in causing today's disjunctions between eastern North America and Mexico.

23 - Quillwort Quagmire

Lytton John Musselman[1], Peter Schafran[2], Jay Bolin[3], Davud Wickell[4]

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Quillwort species are notoriously difficult to identify, sometimes requiring chromosome counts or DNA sequencing—hardly techniques useful for field botanists and ecologists. The quillwort plant is remarkably morphologically uniform across taxa—they all look alike. It is easy to recognize as an *Isoetes* but beyond that even quillwort specialists are flummoxed. Checklists frequently lump them all under *Isoetes* sp. We are regularly asked to name quillworts, advising inquirers to send plants AND the soil around the base which usually contains spores which can provide identification for a few species. But the taxonomy of the southeastern plants is in a state of flux, several taxa being polyphyletic having remarkably similar megaspores so various techniques are needed for even tentative ID or just as likely, no ID because the collection may have a unique genetic makeup. How to proceed?

New studies show a way to reexamine *Isoetes* systematics using a combination of genomics, flow cytometry, cytology, and morphology. In the Pacific Northwest, hexaploid *I. occidentalis* was shown not to be derived from *I. bolanderi* and *I. maritima,* but potentially an autopolyploid with transcontinental roots. *Isoetes engelmannii* and *I. valida* have been confirmed as parents of *I. appalachiana*, but two distinct lineages of *I. engelmannii* were involved in multiple origins of *I. appalachiana* in the northern and southern parts of its range. In an undescribed rock outcrop diploid in southern Georgia, we discovered its autotetraploid and their triploid hybrid, as well as evidence for genetic differentiation between rock outcrop populations. Recent technological advances now allow for higher throughput sampling to begin delineating previously cryptic taxa with greater precision. While no perfect solution for field biologists is in sight, over the next several years we will develop resources to communicate the quickly changing landscape of quillwort taxonomy.

24 - Does artificial intelligence see something else? An initial assessment on what discriminating morphological characters are extracted from images by neural networks during species identification

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There is an ongoing effort to contribute digital biodiversity image data that is easily accessible by humans and analyzable by computers. Within botany, this has resulted in more than 50 million publicly available Plantae images on portals and online citizen science platforms such as iDigBio and iNaturalist. Artificial intelligence, more specifically neural networks, have the capability of extracting discriminating morphological features (e.g., shape, venation, etc.) between taxa from images without prior knowledge of morphological concepts or botanical terms by analyzing patterns in hundreds to millions of images. This may be useful in the extraction of novel morphological traits that may have been overlooked, or allow the description of morphological features within a taxa that are hard to characterize manually (e.g., leaf venation), providing a potentially new set of characters or supporting currently accepted ones. Unfortunately, current neural network-based morphological analyses of botanically-related image data is largely limited to species/character classification, not character extraction. Here, we present an initial assessment of what morphological characteristics are deemed important by state-of-the-art neural network models in identifying/delimiting particular case-study taxa, with data representing both herbarium and live iNaturalist observation images. Additionally, a comparison of how well these morphological characteristics fit within current floristic keys are shown within sister taxa. This assessment and analysis may be helpful both on the data science and botanical fronts—as an initial step towards engineering more performant neural networks for species identification and morphological analyses, as well as providing insight in choosing new morphological features that may currently be overlooked or have yet to be characterized.

25 - Ironing out species boundaries in ironweed (Vernonia, Asteraceae) with phylogenomics

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The taxonomy of the genus *Vernonia* has always been a focal point within tribe Vernonieae. This genus once included upwards of a thousand species and has subsequently been greatly reduced beginning with studies in the 1970s, resulting in an entity with about 20 species mostly restricted to North America. The implosion of *Vernonia* led to other taxonomic issues, such as the creation of non-monophyletic segregate genera with difficult delimitation. Although much of the recent phylogenetic work in Vernonieae has focused on resolving subtribal relationships, few studies have focused on infrageneric relationships or species delimitation in these complicated genera. Little is known about the infrageneric relationships of *Vernonia* and its biogeographic history. Widespread species of ironweed in the Southeastern USA remain a taxonomic complex since they share many morphological features, are sometimes difficult to identify, and may hybridize frequently. With the aim of revealing species relationships and delimiting species boundaries in *Vernonia*, we generated target capture sequences for 525 samples of 29 species of *Vernonia* and 26 outgroups. We ran phylogenetic analyses using a multispecies coalescent approach in ASTRAL and evaluated six biogeographic models to reconstruct ancestral areas. We found that the North American species of *Vernonia* form a monophyletic group, further divided into two clades: one containing species from Eastern USA and the other containing species from Southwestern USA and Mexico. The sister group to this core groupis a clade of Mexican species that have been informally defined as being outside of core *Vernonia.* The delimitation of southeastern species is complicated by their non-monophyly, attributable partly to misidentification in herbarium collections and ongoing taxonomic problems. Ancestral area reconstructions indicate that members of tribe Vernonieae moved from South America to Central America, Mexico and then to eastern North America.

26 - Update on the distribution of the lepidote species of Rhododendron in the Carolinas and Tennessee

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With the description of *Rhododendron smokianum* there are now four recognized lepidote *Rhododendron* species in the southeast. In additional to the above, *R. carolinianum*, *R. minus*, and *R. chapmanii* are regionally located from Tennessee (TN) and North Carolina (NC) south to the panhandle of Florida and west into Alabama. This presentation will concentrate on the first three species as they occur in the Carolinas and eastern TN. Species are distinguished mostly on a combination of floral tube length and flowering time. In addition, variation occurs in flower color within each species range showing colors of purple, pink and white. *Rhododendron smokianum* is restricted to the Great Smoky Mountain National Park, has a very short purple floral tube, and flowers in late June. *Rhododendron minus* is a more southern species and has been documented in TN, NC, and SC. It shows variation in floral tube length and color, with the longest tubes and white flowers in the coastal plain of SC; its flowering time varies by elevation from April to June. *Rhododendron carolinianum* is more northern in its distribution with purple-flowered forms in the Linville Gorge region and white to pink flowered forms in the Green and Broad River drainages of NC and SC. Overall, *R. carolinianum* flowers earlier than *R. minus* when the two are found in vicinity each other. Additional field work is needed to document and clarify NC and TN populations of the New River and Tennessee River drainages.

27 - Relationship Between a Reproductive Polymorphism in the Spotted Salamander and its Unicellular Algal Symbiont

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Spotted salamander (Ambystoma maculatum) egg masses are polymorphic; some females lay clear egg masses while others lay opaque masses. Breeding ponds often contain both mass types, but proportions of clear to opaque masses vary geographically. Over a century of research on this polymorphism has yet to provide a scientific consensus regarding which environmental selective pressures maintain it. Previous studies, including our own, have found evidence for the importance of predation, breeding pond nutrient levels, dissolved oxygen, and other aspects of physicochemistry, but none of these results have been consistently replicated. The spotted salamander also has a singularly unique symbiotic relationship with a unicellular green alga, Oophila amblystomatis. Algae live within the spotted salamander's eggs and photosynthesize to provide salamander embryos with supplemental oxygen that allows them to survive in the often hypoxic, ephemeral breeding ponds. During development, some algae move into the cells of salamander embryos, making this the only known example on earth of a photosynthetic organism living intracellularly within a vertebrate animal. Here, we investigate the relationship between jelly polymorphism, symbiosis, and environmental variation through both observational and experimental designs. We hypothesized that the egg mass polymorphism directly mediates the influence of environmental variables such as light and physicochemistry on the growth and survival of both organisms and the quality of the symbiosis. We sampled A. maculatum breeding sites for egg mass proportions, predators, and water physicochemistry. Additionally, we raised clear and opaque egg masses under two different light treatments, sampled embryonic respiration at two developmental stages, and quantified algal growth. Our study elucidates some heretofore unknown differences between the two mass types, such as differential algal growth, clutch sizes, and hatchling viability. Finally, our data suggest that the polymorphism does fundamentally impact the growth and photosynthesis of O. amblystomatis and thus the quality of the symbiosis.

28 - Habitat Associations of Fishes Across a Gradient of Pool Size and Structure in an Ozark River

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Streams in the Ozark Mountains have experienced an extended period of gravel aggradation, which has been exacerbated by changes in land use. The input of gravel into Ozark streams has resulted in the shallowing and widening of streams along with changes in substrate composition. These changes in stream geomorphology have likely had an impact on fish community structure; however, due to limitations in sampling methodology, few data are available on the abundances of fishes inhabiting pools, particularly in deep, non-wadable habitats. We hypothesized deeper pools in the Kings River with boulder and wood would be optimal habitat for many species, including Smallmouth Bass (*Micropterus dolomieu*). We conducted snorkel surveys, with four to eight snorkelers moving from downstream to upstream, to determine relative abundances of 14 target fish species/life stages. We snorkeled one pool/run reach at each of 20 sites. Community assemblage structure varied across pool/run reaches (NMS) along a gradient of habitat variables with some reaches being deeper with more percent boulder substrate and others shallower with higher percent sand substrate. Associations between habitat variables and individual fish relative abundances and raw abundances were evaluated using regression tree analyses. For example, higher relative abundances of quality-sized Smallmouth Bass (*M. dolomieu*) were associated with boulder volumes equal to and greater than 36.93 m^3, whereas higher relative abundances of juvenile and young-of-year *M. dolomieu* were associated with average depths less than 0.43 m. Regression tree analysis results for other species will be discussed. Increased depths were positively associated with 11 of the 14 target species/life stages examined. Structure (boulder) and substrate were also significantly correlated with multiple species/life stages. Our data highlight the value of large, deep pools for the maintenance of fish diversity in the Kings River and the potential impacts of continued gravel aggradation.

29 - Masculinization of female mosquitofish (Gambusia holbrooki) inhabiting stormwater lakes from communities using reuse water from wastewater for irrigation is more extreme than in fish present in communities using septic tanks for wastewater treatment.

Nora Demers, Charles Billy Gunnels

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Industrialization has led to an increase in hormonally-active synthetic chemicals being introduced into the environment. These chemicals, known as Endocrine Disrupting Chemicals, or EDCs, disrupt the endocrine system in humans, as well as in many aquatic wildlife. Sources of the EDC's include pesticides, pharmaceuticals, personal care products and plasticizers. When exposed to androgenic chemicals, or EDCs, the anal fin of female mosquitofish (*Gambusia holbrooki)* can become elongated and develop into a gonopodium-like structure, which is naturally only seen in male. Since the 1980's masculinized female mosquitofish has been documented worldwide in different waterways, primarily downstream from wastewater treatment facilities and pulp mill that release effluents. In southwest Florida there are many older communities still using septic tanks for their wastewater treatment. In addition, many newer communities are piping in reuse water from wastewater treatment facilities for irrigation of yards, golf courses and other turf including verges. For this study, we compared the anal fin morphology of the female mosquitofish collected from surface waters in a community using septic tanks for their wastewater treatment to anal fins from fish collected from a community using reuse water for irrigation. We found that female fish inhabiting stormwater lakes of the community using reuse water systems showed higher degrees of masculinization than female fish in the drainage canals in the community using septic. We believe this is the first study of this type being done in Florida or comparing septic and reclaimed/ reuse water systems with Gambusia as the model organisms. Our findings emphasize the importance of understanding the implications of EDCs being present in our environment. We believe there is adequate evidence to urge better treatment of wastewater at facilities to prevent the release of potential EDCs at their source into our local environment for the safety of both humans and wildlife.

30 - Analysis of Potentially Diverse Microbial Communities Discovered in Two Central Tennessee Cave Systems

Mattison Fairchild[1], Lauren Camp[2], Aspen Huseman[2], Maya Robles[2], Rocio Alferez[2], James Engman[3], Michael Taylor[3]

[1]Student- Presenter, Arkadelphia, AR, [2]Student-Member, Arkadelphia, AR, [3]Advisor, Arkadelphia, AR

While most biological communities require energy from sunlight, some relying on chemical energy have been discovered, including deep sea hydrothermal vents and some rare caves. Secret Squirrel Cave (SSC) in Central Tennessee is a presumptive chemolithoautotrophic cave. Deep in the cave is the Petroleum Passage, named because of its pervasive petroleum smell. Within it lies a pool, which contains crude oil-releasing "mini vents," surrounded by colored bands of sediment. Metagenomic sequencing (16S) of nine samples identified 593 bacteria and Archaea, including thermophiles/hyperthermophiles, and taxa that oxidize sulfur, methane, ammonia, and hydrocarbons, similar to other chemoautotrophic systems. GC/MS analysis of oil from the pool reveals degraded hydrocarbon chains, five to ten carbons long, compared to "typical" crude oil composed of fourteen to sixteen carbons. Observations of unusually high densities of salamanders and millipedes in the passage further support the hypothesis that chemolithoautotrophy is the basis for supporting multiple trophic levels. Additionally, in nearby Blue Lagoon Cave, is a rimstone pool, located on a boulder that fell from the ceiling long ago. that may contain taxa similar to SSC. The pool is lined with a viscous blue-black material surrounded by white, yellow, and brown jelly-like substances. Further genetic analysis in the pools is proceeding, along with photo documentation recording temporal variation in the SSC pond system and animal populations. Air and water samples for stable isotope carbon analysis, trace metals, anions and cations are being analyzed, with results available soon. δ13C analysis should help determine flow of energy through trophic levels. The microbes present and water chemistry will be compared to determine similarities between the two caves. This survey could provide insight into microbial species in extreme environments on Earth, and may offer a new example of systems previously suggested as potential models for life in subsurface environments on Mars.

31 - In the Face of Climate Change, Does Human Trampling Affect Dune Resilience and Alter Ecosystem Services?

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Sand dunes play a valuable role on the coastline supporting unique native species and protecting beach communities, but are threatened by human intrusion. The City of Tybee Island, Georgia, USA has undergone extensive dune restoration to expand and rehabilitate its shoreline to better defend the town against the increasing frequency of hurricanes and storm surge. New dunes, built eight feet high and a mile long, were constructed using sand pumped from offshore and vegetated with a variety of native species. Beach access points across the new and established dunes include wooden crossovers over the top of the dunes versus footpaths directly through them. To analyze the impact of human trampling on dune vegetation occurring adjacent to footpaths and crossovers in new and established dunes, we measured plant species composition, plant height, and vegetation cover over four months as well as sand accretion or erosion, path width, and colonization of previously trampled regions. Preliminary data analysis shows there is not a significant difference in the cover or species composition, but plant health measured by chlorophyll content was significantly lower next to paths in comparison to those next to crossovers. We also have found that over four months the crossover sites have accumulated twice as much sand as the footpaths, and the width of the footpaths expanded on average. These preliminary results have supported our hypothesis that footpaths negatively affect dune vegetation and its ecological role building and stabilizing the dunes. We will also conduct a greenhouse experiment on the main dune species *Uniola paniculata,* or sea oats, involving various levels of trampling in order to directly observe how it limits plant growth and reduces its photosynthetic capabilities. Full data collection and conclusions of both field and greenhouse observations will be completed in March to present a completed project.

32 - Assessing the Influence of Fire History on Wild American Chestnut Populations on Pine Mountain, Kentucky

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Today, the American Chestnut—functionally extinct by 1950, but dominant in eastern US forests until the arrival of Cryphonectria parasitica triggered mass mortality—has stagnant or declining populations. Chestnuts tend to live in a juvenile state as emergent stems succumb to blight and new sprouts emerge. Restoration efforts rely on wild native germplasm—though it is often inaccessible. Increased access to sunlight often increases germplasm production. To determine fire management's feasibility as a means to increase germplasm production in wild chestnuts, we investigated fire and land management at two Pine Mountain sites in southeastern Kentucky differing in their fire and land management history. Hi Lewis Pine Barrens State Nature Preserve (SNP) experienced three widespread arson fires (2000-2018) and clearing of aggressive native plants and a prescribed burn (2020) in parts. Bad Branch SNP, with no fire disturbances in decades, served as a control. Sampling chestnuts within thirteen 50m x 4m transects at each site, we measured height, diameter at ankle height, number of stems, blight severity, and canopy openness at each chestnut. We then explored statistical associations between fire history or site and canopy openness, chestnut density, blight status, and stem number. Chestnut density did not vary across fire history or site. Chestnuts in the prescribed burn area experienced more open canopies than chestnuts in arson or control areas. While stem numbers were similar between arson and control areas, chestnuts in prescribed burn areas had many more stems. We found no direct relationship between canopy openness and number of stems, suggesting the influence of other factors related to the prescribed burn and species removal. Both fire histories likely increased blight severity. Although we found flowering trees, data were insufficient to test if fire influenced maturity. We recommend further research into the relationship between canopy openness and stem number as well as maturity.

33 - Bird Use of Avocado Farms and Intact Forest in the Dominican Republic

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As the second-largest exporter of avocados worldwide, the Dominican Republic is seeing an increase of avocado farms and a subsequent forest loss. The island of Hispaniola is considered a conservation priority because of its high rates of bird endemism and also serves as an important overwintering ground for Neotropical migrants. Research has shown that agricultural lands can provide viable habitat for birds displaced from forests, but avocado farms have not been studied for this purpose. We conducted point-count bird surveys during the winter of 2021 at two avocado farm sites and two forest sites to determine how avian species richness and diversity differ between avocado farms and intact forest, as well as how vegetation differences between farms and forests could impact bird use. We found that vegetation structure varied significantly between farm and forest sites, but that overall bird diversity and migrant diversity did not differ between site types. However, we found that endemic bird species showed higher species richness and diversity in intact forest than in avocado farm sites and were also influenced by vegetation characteristics such as canopy cover, upper canopy height, vegetation thickness, and plant species dominance, demonstrating the importance of the protection of native dry forest in the region. Migrant birds had less species richness and diversity in the small farm compared to forest sites and the larger farm, eluding to site selection preferences based on other factors than vegetation structure. We conclude that avocado farms provide habitat for generalist bird species, some migrant species, and very few endemic species that can be considered forest-dependent.

34 - Novel detection of *Tritrichomonas foetus* protozoan within the reproductive tract of white-tailed deer in Louisiana

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During the 2013-2014 deer season, hunter harvest data from Sherburne WMA in southcentral Louisiana indicated a decrease in fawn production and lowered lactation rates of adult does. The fortuitous testing of five adult bucks for the presence of *Tritrichomonas foetus* in the following season resulted in a positive PCR (polymerase chain reaction) test from one of the samples. *Tritrichomonas foetus*, a virulent protozoan often found in cattle herds, is responsible for trichomoniasis, a sexually transmitted infection that results in spontaneous miscarriage and infertility in cows after copulation with an infected bull. In cattle, infected bulls are asymptomatic and lifelong carriers, and common practice is to cull these infected males to prevent further infection within the herd, potentially leading to substantial economic loss for cattle farmers and the agricultural industry. *Tritrichomonas foetus* is found in a variety of other animal hosts, but no available literature has been found documenting its presence in white-tailed deer. This research project aims to determine the presence and distribution of *T. foetus* in Louisiana white-tailed deer herds. Hunter harvested bucks of ages 2 ½ years and older have been sampled during the 2019, 2020, and 2021 hunting seasons in multiple locations across the state. These samples have revealed that *T. foetus* is present in herds in southwest, southcentral, and northeast Louisiana, and these findings will serve as a baseline for further research into the pathology of *T. foetus* in white-tailed deer and its potential economic effect on the landscape.

35 - Epidemiological analysis of two Salmonella serovar Kentucky lineages in food animal production and human illness

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Salmonella is a leading bacterial cause of foodborne illness and outbreaks are often linked to food animal products. *Salmonella* serovar Kentucky is polyphyletic with two genetic lineages called, Kentucky-I and Kentucky-II. While serum-based agglutination cannot distinguish between these two groups, their unique CRISPR spacer content can be used to tell them apart. In the United States serovar Kentucky is rarely associated with

human illness despite Kentucky-I isolates being commonly found in poultry. Elsewhere (e.g. Europe and North Africa) serovar Kentucky more frequently causes human illness and these are often Kentucky-II isolates. We sought to develop a surveillance platform to assess the relative incidence of Kentucky-I and Kentucky-II in food animal production and in human cases of salmonellosis in the United States. Publicly available whole genome sequence data of isolates collected by the USDA-FSIS and the CDC were analyzed in this study. We screened a total of 4,929 serovar Kentucky genomes uploaded between January 2017 and December 2021. The two lineages were identified by screening for distinct CRISPR sequences. Kentucky-I was most prevalent in swine 100% (34/34), broilers 99.8% (4687/4698), turkey 60% (9/15), and cattle 55.1% (86/156), while Kentucky-II was most prevalent in human clinical isolates 53.8% (14/26). This data suggests that serovar Kentucky-II is better able to colonize cattle and turkey hosts than swine or broilers, or that cattle and turkeys more often encounter the reservoir (e.g. environment, wildlife) of Kentucky-II. Due to Kentucky-II having a higher association with human illness, its frequency in food animals should be closely monitored, and this study highlights the importance of examining genetic differences within a serovar, rather than relying solely on serotyping data. The CRISPR sequence-based approach presented here provides a baseline for comparing future data and is an ideal way to rapidly screen whole genome sequence data.

36 - Structure-function Studies of Fibronectin Binding Proteins from Relapsing Fever Spirochetes

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The *Borrelia* genus is comprised of many spirochetes, with some species causing disease in humans. One such pathogen is *Borrelia burgdorferi*, the causative agent of Lyme disease. *B. burgdorferi* expresses an outer surface lipoprotein, BBK32, in which the N-terminus binds mammalian fibronectin contributing to adherence of *B. burgdorferi* during infection and promotes spirochetal extravasation. Meanwhile, the C-terminus contributes to evasion of the host's innate immune system by inhibiting C1r, the initiating protease of the classical complement pathway (CP). Another disease caused by related spirochetes of the *Borrelia* genus is Relapsing Fever (RF), and phylogenic analysis indicates that there are up to three separate BBK32 orthologues encoded by RF spirochetes which are termed FbpA, FbpB, and FbpC. Given their relatively conserved overall sequence identity to Lyme BBK32, we hypothesized that these RF spirochetal proteins may also contribute to CP evasion. To test this hypothesis, biochemical assays, structural biology, and surface plasmon resonance (SPR) were used to evaluate inhibitory and binding interactions of RF Fbp proteins. Our data indicate that FbpA and FbpB of *B. miyamotoi* differentially bind zymogen and active C1r protease, and differ in fibronectin binding. Structural data gives insight to why FbpA and FbpB demonstrate differential C1r active state interactions, and a potential molecular mechanism of host adaptation. These results help to better understand how bloodborne pathogens evade the immune systems of their hosts and help to understand how *Borrelia* are capable of surviving and infecting multiple hosts during their life cycle.

37 - Novel Lead Compounds demonstrating anti-biofilm properties in Staphylococcus aureus may act as Nor-A efflux pump inhibitors

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Numerous studies have shown that bacteria quantify their density and collectively carry out a certain response with a communication mechanism known as quorum sensing. Biofilms are a type of virulence factor that forms once a bacterial quorum is reached within the host, preventing the host's immune system from detecting and ultimately eradicating these pathogenic bacteria. Efflux pumps may also be involved in biofilm production. These pumps are transport proteins that are responsible for the extrusion of various substances, including toxins, quorum sensing molecules, and biofilm components. The increased activity of efflux pumps has allowed antibiotic resistant bacteria to increase their survival rates. This study tests certain drugs that were designed to resemble quorum sensing signaling molecules to inhibit biofilm formation. Since these drugs also have structural homology with known Nor-A efflux pump inhibitors (EPI) in *S. aureus,* we tested their activity on this pump. Fourteen of our previously synthesized drugs share this structural homology, with three of them revealing significant biofilm reduction in SA-1199 (wildtype) and SA-1199B (Nor-A overexpressor) but not in SA-K1758 (Nor-A knockout). This indicates that the drugs function in targeting the Nor-A pump rather than as competitive inhibitors at the receptor sites of the *S. aureus.* The conjugated aromatic ring with alternating electron-withdrawing and donating groups on the ortho and para positions appear to have an effect on the inhibitory characteristics of these drugs. Developing a cocktail of drugs that curtail quorum sensing and inhibit efflux pump activity can maximize biofilm inhibition in *S. aureus*.

38 - Honeybee Microbiome Variation Within and Between Colonies Over Seasons

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The microbial community in many animals plays a role in bodily functions such as metabolism, growth, or protection against pathogens. The western honeybee, Apis mellifera hosts a relatively stable 8 microbial symbionts in their gut. Although the composition of the gut microbiome of honeybees is relatively stable across populations, there is variation between colonies. Honeybees from different colonies can differ in the composition or abundance of the core bacteria. The reason for this variation is relatively unknown. Factors that may influence changes in abundance may include colony health or diet which can be impacted by season and location. In this study, we asked two main questions. First, are there differences between the gut and honey microbial communities of colonies? If there are differences, do they change within colonies over time? Second, are there more similarities in the gut and honey microbiome within a colony rather than between colonies over time? In Fall 2014 and Spring 2015, we collected individual bee guts and honey samples from 6 colonies from two locations in Georgia. We sequenced the 16S rRNA gene and characterized the microbial communities of bee guts and honey samples from each colony. We found that season and sample type were the significant drivers of microbial community composition between colonies. We also found that specific bacterial taxa including Bifidobacterium and Neisseriaceae were dominant within colonies across seasons.

39 - Fenbendazole exerts antiproliferative effects on cervical cancer cells by inhibiting mTOR signaling pathway

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Benzimidazole derivatives such as albendazole and fenbendazole are used for the treatment of a variety of parasitic worm infestations. Recently, these deworming drugs have gained considerable attention because of their unexpected effects against cancer. Fenbendazole (methyl N-(6-phenylsulfanyl-1H-benzimidazol-2-yl) carbamate) especially exhibited antitumor effects *in vitro* and *in vivo*. The mammalian target of rapamycin (mTOR) kinase is an important component of PTEN/PI3K/Akt signaling pathway. The mTOR signaling pathway promotes tumor progression and regulates autophagy and apoptotic cell death. Therefore, studies suggest that targeting mTOR signaling pathway could be an effective strategy for the treatment of cancer. Recently, a variety of mTOR inhibitors were developed and entered clinical studies. In the present study, we investigated the growth inhibitory effect and associated mechanism of fenbendazole in HeLa cervical cancer cells. Fenbendazole treatment resulted in significant inhibition of cell viability as measured by MTS, a sulfonated MTT derivative, assay and promoted apoptotic cell death. In cells treated with fenbendazole, we also observed decreased expression of phosphorylated mTOR and mTOR signaling complex constituents such as Raptor and Rictor. The inhibition of mTOR resulted in the inactivation of its target proteins such as ribosomal protein S6. Taken together, these results indicate that fenbendazole could be a potent inhibitor of mTOR signaling in HeLa cells and suggest its potential use as chemotherapeutic agent against cervical cancer.

40 - Impact of L282R on PSEN1 Protein Shape and Phenotype

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Alzheimer’s Disease (AD) is a type of dementia that affects memory and behavior. For our research, we're interested in the genetics of this disease. In previous studies, most patients who developed early-onset AD possessed specific genes or gene variants that were inherited. [1],[2]Our research focused on the mutations in *PSEN1*, which codes for the Presenilin-1. Presenilin-1 forms the catalytic subunit of the gamma-secretase complex whose function is the cleavage of the amyloid protein from APP. Pathogenic mutations in *PSEN1* can lead to an accumulation of the longer, hydrophobic version of Amyloid-β peptide. These accumulations are associated with plaques found in patients with early-onset Alzheimer’s[3]. We examined a *PSEN1* variant of unknown significance (VUS), a point mutation: c.845T>G. This substitution causes an amino acid substitution from leucine to arginine at position 282. The cytogenic location of the variant is 14q24.2 and its genomic location is 14:73198106 (GRCh38).[4] Other variations of *PSEN1* on ClinVar are associated with Alzheimer’s, Pick’s, Acne Inversa, and cardiomyopathy. We used YASARA protein mapping to analyze the 3D features of L282R and completed metrics with sequencing tools, structure and protein dynamics. SIFT, PolyPhen 2 and other algorithms revealed L282R to be likely pathogenic. These will be presented along with cross species multiple sequence alignment, RVIS conservation, and other analysis. It is anticipated that the L282R variant of *PSEN1* will cause a pathogenic phenotype which could include dementia.

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41 - Phosphorus recycling by cyanobacteria

Precious Richard, He Quingfang

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Phosphorus is an element that is required in several (bio)molecules for survival. In organisms, they are obtained as organophosphate. Organophosphates are compounds containing C – O – P linkage. Examples include ATP. Organophosphate esters have been studied for many years, less examined are organophosphonates. Organophosphonates are compounds containing C – P linkage. Understanding organophosphonate metabolism is important for understanding phosphorus cycling. Although other pathway(s) for the uptake and breakdown of organophosphonate has been identified, the common pathway is the C – P lyase's pathway which has its components grouped in the phosphate (Pho) regulon. Multiple studies have pointed that, microbes utilize uncharacterized pathways for organophosphonate metabolism. Such studies led by Gomez-Garcia et al., investigated whether two species of *Synechococcus,* OS-A and OS-B, had the ability to grow when supplied with organophosphonate as their only source of phosphorus. Their result showed that both species survived on media containing methyl-, ethyl-, or aminoethylphosphonate as the sole phosphate source! Both species contain several genes within the Pho regulon, *Synechococcus* OS-A lacks canonical genes for organophosphonate transport and C-P lyase. They inquired, "how does *Synechococcus* OS-A achieves organophosphonate breakdown?" Using a relatively well-characterized *Bacillus cereus* phnase as an anchor for homology searching, they identified 3 putative phosphonatases (phnases) responsible for organophosphonate metabolism.

We propose to study these enzymes by overexpressing them heterologously in the model cyanobacterium *Synechocystis* PCC 6803 and explore their commercial potential in detoxification of fungicides and recycling of unusable phosphonate. We will express and characterize the 3 putative phnases and identify their catalytic products. And further explore the possibility of using these enzymes to breakdown selected fungicides and phosphonates after verifying their roles as phnases and subsequently unravel its novel mechanism of organophosphonate breakdown. Patents will be filed after we achieve significant results.

42 - Development of Transparent Transgenic Zebrafish phenotype to Study NFkB Activity

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NF-κB signaling has broad effects by influencing cell survival, tissue growth and proliferation. NF-κB controls many genes which involved in inflammation and active in many inflammatory diseases and elevation of NF-κB activators and associated with elevated mortality, especially in cancer and cardiovascular diseases. Our laboratory established zebrafish model to study the cell death (Annexin-5) and inflammatory (NFkB) process in cardio-oncology research. In vertebrates, in-vivo spatial resolution is limited due to normal opacification of skin and subdermal structures. For in-vivo imaging skin transparency is primary requirement and to maintain transparency, blocking pigmentation needs to maintain. Blocking of pigmentation can be maintained by chemical inhibition by block melanization. Zebrafish casper mutant maintain transparency throughout life and serve as ideal combination of sensitivity and resolution for in-vivo stem cell analyses and in-vivo imaging. We are developing NF-kB:GFP/Casper transparent transgenic zebrafish cellular phenotype to study an in-vivo inflammatory process by generating transgenic transparent zebrafish progenies. We have designed experimental setup of heterozygous progeny (F1 to F4 generations) and homozygous (F5 generation). We have Cross bred the Casper and NFkB Transgenic adult fish and generated F01 to select and sorting of the transgenic and non-transgenic larvae via fluorescence microscopy. F01 larvae expressed transgenic and non-transgenic expression. Transgenic F01 heterozygous progeny showing only normal skin pattern Newly generated F02 larvae have transgenic and non-transgenic expression showing only normal skin pattern at adult stage. Newly generated F03 heterozygous larvae have transgenic and non-transgenic expression and at the adults of the shows casper transparent and normal skin pattern. For F04 generation only casper background strain selected. Newly generate transparent transgenic zebrafish phenotype will be establish for time lapse in-vivo confocal microscopy to study of Cellular phenotype/pathologies of the cardiomyocytes over time and will quantify the changes in cardiomyocyte morphology and function overtime, comparing control and cardiac injury models

43 - Investigating alternative nursery methods for Spartina alterniflora

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Coastal salt marshes provide significant ecosystem services; however, approximately 50% of salt marshes globally have been lost or degraded, and thus there has been increased effort to restore these habitats. *Spartina alterniflora* is the dominant plant species in salt marshes along the East and Gulf Coasts of the United States, playing a critical role in salt marsh growth and maintenance, and is therefore the primary species used in plantings during restoration. The aim of this research was to utilize a constructed wetland designed to remediate aquaculture effluent for the nursery production of native Georgia *S. alterniflora* for salt marsh restoration. The constructed wetland was divided into four cells, and two cells were stocked with *S. alterniflora* while the other two cells remained unvegetated (control). Effluent from a recirculating freshwater aquaculture system circulated through each cell and then cycled back into the aquaculture tank. *S. alterniflora* plants were also grown using traditional nursery methods on two tables placed near the wetland. Measurements of plant growth and productivity were collected for all plants weekly between May and September 2021, representing the growing season for *S. alterniflora*, and compared between traditional methods and the constructed wetland. Additionally, water samples were collected weekly for measurements of organic nitrogen and phosphorus to identify the remediation potential of the non-vegetated and vegetated wetland cells. Preliminary results suggest that there is no significant difference between wetland and traditional treatments in plant growth and productivity. Additionally, no significant difference was found for remediation between vegetated and non-vegetated cells, but water quality remained in a range conducive to a healthy aquaculture system. These results suggest (1) a constructed wetland can serve as a production method for *S. alterniflora*, providing material for future restoration projects, and (2) *S. alterniflora* does help maintain optimal water quality of an aquaculture system.

44 - Potential and Actual Hybridization between Sarracenia jonesii and Sarracenia purpurea var. montana, Pitcher Plants of Conservation Interest

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Sarracenia jonesii (Jones' pitcher plant), a federally threatened species, is sometimes outplanted into sites with its congener Sarracenia purpurea var. montana (mountain purple pitcher plant), a federal species of concern. Multiple sources suggest 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 led us to ask about the potential for, and realization of, interspecific breeding. For two summers we monitored S. jonesii and S. purpurea var. montana at sympatric western North Carolina field sites. Parental species and their phenotypic hybrids were visited weekly during the flowering season to assess phenological stages and to collect anthers for pollen viability analysis; fruits were collected after floral senescence to analyze seed production. Tissue was taken from all plants for molecular genetic confirmation of hybrid status. 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. 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.

45 - Dominant plant species, not plant species diversity, affects arthropod biodiversity

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When addressing the effects of habitat loss on biodiversity decline, we often assume habitat is lost non-selectively. However, habitat loss is frequently aggregated with respect to the producer species comprising the habitat. Theoretically, selective habitat removal decreases diversity of available resources for organisms at higher trophic levels as well as amount of available habitat. We therefore expect selective habitat loss to reduce biodiversity more than non-selective habitat loss. To test this hypothesis, we implemented two different types of habitat loss at the plant community level and compared arthropod biodiversity between them. In the first type, we reduced habitats by 50% non-selectively, maintaining relative abundance of plant species. In the second type, we reduced habitats by 50% selectively, removing all but one dominant plant species. In each habitat, one of three plant species was dominant: A. tuberosa, S. altissima, or B. alba. While selective habitat loss resulted in greater reduction in arthropod species richness compared to non-selective habitat loss, neither type of habitat loss affected effective number of species (ENS) compared to controls. Instead, differences in ENS between habitats were explained by the identity of the dominant species within the habitat. S. altissima- dominant habitats had higher arthropod ENS than B. alba or A. tuberosa-dominant habitats, indicating that the variety of resources provided by a single, generalist plant species is more important for arthropod evenness than plant species diversity. Our results suggest that presence of generalist plant species may mitigate effects of both selective and non-selective habitat loss on biodiversity at higher trophic levels.

46 - New insights into the reproductive dynamics of the Federally endangered Short's bladderpod (Brassicaceae: *Physaria globosa*)

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Physaria globosa (Desv.) O'Kane & Al-Shehbaz (Short's bladderpod), is a Federally endangered species listed as globally imperiled (G2) and limited to just 33 populations across Tennessee, Kentucky, and Indiana. Habitat degradation and loss appear to be the most significant barriers to long-term survival in *P. globosa*, compounded by limited population sizes and geographical isolation. Pollen limitation has been shown to be a limiting factor for seed production in fragmented populations, affecting smaller populations at higher rates than larger ones. Factors such as resource availability, fragmentation, and plant competition may play a role in simultaneously decreasing both floral density and reproductive success by disrupting mutualistic pollinator interactions. Since *P. globosa* is geographically isolated and currently exists in relatively small populations, it is likely that some populations may be pollen limited. To better inform the recovery of *P. globosa,* relationships between plant density, size of floral display (measured by number of flowering stems per plant), stem diameter, frequency of pollinator visitation, and seed production were evaluated in five populations: two in Tennessee, two in Kentucky, and one in Indiana. Ten plants from each population served as focal plants; for each plant, 10 flowers received pollen via natural pollinator visitation and 10 received supplemental pollen from conspecific donors in addition to open pollination. After 48 h pistils were collected, stained, and visualized under fluorescence to quantify pollen germination and growth. Seed from each focal plant was bagged and counted at the end of the flowering season. Preliminary results indicate pollen limitation is a significant factor in four of the five populations. Relationships between plant density, stem diameter, and overall fecundity are currently being explored. However, a strong correlation exists between stem diameter and number of flowering stems per plant, which may indicate an indirect relationship between stem size and plant age.

47 - Ecophysiological explanations for spatial and temporal variations in autumnal coloration within the canopy of ornamental red maple (Acer rubrum) and Freeman maple (Acer x freemanii) trees

Claire Martin, Howard Neufeld

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Leaves of some urban red maples turn red at the top of the canopy before the bottom (Freeman maples, *Acer x freemanii*), while others have leaves that turn red simultaneously all over (*A. rubrum* 'Armstrong'). Our research investigated ecophysiological mechanisms governing spatial and temporal variation in autumnal red coloration in both tree varieties. We compared leaves from upper (8-9 m) and lower (2 m) canopy locations to see if coloration differences arise from environmental or physiological differences, or both. We used a bucket truck to reach leaves and weather stations to measure microclimates at two heights. Wind speed and solar energy were the only environmental variables that differed between upper and lower leaves, and were higher at the top of the canopy. Lower leaves of Freeman maples leafed out first, reached full size ~13 days earlier, and persisted longer (~18 days) into the fall than upper leaves, resulting in longer leaf lifespans by ~14 days. Mid-summer chlorophyll content in Freeman maples was higher in lower leaves, and in fall, anthocyanins accumulated earlier and to a greater extent, in upper leaves, whereas no such differences occurred in *A. rubrum*. Photosynthetic rates and nitrogen content were higher in lower leaves of Freeman maples, but did not differ in *A. rubrum*. Higher photosynthetic rates in Freeman maples correlated with higher chlorophyll and nitrogen contents, while early and greater accumulation of anthocyanins in upper leaves correlated with lower nitrogen content, a factor known to elevate leaf anthocyanin content. Lower nitrogen in upper leaves could be the proximate driver for early anthocyanin synthesis in upper leaves of Freeman maples, but not *A. rubrum* maples. The results of this study also provide insight into intra-canopy variation in leaf ecophysiology of open-grown trees in an urban environment, which will help with future ecophysiological modeling studies.

48 - Exploring the Photosynthetic Capacity of Various Needle Ages in Fraser Fir (Abies fraseri) Christmas Trees

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Fraser fir (*Abies fraseri*) Christmas trees contribute approximately $100 million to the economy of western NC annually. Unlike *A. fraseri* growing in their endemic, high elevation habitat of the Southern Appalachian Mountains, commercially grown varieties are trimmed annually to create the classic Christmas tree-like canopy. Such trees have denser canopies than their native counterparts, but little is known about how changes in tree architecture affect carbon assimilation. We studied light interception and photosynthetic characteristics of three needle age classes (current, 1, and 2 yr old) on 2 m tall farm-grown Fraser fir trees near Boone, NC. We hypothesized that gas exchange would decline due to aging, but also because of declines in light penetration by the dense canopy. We measured light depletion at three canopy depths using a Li-1500 Quantum Sensor Logger, light response curves on detached planar needles and on twigs with naturally oriented needles using an Li-6800 gas exchange system, and chlorophyll, minimum stomatal conductances, and epicuticular wax content. Direct light intensity on a sunny day near noon was ~2000 µmol m^{-2} s^{-1} for current year needles but decreased to just 3% and 1% at typical canopy locations for 1 and 2 yr old needles, respectively. Apparent quantum efficiency, maximum photosynthesis, and light saturation were lowest in 2 yr old planar needles, while dark respiration, maximum photosynthesis, and light saturation were lower in 1 yr old twigs. Chlorophyll was highest in 2 yr old needles, while minimum stomatal conductances and epicuticular wax content did not differ among needle age classes. A decreased light environment, high chlorophyll, and low photosynthetic rates in 2 yr old needles indicate the need for further research to determine why older needles are retained inside the tree canopy given their low or even negative contribution to the carbon budget of these trees.

49 - Restoring the Roan: Red Spruce Forest Understory Responses to Canopy Gaps at Roan Mountain, NC

Thomas Hennessey

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Red spruce-Fraser fir dominated forests are considered threatened in the southern Appalachian Mountains and are known to support a variety of rare and endemic species. This study explored the effectiveness of different sizes of canopy gaps in boosting seedling and understory growth and recruitment in these forests at Roan Mountain, NC, with the goal of identifying a successful management strategy that mirrors historically natural processes. Seedling survival and soil respiration were monitored over the first growing season after gap creation (June-October 2021) to gain insight into gap effects on seedlings and CO_2 exchange. Soil rings, half of which were scarified to mimic squirrel foraging activity, were established in center and edge of five 10m-diameter gaps, five 3.5m-diameter gaps, and four nearby uncut patches. 1x1m quadrat monitoring at the beginning, middle, and end of the growing season revealed a >90% survival rate of red spruce and Fraser fir seedlings in all plots that contained clusters of them, indicating no immediate negative effect of any gap size on seedling health. Preliminary analysis of weekly soil respiration observations indicates that mean soil CO_2 efflux was significantly lower in 10m multi-tree gaps than in either 3.5m single-tree or uncut areas and that edges of multi-tree gaps had significantly higher efflux than gap centers when soil was scarified. Time had strong effects on soil respiration in all cases, with peak efflux occurring from late July through late August in all cases. This information suggests that multi-tree canopy gaps 10m or greater in diameter may have negative effects on root and microbe processes in these forests that diminish toward the gap edge, and that single-tree 3.5m gaps may be the most beneficial management tool for stimulating red spruce and Fraser fir growth with minimal mortality over multiple seasons.

50 - Examining the Physiological Stress Response of Prairie Lizard, Sceloporus consobrinus, following Extirpation of Keystone Predator, Crotaphytus collaris

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Keystone predators, defined by their pivotal role in food webs, exert top-down control via predation and competition, which promotes biodiversity by regulating population abundances at lower trophic levels. Under the risk of predation, prey organisms must trade off opportunities for foraging, mating, growth, with other physiological requirements for more immediate energetic mobilization. Consequently, these physiological and behavioral trade-offs further alter community dynamics and nutrient cycling, through modified energy allocation and fitness. In the Ozark Highlands of Arkansas and Missouri, regionally-imperiled glade habitat is home to state-threatened keystone predator the Eastern Collared Lizard, Crotaphytus collaris. Habitat degradation has led to local extinctions which enables comparative studies of keystone predator-prey interactions between glades with and without C. collaris. While keystone predator studies often focus on resulting diversity and abundances of prey in response to presence/absence of keystone species, here I investigate the physiological stress responses and life history tradeoffs of collared lizard prey, Sceloporus consobrinus. Specifically, I assess metabolic and reproductive metrics, through corticosterone, glucose, and lactate concentrations and maternal investment, between S. consobrinus populations which are sympatric and allopatric to C. collaris. Results will provide insight to both the ecological and physiological consequences of keystone species loss.

51 - Investigation of a shell-rot disease affecting freshwater turtles in a northeast Louisiana bayou

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Freshwater turtles that inhabit Bayou Desiard have been studied by ULM faculty for 20 years. In this time, researchers have observed turtles in the family Emydidae were exhibiting chronic ulcerative shell lesions. This is to be the first investigative study into the disease in this area. Investigators hope to assess the ecological impact of this event by determining the percentage of total population affected as well as the geographic distribution. Originally, disease distribution was thought to be isolated to the 500 m of bayou that runs through the ULM campus. However, researchers have discovered the lesions are present as far north as the headwaters where Bayou Desiard connects to Bayou Bartholomew. Since June of 2020, 397 turtles have been captured in Bayou Desiard. Of these, every species that is normally found in Bayou Desiard is represented at least once. From the 397 turtles captured, 272 individuals belonged to the family Emydidae. 85 exhibited shell lesions which results in a 21.41% prevalence rate within the total population. However, the captured individuals who exhibited lesions belonged exclusively to Emydidae, resulting in a prevalence within that family of 31.25%. Infected turtles that are captured are held in the lab as behavioral and physical data are collected and then euthanized according to IACUC protocol. All turtles exhibiting lesions are scored according to the method (Total Shell Disease Score) of Hernandez, et al. (2009). Turtles receiving a TSDS of ≥15 (out of 24) exhibited a depressed mentation and slowed righting response. Turtles with a TSDS of ≥20 exhibited severe lethargy demonstrated by absence of a righting response and decreased flexor response. Turtles captured that demonstrated lesions with a TSDS score of <6 were released. Turtles with similar shell lesions have been documented in other states, but none have been successful in documenting a causative agent.

52 - Additional evidence of prey discrimination by Red Hills Salamanders (Phaeognathus hubrichti)

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The Red Hills Salamander (*Phaeognathus hubrichti*) is a large fossorial plethodontid endemic to six counties of south-central Alabama. A nocturnal sit and wait predator, they attempt to consume most invertebrates moving close enough to the burrow entrance for the salamander to attempt capture without it leaving its burrow. Previous work in Monroe Co., AL showed salamanders ignoring chemically protected Opiliones (Harvestmen), a common potential prey, while consuming a variety of other invertebrates suggesting dietary selectivity. In this study, we used six IR capable video cameras to document salamander behavior at a site in Wilcox Co., AL. From four one-day recording sessions (Oct 2012, June 2013, Oct 2013, June 2014), we accumulated 193 camera-hours of salamanders active at their burrow entrances. Depending on camera settings (close or far), one, two or three salamanders were visible on a single tape. Salamanders consumed 65% of prey items they attacked to include xystodesmid millipedes (Polydesmida, Xystodesmidae) which produce cyanide gas as a defensive mechanism. However, they recoiled from *Narceus americanus/annularis* (Spirobolida, Spirobolidae) which produce benzoquinones. We also observed one not attacking a scarabid beetle, yet they consumed carabid beetles (Carabidae), most of which produce defensive chemicals. Red Hills Salamanders appear to be using prey movement as a discriminator, remarkable in that they are usually hunting in near-to-complete darkness (to the human eye) as their habitat is shaded by a hardwood overstory. They are also relatively long-lived (> 11 years) suggesting salamanders learn which prey are palatable, then select or reject potential prey based on how it moves. This study also raises questions about how lungless salamanders react to the variety of defensive chemicals produced by potential prey, especially those that are gas rather than liquid.

53 - Heterochrony and the development of armored dinosaurs (Ankylosauria: Dinosauria): implications for taxonomy and phylogeny

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Ankylosaurs generally form a rare component in most dinosaurian faunas, and thus, their ontogenetic variation is relatively poorly understood. Confidently identifiable juvenile material is especially scarce. The proliferation of bony armor, characteristic for the group, complicates taxonomic inferences by obscuring cranial and other osteological characters. Here we apply paleohistological techniques to juvenile ankylosaur material to examine the ontogeny of their postcrania and armor. In addition, two juvenile specimens, one undescribed, from southeastern North American deposits add information to our understanding of the timing of osteogenic events.

Histologically, all sampled juvenile limb bones show tissues indicative of overall growth rates (azonal fibrolamellar microstructure with incipient primary osteons) slower than other ornithischian dinosaurs (like those suggested for *Stegosaurus*, but higher than those for *Scutellosaurus*). Adult ankylosaur postcrania include entirely remodeled bone and lack any indication of a primary growth record (including any discernible cyclical growth marks).

The use of dermal armor, useful in determining the absolute age of other archosaurs like crocodilians, has some potential for determining relative age in armored dinosaurs. The histology of the cervical half-rings of basal ankylosaurs and nodosaurids indicates metaplastic mineralization of the dermis, which is the expected developmental pathway for archosaurian osteoderms. A deep bony band, only seen in ankylosaurids, lacks metaplastic tissue, and mirrors the development of cranial ornamentation in that family. Analysis of juvenile *Pinacosaurs* specimens indicates that the ossification of this band occurs prior to metaplastic ossification of the overlying dermis.

Combining paleohistological techniques with the few available juvenile ankylosaur specimens (namely the ankylosaurid *Pinacosaurus* from Asia and two nododarurid specimens from southeastern North America) allows us to piece together the timing of skeletogenic events during the development of these animals. A stronger understanding of the timing and progression of skeletogenesis in these animals will better inform taxonomic decisions and phylogenetic interpretations.

54 - A Novel Light Detection and Ranging (LiDAR)-Based Methodology Improves Detection and Monitoring of Green Salamanders (Aneides aeneus)

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Green Salamanders (*Aneides aeneus*) suffer from data deficiency that limits an understanding of the species' geographic distribution and impedes the robust design of species-specific conservation measures. A major driver of this data deficiency is that rock outcrops used by Green Salamanders are often difficult to remotely detect in dense Appalachian hardwood forests, as most outcrops remain hidden under the forest canopy and therefore invisible when relying on aerial orthoimagery to remotely pinpoint habitat features and select survey sites. We developed a novel method using light detection and ranging (LiDAR) point cloud data to remotely identify small rock outcrops harboring potential Green Salamander populations, testing this method during the environmental assessment phase of a proposed USDA Forest Service timber management project within the Cumberland Mountains Physiographic Province. We specifically compared our LiDAR-based approach with the visual identification of rock outcrops across the same area using aerial orthoimagery. Our LiDAR-based approach identified three times as many rock outcrop sites as aerial orthoimagery, resulting in the field verification of four times as many previously unknown populations of Green Salamanders than would have been possible if relying on aerial orthoimagery and expert knowledge of local terrain to guide survey design. Our results indicate that LiDAR-based methods may provide an effective, efficient, and low-error approach that can vastly improve the success of Green Salamander inventory and monitoring methods, especially when researchers lack pre-existing knowledge of local terrain and the location of habitat features.

55 - Preliminary Population Size Estimate of Aquatic Salamanders in Experimental Ponds in the Mississippi Delta

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Amphiuma tridactylum and *Siren intermedia* are pollution sensitive aquatic salamanders that inhabit wetlands, ponds, and ditches. There is very little information on the population dynamics of the two species within the Mississippi Delta. Within Delta State University's Center for Science and Environmental Education, five man-made ponds were used to study A. *tridactylum* and *S. intermedia* to determine population sizes and movement patterns. Modified commercial minnow traps baited with bacon and chicken were used to capture the salamanders as safely as possible without causing too much disturbance in the habitat. Once captured the salamander was placed on a wet foam mat to help prevent injuries and desiccation. Overall length (cm) was measured, and individuals were checked for Passive Integrated Transponders (PIT tags) that may have been inserted during a previous study. If no PIT tag was detected, a PIT tag was inserted into the muscular part of the hip. The salamanders were then returned to the original pond from where they were captured. Few animals were recaptured which may be due to mortality from pollution (crop duster overspray), predation (predaceous diving beetles eating gills), or subterranean movements into nearby drainage ditches. Future studies will include the nearby drainage ditch and chemical analysis of the water. This study could be useful for wetland restoration and wildlife management in the Mississippi Delta.

56 - First Glimpse of Water Fluxes in a Bottomland Hardwood Forest in Northeast Louisiana

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With 2021-22 declared as Water Flux years, it is timely that we make efforts in understanding water and energy fluxes in forested ecosystems. Water and heat flux data was collected for a Bottomland Hardwood Forest (BHF) ecosystem located at Russel Sage Wildlife Management Area in Southeast United States. The site consists of mature closed-canopy hardwood trees with an average canopy height of about 27m. Evapotranspiration (ET) and latent heat data (LE) from 2013 to 2018 from the US-ULM Tower (37.30m) was used to characterize seasonal and annual fluxes. From March to September, the latent heat flux was characterized by a distinct diurnal pattern with the highest values (146 w/m^2) centered around solar noon. Further, the latent heat flux values were higher than sensible heat flux values during late Spring through Summer season (127w/m^2, 145w/m^2) respectively. Sensible heat flux (Δ36w/m^2) was greater than latent heat flux (Δ28w/m^2) during winter-spring transitions where temperature fluctuations are maximum (-5 to 20ºC). The Bowen ratio ranges from 0.12 in Summer to 1.23 in Spring. The average daily evapotranspiration values vary from 0.52 mm/day in winter to 5.20 mm/day during summer. Our findings indicate that total incoming solar radiation, soil moisture availability, vapor pressure deficit (VPD), and temperature collectively determine the rate of evapotranspiration and heat fluxes in these forests. With long-term monitoring of these fluxes, we can improve our understanding of hydrological and energy budgets and develop more accurate climate models for ephemerally flooded forested wetlands; a critical, but understudied ecosystem in this regard.

57 - Loss of relict oak forests along coastal Louisiana: A multiyear analyses using Google Earth Engine

Paurava Thakore, Joydeep Bhattacharjee

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Coastal forests across the Southeast and Gulf of Mexico are known to be diminishing at an alarming rate. The Live-Oak dominant Chenier forests of Southeast Louisiana are amongst those exhibiting the steepest declines. The remnant stands have experienced numerous hurricanes and intense storm events in recent years calling into question the current volume of this resource. Despite their noted ecological and physiographic importance, there is lack of an accurate representation of forest loss and wetland extent for this region in any nationally driven geographic data repository. Supervised Machine Learning algorithms in Google Earth Engine are used to classify and process high-resolution National Agricultural Image Product (NAIP) datasets to create accurate (>90%) Tree Cover Maps of the Louisiana Chenier Plains in Cameron and Vermilion parishes. Three years of data (2003, 2007, 2019) are used to map 2,302 km^2 in series. In this region, between 2003 and 2019, we document a 35.73% loss in forest cover. The majority of the land-use change was to salt-marsh, with losses documented in pastoral lands as well. We find variable rates of loss in regard to elevation. Forest cover losses correspond strongly to rises in Mean-Sea Level. These findings deliver a baseline understanding on the rate of forest loss in this region tying into efforts of restoration and protection of imperiled ecosystems along the Gulf Coast.

58 - Modeling red spruce (Picea rubens) restoration potential in Virginia under current and future predicted climate change

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Global climate change threatens many species across the planet. High-elevation tree species, such as red spruce (*Picea rubens*), face significant and immediate threats from climate change. Red spruce has faced anthropogenic disturbances for over a century and is only recently beginning to regenerate across its range, making it an ideal restoration candidate. Ecological niche modeling has become a common method of identifying the suitable habitat of a species, providing vital information to land managers carrying out restoration efforts. In this study ecological niche models were used in a novel way, predicting distribution and habitat suitability separately to determine the spatial extent to which red spruce can be restored. In addition to models, surveys were conducted to elucidate the current regeneration trends of red spruce. Furthermore, climate projections were used to determine how restoration potential may change over the course of the 21st century. Comparisons between distribution and habitat suitability models indicate that there is additional habitat available for red spruce to expand into. Regeneration surveys show that there is positive regeneration both within and beyond red spruce canopies, validating model comparisons. Climate change projections indicate total elimination of suitable habitat in Virginia by 2100. However, these projections likely predict increased competition for red spruce from low elevation competitors as opposed to physiological limitations imposed by climate change. It is therefore prudent to protect established populations and encourage further regeneration by planting in higher elevations where competition is limited.

59 - Variation in potential spring freezing damage in trees

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Within temperate forests, initiation of leaf-out marks the beginning of the growing season. Climate change is shifting leaf-out dates to earlier in the spring due to milder winter and warmer spring temperatures. While earlier spring phenology can create increased carbon uptake, earlier leaf-out places trees at increased risk of frost damage from late winter or early spring freezing events. Indeed, late spring frost events remain as severe and frequent throughout much of the US even though mean annual temperatures are increasing. Determining which species are more at risk of frost damage throughout the spring will be vital in conservation efforts and provide insight into which species may be winners and losers under future climates.

For this experiment we chose three tree species that are common throughout the eastern United States: *Liriodendron tulipifera, Fagus grandifolia,* and *Acer saccharum*. We sampled six buds from six separate trees located near the Austin Peay State University campus. Samples were collected two weeks prior to the mean last frost date for the sample site (~April 8th). The samples were then subject to a freezing treatment with a sample bud from each species being frozen to a target temperature of 4, -2, -5, -8, -11, or -40°C. By freezing bud samples, we determined the temperature where 50% of the leaf/bud tissues were damaged (LT_{50}) for the three species. Preliminary results for *L. tulipifera* show a LT_{50} of –11.80°C (SD: 3.66; SE: 1.49), *F. grandifolia* at –7.69°C (SD: 5.22; SE2.13), and *A. saccharum* –9.77°C (SD: 4.01; SE 1.64).

When accounting for phenological timing, all three species have sufficient freezing resistance to withstand most late spring frost events. However, as phenology shifts earlier into the spring species with later phenology like F. grandifolia and maintains lower freezing resistance may be susceptible to spring freeze damage under future climates

60 - Correlative modeling for predicting the potential distribution of Maize pests and pathogens within the United States

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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 WoldClim 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 *Heteronychus 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 near an ocean. These maps can be used to efficiently direct preventative action to high-risk areas.

61 - Status and habitat surveys for the critically imperiled Tall Barbara’s Buttons (Marshallia legrandii)

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Tall Barbara’s Buttons (*Marshallia legrandii*) is a critically imperiled perennial flowering herb in the Asteraceae family with just two known population locations: Difficult Creek Natural Area Preserve, Halifax County, VA and Picture Creek Diabase Barrens, Granville County, NC. Surveys were carried out for the two locations in summer 2021. Plant habitat measurements were also performed to provide a more robust description of the species ecology and characteristics of the environment where it is found. At the Picture Creek Diabase Barrens population, we mapped the current size and extent of the sub populations of *Marshallia legrandii* and compared these findings to known occurrences surveyed 9 years earlier. We described the physical environment where the species is found by measuring the range of light conditions, competing vegetation structure, soil moisture, and soil nutrients at each of the sub populations and compared these values to corresponding flowering density. Transects taken across the largest sub population will provide descriptive measures of the physical environment where *Marshallia legrandii* is found flowering and where its flowering and vegetative presence abruptly ends. Patterns at Picture Creek Diabase Barrens are compared with the current size and extent of the population surveyed at Difficult Creek Natural Area Preserve. The results of the study describing the present status and extent of the species will inform conservation efforts by providing guidance for potential plantings to augment the population of this rare plant.

62 - Habitat Suitability Modeling and Site Verification for the White Fringeless Orchid (Platanthera integrilabia) in Alabama

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The white fringeless orchid (*Platanthera integrilabia* (Correll) Luer) assumes a relatively broad but sporadic distribution across the mountainous region of the southeastern U.S. Prior to this project, extant occurrences in Alabama were only documented from 9 sites, although there appears to be a large amount of suitable habitat across the northern section of the state. Habitat suitability models were created, from which medium- and high-suitability sites were selected for ground verification. A total of 71 sites were surveyed and 61 percent of those were verified as having either high or medium habitat for the species. These surveys also led to the discovery of three new occurrences. These three occurrences and four additional occurrences which were part of a separate survey effort were then added to the presence locations used to create a post-survey model. This post-survey habitat model performed best overall and may be useful for guiding future white fringeless orchid surveys.

63 - Preliminary Vascular Flora of the Walls of Jericho in Jackson County, Alabama and Franklin County, Tennessee

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The Walls of Jericho is a 5,062 ha tract of land purchased in 2004 by the Alabama Chapter of The Nature Conservancy through the Forever Wild Land Trust Fund and incorporated into the greater Skyline Wildlife Management area. The greater WOJ spans both AL and TN and occurs on the southern edge of the Cumberland Plateau, which in this area is characterized by sandstone caps transitioning into jagged karst limestone valleys. Throughout many cliff faces and bottomlands is an extensive karst network that support many calciphilic plant species, which are rare or uncommon in the surrounding areas and greater Cumberland Plateau. In 2009, London and Kuehn reported 12 rare, threatened or endangered vascular plant species within the AL WOJ. In 2011, The Alabama Natural Heritage Program documented 29 S1 and S2 vascular plant species in Hytop, an area adjacent to WOJ. To date, 310 species have been documented for the greater WOJ, representing 196 genera and 93 families. Here we summarize the known flora for this two-state protected area as well as report ongoing efforts to more fully document the AL portion, which has a greater karst component compared to the TN side.

64 - Not your grandfather's field manual: Approaches to enhancing plant taxonomy, floras, florulets, field apps, taxon concepts, conservation ranks, and databases for conservation decision-making in the 2020s

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For the broadly defined Southeastern United States (including all or parts of 25 states), we have put together at UNC Herbarium (North Carolina Botanical Garden, UNC-Chapel Hill) a team of botanists, data scientists, and app developers to develop a diversity of flora products for field and office use based on the FloraManager database system. The database uses modern taxonomy, with extensive cross-walking using taxonomic concept mapping principles to regional floras and taxonomic literature. Flora products are being developed for and with Heritage Programs, NGO partners, NPS and other federal cooperators, and with flexible formatting options including paper, pdf, and web formats, with ability to include in products at any scale (from regional to state to tract), include both multiple access (graphic) and traditional dichotomous keys, illustrated or not (with photographs and drawings, including diagnostic photos), with custom fields for local partners (state-specific habitat data, list of natural areas of occurrence, etc.), and useful conservation rankings (GRanks, SRanks, Wetland and CoC rankings, Grasslandiness (heliophily) ratings, etc. We have additionally developed a tool to map names from various digital platforms to a more modern taxonomy using both distribution and the entire list to help narrow the choices down. Managing information on the flora of the region digitally in the flexible FloraManager database provides us the ability to take best advantage of current taxonomy at all scales, and to engage and use data, knowledge, and even wisdom at scales from global to local. We are building out this ability and collaborations with the NatureServe Network as primary, but also strongly with federal conservation and land-managing agencies and with private and public funding.

65 - Standards for conducting an iflora: Using iNaturalist to conduct a vascular flora of the Charles B Henson Cave Preserve in Dade County, Georgia

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Today's rate of biodiversity loss in the face of climate change and human disturbance urges scientists to quickly capture as much biodiversity data as possible. Citizen science is a tool with great potential for aiding scientists in the collection of this information. The citizen science platform iNaturalist simultaneously enables mass data collection and establishes a digital database accessible to scientists anywhere, anytime. The standardization of floras has been a focus of botanists, including Palmer (1995), who listed a complete set of the requirements that all botanists are urged to follow to maximize both data point cohesiveness and broader data quality. The focus of this paper is the evaluation of an iNaturalist project's ability to meet Palmer's standards and the preliminary collection of biodiversity data of the Charles B Henson Cave Preserve in Dade County, Georgia. The goals of this study were to: (1) assess the ability of an iNaturalist project to meet Palmer's standards for conducting a flora, (2) conduct a digital flora of the Charles B Henson Cave Preserve, and (3) evaluate the ability of an iflora of this nature to capture meaningful biodiversity data. Between March and October 2021, fourteen site visits were conducted, resulting in 469 total observations. Of these, 163 were identified to species using iNaturalist's identification tool, and 163 are research grade. The observations identified to species consist of 17 pteridophytes, four gymnosperms, 118 dicots, and 20 monocots. Of these species, seven were determined to have state ranks of S1 or S2. Using the Tennessee Cumberland Plateau species area curve (Huskins and Shaw, 2010), the expected number of species for the CBHCP was determined

to be 580 species, indicating a need for further documentation. Each of Palmer's standards may be met using an iNaturalist project to varying degrees of success.

66 - Of ice and when? A re-evaluation of Southern Appalachian high-elevation rock outcrops as ice age refugia

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Southern Appalachian rock outcrops (SARO) are a unique ecosystem, home to many endemic and rare plant species. They mimic an alpine or arctic tundra environment because of extreme exposure to sun, wind and cold, water saturation and desiccation. Authors have hypothesized that around 17% of the rock outcrop flora may be glacial relict species, based on their growth form, presumed close northern alpine relatives, and their restriction to high-elevation, open habitats with abundant sunlight. But empirical data to support this hypothesis are scarce. I reviewed the literature for studies concerning SARO plant species with presumed northern affinities, including phylogenetic studies, with or without divergence time dating, and population genetics studies that included SARO populations. Results found studies on 22 species and lower taxa. In the phylogenetic studies, only four of these taxa are definitively sister to northern alpine/arctic species or clades, while five others were found to not be closely related to northern taxa. Only one SARO-northern divergence time has so far been dated to the Pleistocene, while two other divergences were estimated to be far earlier (late Miocene). In these latter cases, species association with rock outcrops may be due to intrinsic biological causes, rather than refugial. Seven of the hypothesized northern-affinity SARO taxa have been included in population genetic studies, with the focus being on rare species, which conflates historical biogeographic processes with more recent genetic processes associated with small population sizes. Results from these studies give no consistent picture of their evolutionary history and hypothesized ice age relictual status. More phylogenetic studies with divergence time dating are needed for SARO taxa with presumed northern alpine/arctic relatives, but existing data point to mainly pre-Pleistocene causes for northern disjunctions and intrinsic or coincidental causes for co-distribution between species and habitat, rather than refugial.

67 - The Biodiversity of Nickel Hyperaccumulator Plants in Central America: A 6-Year Retrospective

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Hyperaccumulators are rare and physiologically unusual plants that store high concentrations of specific elements in their leaves. Nickel is the most commonly hyperaccumulated element, with ~500 hyperaccumulator species worldwide, usually growing on nickel-rich ultramafic (serpentine) soils. Until 2016, no hyperaccumulators were known from Central America or Mexico, despite the presence of suitable geological substrates. This paper will summarize the progress since that time. The first evidence for nickel-accumulating plants in Central America was based on screening of herbarium specimens using X-ray fluorescence spectrometry (XRF). Two species of *Psychotria* (Rubiaceae), previously known as hyperaccumulators in Cuba and the Antilles, were shown to have high nickel concentrations throughout Central America; two other members of the genus, endemic to Mexico and Guatemala, were newly reported as hyperaccumulators. Surprisingly, many records from Mexico came from non-ultramafic soils. This prompted fieldwork in the states of Veracruz, Tabasco, and Chiapas. New hyperaccumulators were discovered through these studies. *Blepharidium guatemalense* (Rubiaceae) is a fast-growing tree with foliar nickel concentrations >4%, suggesting its potential for agromining of nickel. In addition, the genus *Orthion* (Violaceae) has at least five species that hyperaccumulate nickel. Fieldwork also allowed soil analysis indicating that, although weathered from sedimentary bedrock, the soils contained high nickel concentrations, perhaps resulting from alluvial transport of lateritic soil particles from ultramafic deposits (ophiolites) along the plate margin known as the Guatemala Suture Zone. Additional XRF screening of herbarium specimens from this region of Guatemala found two additional hyperaccumulator species, *Arachnothryx linguiformis* (Rubiaceae) and *Chionanthus panamensis* (Oleaceae). Fieldwork in Guatemala confirmed the widespread abundance of *B. guatemalense*, *O. subsessile*, *P. costivenia*, and *A. linguiformis* on ultramafic soils, although no living examples of *C. panamensis* were located. Future studies, delayed due to covid-19, will examine other regions, and investigate the relationship between nickel concentrations in soils and plant tissues.

68 - Occurrence of exotic tilapia (Oreochromis spp.) in Alabama.

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The biodiversity of aquatic organisms in Alabama is well known and includes numerous endemic species found nowhere in North America. As with most aquatic organisms, loss of habitat, pollution, and invasive species are among those issues that can result in species decline and loss. Alabama is home to many non-native aquatic species either through introduction or accidental release. Some species of the non-native fishes are non-injurious however some are invasive and impact native populations. Tilapia were introduced into Alabama in the mid-20th century as a potential aquaculture species and several occurrences of the species in the wild have been reported. The species requires tropical temperatures however, and wild populations appear to be established only in the southern regions of the state. Where found, tilapias compete with native species for food and habitat resources and have been documented to negatively impact native sunfish and bass species. In September of 2021, residents of Homewood AL reported an unusually large fish in Shades creek, a tributary of the Cahaba River, near the Homewood Shades creek greenway. Upon examination, the fishes were food size (i.e., >450g) tilapia (*Oreochromis niloticus*, *O. mossambicus*). At the time of observance, water temperatures were above 20 C in the creek. Tilapia were not observed at sites above or below the greenway. Repeat surveys were

conducted in December when water temperatures were below 10 C and no fish were observed. Interestingly a local Asian food market, located 2.2 km from the greenway, sells similar species of live tilapias. We are continuing surveys on the creek and in surrounding tributaries, as well as collecting water samples to probe for the species using eDNA, to determine if established populations exist.

69 - Mortality of Eastern Bluebirds (Sialia sialis) roosting in nest boxes during a severe winter storm in southwest Kentucky and northwest Tennessee

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Eastern Bluebirds (*Sialia sialis*) are secondary cavity users that readily use nest boxes for nesting and roosting. During the winter, bluebirds are known to roost together, presumably to conserve heat, and in severe winter weather, consisting of unusually cold temperatures and freezing precipitation, food resources become less available. Eastern Bluebirds have been found dead in boxes following such storms and these birds often show signs of starvation. Ninety birds were found dead in nest boxes in southwest Kentucky and northwest Tennessee following a severe winter storm that occurred February 9-11, 2021. The storm was followed by nine days of below freezing temperatures. Our goal was to determine the age, sex, weight and overall physical condition of individuals that died. Bluebirds are sexually dimorphic, with males having a brighter hue, therefore sex was determined by looking at the head and back plumage. More males (n = 56) were found dead than females (n = 34). To determine age, we looked at pigment symmetry of the 10th primary covert to age the birds as either second-year (SY) or after-second-year (ASY) individuals. Of the 90 birds collected, 49 were ASY, 39 were SY, and we were unable to age two birds. There was no difference between the mean weight of the sexes. The average weight of a bluebird is 31 grams whereas the average weight of birds collected was 21.75 grams. We ranked the condition of each specimen on a scale from 1 (awful) to 6 (great). The majority were in fair (4) to poor (3) condition The bluebird boxes from which these specimens were recovered have been monitored annually since 1990. By comparing data from past breeding seasons to 2021, it was determined that there was an approximately 70% decrease in breeding success likely due to mortality during the severe winter storm.

70 - 23 and me for turtles: using mitochondrial DNA sequences to determine ancestral lineage and geographical origins for captive Black-breasted Leaf Turtles (Geoemyda spengleri).

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Chelonians are currently one of the world’s most endangered vertebrate groups. Sharp declines in chelonian populations are mostly due to over collection for the pet, medicine and food trades. In Asia, this reduction has been particularly severe over the last 40 years. One species that has been, and continues to be, collected and traded heavily is the Black-breasted Leaf Turtle (*Geoemyda spengleri*) native to southern China, northern Vietnam, and Laos. Large numbers (perhaps tens of thousands, if not more) of *G. spengleri* were imported into the US for pets between the 1970s and the early 2000s. Despite current regulations on international trade, illegal smuggling to the US still occasionally occurs. Previous genetic (mtDNA) work has shown that there are three distinct clades, roughly corresponding to three geographic regions: clade A - Guangxi and Hainan Provinces, China; B - Guangdong Province, China; and C - Vietnam. However, except for the Hainan populations, *G. spengleri* from different regions are relatively uniform in appearance, limiting the ability to easily group captive individuals into ancestral lineages to preserve genetic diversity and differentiation. In this study, we amplified the mitochondrial Cytb gene for captive *G. spengleri* of wild origin and compared it to previously published, and newly collected, known locality samples to determine the clade and geographic origin of the captive individuals. The majority of samples collected to date belong to clade A (82%), while only 10.7% belong to clade B and 7% to clade C. This information can assist captive management programs for this species, and it also provides insight into the impact of the pet trade on specific geographic regions.

71 - Woodland restoration in the Ouachita National Forest: A tale of two management areas

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Restoration of the once-open canopy forests in the southern US is now a common goal of many resource management agencies. The Ouachita National Forest uses both prescribed burning and midstory thinning in the shortleaf pine-dominated forests of Arkansas and Oklahoma to reduce woody stem density and increase ground flora diversity and associated fauna. For over a decade, the USDA Forest Service has worked with The Nature Conservancy to monitor progress toward a desired future condition (DFC) in these shortleaf pine-dominated forests and woodlands. DFC is a planning goal detailing what the structural and composition of a forest should look like after management is implemented. We compare the progress on two management areas: one which received extra funding through a Collaborative Forest Landscape Restoration Project (CFLRP) and one that received only appropriated funding. Since 2010, three measurements were taken three years apart on 200 ten-meter radius plots to evaluate the effectiveness of restoration treatments on stand basal area, tree stem density, and herbaceous species richness and cover. Plots managed with fire and thinning had significantly lower basal area and stem densities, and significantly higher herbaceous species richness and cover per plot. Fire alone or in conjunction with thinning moved plots toward the desired future condition, but plots in the management area with CFLRP funding made more progress towards DFC than those in the management area with no extra funding.

72 - A Comparison of Water Quality, Microbial Ecology, and Antibiotic Resistance of Public Boat Launches in Southeastern Louisiana

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The universal overuse and improper disposal of antibiotics has led to the growing public health concern of antibiotic resistance and the introduction of antibiotic reserves to the natural environment. Louisiana is ranked as the fourth highest state for number of antibiotic prescriptions, which raises the concern for the presence of antibiotic resistant bacteria in waterways and the potential risk of antibiotic resistant infections to water recreationists. The purpose of this study is to monitor the water quality, water microbial ecology, antibiotic resistance, and bacterial biofilm colonization of submerged plastics at two public boat launches in Southeastern Louisiana. Water and biofilm samples were taken in triplicate once a month at Pleasure Bend and Attakapas Landing in Southeastern Louisiana. Water quality measures include testing nitrogen, ammonia, sulfate, phosphate, and carbon levels. Additionally, water and biofilm samples are tested for total and fecal coliform abundance and presence of antibiotic resistant bacteria. The antibiotics tested for resistance include: meropenem, amoxicillin/clavulanic acid, erythromycin, tetracycline, sulfamethoxazole/trimethoprim, bacitracin, and penicillin. The results show that Pleasure Bend has no sulfate in the water, as compared to Attakapas Landing (1-14 mg/L). Many multi-drug antibiotic resistant bacteria were isolated from water and biofilm samples. Bacteria showing multi-drug resistance will undergo genetic analysis for antibiotic resistance genes.

73 - Analysis of potential lead (Pb) mitigating genes on bacterial communities in lead (Pb) contaminated soils

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Heavy metals pose serious threats to organisms due to their mobility and solubility in soil. Bacteria communities are vulnerable to heavy metal stress, but the response of different bacterial groups may vary depending on the level and type of heavy metal contamination. When subjected to heavy metal stress, many bacterial species or populations may become extirpated, while some resistant members survive to form the foundations of a new microbial community. Since the diversity and structure of microbial communities is an important index of soil quality, we conducted a preliminary assessment of the effects of Pb contamination on the bacterial community of a Pb contaminated study site in Cedartown, Georgia. The microbiome present in the Pb contaminated soils did not have lower alpha diversity than non-contaminated reference sites. The toxic conditions at the site did not negatively impact soil bacterial diversity, but the community structure was different from the reference sites. This suggests that bacteria at the high Pb contamination site have a compensatory mechanism or adaptation that allows them to thrive in these toxic conditions. The purpose of this study is to conduct an assessment of the effects of Pb contamination on bacterial communities and measure the presence of possible Pb mitigating genes amongst three operons (pbr, znt, and cad). We predicted that, as Pb levels increased in the soil: (1) Acidobacteria would increase in relative abundance while Proteobacteria and Actinobacteria would decrease in relative abundance, (2) differences in bacterial communities will be associated with differences in soil chemical factors and environmental coverage, and (3) genes known to mitigate the effects of Pb toxicity will increase in abundance with heavy metals in the soil.

74 - Utilization of Restriction Endonucleases as a Diagnostic Tool for Cluster Prediction Before en masse Sequencing of Gordonia phages

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Over the past decade, the number of sequenced Actinobacteriophages has increased as a direct result of the SEA-PHAGES science education program. Multiple Actinobacteria species have been utilized as hosts for the SEA-PHAGES program and the University of Louisiana Monroe has isolated and purified a large number of phages using the host *Gordonia terrae*. Across the program, only a few of the phages isolated can be sequenced due to limited resources. Our lab previously showed that the use of restriction enzyme digestion data could be effective for predicting phage cluster assignments of unknown phages isolated from mycobacteria hosts. In the present study, we combined restriction analysis followed by sequencing en masse to determine if restriction analysis could be used to predict Gordonia phage clusters. Using existing genome sequences and the NEBCutter 2.0 tool, we selected six restriction enzymes that appeared to have potential to discriminate across multiple clusters. We performed restriction analysis with these enzymes on 20 isolated but unsequenced phages followed by sequencing en masse of 10 of the phage DNAs. We were able to get 8/10 complete contigs from the sequencing data. Our initial analysis suggests that restriction analysis can be useful for en masse sequencing of multiple unique phages but that the restriction data performed poorly for prediction. In addition, experimental digestion data often did not match in silico digestion data indicating that restriction sites may be extensively modified in *Gordonia*. Gordonia phage genomes tend to show more sequence diversity within a cluster than do the mycobacteriophages and this, along with restriction site modifications, may render restriction analysis ineffective to make preliminary cluster assignments of unknown Gordonia phage DNA.

75 - Development of Transparent Transgenic Zebrafish Cellular Phenotype to study Cardiomyocytes Function

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Cardiac disease is the most common form of human births defects and abnormalities of the adult heart threaten as the most prevalent cause of morbidity and mortality. In The United States, heart failure considered as epidemic and million new cases are diagnosed annually. Zebrafish provides an excellent platform to study genetic and molecular approach of cellular phenotype-based cardiac research. Recently, we have developed transparent transgenic zebrafish model to study annexin-5 activity in the cardiovascular function by generating homozygous transparent skin Casper (roy$^{-/-}$,nacre$^{-/-}$); myl7:RFP; annexin-5:YFP transgenic zebrafish. Skin pigmentation background of any vertebrate model organism is a major obstruction for in-vivo confocal imaging to study the transgenic cellular phenotype-based study. By developing Casper (roy$^{-/-}$,nacre$^{-/-}$); myl7; annexin-5 transparent transgenic zebrafish strain, we established time-lapse in vivo confocal microscopy to study cellular phenotype/pathologies of cardiomyocytes over time to quantify changes in cardiomyocyte morphology and function over time. Casper contributes to the study by integrating a transparent characteristic in adult zebrafish that allows for simpler transparent visualization and observation. The Casper (roy$^{-/-}$,nacre$^{-/-}$) transgenic progenies developed through crossbreeding with the transgenic strain of *Tg (UAS:SEC-Hsa.ANXA5-YFP,myl7:RFP*). This study protocol is conducting under two sections; 1.1: Generation of homozygous *Tg (UAS:SEC-Hsa.ANXA5-YFP,myl7:RFP); Casper (*roy$^{-/-}$,nacre$^{-/-}$*)* zebrafish (generation F01-F06) and 1.2: Screening and sorting the transparent transgenic progeny and in-vivo imaging to validate cardiac morphology through in-vivo confocal imaging. Confocal and fluorescent microscopy used to obtain accurate, precise imaging and to determine fluorescent protein being activated. In the series of our ongoing project, this newly developed strain *Tg (UAS:SEC-Hsa.ANXA5-YFP,myl7:RFP); Casper (*roy$^{-/-}$,nacre$^{-/-}$*)* is undergoing development of the triple transgenic transparent strain by cross breeding with the NF-kB transgenic line *(Tg(6xNFκB:EGFP)* to develop a cardio-inflammatory study model. These novel results provide an in-vivo whole organism-based platform to design high-throughput screening and establish new horizons for drug discovery in cardiac disease and cardio-oncology

76 - The use of course imbedded research in a senior level undergraduate general toxicology class: The detection of microplastics at the Dauphin Island Sea Lab, Alabama.

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As part of a course in general toxicology, we went on a field trip to dolphin island sea lab and collected sand, sediment, fish, and grass shrimp to bring back to Jacksonville State University for processing. These students used the field trip to select topics for research projects related to the class and microplastics. Some of the students chose to determine if we could detect microplastics in sand sediment, and fish samples. One student group choose to determine if microbeads made of plastic could potentially affect the development of grass shrimp embryos. Each student group had to determine methods and procedures for their analysis. Each group had different problems with different solutions. This project created a lot of enthusiasm in the class and students spent both time in the laboratory and time on their own to ensure completion of projects. Each group created a peer review style paper by the end of class. Although our sample numbers were low the students were able to detect microplastics in the sand, sediments, and fish samples. The group evaluating the developmental toxicity of the microbeads showed developmental effects however there was a confounding issues with the with the test. Overall this work, was very successful in bringing awareness of the problem of microplastics to the class and indicates the more work needs to potentially be done investigate microplastics found near Dauphin Island.

77 - From Then to now: Diversity, Equity, and Inclusion in the Association of Southeastern Biologists: Early History

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In 2021 members of the Association of Southeastern Biologists (ASB) reflected on the association's growth and values and how they relate to diversity, equity, and inclusion. Historical records and oral accounts of the ASB were referenced to evaluate historical perspectives of diversity and inclusion in the early years of the association. Notable figures during the ASB's early history include Dr. Mary Stuart MacDougall of Agness Scott College, who during her presidency, helped to hold the association together while meetings were canceled during World War II. Dr. MacDougall's efforts to maintain the association have been applauded in several histories of the association, and have been highlighted as one of many important roles of women in the history of the ASB. The association's adherence to Jim Crow laws in the 1950s unfortunately limited the participation of prominent Black scientists in various functions in the annual meeting. Racial integration of the ASB would not occur until 1958, when Dr. Lafayette Frederick attended the Gainesville, FL meeting with several of his students from Southern University. Dr. Frederick's persistence in encouraging his student's participation in the ASB in subsequent years was essential in making the association a more diverse and open venue for scientific collaboration.

78 - From Then to now: Diversity, Equity, and Inclusion in the Association of Southeastern Biologists: Contemporary History

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During intentional reflection of our early history and future directions during 2021, members of the Association of Southeastern Biologists (ASB) also did an inventory of the contemporary history of our association. We used 1990, the year of the American Institute of Biological Sciences (AIBS) Conclave of Presidents, as a key turning point in the Associations' transition from reactive to proactive in diversity, equity, and inclusion efforts. In 1991, under the leadership of ASB President Frank Day, the Association established an ad hoc committee on Women, Minority, and Handicapped Affairs which is the origin of the current Human Diversity Committee. Over the next several years, this committee, which experienced several name changes to reflect its goals, organized symposia, workshops, luncheons, and invited speakers at the annual meeting to engage the membership in topics related to diversity, equity, and inclusion. In 1999, during participation in the National Science Foundation's President's Summit, ASB President Pat Parr indicated that ASB was one of only two organizations of 53 participating groups to have a formal committee focused on diversity and minority involvement. In 2016, the now renamed, Human Diversity Committee, made another large step in increasing minority participation in the annual meeting by establishing the Support Awards for First-Generation Student Members of ASB and in 2017 worked with Past-President Dr. Lafayette Frederick, his family, and Dr. Luther Williams to establish the Dr. Lafayette Frederick Underrepresented Minorities Scholarship. Since the inception of these awards, the first-generation and Lafayette Frederick Underrepresented Minorities Scholarships have supported thirty and three students, respectively.

79 - From Then to now: Diversity, Equity, and Inclusion in the Association of Southeastern Biologists: Moving Forward

Matt Heard[1], Chris Havran[2], Kimberly Hays[3], Ashley Morris[4], Loretta Ovueraye[5]

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Building and maintaining a scientific society that is diverse, equitable, and inclusive requires continual work and strategic planning to be successful. Therefore, over the past few years, the ASB Executive Board has begun directed efforts to prioritize creating a more open and inclusive environment at our annual meetings. In 2020, the ASB Executive Committee entered into a collaboration with the Alliance to Catalyze Change for Equity in STEM Success (ACCESS) via co-principal investigator and member of the ASB Executive Committee, Dr. Verónica Segarra (High Point University). Building on this work with ACCESS and their recommended best practices, the ASB Executive Committee chose to focus the plenary session of the 2021 annual meeting on diversity in STEM and how it relates to the ASB and biologists in the Southeastern US. The plenary session was titled "Including Diversity in STEM" and was moderated by an African American ASB Executive Committee member, Dr. L. Ovueraye, Vice Provost for Workforce Programs and Professional Learning at Miami Dade College. In the session, Dr. Ovueraye led a conversation with a group of ethnically and socially diverse individuals with science education and research backgrounds: Dr. Edward Moreira Bahnson from the University of North Carolina at Chapel Hill, Dr. Kelly Mack from the Association of American Colleges and Universities, Dr. Veronica Segarra from High Point University, and Dr. Selwyn Williams from Miami Dade College. Though these efforts and conversations represent the first steps on this journey, the ASB board hopes that they will provide a blueprint for creating a more inclusive environment within the ASB and at the meetings the society hosts each year.

80 - Development of a Novel Purification Protocol to Isolate and Identify Brain Microglia

Jennifer Bradford

Department of Biological Sciences, Augusta University, Augusta, GA

Microglia, the tissue-resident macrophage of the central nervous system (CNS), play a paramount role in brain health and disease status. As microglia are crucial in multiple aspects of biology, such as in normal brain development/function, immune response, neurodegeneration, and cancer, isolation of these primary cells is important for multiple lines of research. Also important is the establishment of reliable markers to distinguish microglia from other macrophages, something the field lacks and desperately needs. Here, we describe a novel method for enriching and isolating primary microglia from mouse brain tissue. This isolation method yields a high number of cells from either young or adult mice, and importantly, maintains the health of the cells for subsequent cell culture. We also describe flow cytometry methods using novel cell surface markers including CX3CR1 and Siglec-H to specifically label microglia while avoiding other bone marrow and/or non-CNS derived macrophages and monocytes, which has been historically difficult to achieve. This novel isolation technique could greatly benefit a wide range of studies in human CNS biology, health, and disease mechanisms. Being able to isolate a largely pure population of microglia could also allow for a more comprehensive understanding of their functional dynamics and role in disease mechanisms, advancement of potential biomarkers, and development of novel therapeutic targets to improve prognosis and quality of life in multiple diseases.

81 - Tumor Microenvironment Altered by Lung Carcinoma Exosomes

Jade Dorman

Ouachita Baptist University, Arkadelphia, AR

Cancer uses intercellular communication to induce tumor growth and metastasis. Fibroblasts can become specifically transformed and associated with cancer to aid in the process. Extracellular vesicles, specifically exosomes, contain proteins, RNA, and DNA that are taken up by local cells to affect cellular behavior. Exosomes were isolated from lung carcinoma using total exosome isolation reagent and quantified. These exosomes were used to treat lung fibroblasts and enrich lung carcinoma cells, and the effects of exosomes on cancerous properties, cell viability and cell migration, were studied. An increase of cell viability was found with exosome treatment for both cell lines while migration only increased for enriched lung carcinoma cells. Additionally, mass spectrometry-based proteomics of exosomes isolated from hepatocellular carcinoma was analyzed. Through a survey of differentially expressed proteins between high and low grade hepatocellular carcinomas against normal liver cells, several pathways of interest were identified. Some common motifs in underexpressed genes were the regulations of cell signaling, cell metabolism, and cell death.

82 - How the ‘horrid prison’ eats: comparative transcriptomics in the Venus flytrap (Dionaea muscipula) at various points of prey capture and digestion.

Jeremy Rentsch

Francis Marion University, FLORENCE, SC

Darwin described the Venus flytrap as both “one of the most wonderful [plants] in the world” and a “horrid prison with closing walls”. The Venus flytrap closes in response to the stimulation of mechanosensing trigger hairs, which can be found on the adaxial side of the trap. Stimulation of these hairs in rapid succession causes the generation of action potentials, two of which triggers trap closure. While Venus flytraps almost certainly evolved carnivory to deal with nutrient deficiencies in the soil, research also suggest that these plants use prey-derived carbon as a substrate for cellular respiration even with an abundance of atmospheric CO2. To better understand how the Venus flytrap behaves, we isolated RNA at various stages of prey capture and digestion. We propose to use comparative transcriptomics to understand which genes are up and down regulated at various stages of the flytrap’s predatory cycle.

83 - A Drosophila platform to investigate the force tuning of mechanosensitive Notch receptors and the requirements for Notch activation in C. elegans.

Paul Langridge

Augusta University, Augusta, GA

The conserved transmembrane receptor Notch has diverse and profound roles in controlling cell fate during animal development. In the absence of ligand, a Negative Regulatory Region (NRR) in the Notch ectodomain adopts an autoinhibited confirmation, masking a protease cleavage site. Transmembrane protein ligands presented on the surface of neighboring cells can bind the receptor, relieve autoinhibition and induce cleavage of the NRR, the initiating step of signal transduction. In Drosophila and vertebrates, recruitment of ligands by the endocytic adaptor Epsin, and their subsequent internalization by Clathrin-mediated endocytosis, exerts a "pulling force" on Notch that is essential to expose the cleavage site in the NRR. We show that Epsin-mediated endocytosis of transmembrane ligands is not required to activate the two C. elegans Notch proteins. Using an in vivo force sensing assay in Drosophila, we present evidence (i) that the C. elegans NRRs are tuned to lower force thresholds than the NRR of Drosophila Notch, and (ii), that this difference depends on the presence of a “Leucine plug” that occludes the cleavage site in the Drosophila and vertebrate Notch NRRs but is absent from the C. elegans Notch NRRs. Our results thus establish an unexpected evolutionary plasticity in the force-dependent mechanism of Notch activation and implicate a specific structural element, the Leucine plug, as a potential determinant. The work also demonstrates the feasibility of a systematic investigation of force sensitive domains using the Drosophila force sensing assay.

84 - Bringing In More Voices Through Podcasts and Scientist Spotlights

Darlene Panvini

Belmont University, Nashville, TN

Incorporating a variety of scientist perspectives and voices in STEM courses can both promote student learning and enhance science identity. Science identity is a sense of belonging and affiliation with the content and/or scientists presented in a course. As student populations become more diverse, including different voices in the classroom is one way for students to feel a greater sense of connection. Using readily available podcasts and implementing “Scientist Spotlights” provides an opportunity for students to identify with scientists from diverse backgrounds. Podcasts and Scientist Spotlights can be combined with corresponding activities to analyze data and/or graphs from the scientists’ research to enhance students’ quantitative skills. However, finding time to search for and develop these resources can seem daunting to faculty. This session will describe resources available to faculty interested in incorporating podcasts, scientist spotlights, and related quantitative analyses into their courses, while providing some tips for facilitating this process. Examples from introductory and upper-level biology courses will be included. The session will also introduce faculty to the benefits of participating in a faculty mentoring network (FMN) and the open educational resources (OERs) at Qubes. A sample DEI (Diversity, Equity, and Inclusion) syllabus statement will be shared that was an outcome of participating in an FMN.

85 - How an online practice tool, ILEX (Identify-Learn-EXplore), helps students learn and practice sight identification skills

Stephanie Jeffries[1], Maccoy Kerrigan[2]

[1]NC State University, Raleigh, NC, [2]NC State University, RALEIGH, NC

Many natural resources programs and careers require sight-identification skills. At NC State, Dendrology (a required class for Forestry, Natural Resources, Wildlife, and the Field Botany certificate) teaches students to sight-identify 170-180 species of trees, shrubs, and woody vines using scientific names, common names, family names, and natural history. Learning identification is intensive, requiring both a growth mindset as well as observation, study, and practice for students to distinguish among similar species and remember unfamiliar scientific names. Given the fast pacing, it is easy for students to fall behind, and the course has a high failure rate. In Fall 2020, during the COVID-19 pandemic, we realized we needed more options for teaching identification when we could not take students out in the field, or when students had to miss class. During the past year, we worked with a team of instructional designers at NC State to create ILEX (Identify-Learn-EXplore), a practice tool that uses an extensive photograph database to enable students to study and filter species and create their own sets of practice quizzes. Users can sort species by leaf arrangement, simple/compound leaves, family, or genus and can practice identification by choosing the correct scientific name or spelling it correctly. In Fall 2021, students listed ILEX as the most helpful study tool outside of our weekly outdoor labs, with most using the “identify by spelling” option most often. While online tools will never substitute for field experience, we have found that the ILEX tool is a valuable addition to our repertoire of study tools. Based on student feedback, we plan to make some additional revisions, and we hope to create a public-facing version for anyone who wants to practice and sharpen their tree identification skills.

86 - Rooting students in their botanical history: a collaborative curriculum for herbarium curators and high school students and educators

Shawn Krosnick, Kelly Moore

Tennessee Tech University, Cookeville, TN

It has been well documented that students often overlook plants when they consider the natural world. Early interventions in elementary education have shown that students not only enjoy botanical learning experiences but may also gain long-term benefits. However, botanical curricula are rare in K-12 education and especially so at the high school level. This can result in university students who fail to appreciate the critical role plants play in understanding topics such as ecology, conservation, and climate change. Equally important is the need for student exposure to natural history collections given the wealth of information they provide about both the past and future of life on earth. To address the deficit of botanical preparation in K-12, we have created a collaborative educational program for use in high school curricula. The program brings together herbarium curators and high school educators for learning experiences that take place in the classroom, the field, the herbarium, and online. The core concept underlying the project is that everyone has a connection to plants – their own botanical history – and this is fundamentally connected to their family history. Students connect to their botanical history, where they identify specific plants that are significant to them or their family. They work with these plants in the field and in the herbarium, learning how to collect plants, prepare archival specimens, and digitize them. Moving through 10 educational modules, students will work with many types of digitized specimen data and explore career options in natural history collections. Each module is critically reviewed, tested, and improved through direct collaboration with high school biology teachers and students. Instructional videos, teacher guides, student worksheets, and supplemental activities are being made available via QUBES and Google Sites for use across the country, with final release of the entire project estimated in January 2024.

ASB Symposia

Symposium: From Cookbooks to Cell Blocks: Developing a Research-centered Undergraduate Curriculum

Lori Hensley, Jacksonville State University, Jacksonville, AL and Nathan Reyna, Ouachita Baptist University, Arkadelphia, AR

87 - From Cookbooks to Cell Blocks: Developing a Research-centered Undergraduate Curriculum

ORGANIZERS: Nathan Reyna[1], Lori Hensley[2]

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For faculty to be successful in developing a research-based curriculum, they must have a viable research program themselves and the confidence to move their research into course-based labs. To address such needs, the Cell Biology Education Consortium (CBEC/www.cellbioed.com) created a comprehensive model that provides faculty with the resources they need to incorporate mammalian cell culture into the undergraduate classroom. By providing resources in the form of Cell Blocks, even inexperienced faculty members can successfully make the move. Cell Blocks consist of video protocols, written protocols, classroom implementation strategies, and assessments for common cell culture experiments. Most current CURE initiatives focus on students conducting predefined projects; however, this often limits student creativity and the ability to scaffold research throughout a program's curriculum. Because Cell Blocks are all similarly formatted, they serve as mix-and-match modules, allowing faculty and students to develop projects that are of interest to them, relevant to their course content, and feasible at their institutions. In addition, Cell Blocks are freely available to everyone through the CBEC website, our YouTube channel, and Google Classroom. Taking a collaborative approach and offering vouchers to both faculty and students for resource development, the CBEC has grown nationally and incorporates a diverse group of institutions throughout the U.S. and Puerto Rico. In this presentation, I will discuss how Cell Blocks were used to change the focus of my research and better impact my students' learning. By blurring the lines between the classroom and the research lab, the CBEC seeks to improve undergraduate research and positively impact science education. I will present how I used Cell Blocks to change the trajectory of my research and how others can get involved with the CBEC.

88 - Ciprofloxacin as treatments for non-small cell lung cancer (A549): CUREs in Action

Emma Bynum, Kaitlyn Montgomery, Chase Foiles, Elysian Majeske, Andrew Tarlton, Nathan Reyna

Ouachita Baptist University, Arkadelphia, AR

Non-small cell lung cancer is regionalized to the lungs and has a 5-year survival rate of 25%. As a class research project, we investigated the role of Ciprofloxacin on A549 lung cancer cell lines. Due to its membership in fluoroquinolones, Ciprofloxacin stands as a potential treatment for cancer. Recent studies have shown that Ciprofloxacin treatments ultimately slow tumor growth by affecting cell viability, disrupting redox balance, increasing p53 expression, altering BAX and Bcl-2 expression, inhibiting topoisomerases, arresting cells in the S phase, and inducing apoptosis. Our research used a combination of cell viability assays (MTT) and scratch assays to determine how Ciprofloxacin HCl affects cell proliferation and cell mobility in A549 non-small cell lung cancer cells. Bioinformatic analysis of The Cancer Genome Atlas (TGCA), using cBioPortal, was used to help identify pathways and genes affected by Ciprofloxacin. The initial MTT assay showed a concentration of 0.001M produced a lethal dose 50 (LD50), where 50 % of the cells were arrested in S phase. Over 24hr, 48, and 72hrs, cell viability and mobility were tested at 0.001M concentration of Ciprofloxacin. The results show that Ciprofloxacin decreased cell viability by 50% and decreased cell mobility at 24-hour dosages. These results concur with previous research on the effects of Ciprofloxacin in the cellular apoptosis cascade and further shine light on its various reducing properties that make it a promising drug for future cancer research. Our research was conducted as a Course Embedded Research Experience (CURE) through the Cell Biology Education Consortium (CBEC).

89 - CURE Assessment: Impacts and Outcomes from the Cell Biology Education Consortium

Jaime Sabel

University of Memphis, Memphis, TN

This presentation will focus on assessment of Course-based Undergraduate Research Experiences (CUREs) using the Cell Biology Education Consortium (CBEC) as an example. The CBEC is a network of faculty and students incorporating cell culture-based research into the classroom. Project coordinators have collected information on the experiences of both faculty and students, the impact of the research on students, and how the research and educational materials are disseminated. In this session, I will present results from analyses that have assessed the impact of the project and the outcomes for students and faculty. These results will be of interest to anyone involved or interested in developing assessment for CUREs, becoming involved in the CBEC , or building assessment into the development of similar types of networks.

90 - From Genetics to Biotechnology: Synthetic Biology as a flexible course-embedded research experience

Kristen Johnson[1], Jaime Sabel[2], Judith Cole[2], Christin Pruett[3], Ruth Plymale[3], Nathan Reyna[3]

[1]UNH Manchester, Manchester, NH, [2]University of Memphis, Memphis, TN, [3]Ouachita Baptist University, Arkadelphia, AR

Course-embedded Undergraduate Research Experiences (CUREs) have gained much traction in the STEM educational community, as they enable equitable access for students to research experiences. Through CUREs, students engage in projects and make discoveries that are of interest to the broader scientific community. We will report on the development, implementation, and evaluation of a synthetic biology CURE. Synthetic Biology involves systematic engineering of novel organisms, such as bacteria and plants, to work as functional devices to solve problems in medicine, agriculture, and manufacturing. The value of synthetic biology and its ultimate utility as a teaching tool relies on reusable, standard genetic parts that can be interchanged using common genetic engineering principles. This synthetic biology CURE effectively achieves 5 essential goals: 1) a sense of project ownership; 2) self-efficacy: mastery of a manageable number of techniques; 3) increased tolerance for obstacles through challenging research; 4) increased communication skills, and 5) a sense of belonging in a larger scientific community. Based upon student assessment data from this CURE implemented in a mid-level cellular biology course and two advanced-level genetics/molecular biology courses across three distinct institutions, we demonstrate that this course-based synthetic biology laboratory engages students directly in an authentic research experience and models important elements of collaboration, discovery, iteration, and critical thinking. While developed as a semester-long CURE, the lab's flexibility allows faculty to design projects that fit into their curriculum's learning goals and student-oriented outcomes.

91 - Enhancing undergraduate student engagement in cancer research through use of cBioportal patient database

Dr. Lyndsay V. Rhodes, PhD

Florida Gulf Coast University, Fort Myers, FL

Effectively teaching the molecular biology of cancer at the undergraduate level can be challenging. Students are often overwhelmed with the amount of information and the seemingly unconnected genes, mutations, and pathways associated with cancer. The data portal cBioportal was used to create opportunities for students to connect more deeply with the topic by directly investigating patient data. This pilot study was run in Honors Cancer Biology, a 4000-level elective course, of 15 students over the span of 4 weeks. The goals of this project were to 1) use molecular patient data to correlate gene changes to patient outcomes, 2) identify trends in data, 3) connect content knowledge from class to actual patient data, and 4) to effectively communicate scientific findings to peers. Each student chose a cancer dataset of interest available in cBioportal that included genomic sequencing, gene expression, proteomic data, as well as clinical and demographic information such as age, race, gender, tumor stage, grade, and survival data. Students were given a series of questions to guide them in mining their selected dataset to determine associations between particular gene mutations and patient outcomes. Students then generated a written report and oral presentation of their findings to share with their peers. While students were excited for the opportunity to interact with and analyze actual cancer patient data, for the majority this was the first time they had been exposed to -omic data sets. Most students felt challenged and somewhat overwhelmed with the amount of information presented and the prospect of learning to navigate a new system. However, student final reports and presentations indicated a strong understanding of cancer signaling pathways, ability to classify mutations and correlate specific mutations status to patient outcomes. cBioportal is a valuable resource for cancer biology education and engagement in addition to traditional independent research applications.

92 - Cell and molecular biology bilingual tools for a more inclusive scientific workforce

Elizabeth Padilla-Crespo[1], Edwin Girald[1], Lori Hensley[2,3], Nathan Reyna[3,4]

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Inclusive science communication has been described as any effort that aims to engage individuals in STEM grounded in equity, inclusion, and intersectionality. Studies have shown that multilingual learners are more responsive in integrating the understanding of preliminary concepts, initial exploration, and inquiry, when these concepts are presented in their familiar language Different challenges exclude highly capable multilingual learners from engagement, the use of diverse methods and vocabularies that create barriers, lack of formal curricula and/or training activities to expose individuals. Language can be a major barrier for inclusivity, therefore multilingual learners may be more responsive when initial concepts, exploration and inquiry are presented with their mother tong, familiar language(s) and language practices. The changing demographics in the U.S., call for new approaches and resources to overturn this inequity in science education. To make science more culturally and linguistically responsive we have developed a series of Spanish science communication videos and workshops introducing the fundamental concepts of Cell and Molecular Biology, and opportunities in Synthetic Biology through inquiry and hypothesis-driven questions using the cBioPortal Cancer Genomics Portal (http://cbioportal.org). Preliminary data on Puerto Rican students indicates that the activities in their mother-tongue language (Spanish) had a positive impact, as shown trough the Persistence in the Sciences assessment survey (designed to measure student psychological outcomes in course-based research experiences). Also, most students (>70%) expressed that having the Spanish videos was helpful and advantageous to complete their projects successfully. Our efforts will shed light into the dissemination, application and best practices of science bilingual resources and outreach communication efforts.

93 - Tissue Culture Based Research in the Undergraduate Classroom: You can do it. The CBEC can help.

Lori Hensley[1], Nathan Reyna[2]

[1]Jacksonville State University, Jacksonville, AL, [2]Ouachita Baptist University, Arkadelphia, AR

The Cell Biology Education Consortium (CBEC) is an NSF-funded network of faculty and students working to incorporate tissue culture-based research into the undergraduate classroom. While isolated groups are introducing cell culture techniques into such experiences, until now, there has been no coordinated effort to compile resources and provide training that makes creating customizable research projects easier to implement at smaller, primarily undergraduate institutions (PUIs) and community colleges (CCs). CBEC members are developing Cell Blocks—technique-specific modules consisting of written and video protocols, classroom implementation strategies and assessments. Because all Cell Blocks will have similar basic components, faculty and students will be able to mix and match multiple blocks to address novel research questions in semester-long course-embedded research experiences (CUREs). These protocols and materials are developed by people at PUIs and CCs for use at these types of institutions with protocols optimized for once/week labs. In this session, students and faculty involved with this project will provide guidance and answer questions related to such CUREs, including how to receive technical and financial support, the use of peer instructors, and how to advocate to administrators. This session is designed for both the beginner, "I do not have a hood," to the seasoned expert.

This work was funded through the NSF Award #1827066, RCN-UBE: Cell Biology Education Consortium

Symposium: Plant Conservation Genetics (1/2)

ORGANIZERS: Matt C. Estep, Appalachian State University, Boone, NC

Genetics is a powerful tool that can be used to address many questions in Biology. Our goal is to bring together the botanists within the southeast that are using genetic techniques to address questions concerning the conservation status of our native plants. We hope to provide an inviting platform for labs to discuss their work and build a network of botanists focused on the conservation of our local flora.

94 - Building a network to enhance plant conservation genetic studies in the southeast

Matt C. Estep[1], Ashley Morris[2]

[1]Appalachian State University, Boone, NC, [2]Furman University, Greenville, SC

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

Erika Moore[1,2], Carolina Siniscalchi[3], Jennifer Mandel[1,2]

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Estimating the population genetic diversity and structure of fragmented or isolated species is crucial when designing a conservation strategy. Knowledge of the genetic composition and variation among populations of rare or endangered species can aid conservation managers in understanding how, and which, populations to protect. The whorled sunflower, Helianthus verticillatus (Asteraceae), is an endangered sunflower species endemic to the southeastern United States. It was previously known to consist of four populations spanning three states: Alabama, Georgia, and Tennessee (McNairy County and Madison County). Recently, two new populations were discovered in Marshall County, Mississippi (2017) and Franklin County, Virginia (2019). Here, we present the results of a population genetic study on these new populations using nuclear microsatellite markers and compare those results to previous studies, with hopes of determining genetic diversity and population structure of this rare species. We found that both newly discovered populations contain unique genetic variation, with the Mississippi population being the most diverse, both genetically and morphologically. We also found that the Virginia population is genetically similar to the previously known populations but is potentially under the most conservation concern given the recovery of only two unique genets within the population. These results indicate that the new populations are worthy of protection and conservation efforts given the genetic variation that they harbor. We hope that this study sparks more research into understanding the history and population structure of this rare species, as well as provide genetic data that will aid in its conservation.

96 - Genetic Diversity and Population Genetic Structure in American Ginseng, a Commercially and Culturally Valuable Medicinal Herb

Bassam Shawamreh[1], Tiana Miller[2], Emmanuella Afrane[1], Alisa Hove[1], Jen Rhode Ward[2]

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American ginseng (*Panax quiquefolius* L., Araliaceae) is an herbaceous medicinal plant that is uncommon to rare in eastern deciduous forests of North America. This species is grown worldwide as a commodity crop, but in the Americas it has been wild-collected for centuries, primarily for export to traditional Asian medicine markets. In recent years, ginseng overharvest has led to its designation by CITES (Convention on International Trade in Endangered Species) as a species at risk of extinction. Ginseng may be particularly vulnerable to extirpation events

because harvesting often removes larger, older individuals from populations, and plants take at least five years to reproduce sexually. We sampled leaflets from 10-30 individuals per population in 17 western North Carolina ginseng populations; harvest pressure and census data varied among populations. We are analyzing microsatellite diversity at seven polymorphic loci in order to understand population genetic structure, estimate genetic diversity, test for gene flow among populations, and relate these factors to harvest pressures. Results can indicate populations' and species' potential for evolutionary response to regulatory protection, harvest, and climate change.

97 - Locust Pocus: Morphological and Molecular Tests of Species Delimitation in Robinia L. of the Southeastern United States

Brandon Wheeler

Western Carolina University, Cullowhee, NC

Robinia L. is a genus of trees and small shrubs native to North America, with several species that are of conservation concern within the Southern Appalachians. The genus has been re-circumscribed utilizing morphologically based taxonomic treatments several times in the last century, though no molecular study has focused solely on the genus. Restriction Site Associated Sequencing (RADSeq) is a method of rapidly sequencing short reads from the genome that are generated by digesting the DNA with restriction enzymes to generate short sequences from the same loci in many samples. I plan to sample the entirety of Robinia L. species native to the Southeastern United States and employ both RADSeq and morphological methods provide an updated taxonomic treatment. This work will generate a thorough understanding of the genus, which will be integral to conserving populations of several rare species in their native ranges in the Southern Appalachians.

Symposium: Plant Conservation Genetics (2/2)

Matt C. Estep, Appalachian State University, Boone, NC

98 - Conservation genetics of Spiraea virginiana

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Spiraea virginiana Brit. (Rosaceae) is a rare clonal shrub restricted to the Cumberland, Tennessee and Ohio River drainages in isolated populations. Reproduction is thought to be mostly asexual by ramet formation, suggesting that the major means of dispersal is by dislodged rhizomes. In order to facilitate future recovery efforts where augmentation or translocations are employed a comprehensive understanding of genetic diversity and population structure is required. The aim of this study is to conduct an independent genetic analysis of diversity across a broader geographic range (GA, TN, NC, VA, KY, WV) using the same microsatellite markers to connect with earlier data sets within the northern range (OH and KY). Our analysis of more than 400 individuals confirms the low genetic diversity and clonal nature of reproduction reported for this species. The data failed to reveal strong population structure within major river drainages or across the range of the species. The implications of our analysis on conservation actions that could facilitate recovery will be discussed.

99 - Genetic diversity and structure of three rare and imperiled Southern Appalachian conifers

Kevin Potter

North Carolina State University, Research Triangle Park, NC

The Southern and Central Appalachians are home to three endemic conifer tree species of conservation concern: Carolina hemlock (Tsuga caroliniana), Fraser fir (Abies fraseri), and Table Mountain pine (Pinus pungens). Each faces a threat to its persistence in natural forests: non-native insects killing Carolina hemlock (hemlock woolly adelgid [Adelges tsugae]) and Fraser fir (balsam woolly adelgid [A. piceae]), and the absence of fire preventing sustainable regeneration of Table Mountain pine. Range-wide genetic diversity studies using microsatellite molecular markers have quantified patterns of genetic diversity and genetic differentiation for each of these species. The three conifers exhibited different patterns of population-level diversity, inbreeding, and differentiation despite all having wind-dispersed pollen and seed. Fraser fir exists as a set of low-diversity and moderately inbred populations that are not much differentiated from each other. Carolina hemlock populations are characterized by high inbreeding, low diversity, and extremely high differentiation. Table Mountain pine populations have moderate levels of diversity, inbreeding, and differentiation. These results suggest a high level of interpopulation gene flow in Fraser fir, an intermediate level in Table Mountain pine, and a low level in Carolina hemlock. The Carolina hemlock findings further suggest that it has long been below the threshold of interpopulation gene flow necessary to avoid genetic drift and high inbreeding. Topographic position, population size, biogeographic history, and seed and pollen morphology may explain the differences in gene flow and genetic structure among these three conifers. The results have been used to guide the ex situ conservation of each species, including seed collections by the USDA Forest Service and the Camcore conservation cooperative at North Carolina State University.

100 - Assessing the Health of Gray's Lily (Lilium grayi) with Demographic Monitoring

Ben Brewer, Matt C. Estep

Appalachian State University, Boone, NC

Lilium grayi S. Watson, Gray's Lily, is a threatened perennial herb endemic to high elevations in the Southern Appalachians of Virginia, North Carolina, and Tennessee. *L. grayi* is an iconic species in the grassy bald plant community, and also grows in bogs, mesic forests and meadows. L. *grayi* faces multiple challenges, including continued habitat loss, many small and isolated populations, and disease caused by a fungal phytopathogen. First monitored in *L. grayi* in 1998, Lily Leaf Spot (LLS) disease results in early senescence of aboveground tissues and often prevents individuals from reproducing successfully. Early season collapse resulting from LLS has been observed at a large scale in multiple populations of *L. grayi.* Demographic monitoring of *L. grayi* across the range of the species is necessary to fully understand how the disease is affecting populations and reproductive output. During the growing seasons of 2020 and 2021, flowering *L. grayi* individuals at 22 sites were monitored for reproductive success. Each site was visited twice: first while plants were flowering in June and early July, then when plants were producing capsules in September and early October. Data was collected on plant size, number of flowers, severity of disease infection, shading strata, and reproductive success. In 2020 207 plants were monitored at 17 sites, with 67 (32.37%) successfully producing capsules and 97 (46.86%) prematurely senescing to LLS. In 2021 347 plants were monitored at 22 sites, with 45 (13.00%) successfully producing capsules and 280 (80.69%) prematurely senescing to LLS. LLS was present at all sites visited. These results suggest that reproductive output in *L. grayi* is very low across the range of the species. These data will be instrumental to Federal and State governments in determining the conservation status for this species and informing future management decisions.

101 - Extremely limited genetic variation observed in Illinois occurrences of the federally endangered leafy prairie clover (Dalea foliosa; Fabaceae)

Ashley Morris[1], Clayton Visger[2], Cathy Pollack[3]

[1]Furman University, Greenville, SC, [2]California State University, Sacramento, CA, [3]US Fish and Wildlife Service, Chicago, IL

Leafy prairie clover (*Dalea foliosa*; Fabaceae) is a federally endangered legume associated with limestone glade habitats in Middle Tennessee and northwest Alabama and dolomite prairies in Illinois. The Illinois occurrences represent the most geographically disjunct and ecologically differentiated occurrences within this species. Previous work using allozymes alluded to lower-than-expected levels of genetic variation across the species' range, with lowest levels detected in Illinois, but only three IL sampling locations were included. Here, we use six novel nuclear microsatellite loci to assess genetic structure within and among nine sites: four naturally occurring sites, two naturally occurring sites that have been augmented, and three introduced sites. All loci included here were shown to be polymorphic in screens using individuals from across the species' range. However, five sites included here were monomorphic for all but one locus; two sites were monomorphic for all but two loci, and one site was monomorphic for three of the six loci. Three additional loci were genotyped for four of the sites from the present study as part of a broader survey of the species range, and all four sites appear to be monomorphic for those three loci, indicating that low levels of genetic diversity observed here are not the result of low genetic resolution, but are instead an accurate reflection of the system. Furthermore, environmental analyses forecast increases in mean precipitation and mean temperature within the next 50 years. These concerns combined lead us to question the potential impacts this could have on long-term survival of these isolated populations, and future directions are discussed.

Symposium: Progress Update from the SE Pulse III Institute

Christopher Finelli[1], Judy Awong-Taylor[2], Cerrone Foster[3], Mark Lee[4], Kristen Miller[5], Katie Northcutt[6] and Jen Rhode Ward[7], [1]University of North Carolina Wilmington, Wilmington, NC[2]Georgia Gwinnett College, Lawrenceville, GA[3]East Tennessee State University, Johnson City, TN[4]Spelman College, Atlanta, GA[5]University of Georgia, Athens, GA[6]Mercer University, Macon, GA[7]University of North Carolina Asheville, Asheville, NC

The Southeastern Region (SERP) of the Partnership for Undergraduate Life Sciences Education (PULSE) hosted the third SERP Institute during May 24-27, 2021. Fourteen teams of faculty and administrators met virtually over the course of the Institute to interact with experts in advanced pedagogy, building equitable learning environments, and departmental transformation. Each team developed an action plan to improve learning outcomes for undergraduate students. At this invitation only symposium, teams will share the progress, challenges, and insights from their work. As part of our IRB for this work, this session is by invitation only. Posters and a separate symposium will also be presented for attendance by the general ASB membership.

Symposium: The surprising frequency, diversity, and relevance of southeastern grasslands (and why we need to save them). (1/3)

Sponsored by and supported by the Southeast Chapter of the Ecological Society of America

Dwayne Estes[1,2], Theo Witsell[3] and Scott A. Woolbright[4], [1]Center of Excellence for Field Biology, Austin Peay State University, Clarksville, TN[2]Southeastern Grasslands Initiative, Clarksville, TN[3]Arkansas Natural Heritage Commission, Little Rock, AR[4]University of Arkansas at Little Rock, Little Rock, AR

The purpose of our symposium is to create a forum for researchers, land managers, historians, and others to increase awareness of the unique but largely overlooked ecology of southeastern grasslands. For most North Americans, the term 'grassland' likely evokes images of the prairies of the Great Plains or other western locales. But grasslands in the southeastern US are more frequent and more biodiverse than most realize. Southeastern grasslands also have unique and rich cultural histories, and preserve information and artefacts that can span millennia. Grassland ecological research has been overshadowed in the southeast by studies that focus on forest, coastal, and other systems that are more commonly associated with the region. However, a recent resurgence in interest has revealed levels of biodiversity in southeastern grasslands that can rival those in western environments. Such studies expose both a need and an opportunity for transformative research on the processes that shape grassland environments in southern US--environments that differ significantly from those in the more familiar west. Unfortunately, agriculture, development and other anthropogenic forces have reduced grasslands in the southeast by an estimated ninety to ninety-nine percent, and this loss is thought by some to represent the greatest threat to biodiversity in the eastern United States. Remaining grasslands face these same threats but are also vulnerable to climate-driven changes in temperature, moisture, and fire frequency as well as the often related encroachment by invading species and communities. As grassland communities disappear, so do countless opportunities for research because southeastern grasslands are also repositories of novel genetic, ecological, and evolutionary information. With those opportunities in mind, we hope that this symposium will serve to educate and inspire others in the ASB to forge new opportunities for collaborative research, and to take an interest in exploring and preserving novel grassland ecosystems in their own communities.

102 - Saving Southeastern Grasslands: Recalibrating Priorities for Science and Conservation in a Global Biodiversity Hotspot

Dwayne Estes[1,2], Reed Noss[1,3], Theo Witsell[1,2], Alan Weakley[1,4], Pat Comer[5], JoVonn Hill[1,6], Evan Rehm[1,7], Marcello DeVitis[1,2]

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Grasslands represent one of the most endangered ecosystems on Earth. While the grasslands of central North America (the Great Plains and Midwestern Tallgrass Prairie), Africa, Asia, Australia, and South America are well known, the significance of grasslands in eastern North America, has been under-appreciated. These grasslands, particularly those of the southeastern U.S., are the most biodiverse in temperate North America. The 10 major categories of southeastern grasslands (balds, barrens, dunes, fens, glades, marshes, meadows, prairies, riverscours, and savannas) collectively comprise 118 NatureServe ecological systems and hundreds of National Vegetation Classification (NVC) associations. Southeastern grasslands owe their origins to Temperate, Boreal, Neotropical, and Madrean biogeographic influences and their maintenance to fire, megafauna, edaphic factors, hydrology, and recent anthropogenic factors. Their high degree of endemism suggests an antiquity that spans thousands to millions of years. Unfortunately, southeastern U.S. grasslands have undergone millennia of management by Native Americans and nearly 500 years of degradation following Euro-American settlement. As such, southeastern grasslands have declined by >90 percent with many types experiencing losses approaching 100 percent. A few represent extinct or functionally extinct ecosystems and nearly all existing types are rare or endangered. The late E.O. Wilson, of Harvard University, considered conservation of the “Southern Grassland Biome” to be a priority goal in America’s environmental movement. Yet, despite supporting more than half of the terrestrial species of conservation concern throughout the region, grassland ecosystems often are considered of lower priority compared to forests, forested wetlands, streams, and coastal ecosystems. We review the current state of science of southeastern U.S. grasslands and provide updates on efforts to: classify and map them, document their biodiversity, assess their role in climate change and landscape resilience, determine their importance as migratory corridors, explore innovations in their restoration/re-creation, and we emphasize key knowledge gaps that need further study.

103 - Grasslands of Arkansas: An Overview of the State's Naturally Open Habitats

Theo Witsell

Arkansas Natural Heritage Commission, Little Rock, AR

While Arkansas is often thought of as a naturally forested landscape, several lines of evidence indicate that millions of acres of grasslands were present at the time of Euro-American settlement. These grasslands were scattered throughout the state and included several types of prairies, barrens, deep sand grasslands, flood-maintained riparian grasslands, marshes, open seeps and fens, savannas, open woodlands, and a variety of edaphic to semi-edaphic glade and rock outcrop communities. Many of these types contained significant variation along gradients of geology, slope, aspect, soil depth, soil chemistry, hydrology, and disturbance regime. These grasslands were disproportionally biologically diverse when compared to forested matrix communities and supported many endemic, disjunct, or otherwise rare taxa. They have also declined dramatically, with some types experiencing near total loss following Euro-American settlement, and protecting grassland remnants and restoring degraded or converted sites are among the highest conservation priorities in the region. The Arkansas Natural Heritage Commission is working on a reclassification of Arkansas grassland natural community types to align with concepts being employed across the broader "Biogeographic Southeast". This presentation will provide an overview of grassland types recognized for the state under this reclassification, comment on their conservation status, and highlight species of conservation concern that depend on them.

104 - (Red-cockaded Woodpeckers) In the pines, in the pines, where the sun always shines at Pine City Natural Area, Monroe Co., Arkansas

Diana Soteropoulos[1,2], William Holimon[1], Joseph Ledvina[3], Travis Marsico[2], Theo Witsell[1]

[1]Arkansas Natural Heritage Commission, Little Rock, AR, [2]Arkansas State University, Jonesboro, AR, [3]Arkansas Department of Transportation, Little Rock, AR

The Mississippi Alluvial Plain (MAP) Ecoregion of eastern Arkansas has had >90% of its land area converted to agriculture and has historically been under-collected floristically, including the ecologically unique site, Pine City Natural Area (PCNA). Actively managed by the Arkansas Natural Heritage Commission, PCNA contains some of the last known saline barrens in the MAP and diverse, open loblolly pine-post oak flatwoods. This site is home to the only population of Red-cockaded Woodpeckers (RCW), a federally endangered bird, in the MAP Ecoregion. This RCW population has grown from a single breeding group in 2003 to four in 2017 through active translocation and habitat management. Population changes and breeding success of the RCWs will be presented in addition to a vascular flora of PCNA and the surrounding area from 2018-2019 that documented 576 taxa, including 9 taxa of state conservation concern. In comparing the flora of PCNA to the known flora of the ten counties surrounding it, 27 taxa (4.7%) documented at PCNA had not been vouchered in the region, and 196 taxa (34.0%) are known from half or fewer of the surrounding MAP counties. The richness in the PCNA flora, in comparison to the broader MAP, demonstrates the need for continued ecological and floristic inventory in eastern Arkansas to find areas of high conservation value for protection, most of which persist as remnant grasslands in an agricultural landscape.

Symposium: The surprising frequency, diversity, and relevance of southeastern grasslands (and why we need to save them) (2/3) *Sponsored by and supported by the Southeast Chapter of the Ecological Society of America*

Dwayne Estes[1], Theo Witsell[2] and Scott A. Woolbright[3], [1]Austin Peay State University, Clarksville, TN[2]Arkansas Natural Heritage Commission, Little Rock, AR[3]University of Arkansas at Little Rock, Little Rock, AR

114 - Using witness trees to infer the presence of pre-settlement grasslands in central Tennessee

Chip Morgan[1,2], Kurt Bryant[3], Dwayne Estes[1,2], Laura Hunt[1,2], Jodi Morgan[1,2], Michael Wilson[3]

[1]Southeastern Grasslands Initiative, Clarksville, TN, [2]Center of Excellence for Field Biology, Austin Peay State University, Clarksville, TN, [3]Austin Peay State University GIS Center, Clarksville, TN

Reconstructing the historical distribution of Southeastern grasslands requires detective work—looking for existing remnants, determining the distribution of conservative grassland-dependent species, and sifting through early historical documents, maps, and land surveys. There is a wealth of historical land survey data from the southeastern U.S., much of which remains buried in hard-to-access state archives and libraries. Some parts of the Southeast, such as Arkansas, were mapped by Government Land Office (GLO) surveyors who divided the landscape into square-mile blocks of townships, ranges, and sections. In other states, such as Tennessee, surveyors used the "meets and bounds" system where individual land tracts (plats) were mapped, and the types of trees at property corners were recorded. During the past 30 years, historians systematically mapped and published more than 1,500 plats (ca. 14,000 trees and 3,000 stakes) from central Tennessee dating from 1783 to 1816. References to "witness" trees could be specific (e.g. "white walnut" for Juglans cinerea) but more frequently were general (e.g. "hickory" which could be any one of several species). Certain trees, such as post oak (Quercus stellata) and blackjack oak (Q. marilandica), were often indicative of savanna, grassy woodlands, or prairies. When trees were absent, surveyors would often use wooden stakes or rock stacks to mark a boundary.

The relative abundance of stakes used in an area may provide clues to the openness of the landscape. In rare cases surveyors actually referred directly to grasslands, such as “stake in the barrens.” We discuss the utility of using these land survey records for inferring pre-European settlement vegetation across five ecoregions spanning a 15,000 km2 area of central Tennessee, representing one of the largest mapping efforts of its kind in the eastern U.S. Furthermore, we identified key challenges and limitations to using witness tree data for understanding grassland distribution in the region.

115 - “The Bright, Sunny South” -- obligate heliophily and the still underappreciated grasslandiness of the Southeastern flora

Alan Weakley

University of North Carolina Herbarium, Chapel Hill, NC; Southeastern Grasslands Initiative, Chapel Hill, NC

Despite the assumption that the Southeastern United States was historically and "naturally" a densely forested landscape, an analysis of the ecological requirements and associations of the full regional flora tells a different tale. A large proportion of the native flora of the SEUS (defined broadly as south of Pleistocene glaciation and east of the "dry line") are heliophytes dependent on naturally open and sunny habitats: grasslands, prairies, fens, bogs, dunes, pyrophytic woodlands and savannas, etc. Even in ecoregions of the Southeast formerly areally dominated by forests (e.g. the higher elevation, moister, and less fire-prone Southern Blue Ridge), heliophytes occupy patch communities that add very substantially to the community and species diversity of the landscape, and additionally support animal and other species diversity by providing landscape, habitat, and plant species heterogeneity and diversity. In collaboration with botanists across the region and with support from the National Park Service and others, we are developing a Grasslandiness Fidelity Index to assess the heliophily (dependence on open habitats) of the 11,000 plant species in the region. The Grasslandiness Fidelity Index will be useful in conjunction with other ratings (Wetland Status, Coefficients of Conservatism, etc.) to characterize the species themselves, and more importantly the sites in which they occur. Such a tool provides the conservationist and land manager a basis for monitoring the effects of management in restoring appropriate structure and species composition. For instance a manager might use a combination of FQI (Floristic Quality Index) and GFI (Grasslandiness Fidelity Index) to assess the effects and progress of management tools (prescribed fire, seeding of natives, etc.) on the restoration of a savanna community dominated by conservative, native heliophytes. This effort is part of the ongoing work of the Southeastern Flora Project (UNC Herbarium, North Carolina Botanical Garden) and Southeastern Grasslands Initiative (Austin Peay State University).

116 - Chronic Drought effects on mixed-grass prairie structure: above- and belowground production responses

Lara Souza[1], Karen Castillioni[2], Mariela Encarnacion[1], Gregory Newman[1]

[1]University of Oklahoma, Norman, OK, [2]University of Minnesota, Minneapolis, MN

The intensity and frequency of extreme precipitation events, including the severity and duration of drought, is expected to increase with climate change. Much attention has been paid to understanding the effect of climate variation, including drought on aboveground production (ANPP). Yet, fewer experiments have explored the impact of drought on total net plant production (NPP), including belowground productivity (BNPP). We have been experimentally testing drought effects on above- and belowground plant responses in a mixed-grass prairie ecosystem in Oklahoma, USA, since 2016. Our experimental design manipulates a precipitation gradient with seven treatment levels: +50%, 0%, -20%, -40%, -60%, -80%, and -100% change from ambient precipitation, replicated three times for a total of 21 2 x 2 m plots. In each year from 2016-2018, ANPP was determined by harvesting standing vegetation, while BNPP was determined via in-growth cores.

There was a decrease in ANPP and increase in BNPP with more intense chronic drought conditions, creating an aboveground-to-belowground shift in plant allocation ($p=0.029$). However, changes in ANPP:BNPP ratio resulted in no effect of precipitation on total NPP, but a shift in where productivity was distributed. ANPP:BNPP ratio was 0.46±0.22 (mean±se) in extreme dry conditions (-100% precipitation), while 1.17±0.51 in wet conditions (+50% precipitation) in 2017 (year of significant change). ANPP ($p<0.001$) and BNPP ($p<0.001$) varied among years. ANPP decreased nearly two-fold in extreme dry plots (256±90 $g.m^{-2}$ in 2017, 262±93 $g.m^{-2}$ in 2018) in relation to wet conditions (419±105 $g.m^{-2}$ in 2017, 372±79 $g.m^{-2}$ in 2018). In contrast, BNPP in extreme dry plots decreased approximately two-fold from 621±74 $g.m^{-2}$ to 418±105 $g.m^{-2}$ wet conditions in 2017. Thus, grasslands subjected to drought could shift carbon allocation towards belowground, as an advantageous trait during drought periods In normal or wet conditions, more investment will likely occur toward aboveground productivity.

Symposium: The surprising frequency, diversity, and relevance of southeastern grasslands (and why we need to save them). (3/3) *Sponsored by and supported by the Southeast Chapter of the Ecological Society of America*

Dwayne Estes[1], Theo Witsell[2] and Scott A. Woolbright[3], [1]Austin Peay State University, Clarksville, TN[2]Arkansas Natural Heritage Commission, Little Rock, AR[3]University of Arkansas at Little Rock, Little Rock, AR

117 - Experimental tests on the importance of soil-borne microbes to community assembly of tallgrass prairies.

Scott Mangan[1], Rachel Becknell[2], Claudia Stein[3]

[1]Arkansas State University, Jonesboro, AR, [2]Washington University in St. Louis, St. Louis, MO, [3]Auburn University at Montgomery, Montgomery, AL

Species-specific interactions between plants and their soil-borne microbes have the potential to maintain plant species diversity, as well as determine which plant species are common, and which are rare. In this talk, I will outline experiments designed to determine the strength of plant-soil feedbacks formed among 18 tallgrass prairie grasses and forbs native to Missouri. I will then link these results to the temporal dynamics measured over 7 years in an outdoor mesocosm experiment where we established mixed-species plant assemblages, initially with and without soil microbes. Collectively, results from these experiments were used to determine the extent to which variation in strengths of plant-soil feedbacks predicted plant community change, and to what degree plant phylogenetic relatedness mediated these patterns.

We found strong evidence that 1) our tallgrass prairie system is dominated by strong negative interactions formed between plants and their soil microbes, 2) the strengths of these diversity maintaining interactions are often stronger than those generated via plant-plant competition, 3) plant phylogenetic relatedness mediates the strength of plant-microbial interactions, and 4) variation in strengths of these interactions predicts temporal change in biomass in mixed-species assemblages. Specifically, in the greenhouse experiment, 10 of the 18 plant species exhibited negative plant-soil feedbacks when grown with live soil biota, and the variation in strengths of feedback were correlated with plant phylogenetic distance. When soil microbes were eliminated, these negative feedbacks vanished. When linking results from the greenhouse to those from the mesocosm experiment, we found that annual increase in biomass was higher for plant species exhibiting weak negative feedbacks, while such increase was less for those species exhibiting strong negative feedbacks. There was no relationship between feedback strength and annual change in biomass when soil microbes were eliminated. Our findings provide strong support that plant-microbial interactions can shape temporal dynamics of tallgrass prairies.

118 - Relicts, remnants, and other natural experiments as ecology and evolution labs

Scott A. Woolbright

University of Arkansas at Little Rock, Little Rock, AR

Climate relicts and other remnants have long been recognized as important components of local or regional biodiversity. Efforts to protect relicts and remnants are often focused on preservation of endemic or rare taxa that are unique within the context of state or other administrative boundaries. But relicts are also *de facto* experiments and natural ecology and evolution labs. Such experiments help to overcome the challenges inherent to experiments that mimic climate change at relevant temporal and spatial scales. By preserving a record of ecological and evolutionary change, climate relicts create tools for understanding how species, communities, and ecosystems have responded to past, long-term environmental change. Using data from ongoing projects as well as examples from the literature, I highlight the dual roles of relicts and remnants as both natural history museums that preserve native biodiversity *and* eco-evo laboratories that provide windows to future environments.

119 - Ecology and Conservation of Crawfish Frogs in Remnant Prairies of Northwest Arkansas

J.D. Willson

University of Arkansas, Fayetteville, AR

Wetlands within tallgrass prairie are among the most endangered ecosystems in North America and serve as critical habitat for many sensitive and endemic species. An iconic, but disappearing species of tallgrass prairie and its associated wetlands is the Crawfish Frog (*Lithobates areolatus*). Although Crawfish Frogs require fishless wetlands for reproduction, they spend much of their adult lives in terrestrial crayfish burrows, often >1 km from water. These unique habitat requirements make Crawfish Frogs vulnerable to numerous anthropogenic stressors and they are listed as endangered, threatened, or of greatest conservation need in every state where they occur. In most regions, however, the precise causes of Crawfish Frog declines remain unclear. This presentation synthesizes a series of field, mesocosm, and modeling studies aimed at understanding the status, biology, and conservation of Crawfish Frogs in historic prairies of western Arkansas. We find that Crawfish Frogs are declining in the region and are threatened by urban expansion, habitat fragmentation, and degradation of historic prairies. Additionally, we explore diverse mechanisms driving negative effects of exotic Tallgrass Fescue vegetation on Crawfish Frog populations, including alternation of water chemistry and disruption of stabilizing density-dependent population regulation.

Symposium: SE Pulse Institute: Departmental Strategies for Change in Life Sciences Education

Christopher Finelli, University of North Carolina Wilmington, Wilmington, NC

The Partnership for Undergraduate Life Sciences Education (PULSE) provides academic departments with resources and training that promote alignment of undergraduate life sciences programs with best educational practices, including those recommended in the Vision & Change Report (2011). The Southeastern Region of PULSE (SERP), which coordinates PULSE's efforts across the southeastern US, has led fifty-four teams of faculty from colleges and universities in a process of reflection, planning, and action to improve outcomes for undergraduate students. During this symposium attendees of previous SERP Institutes will share insights and results from their departmental change efforts. Talks will include topics such as advanced pedagogy, designing inclusive curricula, navigating departmental change, incorporating undergraduate research, and other topics of interest to the ASB membership.

105 - PULSE: Empowering Departments and Transforming Education

Christopher Finelli[1], Judy Awong-Taylor[2], Jung Choi[3], Cerrone Foster[4], Ashley Haines[5], Gail Hollowell[6], Nitya Jacob[7], Mark Lee[8], Kristen Miller[9], Katie Northcutt[10], J. Scott Stauble[11], Jen Rhode Ward[12], Angela White[13], Michael Wolyniak[14]

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Join us to learn about the Partnership for Undergraduate Life Sciences Education (PULSE) and the Southeast Regional PULSE Network (SERP). PULSE is a national network of university faculty and administrators launched in 2012 as a collaboration between the National Science Foundation, the National Institutes of Health/National Institute of General Medical Sciences, and the Howard Hughes Medical Institute to stimulate department-level implementation of the changes recommended in the 2011 publication *Vision and Change in Undergraduate Biology Education: A Call to Action*. PULSE helps life sciences departments at all institutions of higher education align with national education initiatives so they can develop inclusive, student-centered, evidence-based teaching and learning in order to cultivate the development of scientists who reflect the diversity of American society. PULSE focuses on the department as the unit of change because this is the level at which many decisions are made that affect curriculum as well as teaching and learning practices. Importantly, to effect change, departments need to engage in a cycle of continuous, data-driven self-assessment and improvement. As such, PULSE programs provide tools and strategies for self-assessment and teach collaborative strategies that foster cycles of improvement. We will introduce you to PULSE's key programs and showcase some of our recent efforts from the third Southeast Regional PULSE Institute held virtually in May 2021. The other presentations in this session highlight work completed by faculty alumni of SERP's three regional institutes and reflect ways in which departments have adapted to meet the needs of their students. We encourage ASB members to stop by to learn how PULSE and SERP can inspire their own departments to implement the recommendations of Vision & Change.

106 - "You talkin' to me?" and other things your students MAY think and say.

Mark Lee

Spelman College, Atlanta, GA

Inclusive teaching is a leap beyond what most of us think about when we consider diversity, equity and inclusion in higher education. Inclusive teaching is an intentional consideration of the lived experiences of your students as you conceptualize what you will say and what constructs will be effective in expanding on class topics. Teaching bereft of inclusivity may be selecting successful students based on other criteria than content mastery. As instructors, we are not expected to know each students lived experience. We are, however, implored to be curious about how our students see the world and our subject matter. This short talk will share some insights on how inclusive teaching was incorporated in large class and small classrooms to improve student learning while maintaining rigor. Additionally, some examples from biochemistry texts can show us how course content may need recontextualizing to speak to students as opposed to speaking "at them". To that end, inclusive teaching is not fostered by lowering expectations of our students. Inclusive teaching is only possible when we raise our expectations of ourselves in a way the provides the opportunity for student success.

107 - Low Cost CUREs using Biological Collections Data

Tiffany Doan

New College of Florida, Sarasota, FL

Course-based Undergraduate Research Experiences are well known to provide benefits to students and faculty, including self-confidence in scientific thinking, improving persistence in science and medicine, and increasing inclusivity in research. BCEENET is a National Science Foundation-funded group of biology educators, natural history collections professionals, education experts, and data experts who have developed and implemented CUREs utilizing digitized natural history collections data. The major benefits of BCEENET CUREs are that they use freely available public data and only require a computer and internet access. Unlike traditional laboratory-based CUREs, departments do not have to spend funds on expensive equipment and supplies. Students are able to participate through in-person, hybrid, or online instruction. Students gain transferable skills and experience with big data tools and techniques. Four distinct CUREs were created in summer of 2020 and have been used in 30 courses at 24 institutions, including community colleges, minority-serving institutions, liberal arts colleges, and research-intensive universities with over 1200 students participating in CUREs. The BCEENET network provides training for new implementers and support throughout the CURE process. Faculty have the option to select the CURE that suits the goals and level of their course, with funding available for new implementers. The BCEENET CURE that I developed is called Species Distributions and Their Drivers. In this CURE, student groups select a species they are interested in, download the data, map the data using QGIS, conduct spatial analysis, and determine if the species range has changed over time. Students ask questions about climate change, invasive species, and other phenomena and have found novel results about a wide variety of species. Students learn the process of science by conducting original research from inception through analysis and writing of a scientific article. All faculty are welcome to join the BCEENET community to implement CUREs in their classes.

108 - Curriculum Mapping with Vision and Change

Dwight Dimaculangan

Winthrop University, ROCK HILL, SC

Departments may want to determine how their programs' curricula relate to the ideals of the Vision and Change (V&C) doctrine. In this presentation I describe the curriculum mapping project undertaken by the Biology Department at Winthrop University to determine how our curriculum aligns with our program's Student Learning Outcomes (SLOs), the institution's University Learning Competencies (ULCs), and the V&C recommendations to improve undergraduate biology education. The exercise included participation from faculty teaching courses through the use of Excel data sheets specifically designed to capture information about how the biology courses correlate with the core competencies and core concepts with sub-disciplines articulated in the BioCore guide. Each course was scored through a number of tasks according to whether or not it addressed the core concept or core competency and at what level or amount of emphasis. The complied data was then illustrated using a heat map to emphasize how these core elements progress through the overall curriculum. The department is using the results of this study to help make adjustments to address program weaknesses related to curriculum structure and plans for future curriculum development.

109 - CURE in General Science: Weather Investigation

David Campbell, Stefka Eddins

Gardner-Webb University, Boiling Springs, NC

Apart from a few environmentally-focused science majors, most students in Oceanography and Meteorology are getting their science requirement. We developed a series of labs where students identify a question and assess it through measuring around campus. In addition to giving students a research experience, this reinforces the concepts behind the measurements and provides a template for learning to write lab reports.

Students encounter the portable electronic weather meters in the first lab, where they make an assortment of preliminary measurements and observations. Before the first targeted weather measurement lab, they receive a brief explanation of the measurements used (average wind speed, air temperature, wind chill, relative humidity, heat index, dew point, barometric pressure, and altitude) and think of a question that can be addressed with those measurements. They also select five places to measure to help them to answer the question. Measurements are taken on three days, spaced about a month apart, to provide variety in general weather conditions. In addition to the quantitative measurements, students record qualitative weather data in case that affects the pattern (*e.g.*, Day 2 was different – oh, that was the rainy day). After each of the first two rounds of measuring, there are questions to answer aimed at helping them to think about the data – how fast is wind speed in more familiar miles per hour? Does a graph show a relationship between temperature and humidity? They also have directions for the final report, as a reminder to keep the necessary data until then.

The opportunity to investigate their own question is popular, and many students identify this as their favorite lab. Some students require assistance with graphing, and some fall for the temptation to skip the homework component of the assignment as just another lab grade, but overall the students do well.

110 - Integrating introductory biology courses with mathematics

Katharine Northcutt, Jeffrey Pullen

Mercer University, Macon, GA

Most biology programs require mathematics courses, but often students have difficulty seeing the interrelationship between science and math. This is particularly difficult for students who begin college with less mathematics preparation, who often view math as a hurdle to their success. At Mercer University, we have developed an integrated science and mathematics program (PRISM) that seeks to train students to see and use the overlap in content and skills between biology, mathematics, and other scientific disciplines. We were inspired and assisted by the faculty who have developed integrated programs at the University at Richmond. PRISM is specifically targeted towards students who have less mathematics preparation and are not ready to begin science courses; the program allows them to begin biology courses sooner and gives them an alternative pathway for success in our curriculum. Faculty from Mercer's College of Liberal Arts and Sciences have collaborated on two versions of the program: 1) a year-long intensive version that combines concepts from Introductory Biology I (evolution, diversity, ecology, and physiology), Introductory Psychology, Introductory Physics I, Statistics, and Pre-calculus, and 2) a semester-long version that combines Introductory Biology I and Statistics. Students learn concepts and skills from each discipline, and then they practice the integrated nature of science and mathematics through assignments and an intensive research project. Our students' research projects have investigated the ecology of campus squirrels, particularly related to predator avoidance. They use concepts from statistics (and physics, when included) to plan their experiments and analyze their data. After completing the program, many students have decided to pursue interdisciplinary majors, such as neuroscience, as well as independent undergraduate research in a research lab. The challenges of designing and implementing integrated programs primarily relate to the time investment required by faculty; investment from the administration, including course releases, are critical for their success.

111 - Introductory Biology CURE labs have positive effects on student skills and attitudes toward research

David Remington, Iglika Pavlova, Malcolm Schug

University of North Carolina at Greensboro, Greensboro, NC

As part of a wider effort to integrate course-based undergraduate research experiences (CUREs) throughout our Biology curriculum, we introduced CURE modules into a large-enrollment introductory-level lab course for Biology majors starting in Fall 2017. For four semesters, some lab sections consisted of two or three CURE modules depending on semester in which the students designed, implemented, and analyzed data from experiments. The remaining sections followed a traditional lab curriculum with prepared lab activities. Students had no prior knowledge of which sections were CURE-based or traditional, allowing for a quasi-random experimental design. Students in both types of labs were evaluated using standardized instruments to measure statistical analysis and research design abilities consistent with departmental student learning outcomes, and were also evaluated for research mindsets and confidence in research skills. Analyses of data from propensity-matched cohorts showed that students from the CURE sections showed higher levels of proficiency in scientific inquiry compared to students in traditional labs, and also showed more expert-like scientific mindsets and greater confidence in their research abilities. These positive effects were consistent across all semesters and demographic groups including sex, race and ethnicity, and income level. Since skills, mindsets and confidence have all been identified as factors in student STEM persistence and interest in research careers, these result highlight the potential benefit of CURE experiences to broaden representation of diverse groups in STEM fields.

112 - One Size Does Not Fit All: Leveraging Multiple Metacognitive Strategies to Improve Student Learning and Mindsets

Cerrone Foster

East Tennessee State University, Johnson City, TN

As we continue to adapt to changes in the 21st century, it becomes increasingly important that students become science literate and develop a toolkit for academic success. The need for these skills is highlighted by recommendations outlined in the Vision and Change in Undergraduate Biology Education: A Call to Action in core competencies for undergraduate education. Common challenges during the transition to college include student motivation and engagement, difficulty to adapt to high course structure, critical thinking, and communication skills. Metacognition, which is "thinking about thinking", has become a successful tool with intentional actions to monitor and improve student learning. Participants in this interactive session will learn how to incorporate metacognitive practices into daily classroom instruction and assess changes in student mindsets and learning. We will also discuss student self-efficacy and its role in academic achievement and strategies to help students develop healthy mindsets about their intelligence and success.

113 - An Integrated Introductory CURE for Sophomores Increases Research Interest, REU Applications, & Academic Success

Linda Hensel[1], David Goode[2]

[1]Mercer University Department of Biology, Macon, GA, [2]Mercer University Department of Chemistry, Macon, GA

Course-based undergraduate research experiences (CUREs) have positive effects on student learning, retention in science, and understanding of research. In addition, we report an increase in post-CURE research participation. A small proportion of CUREs in biology are interdisciplinary or at the introductory level. Our CURE fills those gaps by integrating the laboratory components of O-Chem and Intro Biology; students spend 6-7 hours per week with drug design, synthesis, and testing of potential biofilm inhibitors. CURE students are compared to students in a control with a traditional "cookbook" lab experience (CBLE). Instructors and all course materials are identical for CURE and CBLE cohorts; only the laboratory experiences differ. CURE students perform better overall, and the number of students leaving science is reduced (by 45 % for Biology and 93 % for Chemistry). Student responses reveal that the increased academic success may result from understanding the relevance of the material to "real world" applications. An impressive outcome is the large numbers of students that gain an understanding of authentic research and build confidence in their own abilities. Two to 4.5 times more students in CURE versus CBLE participate in post-CURE undergraduate research. Student responses also indicate that over 90 % of the participating students gained an understanding of the discovery and applied natures of research, as well as the authentic frustrations present in research. The first two renditions of this CURE had small cohorts (23-27) while the last two renditions were double in size to test scale. Initial analyses indicate the scaled-up version will afford the same successes. In the future, transferability will be tested. Finally, in six renditions of the CURE 400+ compounds were synthesized and 30+ of these new compounds specifically inhibit biofilm formation in one of the 5 bacterial species tested benefiting the undergraduate research programs of both instructors.

ASB Lightning Talks

LT 1 - Estimation of snag density using UAV based imagery in a declining green ash swamp forest

Emma Halstead, Arilyn Lynch, Jay Bolin, Andrew Jacobson

Catawba College, Salisbury, NC

We used a SenseFly fixed wing UAV to capture aerial imagery of the Fred Stanback Jr. Ecological Preserve (FSJEP) in the central piedmont of North Carolina. Plot sampling has confirmed the decline of this green ash (*Fraxinus pennsylvanica*) dominated swamp forest due to widespread infection by the emerald ash borer (EAB). Deadwood monitoring is of central importance to monitoring forest health, biodiversity and EAB-related mortality. Aerial-based monitoring of deadwood holds several advantages over ground-based monitoring such as limited accessibility on foot and reduced time. UAVs are an incredibly accessible tool to monitor forests from the air. With substantial reductions in the difficulty and cost of capturing aerial-based imagery from UAVs, the next primary challenge is to easily process and analyze UAV data for use decision-making. Our goal is to create a simple workflow that forestry managers can implement to create and analyze orthomosaics from UAVs to estimate snag density in deciduous forests.

LT 2 - Phylogeny of Hemiparasitic Genus *Seymeria* (Orobanchaceae) Inferred from *matK* and *rps2*

Benjamin Gahagen, Caroline Shaw, Sharon Spiess

Abraham Baldwin Agricultural College, Tifton, GA

Seymeria is a small genus of annual or perennial root hemiparasites in the Pedicularideae tribe of Orobanchaceae. Members of this genus are distributed from southeast United States to central Mexico. Taxonomic work on Seymeria has been limited to a genus revision by Pennell in 1925, a revision by Turner in 1982 focusing on species distributed throughout Mexico, and new species described in 1995 by Turner and in 2017 by Carranza and Medina. Phylogenetic work has been limited to a few members of Seymeria being included in larger family studies or studies investigating the evolution of parasitism, in general. This project used the plastid gene regions matK and rps2 to infer the phylogenetic relationships between 14 species of Seymeria.

LT 3 - Using RADseq to Determine the Provenance of Longleaf Pine (*Pinus palustris* Mill.) at Blackwater Ecological Preserve

Lauren Heyd[1], Nicholas Flanders[1], Peter Schafran[2]

[1]Old Dominion University, Norfolk, VA, [2]Boyce Thompson Institute, Ithaca, NY

Longleaf pine (Pinus palustris Mill.) is estimated to have a genome size of 23.6 Gbp, which creates difficulties for sequencing. Eight needle samples were collected from three sites (two in Virginia and one in Alabama) and analyzed using RADseq with five sets of restriction enzymes, in order to determine an adequate sequencing depth for identifying genetically distinct populations. This preliminary study is part of an ongoing longleaf fingerprinting project focused on Blackwater Ecological Preserve in Isle of Wight County, Virginia. The site is of both ecological and historical importance, however the genetic provenance of trees there is unknown. The end goal of the project is to determine whether previous land owners imported any individuals from other parts of the longleaf pine range. Those results will guide future restoration efforts as longleaf is replanted across Virginia.

LT 4 - Let's be real; new experimental approaches for more realistic climate simulations in grasslands

Evan Rehm[1], Gabriella Lefevre[1], Bryan Gaither[1], Dwayne Estes[1,2,3]

[1]Austin Peay State University, Clarksville, TN, [2]Southeastern Grasslands Initiative, Clarksville, TN, [3]Center of Excellence for Field Biology, Austin Peay State University, Clarksville, TN

Open-top chambers (OTCs) are used to warm low-stature vegetation plots, simulating climate warming. However, climate change will alter more than just temperatures. We've developed a novel automatic retractable rain shelter to create a more realistic simulation of climate change. In combination with a specialized OTC for tall-stature grasslands, our approach warms plots between 1-1.5°C while also allowing us to manipulate precipitation (30% reduction) to better match climate projections for our region.

LT 5 - Grassland restoration success in a changing world: the roles of climate change and invasive species

Gabriella LeFevre[1], Dwayne Estes[2], Evan Rehm[1]

[1]Austin Peay State University, Clarksville, TN, [2]Center of Excellence for Field Biology, Austin Peay State University, Clarksville, TN

Climate change is hypothesized to favor invasive over native species because invasives tend to have wider climatic tolerances and greater phenological plasticity. These invasive species may be at an advantage under future climates, potentially altering the long-term success of grassland restoration efforts. We are using a fully factorial design of simulated future climates (open-top chambers for passive warming [+1.5 °C above ambient] and automatic rainout shelters [30% precipitation reduction]) and the presence of a detrimental invasive species (*Sorghum halapense*) to track restoration success in a simulated future. While plant communities are identical at the start of the experiment, we expect climate change and invasive species to act synergistically to reduce overall native biodiversity. We will discuss this novel experimental approach, preliminary findings, and what this means for conservation efforts moving forward.

LT 6 - Small World Initiative: Innovative Tool for Student Laboratory Engagement

Megan Meade, Richard Watkins, Jocelyn Moore, Jenna Ridlen

Jacksonville State University, Jacksonville, AL

This project represents results of the introduction of the Small World Initiative Course based undergraduate research experience (CURE) to Jacksonville State University (JSU) Biology I laboratories. The Small World Initiative CURE was originally piloted at Yale University from 2012-2013 before being introduced to over 300 schools in over 15 countries by 2019. We joined the initiative in 2021 as student rejoined face-to-face laboratory classes after a year of virtual class instruction in high school and/or college. We set up four laboratory sections to investigate the discovery of antibiotics following the World Health Organization's (WHO) prediction of potential premature deaths associated with superbug growth in immunocompromised patients by the year 2050. Students took local soil samples and cultured their own strains of bacteria. Along the way they learned important microbiology and laboratory techniques as well as enhanced scientific communication. This CURE was aimed to increase student engagement in research and matriculation in the face of an enrollment increase at JSU. We will present our SWI start-up challenges, first semester debrief, current setup, and future plans for this program in JSU curriculum.

LT 7 - Pie charts are evil

Patrick Cain

Georgia Gwinnett College, Lawrenceville, GA

Data visualization in science is an art. We must present complex data in such a way that our reader can quickly, easily, and most important, convincingly, see and understand the important trends our hard work and stalwart dedication has discovered. The human ability to detect patterns in complex data sets is severely limiting. Therefore, we must present our findings in figures that are able to catch the reader's attention while being clear and concise enough to limit the work the reader needs to grasp the trend we are proposing. Pie charts do none of this. In fact, there are few, if any, examples of when a pie chart is the best data visualization option. Here, I contend that pie charts should be boxed, put on ice, and taken off the menu forever.

LT 8 - Elucidation of Honey's Antimicrobial Mechanism

Jonah Dennis[1], Dr. Sarah Beno[2]

[1]Birmingham Southern College, Birmingham, AL, [2]Birmingham-Southern College, BIrmingham, AL

Rising prices of antibiotics and an uptick in rates of antibiotic resistance in veterinary medicine have prompted an investigation into lower cost and effaceable alternatives. Unpasteurized honeys are known to have antimicrobial properties and thus, may prove a low-cost asset to animal owners. Sixty bacterial isolates, collected from infected wounds of four horses, were characterized and identified, and then tested against a triad of orange blossom, dark, and Manuka honeys. It is hypothesized that honey's antimicrobial mechanism is a combination of three factors: prebiotic oligosaccharides from the bees, in unison with the chemicals: hydrogen peroxide, and HMF, contained in the honey. Together, these factors allow honey its antimicrobial properties, even against bacteria resistant to traditional antibiotics. This research analyzes each cofactor to elucidate the driving aspects of the mechanism. Kirby-Bauer and minimum inhibitory concentration assays were used to assess the effectiveness of each cofactor. A *Staphylococcus* isolate and an *Escherichia coli* isolate were resistant to both tetracycline and carbenicillin, yet, showed sensitivity to 5% honey aqueous solutions of both dark and Manuka honey on disk diffusion assays. Honey may serve as a promising treatment for inhibiting bacterial growth at a significantly lower cost.

LT 9 - Chirping in a Noisy World

Natasha Vanderhoff

Jacksonville University, Jacksonville, FL

Man-made noise (anthropogenic sound) creates excessive noise levels above ambient norms and high noise levels can negatively affect organisms in the environment. Anthropogenic sound pollution can alter foraging, anti-predator and mating behaviors and is particularly important for animals that communicate with vocalizations, like birds. Anthropogenic sound can mask vocalization at lower frequencies and some birds will increase the frequency and/or amplitude of their vocalizations to compensate. While the effect of anthropogenic noise on birds' songs has been widely investigated, fewer studies have examined how noise might impact the calls birds use year-round.

LT 10 - Determining Longleaf Pine (Pinus palustris Mill.) Naval Store Production at its Northern Range

Nathan Teel

Old Dominion University, Norfolk, VA

Longleaf pine (*Pinus palustris* Mill.), ranging from southeastern Virginia to the Atlantic and Gulf Coastal Plains into central Florida and extends into eastern Texas, supported a naval stores industry from the earliest European settlement. Initially, dead pine wood laden with resin, known as "lighter wood" or "lightwood", was collected and heated in structures called tar kilns which was used to create naval store products: tar, pitch, and turpentine. Situated in the northern-most part of longleaf pine's range, Blackwater Ecological Preserve (BEP) in Isle of Wight County, Virginia is home to the best preserved and largest number of tar kilns in the region. LiDAR and historical records were used to to determine the density of tar kilns at BEP. Using tar kilns as a proxy, we were able to compare the productivity of longleaf pine for naval stores at BEP with sites further south, with differences possibly attributable to regional variation in both ecology and history.

ASB Posters

SE-PULSE1 - MGA Checks Its Pulse: Flatline or Healthy Rhythm?

Dr. Dawn Sherry, Ph.D[1], Donna Balding[1], Christie Canady[2], Thomas Hancock[1]

[1]Middle Georgia State University, Macon, GA, [2]Middle Georgia State University, Cochran, GA

The purpose of our project was to examine the Middle Georgia State University (MGA) biology curriculum and bring it into alignment with the goals and objectives outlined in *Vision and Change in Undergraduate Biology Education* (NSF 2009). The first step in this process was to address the status of the curriculum. We called a voluntary meeting for biology faculty who teach upper-level courses and who were interested in discussing and updating our curriculum. In this meeting we presented the goals and objectives outlined in *Vision and Change*. All fourteen faculty who teach upper-level courses participated. Following the meeting, faculty were sent surveys that asked them to identify content covered in each of the upper-level biology courses offered by MGA. If a faculty member was an instructor for a specific upper-level course, they were asked to identify content covered in their course. If the faculty member was not an instructor of a specific course, they were asked to identify areas of overlap from other courses they teach. Faculty were also asked to describe at what level and by what methods content was covered (e.g., low, high, laboratory activity, assignment, exam, paper, project, etc.). From the data, we created a heat map that characterized content coverage across all upper-level courses. Next steps will include mapping content coverage to the goals and objectives outlined in *Vision and Change*. Future plans include sharing this with the faculty and conversations on how to implement any strategic changes.

CURE1 - Enhancing STEM skills relating to analysis, reasoning and communication

Patrick Cain, Maribel Fernandez, Mia Malloy, Jill Penn

Georgia Gwinnett College, Lawrenceville, GA

It has been the experience of this group of researchers that students reach their senior year without being competent in data management, including analysis and interpretation of results. We have experienced this over several semesters in students taking STEC4500 and BIOL4570. This is despite these skills being specifically addressed in the BIOL1108K gateway course through 2 laboratory sessions on scientific method and one large semester long group project. The objectives of this project are to increase students' proficiency in data management, including: organization, analysis, reporting and interpretation. These will contribute to the following STEM skills: Scientific Communication, Problem Solving & Critical thinking, Data Analysis and Quantitative Reasoning. The questions is if performing frequent activities on data handling during a gateway course will help students be more proficient when they reach their senior year and hopefully beyond. We propose to have one additional lab session as well as weekly data management activities that students will perform as home works, with a brief in-class discussion of the results in small groups and as a class. These data management activities will include basic data set management – such as sorting, organizing and reformatting data, as well as basic statistical analysis and graphing with Excel, and finally interpretation of the results. In order to find out if these interventions are effective, we will develop a set of questions related to these skills to be included in the lab practical of the control and the experimental sections.

P1 - eBio: The Official Peer-Reviewed Experimental Life Science Journal of the Association of Southeastern Biologists (A)

Judy Awong-Taylor[1], Holly Boettger-Tong[2], Chris Gissendanner[3], Dr. Lyndsay V. Rhodes, PhD[4], Veronica Segarra[5], Ted Zerucha[6]

[1]Georgia Gwinnett College, Lawrenceville, GA, [2]Wesleyan College, Macon, GA, [3]University of Louisiana Monroe, Monroe, LA, [4]Florida Gulf Coast University, Fort Myers, FL, [5]Interim Chair and Assistant Professor of Biology, High Point University, High Point, NC, [6]Appalachian State University, Boone, NC

The re-envisaged eBio is a laboratory-based biological research journal and an official journal of the Association of Southeastern Biologists (ASB). eBio publishes full length articles as well as shorter notes including micro-publication style publications in the experimental life sciences, and the scholarship of teaching and learning relating to laboratory-based biological sub-disciplines. The focus of the journal is the biology of organisms in the context of the structure, function and development of their internal systems. This focus encompasses biological sub-disciplines including biochemistry, biotechnology, cell biology, genetics and genomics, immunology, microbiology, molecular biology, neurobiology, physiology, parasitology, and toxicology. eBio is now accepting manuscript submissions as well as proposals for special issues. We welcome manuscripts that add to the conversation of subfields that fall within the scope of the journal including data that does not support the original hypothesis. Manuscripts accepted for publication by eBio are published online on an article-by-article basis facilitating timely publication. eBio is an excellent destination for research projects of undergraduate students, honors students, masters students as well larger scope projects. In addition, ASB members receive special page rates and are encouraged to consider submitting manuscripts based on ASB presentations.

P1 - eBio: The Official Peer-Reviewed Experimental Life Science Journal of the Association of Southeastern Biologists (B)

P1 - eBio: The Official Peer-Reviewed Experimental Life Science Journal of the Association of Southeastern Biologists (C)

P1 - eBio: The Official Peer-Reviewed Experimental Life Science Journal of the Association of Southeastern Biologists (D)

CURE2 - Identification of Fluorescently-Tagged Cell Populations in a Biotechnology Lab Course

Shoshana Katzman, Jennifer Hurst-Kennedy

Georgia Gwinnett College, Lawrenceville, GA

Course-based undergraduate research experiences (CUREs) are high-impact practices that promote student gains in performing hypothesis-driven research. We established a new inquiry-based CURE at Georgia Gwinnett College (GGC) in our Biotechnology Laboratory course. This laboratory-based course includes a semester-long research project in which students design experiments and apply biotechnology laboratory skills to address a research question. We implemented a new CURE in the fall of 2021, wherein students investigated fluorophore gene expression in stably- transfected B16F10 murine melanoma cell lines. Each cell line expressed a unique fluorophore (i.e., GFP, YFP). Students were tasked with designing experiments to determine which fluorophore was expressed in each cell line at the DNA and protein levels. Students performed PCR to detect the presence of various fluorophores, while flow cytometry and fluorescence microscopy were used to confirm that the fluorophore present at the protein level. Student engagement in the project throughout the semester was high and feedback on the newly introduced CURE was positive.

SE-PULSE2 - Harmonizing Undergraduate Biology Education with Best Practices at The Citadel

Kathy Zanin[1], Dena Garner[2], Andrea Gramling[2], Darin Zimmerman[2], John Weinstein[2]

[1]The Citadel Military College, Charleston, SC, [2]The Citadel, Charleston, SC

The Citadel is a comprehensive, public, four-year college, with an undergraduate enrollment of approximately 2,300, including 115 biology majors. The Biology Department consists of 11 full-time and 9 adjunct faculty, with a total undergraduate credit hour production of around 2,650, with about 850 of those in Biology major courses and 1800 in service/general education courses for nonmajors. The degree programs offered include the B.S. in Biology and the M.A. in Biology. The Biology Department's goals are to 1) improve recruitment and retention, especially of at-risk students, 2) improve the quality of graduates and their ability to gain employment within STEM fields, and 3) improve students' graduate school acceptance rates. We hope to make progress toward those goals by instituting greater alignment between our teaching practices and the principles of Vision & Change. After learning about Vision & Change at SERP II, these principles were introduced to faculty at a summer Departmental retreat. Faculty agreed to begin in the Fall 2021 semester by integrating measurable objectives into one course per semester and to incorporate a few high-impact practices that they had not tried before.

P2 - Exploring the Growth Behavior of Fungal Pathogen *Candida albicans* and Biofilm Formation on Various Nanomaterial Coatings

Hunter Tinker[1], Sahar Hasim[1], Parvin Fathihafshejani[2], Masoud Mahjouri-Samani[2]

[1]Mercer University, Macon, GA, [2]Auburn University, Auburn, AL

Biofilm formation on abiotic surfaces is a serious problem playing an important role in healthcare-associated infections, especially those related to prosthetic and indwelling medical devices. Despite efforts to maintain sterility, implantable and prosthetic medical devices can quickly become contaminated, leading to device failure, chronic infections, and high mortality rates. *C. albicans* is the most common source of fungal infections in humans, often proving to be fatal in immunocompromised patients, as it results in the development of candidemia, a systemic bloodstream infection. Therefore, the research interest of inhibiting fungal adhesion and biofilm formation, on the surface of medical devices, is of interest to reduce the risk of surgical site infection. In this study, several transition metal dichalcogenides (TMDs) were tested, among them TiS2 (Titanium Disulfide) and MoS2 (Molybdenum Disulfide), which showed decreased metabolic activity of *C. albicans*, as confirmed by the XTT cell viability and proliferation assay. Further examination of the unique properties of Molybdenum may allow for its eventual application as a material or coating for implanted devices; however, its potential impact on the naturally occurring cells within the human body is elusive at this time.

CURE3 - Integrating PBL to Enhance Student Learning of Precalculus Concepts

Rabia Shahbaz

Georgia Gwinnett College, Lawrenceville, GA

The purpose of this project was to integrate project-based learning in Precalculus classes to enhance students' understanding and aptitude about mathematics. Precalculus is a prerequisite course for Calculus I, which is a required math course for many STEM majors at Georgia Gwinnett College, and other institutions across the nation. Precalculus, and in general all math, students struggle with skills such as modeling, analyzing and interpreting graphs and data, drawing conclusions and making projections. Students also have trouble applying mathematics in real world situations and across other disciplines. With the integration of project based learning our students used trig and exponential functions to model real life data, used research skills such as collecting and analyzing data, interpreted results and drew conclusion. This project was implemented in fall 2020, spring 2021 and fall 2021. Each investigator used one of their sections as a control group and other as treatment group. We conducted pre and post attitudinal surveys as well as compared students grades on the targeted standards. In this presentation, our poster will include a description of our project, samples of students' work and the summary of our pre and post survey results demonstrating the impact of these projects on our students' attitude towards mathematics. The poster will also include a reflection of the successes and challenges that we, as instructors, faced during the development and implementation of these projects.

SE-PULSE3 - Improving Assessment and Infrastructure for New College of Florida's Biology Discipline

Tiffany Doan, Amy Clore, Erika Diaz-Almeyda, Sandra Gilchrist

New College of Florida, Sarasota, FL

After completing the SERP III Institute, the biology discipline at New College of Florida identified three major areas of improvement that would bring our programs more in line with Vision and Change principles. (1) Course-level assessment, (2) program-level assessment, and (3) infrastructure and climate. Since the institute, we held a meeting with the entire biology faculty to go over the results of the snapshot rubric and to share the areas that we sought to improve. We had very positive reactions from the other faculty and got volunteers to work on each of the initiatives. We have made progress in consulting with institutional research to get data from mid-semester progress reports for students taking biology classes, which helps us see numbers of students struggling at midterm and identify some of the reasons they are doing so. This information should allow us to devise appropriate interventions. For infrastructure and climate, we discussed conducting formal peer evaluations with faculty from the entire Division of Natural Sciences to get a broader idea of the points of view of faculty from throughout the sciences. One of our faculty colleagues has been in discussion with facilities about grants for renovation of our building and consulting the strategic plan of the college to determine how renovation or a new building fits into the strategic plan. Although we have made some progress, much more work needs to be done. We plan to investigate more tools for course-level assessment, compile and analyze the assessment data we already have, develop a set of mindset interventions, and work with the alumni foundation and the Center for Engagement and Opportunity to better compile outcomes from our alumni and make connections to between NCF biology alumni and our current students.

P3 - Analysis and identification of lipolytic bacterial species for the degradation of wastewater lipids

Lindsay Smoak, Tiehang Wu

Georgia Southern University, Statesboro, GA

Though the bioremediation of lipids in wastewater is not a novel concept, the process typically requires a regular addition of the bacteria involved in lipolysis to the treated water because the introduced organisms cannot compete with native organisms. Isolating lipolytic bacteria from the wastewater itself ensures the bioremedial agent will not be outcompeted by other native organisms. Previous studies into the matter found that *Bacillus* and *Pseudomonas* tend to have higher levels of lipase, and these bacteria can additionally be used to break down a variety of other contaminants.

The aim of this study was to isolate bacteria sampled from Statesboro wastewater treatment facilities to identify native lipolytic strains. Lipolytic strains were isolated then assessed via morphological, biochemical, and molecular methods to determine their enzymatic capabilities. Use of the detergent Tween-20 in growth mediums was the first alert to lipase activity, and these isolates were further investigated to quantitatively measure lipase presence and activity. Lipase protein was precipitated and dialyzed to properly perform a lipase activity assay, followed by Sodium Dodecyl Sulphate–Polyacrylamide Gel Electrophoresis (SDS-PAGE) to confirm the protein's presence. Sanger sequencing was then employed to determine the bacteria's identity.

Results indicated lipolytic activity, as displayed by Tween-20 indication. Activity quantification found that industrial agents have a weaker lipolytic capability than the isolated bacteria. The isolates with the highest levels of enzymatic activity were identified as *Bacillus* spp. through Sanger sequencing. This analysis showed that the bacteria specific to a wastewater plant can be successfully employed to improve water quality while also causing fewer downstream effects because they process lipids without the addition of harsh chemicals.

CURE4 - A CURE in an introductory biology course improves students experimental design skill.

Allison D'Costa, Cindy Achat-Mendes, Judy Awong-Taylor, Joshua Edwards, Latanya Hammonds-Odie, Pat Uelmen Huey, Elisabeth Javazon, Candace Timpte

Georgia Gwinnett College, Lawrenceville, GA

The Principles of Biology I BIOL1107K labs were redesigned with a course-embedded undergraduate research experience (CURE) to provide multiple opportunities for students to learn and practice experimental design, a valuable STEM skill. As part of the CURE, students conducted in-depth investigations on two topics: (a) effect of UV radiation on yeast survival, and (b) enzymatic reactions and factors affecting enzyme activity. Using minimal handouts and instruction, students had at least three opportunities to design controlled experiments iteratively. To assess the effectiveness of the CURE on improving students' ability to design an experiment, Control lab sections continued in the traditional cook-book format, with students following step-by-step instructions in a lab manual and having just one opportunity to design an experiment. A validated Experimental Design Ability Test (EDAT) was administered to students in both the CURE and Control sections as a pre-test during the first week of the semester and as a post-test at the end of the semester. At the end of the semester, each student's pre and post-tests were graded by two faculty members using a validated rubric. Faculty graders were randomly assigned a mix of pre- and post-EDATs from both Control and CURE sections to minimize scoring bias. Data analysis shows that students in both CURE and Control sections began the semester with similar pre-EDAT score averages. However, at the end of the semester, only students in CURE sections show a significant increase ($p = .035$) in their post-EDAT scores. Impact of the CURE on various aspects of experimental design such as multiple variables, multiple trials, or appropriate controls will be presented.

SE-PULSE4 - Yes, you belong! Creating a more inclusive learning environment in a Principles of Biology Course.

Jasmin Feimster, Kimberly Miller, Lisa Spring

Central Piedmont Community College, Charlotte, NC

Central Piedmont Community College is a diverse institution with enrollment exceeding 55,000 credit and non-credit seeking students. The Natural Sciences Division offers a Principles of Biology course (BIO-110), which largely serves to fulfill the science requirement for the Associate in Arts degree. Previous redesign efforts yielded great success in incorporating more innovative learning strategies, however they did not address the needs of our unique student population. Thus, the Biology leadership at the college envisions creating a more inclusive learning experience for students in our BIO-110 course. We began with reflecting on what inclusivity means for our students. Key faculty stakeholders were availed to professional development centered on reducing learning barriers and improving equity. Faculty also participated in an Opportunity Walk activity, which mimicked many of the challenges our students face while navigating their education. We then decided to revise the learning outcomes for BIO-110 and began exploring changing the required course text for the class. Criteria for the new text include quality, cost, accessibility, and inclusion of culturally diverse ideas. Currently, a new text is being piloted in 2 sections of the course. The next steps in our plan include reviewing success data in the sections piloting the courseware, collecting qualitative data about the students' experience with equity in their learning environment, and assessing how the diverse approach facilitated their learning. We are aware that course texts are a small portion of the plan; faculty buy-in, accompanied by data that supports the continued use of inclusive practices will make for a well rounded student experience. In the future, we hope to make professional development relative to inclusive teaching an integral part of the faculty annual evaluation process, revitalize the syllabus with more learning-centered language, and incorporate tiered assessments that engage students in real world, meaningful work.

P4 - Retention ponds are a breeding ground for bacteria populations that can be manipulated into antibiosis.

Cheyenne Bailey, Deilan Estrada, Ericka Walczak, Hugo Coronado

Georgia Highlands College - Rome, GA, ACWORTH, GA, GA

Retention ponds hold a permanent pool of water designed to store runoff. Thus, they are a breeding ground for prokaryotic organisms that are continually being fed from carried nutrients and waste. The focus of this study will be to analyze and compare bacterial populations using the 16s rRNA gene sequencing and create a database of bacterial populations. Chemical analysis of the retention pond will evaluate dissolved oxygen, nitrogen, total phosphorus, and other parameters while analyzing bacteria populations. Antibiotic production of each species will be tested in an asocial and social growth experiment to further understand the social interactions of bacteria and antibiosis.

Antibiotics work by ceasing vital processes in bacteria and inhibiting them from multiplying. The methods of antibiotics differ from destroying bacterial cell walls, such as penicillin, or affecting the way the bacterial cell's function. Due to an increase of antibiotic resistant infections, such Methicillin-resistant Staphylococcus aureus (MRSA), more studies on how additional new bacteria that can produce antibiotics are needed. As we investigate the type of bacteria capable of producing antibiotics, we also investigate the environment that helps increase the likelihood of it occurring. When faced with competition, certain bacteria have signaled that trigger antibiotic production as a defense mechanism. Observing these defense mechanisms, in an asocial and social environment, we can see how bacterial signals can trigger an increase in antibiotic growth.

Our objective is to investigate the interaction between various types of bacteria found in the retention pond at GHC-Cartersville. Our goal is to investigate the types of bacteria present in the retention pond and their interaction between competing bacterial colonies and to see if certain bacteria can produce antibiotics in different environments.

CURE5 - CUREs: part of a holistic approach to learning, inclusivity, and sense of belonging in STEM education

Clay Runck[1], Judy Awong-Taylor[1], Allison D'Costa[1], Tirza Leader[1], Cindy Achat-Mendes[1], Chantelle Anfuso[2], David Pursell[1], Mohamed Jamaloodeen[1]

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We have incorporated Course-embedded Undergraduate Research Experiences (CUREs) for 10 years as part of a comprehensive systems approach model to transform STEM learning, student engagement, and inclusivity for our student population. CUREs increase inclusivity because they offer research experiences to all students enrolled in the course irrespective of their background and skills. Our model incorporates multiple CUREs throughout all four years of matriculation for all STEM majors. This provides a mechanism for successfully engaging large numbers of students in undergraduate research and provides them with the skills and confidence to seek out independent, faculty-mentored research. We recently analyzed five semesters of quantitative and qualitative assessment data on the impact of CUREs in gateway STEM courses on student success and engagement. Results show: (1) CUREs led to a more positive belief in self-efficacy in communication, experimental design, career choices, and critical thinking/problem solving; (2) CUREs had little to no significant effect-size on ABC/DFW percentages; and (3) CUREs are inclusive and allow for repeated exposures to research experiences. However, CUREs are not a single cure-all to address underlying educational inequities that affect academic performance, retention, and sense of belonging of students from historically underserved populations in STEM. A more holistic approach is needed. For example, our Peer Supplemental Instruction (PSI) Program has had positive effects on academic performance, mindset, and sense of belonging, particularly for students that come to GGC less well prepared for college-level work. For the past 5 years we have had formal collaborations with 3 external institutions to assist them in implementing CUREs into their curriculum, as well as several additional informal collaborations with other institutions in the University System of Georgia. These collaborations indicate that our model is transferable to different institution types.

P5 - Effects of Copper and Silver on *Candida albican* and *Candida auris*

Victoria Gomez, Lauryn Mcgahee, Jheel Patel, Dorina Mihut, Sahar Hasim

Mercer University, Macon, GA

In recent years, the availability and use of various antifungal agents have increased drug resistance in *Candida* species. *Candida auris* and *Candida albicans* are worldwide hospital-acquired fungal pathogens that cause a broad spectrum of infections and commonly colonize medical devices such as central venous catheters. Developing different coatings with antimicrobial and antibiofilm agents is a promising approach that can inhibit the initial attachment of planktonic cells on the surface of medical devices. In this study, copper and silver-plated filter paper will be used to test its efficacy of resisting growth of *Candida* species. Copper is found to be the most effective at preventing the growth of the three strains that it was tested against while silver is less effective. These findings lead to the conclusion that copper and silver can prevent *Candida* growth and could be used to prevent infections. Future studies should focus on ultraviolet light resistance that is prominent in *Candida auris* and combining UV treatment with copper and silver treatments for increased efficacy at reducing the growth of the cells.

SE-PULSE5 - SERP GPS: Recalibrating ...

Meredith Rowe, David Judge, David Campbell

Gardner-Webb University, Boiling Springs, NC

At the SERP meeting, we identified three main targets for our Gardner-Webb PULSE Strategy: develop effective supplements to student learning (assessment and learning modules), increase student research (CUREs and independent), and improve student connection to the department and each other. A wide assortment of challenges has slowed implementation, but we are moving forward and hope to have more extensive progress in the future, especially as the department as a whole has more time to discuss ideas and get involved.

Several university-level revisions to assessment are underway. Implementing large changes makes it challenging for us to focus on refining our assessments, but it also represents an opportunity for innovation and review. We are starting to develop some learning modules, building on the experiences of creating new materials in the wake of COVID.

For research, we have begun to synthesize information on existing CUREs and independent research opportunities. Several classes have some open-ended research components, but we hope that sharing ideas will increase the use of CUREs and allow the development of greater continuity, integrating the student data into larger projects. Likewise, we are investigating how to expand our existing independent research opportunities to involve more students.

To promote student connections, we had a new event to welcome new and returning students, and hope for higher participation next year. We are identifying areas that deserve greater support and guidance for the students. A new one-credit class focuses on professional readiness, and seems successful after one semester. As the university is changing its new student introductory programs, we hope to implement an “Introduction to Natural Sciences” course to help get students off to a well-guided start.

P6 - Staphylococcal contamination in a Neonatal Intensive Care Unit after earlier remediation efforts

Loren Captain[1], Daniel See[1], David Levine[2], Anuj Sinha[3], Henry Spratt[2]

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Methicillin-resistant *Staphylococcus aureus* (MRSA) continues to plague hospital units with nearly 29% of MRSA infections being fatal. Contanimation of MRSA is common in neonatal intensive care units (NICUs) and effective infection management requires early detection to prevent transmission in the neonates. Our research group had conducted a study of Staphylococci in this NICU unit five years earlier, which led to the institution of measures to reduce Staphylococcal contamination. The goal of this study was to validate the earlier interventions, and to determine if contamination by MRSA and Methicillin-susceptible *Staphylococcus aureus* (MSSA) remain in this NICU. During 2021 we collected swab samples from 20 sites in seven NICU pods over fourteen weeks, with a total of 966 swabs collected. The swabs were used to

inoculate Hardy CHROM MRSA agar and Mannitol Salt Agar to indicate growth of MSSA. Presence of Staphylococci for a swab was determined by observing unique colonies on either the CHROM MRSA or MSA agar after 48 hour incubations at 37 ºC. Our findings showed that even after measures to address Staphylococcal contamination in this NICU had been instituted, areas of the NICU remained highly contaminated by MRSA and MSSA. Two areas with very high levels of contamination were found. The greatest Staphylococcal contamination was found on the floors by the sinks with 76.2% positive for MRSA, and 87.3% positive for MSSA. The other area with high levels of Staphylococcal contamination was the Yankauer suction devices found inside isolette beds, with 25.7% of the devices contaminated by both MRSA and MSSA. These results suggest that initial measures to reduce the amount of Staphylococci in the unit, particularly for the floors by the sinks have not been completely effective. We have helped establish a new baseline of Staphylococcal contamination in this NICU to help direct future remediation efforts.

SE-PULSE6 - SERP 2022: Service Learning, Theme-Based, and Virtual Pedagogies Before and During a Pandemic

Kartz Bibb

Alabama State University, Montgomery, AL

Theme-based teaching, online teaching and service learning are three pedagogies utilized at Alabama State University to keep students engaged in the learning process. It is beneficial to explore new strategies of teaching and to improve existing strategies for students during these challenging times. The COVID-19 Pandemic has forced educators to become more innovative in providing learning opportunities on every level of matriculation. The effectiveness of service-learning can be attributed to its impact on the community and services it provides. It is a strong pedagogy to connect students with academic concepts. Colleges and universities have implemented higher numbers of services learning courses for students as well as other programs like it to provide community engagement and development. One of our Biology 127 courses was built around 3 major themes: Cancer, Energy Drinks and Sickle Cell. Students used writing modes like case studies, journal writing, storytelling, and other ways created by the students to understand concepts. The writing modes became the major assessment instrument instead of the traditional exams. Initial results indicate that students prefer this method if they are given ample time to write and clear instructions. Due to the ongoing pandemic and its impact on higher education, the necessity of online learning cannot be over emphasized. Effectiveness must not be sacrificed for convenience therefore course designers must rethink learning strategies to maintain positive student learning outcomes. Studies have shown that there are only negligible deviations in learning effectiveness between traditional and virtual learning platforms given the course well-designed (Igelsias-Pradas, 2021). Our objective is to explore these pedagogies and their value to course learning objectives at ASU in our freshman biology classes.

CURE6 - Impacts of a SARS-CoV-2 Bioinformatics CURE in an Introductory Genetics Course on Learning Outcomes and Science Attitudes

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

Georgia Gwinnett College, Lawrenceville, GA

The Department of Biology at Georgia Gwinnett College (GGC) incorporates Course-based Undergraduate Research Experiences (CURE) in many of our biology lab courses. In order to retain high impact lab practices while following social distancing requirements during the COVID-19 pandemic, we created a multi-week bioinformatics lab module that has students analyze variant genomes and possible routes of transmission/migration of SARS-CoV-2, the virus that causes COVID-19. We piloted this CURE in 2020 and have offered it both virtually and face to face in all sections of the genetics course since the spring 2021 semester. The CURE begins by teaching the history and biology of the SARS-CoV-2 virus. Students are then introduced to the field of bioinformatics including basic techniques and tools used to assess genome sequences and variants including collaborative databases such as NCBI and GISAID. GISAID is internationally recognized as one of the leading consortium databases experts use to investigate the novel coronavirus. Students complete individual research projects comparing 15+ genomes and at least one protein sequence from two different regions of the world to the original COVID-19 variant. Students develop multiple hypotheses, gather and analyze data to reach conclusions and present their projects either orally or in written form, thus engaging in all aspects of the scientific method. Here we present three semesters of data exploring if this CURE impacts students' long-term retention of basic concepts used in bioinformatics by assessing students at least one semester after being exposed to the CURE. We will also present our current effort in determining how this CURE impacts students' perceptions regarding their ability in science.

CURE7 - CURE: Learning and Applying the Scientific Method Through Experimentation with Bayou Microcosms

Timothy McMahan, Tom Sasek, Srinivas Garlapati, Ann Findley, Chris Gissendanner

University of Louisiana Monroe, Monroe, LA

The freshman biology laboratory for majors at the University of Louisiana Monroe is an introductory lab covering basic biological principles. The lab includes a 10-week experiment where students explore the effects of environmental water pollutants on the trophic levels within a "Pond in a Jar" aquatic microcosm constructed by students using bayou water. Before implementing this CURE, the experiment was limited to qualitative metrics, which were hindering students' ability to evaluate their unique findings. The goals of this CURE are to update the methodology to collect quantitative data, develop lab skills that carry over into upper level biology curricula, improve attitudes towards scientific research, and give students experience with the requisite critical thinking involved throughout the scientific process. In implementing these

changes, we started with improving the experimental design of the “Pond in the Jar” experiment by requiring students characterize the bacterial microbiome and monitor water quality throughout the 10-week experiment. Through these procedural additions, students gain valuable lab skills while collecting novel data that allows for scientific analysis. We also began utilizing Bayou DeSiard, which runs through campus, as our source of water, soil substrate, and aquatic life, in an effort to generate student interest. To assess the effects on student attitudes and level of expert understanding regarding the scientific method, we plan on utilizing the CURE survey and the Biological Experimental Design Concept Inventory (BEDCI). By comparing results from control and experimental sections, we hope to accurately assess the impact of the CURE. Currently, implementation of the CURE has improved the quality and relevance of the data collected during the course of the experiment. However, instructor observations indicate only marginal improvements in critical thinking within most groups. The scheduled assessments should help us diagnose this shortfall and craft programmatic improvements within our CURE.

SE-PULSE7 - ACTIVATE Bio: Assessing Curriculum To Improve Vision And Transform Education in Biology

Elizabeth Deimeke, Joann Powell, Danielle Gray-Singh

Clark Atlanta University, Atlanta, GA

The Biological Sciences Department at CAU has made steady progress in achieving the goals identified at the PULSE SERP Institute in May 2021. The top priorities were generating program assessments to align core concepts with Vision and Change standards and producing a department culture that encourages the use of student-centered pedagogies and evidence-based teaching. To create a collaborative environment, the department hosted a SERP Ambassador Workshop resulting in the identification of three primary goals: design a dashboard to track faculty service roles and workloads with an aim towards equitable distribution of responsibilities and opportunities; develop and implement a career-focused curriculum to prepare students for diverse opportunities; and improve faculty communication to facilitate student learning and success. Since August, the undergraduate standards and assessment committee has updated program learning outcomes to reflect Vision and Change content areas and competencies and is identifying assessment methods and criteria at each programmatic level to track student retention and success. The committee also surveyed faculty to assess current alignment with Vision and Change standards, the results of which will be used to inform curriculum mapping and changes. The curriculum committee resolved an outstanding core course issue and is reviewing proposals for the development of two new courses in cancer biology. The Department is creating cross-disciplinary BioEd Program that will allow graduates to become a certified teacher in biology. Technology has been leveraged to streamline departmental processes, documentation, and communication. Finally, resources and funds have been identified to support course (re)design and renovate shared lab space for teaching faculty to engage undergraduates. Looking toward the future, the department will turn its attention to generating a peer mentoring community in which faculty can enhance teaching by learning from colleagues and increasing capacity to use assessment data to reform teaching and curriculum and boost student retention and outcomes.

P7 - Characterization of Entomopathogenic Fungi Metabolites Isolated from North Carolina Soil

Hannah Walsh, Michelle Thomas, Jordan Womick

Campbell University, Buies Creek, NC

Entomopathogenic fungi *Metarhizium anisopliae* and *Beauveria bassiana* are used worldwide as alternatives to pesticides in agriculture and are known for pathogenic metabolite: destruxins. Dtx are vacuolar H^+-ATPase inhibitors, suggested to be lethal targets for cancer cells. Dtx may also provide solutions to antibiotic resistance, as fungal metabolites have been explored for antibiotic use before. Existing data on uses of soil fungi isolates are underexplored. Applications of soil fungi were investigated using antimicrobial assays, and insect baiting. 50 mL of soil, and 3-inch root samples were taken from 27 plants at Hannah Forest Farms (34°47’31.388” N, 78°12’32.955” W) 2 feet deep into blueberry shrub soil. Cultivations utilized 10% Potato Dextrose, 0.1% cycloheximide and 0.03% chloramphenicol plates. To screen for pathogenicity, *Galleria mellonella* interacted with 3-day old fungal plates, sterilization with 1% Na-Hypochlorite occurred upon death. Comparing entomopathogenic fungi studied by Richard Humber to slides of spores suggested unknown fungi’s genus were *Nomuraea, Gibellula,* and *Metarhizium*, and confirmed identities of *Beauveria bassiana* and *Metarhizium anisopliae* (MetMaster). Antimicrobial assays of fungal colonies provide information on side effects on human microbiota if exposed to the isolates and any antimicrobial properties present in a growing antibiotic resistant state. Fungal colonies overlaid 1.5×10^8 CFU/mL of *E. coli, P. putida, B. subtilis, E. aerogenes, E. , E. raffinosus, P. aeruginosa, A. baylyi* and incubated at 37 degrees for 6 days called to question if nutrients and/or quorum sensing mediate production of secondary metabolites. Crude extractions of dtx were harvested using centrifugation of 2 L of culture, separation with ethyl acetate, rotary evaporator, and characterization by 1H NMR spectroscopy ‘H NMR 60 MHz σ: m (0.8-1.8 ppm), m (2.1-3.0 ppm), m (3.9-4.4 ppm), s (5.8 ppm), m (6.8-7.0 ppm), s (7.3 ppm). This allows for apoptosis assays of dtx against normal and cancer cell lines in future research.

CURE8 - Cloud Computing Resource-Based Quest Series of Learning

Hongsik Choi, Sean Yang, Heysung Park, Umar Khokhar
Georgia Gwinnett College, Lawrenceville, GA

In today's ever-increasing complex world, it is more important than ever that our students are prepared to use knowledge and skills to solve problems, think logically, and know how to gather and evaluate data to make decisions. Data or information is produced daily by organizations and individuals, and many jobs, including scientists, nurses, climatologists, political scientists, and engineers, take advantage of analyzing data. Data-driven decision making, argumentation, and problem-solving skills are some of the most important skills for students in STEM, and US universities are expected to produce only 29% of the required number of graduates. The Information Technology discipline supports 1400 students (based on Fall 2019). ITEC 2201 Introduction to Information Systems course is a required course for all IT track students and provides fundamentals of information systems in today's digitized world. The course describes the basic concepts of systems and system thinking and the use of information systems, as well as describes concepts and the development of information systems applications that manage data and make decisions. Thus, we *developed and implemented a scientific inquiry method and hands-on activities using cloud-based big data analytics*. Students were exposed to available cloud services, such as Amazon Web Service, Google Cloud, MS Azure, etc., to manage data to support better decisions. They examined the different tools offered by available cloud services, picked the tools that best fit them, integrated the chosen tools to manage data, and visualize the data to produce meaningful information for decision making. This allows them to become familiar with the publicly available, free online data, tools, and services needed to improve data-driven decision making and information analysis skills, and improves students' confidence in solving problems and answering inquires based on big data analysis

P8 - The Effects of Antibiotics and Honey on Bacteria from an Equine Wound Infection

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Antibiotic resistance is a growing problem in medical and veterinary settings that threatens public health. Careful use of these powerful tools is necessary and identifying alternative drugs may be critical. Manuka, and other forms of honey, have traditionally been used in medicine to fight infection and heal wounds. We aim to test the susceptibility to antibiotics alone, as well as antibiotics in synergy with Manuka honey and a generic store brand honey, against bacteria isolated from an equine wound. Selected bacteria from an equine leg wound were Gram stained to determine the thickness of the cell wall and identify potentially effective antibiotics. Once identified, six different species of bacteria were selected and tested against erythromycin, carbenicillin, tetracycline, trimethoprim sulfamethoxazole, imipenem, and gentamicin using a Kirby Bauer test. In addition, plates of honey agar were made to test the synergetic antimicrobial effects when honey was added to the antibiotics. Zone of inhibition was measured around each antibiotic to see if the bacteria presented as sensitive or resistant to the respective antibiotic. From the antibiotic tests, imipenem proved to be the most successful against *Staphylococcus* species, Escherichia coli, certain *Bacillus cereus* group species, *Salmonella enterica,* and *Pseudomonas aeruginosa.* We were unable to obtain consistent results from the honey plates and will troubleshoot this method. In future studies we plan to explicitly analyze synergy between antibiotics and honey against bacteria commonly found in equine wounds, including *Klebsiella*, *Staphylococcus*, *Salmonella*, *Pseudomonas*, and *E. coli*.

SE-PULSE8 - Promoting Student Metacognition to Increase Student Success across a Community College Biology Curriculum

Marlena Yost, Anne Allison, Melinda Clark, Donna Hoefner, Nicole Winkler

Piedmont Virginia Community College, Charlottesville, VA

There is compelling evidence that shows how metacognitive approaches propel learning outcomes for most students. We introduced metacognitive exercises in a sampling of biology courses in the Science Program at Piedmont Virginia Community College: Life Science (BIO 106), Microbiology for Health Sciences (BIO 150), and Anatomy and Physiology (BIO 141, 142). In Life Science, a course designed for general education, students learn about and practice targeted reading skills and complete low-stakes assignments to reinforce reading comprehension. In our Microbiology for Health Sciences and Anatomy & Physiology course, students think seriously about their strategies, study habits, and approaches to learning material through reflection posts after exams. With their reflections, students consider their preparation activities for the test and if each activity was effective. If the preparation activity was not effective, students are asked to consider other study methods that may be more beneficial before taking the next high-stakes assessment. To assess if the exercises within our courses are beneficial, we would like to implement either the SMASH survey or the Motivated Strategies for Learning Questionnaire (MSLQ). The survey will deploy in two sections of Life Science, one section with metacognitive interventions, and one section without as well as in Microbiology for Health Sciences and Anatomy and Physiology as a repeated measures instrument at the beginning and end of the semester. The responses will be analyzed to see if students demonstrate an increase in positive associations with the learning process, which is a component of student success.

P9 - An analysis of the antibacterial properties of the Indian Tulip tree, *Thespesia populnea*, on clinical isolates of *Acinetobacter baumannii*

Carlie Dollar

Columbus State University, Columbus, GA

For the past eighty years, antibiotics have been a frontline defense against many common bacterial infections. However, due to the rise in multi-drug resistant bacterial strains, the efficacy of antibiotics is rapidly decreasing. Considering this issue, the search for therapeutic options for bacterial infections is rising in importance. With plants being a potential source of antimicrobial benefit, researchers across the world have been investigating the antimicrobial activity of medicinal plants, specifically those used in traditional or alternative healthcare. In this study, we are investigating the antibacterial potential of extracts of Thespesia populnea, a rapid growing evergreen shrub found in tropical areas in South Asia, Africa, and the Pacific Islands, on Acinetobacter baumannii, an opportunistic bacterial pathogen known for causing nosocomial infections. T. populnea is known for exhibiting antimicrobial properties due to the presence of several phytochemicals, such as flavonoids and tannins, in various extracts of the leaves and woody tissues. Various botanical extracts using different solvents will be analyzed for select phytochemicals and tested on multi-drug resistant (MDR) and non-multi-drug resistant (non-MDR) human wound isolates of A. baumannii by measuring

minimum inhibitory and bactericidal concentrations. The purpose and hope for this study is to evaluate the efficacy of T. populnea extracts in combatting antibiotic resistance by serving as an alternative treatment to traditional antibiotics.

CURE9 - Antlions - A Field and Laboratory Model Organism for CURE

Mark Schlueter, Patrick Cain

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Antlions are insects in the Family Myrmeleontidae. They are best known for their fierce prey-capturing behavior exhibited by their larvae. Antlions lay their eggs in dry sand in sheltered places, such as under highway bridges or the edges of buildings. These insects can be found throughout the Southeastern United States and throughout the world. Antlion larvae can easily be captured using a hand sieve to separate them from the dry sand they inhabit. Thus, live specimens can be easily collected or experimented on at field sites or taken back to the laboratory. During the past several semesters, students enrolled in the Georgia Gwinnett College General Biology course have performed numerous course embedded research projects using antlions. These CURE projects were designed to increase student engagement in the course and to provide students a more hands-on approach using the scientific method. In this project, we first introduced students to the basic biology, life history, and behavior of antlions. Next, students in each laboratory section were divided into groups of three or four students to complete an initial introductory training experiment. Next, students developed and conducted a second experiment with antlions of their own design. We compared survey data covering basic biology, experimental design, and antlion biology between three General Biology sections that used antlions and two sections that conducted traditional guided experiments (control groups). The GGC general biology course has three STEM skills assigned to it (data analysis, effective communication, ability to apply evolutionary concepts). During the 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. The results of the student survey indicated that students benefited from preforming independent research studies with antlions.

SE-PULSE9 - Changing the PULSE: an inquiry-based curriculum in STEM at UNCG

David Remington, Malcolm Schug, Jerry Walsh, Andrew Hamilton

University of North Carolina at Greensboro, Greensboro, NC

At UNCG, our vision is to be a Department with a student-centered curriculum focused on research experiences. In consultation with the NSF-funded Council on Undergraduate Research Transformations Program (CUR-TP), the Departments of Biology and Chemistry and Biochemistry have been scaffolding undergraduate research experiences throughout our curriculum since 2018. Participation in the SERP Institute helped us identify opportunities to strengthen our approach to this project. Two key steps in our Action Plan are to assess our integration of active learning strategies in our curriculum, and to integrate student metacognitive development more intentionally into our courses. To accomplish this, we have added items related to these steps to the Departmental Strategic Plan. One item is to have departmental seminars devoted to sharing pedagogy and curriculum insights each semester, and we are planning the first of these seminars for Spring 2022. One of the biggest challenges we face is to develop a basic awareness of student metacognition among our faculty – what it is, why it is important, and what we can do about it. We believe that the insights we gained at the SERP Institute provide the foundation for these efforts.

CURE10 - A CUREs Take on Class Design: Field Herpetology

Christopher Manis, Daniel Gaillard

Dalton State College, Dalton, GA

The CUREs (Course-Embedded Undergraduate Research Experience) program integrates research experiences into early STEM curricula that students encounter in their programs. The application of research skills engages and prepares students for later development as they progress in their disciplines. During Spring 2020, Biology 3900 Field Herpetology was given approval to be offered during the following Spring 2021. Over the next year, the opportunity was taken to design for and apply the CUREs program concepts to the lab portion of this class section. Students were involved in multiple field sampling techniques during the January-April field season. Terrestrial sampling activities included drift fence installation, wood/ metal cover board deployment, and visual surveys. Aquatic sampling efforts consisted of turtle trapping via hoop nets and visual surveys. Various habitats sampled included ridges, valleys, wetlands, ponds, and creeks. Herpetofaunal specimens were collected and released on site. Specimens were identified with keys/ field guides and morphometric data was recorded. This inaugural class's efforts have become foundational in nature as the drift fences and cover boards will yield data for years to come. Anonymous reviews of the class by the students were overwhelmingly positive. Students readily identified the field sampling activities as the highlights of the class. Further, some of the students have developed a deeper passion for field herpetology and are pursuing more education, more research opportunities, and careers in the subject.

P10 - The effects of high-efficiency *N,N'*-bis-substituted triazolium salt analogs on multidrug-resistant *Acinetobacter baumannii*

Julie Wilson, Kerri Shelton, Lauren King

Columbus State University, Columbus, GA

The emergence of antibiotic resistance in bacterial pathogens is a growing public health crisis, particularly regarding increasing multidrug resistance (MDR) seen in clinically significant species causing hospital-acquired infections. These infections are prevalent in immunocompromised patients, such as those admitted to the intensive care unit, and are usually associated with invasive medical devices such as respiratory intubation and intravenous catheters. These devices provide the ideal environment for biofilm formation, which aids in the spread of infection among patient populations. Of note, increasing MDR in Acinetobacter baumannii presents a looming threat to healthcare that warrants the investigation of therapeutic alternatives. One such possible alternative to traditional antibiotic therapy is the use of azolium salt derivatives such as imidazoles and triazoles. These derivatives have been found to exhibit promising broad-spectrum pharmacological activity, particularly in their development as antiviral and antifungal therapies. In this study, we examined the interaction of a series of previously identified high-efficiency triazolium salt analogs with A. baumannii clinical isolates. We characterized the bacteriostatic and bactericidal effects of the derivatives, their synergistic activity with antibiotics, and their effects on biofilm formation and dispersal. All clinical isolates used in this study were resistant to commonly prescribed antibiotics and are all considered to be MDR. Further studies must be conducted to elucidate the true value of these alternative treatments, but these results suggest that A. baumannii's susceptibility to triazolium salt derivatives may result in novel therapeutics to prevent infection in immunocompromised patients.

SE-PULSE10 - Engaging Distance Learning Students Through Hands-On Science

Megan Meade

Jacksonville State University, Jacksonville, AL

Contemporary collegiate science educators are increasingly challenged to provide quality remote learning experiences to students. Student centered instruction, specifically active learning, has become the norm for science courses. Connectivity, multi-tasking, and social interaction/group activities have proven requisite to successful online learning. Comparisons were made across two-like semesters; one before (Fall 2019) and one after (Fall 2020) implementation of instructional redesign. The new development included adoption of hands-on online laboratory curriculum, modified assessment strategies including formative and summative assessments, and optimized LMS delivery. The results of these tests showed an increase in comprehensive performance when using the newly adopted laboratory program in both Biology I and II labs. A significant difference was observed in page views in Biology I as students viewed on average twice as many pages per week in the newly designed, hands-on course. A significant difference was not observed in Biology II courses. A possible explanation is that students who matriculate to Biology II understand course expectations and thus engage equally, regardless of delivery method. A course questionnaire was administered as an assessment of overall student perspective on the updated course delivery. In all instances, student responses favored the new course design and delivery in comparison to other online courses. Overall, student engagement and success were increased with the implementation of the new course curriculum and delivery.

P11 - Biofilm Control Using Chemical and Biological Barriers

Zoya Faruqui
University of Arkansas at Little Rock, Little Rock, AR
Abstract
Biofilms are a menace that are generally difficult to tackle. Biofilms are formed by the adherence of a cluster of microbes that create complex communities on surfaces and are resistant to removal. They can cause biofouling, spoilage of materials, and illnesses, including antibiotic resistance aggravation. Biofilm removal, inhibition, and control without using chemicals and antibiotics are critically needed. Therefore, first, we have studied carbon-based materials like chemically modified graphene membranes and composites. These materials were found to have inhibitory effects upon bacterial growth. Silver coupled graphene composites were most effective in bringing down bacterial growth. Graphene and its composites can suppress biofilms' growth by filtration of bacteria, adsorption, chemical disinfection by ROS generation, and physical damages to the cell wall. Second, we have studied the NIH-approved model organism, Dictyostelium discoideum (slime mold/social amoeba), to bring down the bacterial load. Dictyostelium primarily feeds upon bacteria, yeast, and their biofilms through phagocytosis without forming biofilms itself. The utilization of Dictyostelium discoideum to eliminate biofilms from surfaces is a relatively unexplored area of research. It can aid in finding a natural and sustainable way to control biofilms without endangering human health or corroding any materials.

Biography:
Zoya N. Faruqui and Michael Appiah-Kubi are graduate students in the Departments of Biology and Chemistry, respectively. Dr. John Bush is a Professor of Biology, and Dr. Wei Zhao is a Professor of Chemistry at the University of Arkansas at Little Rock, USA.

CURE11 - Learning Programming Concepts in Digital Media Course

Adrian Heinz, Xin Xu, Shuhua Lai

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This project consists of the creation and adaptation of scripts to generate vector graphics. A script is a block of programming code to perform a specific task. The target course is ITEC2110 Digital Media, which deals with multimedia applications. As most students in the course are non-IT

majors, they are usually not familiar with computer programming. Therefore, they learn to use applications to manipulate computer graphics such as shapes, symbols, text, colors, and gradients without writing any computer code. While this simple approach works most of the time, our project intends to show them how much more can be accomplished by learning how to create and modify scripts that can quickly perform tasks that would otherwise be very tedious and time consuming. In this way, students will be given simple scripts for Adobe Illustrator so that they can experiment with them and get to see firsthand how useful they are. We will also introduce elementary programming concepts such as variables, conditional statements, and loops so that they can also modify those scripts and eventually create their own. Sample scripts include creation of random distinct geometric shapes, buildings, stars, clouds, trees, etc. with different colors. We believe that this project will make students appreciate the value of computer programming, foster critical thinking skills as well as to encourage them to pursue a major or minor in Information Technology.

SE-PULSE11 - Striving Towards Extraordinary!

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The Biology Department at High Point University (HPU Biology) recently redesigned its foundation biology curriculum, moving to a three-course biology core course system that models the AAAS Vision and Change recommendations for undergraduate biology education. HPU Biology participated in the 2021 SERP-III Virtual Institute with the goal of creating an action plan to identify additional changes that would supplement curricular changes to maximize student success. In the 2021/2022 academic year, HPU Biology has made progress towards the implementation of its action plan. For example, we have strengthened the use of assessment tools to determine if changes in our practices are successfully impacting student outcomes and preparing our students for professional health programs and the job market. As part of this poster presentation, we describe our progress and assessment strategies. We also describe next steps in action plan implementation.

CURE12 - Practices to engage students in the class project in a pandemic-altered world

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The project in Introductory Physics II (PHYS 1112K) at GGC was designed and proposed before the pandemic. In the original plan, students were required to work in groups to conduct a mini-research project related to their major with an oral presentation component. Faculty with backgrounds in physics, exercise science, and chemistry guided each group through the process of the project. After the pandemic began, it was challenging to conduct the class project as planned due to the public health concerns, such as social distancing and mask-wearing. To address this issue, some adjustments were made to the project requirements to make it feasible, such as shifting the focus to literacy research, prerecording and sharing the presentation in video format on Desire2Learn, and requiring review reports after students watched others' presentations. In addition, several strategies were used to ensure a similar level of students' engagement in the project, such as one-to-one live or online meetings with project advisors, faculty feedback along the way from the initial project proposal to the daft of the presentation. This revised way to conduct class projects has been implemented in both in person or online modality and is adaptable in the constantly changing situation during the pandemic. Despite some technical difficulties along the way, all students adapted to the new format and received most of the deliveries of the class project as originally designed.

P12 - The Discovery of Novel Biofilm Inhibitors in *Staphylococcus aureus* and *Pseudomonas aeruginosa*

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Antibiotic resistance has become an increasing concern worldwide due to the over-prescription and misuse of antibiotics. To combat the medical dilemma, novel lead compounds were synthesized via a dehydration reaction of an amino acid and carboxylic acid, as well as tested for competitive inhibition of signaling molecules responsible for the formation of biofilm, a virulence factor. By allowing the bacteria to live unharmed and reducing pathogenicity, the compound would treat the illness without harming normal flora. Biofilm production is activated by quorum sensing molecules binding to a cell surface receptor to initiate a signaling cascade once a bacterial population has reached a set population density. The biofilm production of the bacterial species was measured with a standard Crystal Violet Assay. Furthermore, the drugs were tested to ensure they were not merely inhibiting bacterial growth rates via Disk-Diffusion, Use-Dilution, and Growth Curve Assays. The preliminary results revealed that three tyrosine derivatives displayed inhibition of biofilm in Gram-positive *Staphylococcus aureus*, while phenylalanine and glycine derivatives caused reduced biofilm production in the Gram-negative *Pseudomonas aeruginosa*. The biofilm inhibition will be quantified with two alternative assays in future experiments. In addition, the shared structures in these potential inhibitors will be expanded upon in future drug design trials.

SE-PULSE12 - Vision and Change at the University of Mary Washington

Ginny Morriss, Lynn Lewis

University of Mary Washington, Fredericksburg, VA

The University of Mary Washington is a liberal arts college of approximately 4,300 students, located halfway between Richmond, VA to the south and Washington, DC to the north. The Department of Biological Sciences has 15 full-time faculty members, with 5 full professors, 3 associate professors, 6 assistant professors and 1 senior lecturer, with 19% of our Departmental faculty self-identifying as minorities. We offer three majors – Biology (109 students), Conservation Biology (44 students) and Biomedical Sciences (137 students). The overall student body identifies as 28% minority. The Department had been engaged in assessing our Biology major, when we began offering Conservation Biology in Fall 2019, and then Biomedical Science in Fall 2020. We are now assessing all three majors, while attempting to incorporate as many of the AAAS' Vision and Change learning objectives as practical into all of our courses. In the past, we have struggled with incorporating assessment into courses in a way that can be easily extracted and analyzed, as well as with the actual analysis of the data we have already collected. During the SERP conference, we identified several ways to streamline our data collection and analysis. We discussed both data collection and analysis at our Department retreat during the summer of 2021, and have engaged in "norming" our definitions of the V&C learning objectives and data to be collected at each Department meeting during the academic year 2021-22. Our shared courses (introductory biology, Biostatistics and Proposal Writing, Cell Biology and Genetics) are developing shared assessments which can be delivered through our learning management system (Canvas) to facilitate collection and analysis. We will report on our progress and issues with our poster.

P13 - An Opponent During Bacterial Invasion: *Staphylococcus aureus* Recognizes Heparin During Growth and Biofilm Formation.

Allison Tucker, Aurijit Sarkar

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Glycosaminoglycans (GAGs) are acidic complex polymeric biomolecules, most of which are highly sulfated. Present in the extracellular matrix and on host cell membranes, GAGs are amongst the most prominent structures encountered by bacteria during the process of invasion. Bacterial responses to glycosaminoglycans have not been explored adequately in the past. Here, we investigate how Staphylococcus aureus and Escherichia coli respond to heparin, a model glycosaminoglycan, and other highly sulfated chemicals. We found that S. aureus can sense heparin under stressful conditions, specifically those simulated by high fever temperature. Contrary to previous studies, we found that heparin-based growth inhibition is not due to annexation of divalent cations required for survival. This growth inhibition can be overcome by specific gene knockouts (kdpD, hssS and nreB histidine kinases), but not others, suggesting S. aureus senses the polymer through specific signaling mechanisms. Other GAGs fail to induce similar growth inhibition. We also uncovered that S. aureus produces more biofilm upon heparin exposure under regular incubation temperatures, a critical virulence response. We therefore hypothesize that this bacterium is able to sense heparin during invasion of the host cell and responds by increasing self-preserving virulence activities like biofilm formation. We also propose that further investigation into glycosaminoglycan-bacterial interactions is critical in light of this new evidence.

SE-PULSE13 - The Roadmap for Implementing Change in Biology at Georgia State University

Jonathan Sylvester, Therese Poole

Georgia State University, Atlanta, GA

Last year at SERP 2021, the team at Georgia State University outlined the following goals for the department: i) achieve curriculum alignment, ii) initiate programmatic assessment, iii) rebuild departmental climate and infrastructure, and iv) increase student success. These goals follow a roughly near-term to far-term organization. This poster serves to update our progress in each of these goals over the past year. For the first two, near-term goals, we have had demonstrable progress, particularly in the standardization of course content (goal i) and in a multi-course assessment of course learning goals and student outcomes (goal ii). Recent attrition in faculty numbers have prevented any meaningful progress on goal iii, but we have begun some preliminary steps for goal iv. The team hopes new hiring and policies within the department will allow up to increase our progress on these long-term goals. We remain confident that we will continue to progress in the year to come.

CURE13 - Implementing CUREs in the Principles of Biology I Course at SSU

Andrea L. Moore, Takayuki Nitta, Xiaorong Zhang

Savannah State University, Savannah, GA

Curriculum redesign and implementation of CUREs requires individual, departmental, and institutional support to be successful and sustainable. The SSU CURE team established three inquiry-based research projects in the Principles of Biology I Lab course with the stated purpose of enhancing analytical and critical thinking and enhance technical skills of Biology majors. The three CUREs focused on the following STEM Skills: engage in the process of science by designing, conducting, and reporting scientific findings (apply the process of science), have quantitative competency and an ability to interpret data by creating graphs and/or tables and using that data to draw conclusions, and provide alternative explanations (data analysis). The designing and implementation of these CUREs presented strengths, barriers, resources, products and sustainability issues at the instructor, course, and departmental level. As a result of our efforts over the past three years, the CURE projects formed the supporting community, provided the data for assessment and identified successes as well as challenges the team needed to overcome. As a result, BIOL1107L (Principles of Biology I Lab) has been revised to include the new learning outcomes and a research component.

CURE14 - Experimenting with osmosis

Martiana Sega

East Georgia State College, Augusta, GA

Course-based Undergraduate Research Experiences (CURE) pedagogy exposes students, non-majors, and majors, to experiences related to science and research careers that helps develop their scientific identity. We use CURE in a majors' introductory courses, BIOL 1107, to teach them how to design and perform an experiment and communicate their results. The project involves using the scientific method as guide to transform one of our previous labs on osmosis. The students will introduce a change in the experiment that will help them answer their specific scientific questions. Students will repeat the experiments and collect data, learn how to represent, and analyze data and finally develop their written communication skills by writing a lab report in the form of a scientific paper.

P14 - Honey: A Natural Antibiotic An Evaluation of Honey's Antibiotic Efficacy

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Rising prices of antibiotics and an uptick in rates of antibiotic resistance in veterinary medicine have prompted an investigation into lower cost and effaceable alternatives. Raw honeys are known to have antimicrobial properties and thus, may prove a low-cost asset to animal owners. Sixty bacterial isolates, collected from infected wounds of four horses, were characterized and identified, and then tested against a triad of orange blossom, dark, and Manuka honeys. It is hypothesized that honey's antimicrobial mechanism is a combination of three factors: prebiotic oligosaccharides from the bees, in unison with the chemicals: hydrogen peroxide, and HMF, contained in the honey. Together, these factors allow honey its antimicrobial properties, even against bacteria resistant to traditional antibiotics. This research analyzes three raw honeys to assess their levels of antimicrobial properties. Kirby-Bauer and minimum inhibitory concentration assays were used to assess the effectiveness of each tested honey. A Staphylococcus isolate and an Escherichia coli isolate were resistant to both tetracycline and carbenicillin, yet, showed sensitivity to honey aqueous solutions of orange blossom, dark, and Manuka honey on disk diffusion assays. Honey may serve as a promising treatment for inhibiting bacterial growth at a significantly lower cost.

CURE15 - Enhancing Web Programming Skills by Creating Animations

Shuhua Lai, Shuting Xu, Adrian Heinz, Cuilan Wang

Georgia Gwinnett College, Lawrenceville, GA

Web development is a fast-growing field and there is a high demand on job market for web developers. Web programming using JavaScript is one of the most important skills for web developers. However, like other programming languages, students feel JavaScript difficult to learn because it is hard for them to setup a mental model, and they lack the encouragement, motivation, and the mode of study in learning. To meet these challenges, we integrate animation creation in teaching JavaScript in Web Technologies course. Creating animation can inspire students' interest in applying JavaScript skills. We also developed an undergraduate research project for students to create a web site using JavaScript-based animations. One objective of the research project is to get students involved in conducting research at the sophomore or junior level. We believe that such a research experience will promote a sense of excitement and engagement for students, and consequently, promote success in college education. We expect the research experience will impact students by increasing their interest in web programming, which in turn will attract more students to our IT program.

Animation-based JavaScript learning materials and the undergraduate research project were used in two sections in fall 2020 and two sections in spring 2021. Surveys were conducted for the assessment after learning JavaScript. 86% of students thought the animation-based JavaScript activities helped them better understand how to use JavaScript. 91% of students thought the animation-based JavaScript activities were exciting. 88% of students would like to learn more about JavaScript in the future. The survey results suggest that creating animations is an effective method in teaching JavaScript and in stimulating students' interests.

P15 - Sex and Starvation Influences Latrotoxin Expression in the Brown Widow Spider

Mattie Harris, J. Scott Harrison

Georgia Southern University, Statesboro, GA

The production of venom in spiders is ecologically and metabolically expensive. Selective use and regulated production are mechanisms to control the potential cost. Spiders in the genus *Latrodectus* (widow spiders) produce a venom consisting of a complex mixture of proteins and other small molecules. Latrotoxins are a group of protein neurotoxins serving as the main active component of *Latrodectus* venom. Latrotoxins are taxa specific in their effects. For example, α-latrotoxin is vertebrate specific and α-latroinsectotoxin is insect specific. Regulation of latrotoxin gene expression is not well understood but sex and feeding could be factors influencing production. The development of widow spiders varies between males and females with males maturing in four molts compared to six molts for females. The average male lifespan is four to ten weeks, while the females are known to live two years. At sexual maturity, males reduce or stop feeding, and pedipalps transition to reproductive organs. These developmental patterns make latrotoxins a good candidate to study sex-biased gene expression. Prey encounter or prey type may also serve as a signal for expression regulation as venom is important for prey capture. In this study, we used quantitative qPCR to (1) characterize the expression patterns of both the insect and vertebrate specific latrotoxins in male and female brown widow spiders to characterize sex-biased expression and (2) to study the expression pattern of insect-fed and starved female spiders for both genes of interest. Our findings indicate sex-biased expression with an average of 30-fold higher expression in females for both genes. Preliminary data for the fed vs. starved experiment suggest that the α-latroinsectotoxin is downregulated while starved and upregulated following feeding, and that α-latrotoxin expression does not change regardless of the condition.

P16 - Arf6 Regulates Release of Murine Leukemia Virus Gag

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The ADP-ribosylation factor 6 (Arf6) is a small GTPase and has several important functions in regulating intracellular trafficking of vehicles and cargos. GTPases are active when bound to GTP and inactive when bound to GDP. Retroviruses are double-stranded RNA viruses encoding basic three genes, *gag, pol*, and *env*. Translated retroviral proteins are trafficked to the plasma membrane and assembled into virus particles, but the detailed mechanisms remain elusive. A previous report demonstrated that a constitutively active form of Arf6, Arf6Q67L inhibited release of human immunodeficiency virus (complex retrovirus) by redistributing intracellular phosphatidylinositol 4,5-bisphosphate (PIP_2). We here investigated how Arf6 affected release of a simple retrovirus, murine leukemia virus (MuLV). Viral structural protein Gag in cells and media was monitored by western blots to evaluate virus release. Overexpression of Arf6Q67L showed accumulation of Gag in 293T cells and impaired Gag release to cell culture media. Arf6Q67L did not show major changes in production of intracellular Gag. It is reported that Arf6 enhanced production of PIP_2 through activation of phospholipase D (PLD) and phosphatidylinositol-4-phosphate 5-kinase (PIP5K). Treatment of the chemical inhibitors targeting these molecules attenuated inhibitory effects of Arf6Q67L and released more MuLV Gag into media, suggesting that regulation of PIP_2 through PLD and PIP5K pathways regulates MuLV release. We also assessed if Arf6Q67L could enhance degradation of Gag through autophagy which is a cellular system eliminating invading pathogens through autophagocytosis. The inhibitors targeting autophagosome and autophagolysosomes formation did not alter inhibitory effects of Arf6Q67L on MuLV Gag release. Interestingly, these chemical inhibitors did not change viral release from the control cells. Our data demonstrated that Arf6, PIP_2 but NOT autophagy and PI3K are determinants in MuLV Gag release.

CURE16 - Virtual Labs and Research Project for Information Security Course

Shuting Xu, Umar Khokhar, Yi Ding, Karen Benson, Lorraine Jonassen

Georgia Gwinnett College, Lawrenceville, GA

Georgia Gwinnett College (GGC) System and Security rising graduates must complete an Information Security class. As a junior-level class, the expectation is that students will learn to implement the key concepts of system security and gain knowledge of cryptography, access control, attacks, policies and procedures for Internet security, and more. Knowing that students learn best with real-world, hands-on experiences, the PIs researched online security training providers aligned with the course goals. Evaluation of several options led to the selection of InfoSec because of its flexibility to customize the online networking environment for virtual labs and projects. We selected 10 InfoSec virtual labs to train students' hands-on security skills and designed a Course-based Undergraduate Research Experience (CURE) project. CURE Projects are known for their various advantages such as increased students' interest and retention, enhanced critical thinking skills, and improved self-confidence. Specific to this CURE project, the objectives were to expand students' knowledge and skills in server vulnerability scanning and expose students to conducting research. The PIs designed a virtual network environment for the research project and provided a detailed research procedure to students including literature review, research planning, research implementation, result analysis, and research summary and documentation. The labs and projects were used in Fall 2020 and Spring 2021 with a total of 64 students participating. Surveys were conducted for the assessment of the virtual labs and the research project. For the virtual labs, 1) 76% stated improved hands-on abilities, 2) 67% stated improved problem-solving skills, and 3) 73% recommended the labs to be used in other information security sections. For the research project, 1) 66% stated better understanding on how to do research, 2) 65% stated improved problem-solving skills, and 3) 70% recommended the research project to be used in other information security sections.

CURE17 - Comprehensive Game-based Learning Modules for Programming Fundamentals

Hyesung Park, Adrian Heinz, Evelyn Brannock, Wei Jin, Xin Xu

Georgia Gwinnett College, Lawrenceville, GA

In general, many students believe programming classes are challenging because each layer of the learning process is complicated. It is not easy to motivate students to persist in learning. This project presents a platform for students to learn complex programming languages interactively while positively changing the perception through integrating game development in the learning process. Traditionally, game development has only been done at upper-level courses. In this project, students of the fundamental programming courses analyze and reproduce games that their seniors have already developed using Processing as the platform. This process increases the engagement and retention of students in the computing

education area. In this presentation, we will share the result of the data, including analysis of student attitude, student experience, and student motivation.

P17 - An Exploration into the Effect of the Clinical VUS T147A in CTLA4

Elin Zaman, Jenna Ridlen

Jacksonville State University, Jacksonville, AL

Viral infections have always had an impact on health conditions, COVID being one of the more recent viral infections that has shown the unforeseen health complications after contracting the virus. A recent study from the CDC had shown a complication of an increased risk of newly diagnosed diabetes in the 30 days following SARS-coV-2 infection[1]. This allowed for genetic inquiry into the risk between autoimmune diseases and viral infections which had been observed and documented thoroughly. As well as inquiry into the genes of the immune system. CTLA4, located at 2q33.2, is a gene that is also known as cytotoxic T- lymphocyte associated protein 4, is among the immunoglobulin superfamily that produces a T cell inhibitory protein. This gene is a protein receptor that functions as an immune checkpoint and is vital in the immune response to viral illnesses. Mutations of the CTLA4 gene have been implicated in type 1 diabetes (DM1), autoimmune thyroiditis, celiac, lupus, Grave's disease and other autoimmune illnesses. My CTLA4 variant, T174A, is a missense, point mutation of A>G which resulted in an amino acid switch from threonine to alanine at position 174. Multiple bioinformatic tools such as YASARA protein mapping, SIFT, GerpS, Provean, Align-GVGD, PolyPhen2 and other analyses were utilized to compile metrics of sequencing, structure, and protein dynamics. These have revealed that the T147A variation would most likely be pathogenic. These bioinformatic results will be presented along with cross species multiple sequence alignment and other variant analysis.

1. https://www.cdc.gov/mmwr/volumes/71/wr/mm7102e2.htm

P18 - Understanding Caspofungin mechanisms in the Emerging Drug-resistant *Candida auris*

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Over the last few years, *Candida auris* infections have been increasingly recognized as a severe concern to human health, especially for immunocompromised patients and those hospitalized with severe underlying diseases. Echinocandins are the newest antifungal drugs in clinical use to inhibit the synthesis of β-glucan, an essential fungal cell wall component. *C. auris* has exceptionally high MICs for the main classes of antifungal drugs, echinocandins, such as caspofungin. Resistance of *C. auris* to the caspofungin is linked to mutations in short, conserved regions in the *FKS1* gene. In this poster first, we report the ideal condition for *C. auris*growth followed by testing the effect of two-drug combinations *in vitro* against nine *C. auris* clinical isolates. Then, *C. auris* susceptibility to antifungal drugs was determined by sequencing the "hot-spots" region of *FKS1*. Strains with higher caspofungin resistance show a mutation in the region of the *FKS1* subunit with a reduced maximum catalytic capacity of their glucan synthase complexes.

CURE18 - NSF HBCU-UP Targeted Infusion Project: Drosophila Behavioural Genetics (EUSTEM-DaBuGs) Engineering & Research CUREs

S. Catherine Silver Key[1], Tanina Bradley[2], Aileen Reid[3], Eric T. Saliim[4]

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The purpose of the Engaging Undergraduates in STEM through Drosophila Behavioural Genetics (EUSTEM DaBuGs) is to increase underrepresented minority STEM retention. The project at North Carolina Central University (NCCU) seeks to develop an integrated undergraduate education, training, and research initiative in behavioral genetics and engineering design by creating Course-based Undergraduate Research Experiences (CUREs) in two courses: a sophomore elective and a junior required course. Additionally, the DaBuGs summer internship opportunity provides a formalized mentorship program with external speakers from neighboring Research 1 institutions along with a tri-disciplinary research experiences: biology, fabrication and electrical engineering. This poster reports student gains in three categories: 1) experimental design ability gains as measured by pre-/post-EDAT, 2) intellectual knowledge gains as measured by pre-/post-quizzes, and 3) oral presentation gains (measured by summative rubrics). Additionally, external evaluation suggests that the courses are well-received and that students are most interested in the hands-on research component of the courses. Finally, a subset of the 40+ student artifacts created by 3D fabrication and/or engineering will be showcased. In summary, this NSF-funded targeted infusion project is preparing students for the 21st century workforce. NSF HBCU-UP Targeted Infusion Project (TIP) grant # 1912188

CURE19 - Three Sequential Course Undergraduate Research Experiences (CUREs) implemented at Winthrop University.

Course 1: SEA-PHAGES Discovery

Victoria Frost, Kristi Westover

Winthrop University, Rock Hill, SC

Winthrop University is a public comprehensive university that considers undergraduate research to be a vital part of required student training. Three course undergraduate research experiences (CUREs) have been established at Winthrop as part of the Science Education Alliance (SEA) Program, developed by the Howard Hughes Medical Institute (HHMI). The program aims to increase undergraduate interest and retention in the biological sciences through immediate immersion into genuine research that is achievable at most public institutions. The discovery and investigation of novel bacteriophages (phage) is at the heart of the program and allows the course experiences to be delivered sequentially to optimize a student's full engagement. Motivated students are encouraged to apply to be part of the cohort. During the preliminary course experience, SEA-PHAGES Discovery, first-semester freshmen "hunt" for their own novel phage from the local environment. Students then use microbiological techniques to successfully replicate and isolate their phage in host bacteria. Molecular techniques and transmission electron microscopy enable preliminary characterization of the class's phage collection before selecting two representative viruses to be sequenced by the SEA team at the University of Pittsburgh. To date, as a result of the Discovery course, Winthrop students have collected, isolated and initially characterized 60 novel phages from the soil. Pairing students from the beginning establishes strong cooperative relationships with members of the class and, since the cohort remains together as a team throughout the program, the entire cohort evolves as a collective. The establishment of this CURE over the past 6 years has resulted in a core of highly trained and capable undergraduate students, the majority of whom are interested in remaining in the realm of science and/or the field of basic scientific research.

P19 - Isolation of Novel Mycobacteriophages as Potential Sources of Phage Therapy Candidates

Elin Zaman, Chris Murdock

Jacksonville State University, Jacksonville, AL

Bacteriophages are ubiquitous in nature and can are found in all habitats across the globe. The goal of this study was to isolate novel mycobacteriophages from soil samples. These particular viruses target and infect mycobacteria. A notable mycobacteria species includes the one responsible for tuberculosis, known as *Mycobacterium tuberculosis,* this where the bacteria multiplies and attacks the lungs and other portions of the body such as the kidney, lymph nodes, brain and spine. Another notable mycobacteria species would be *Mycobacterium leprea* which causes leprosy. Leprosy is a chronic infectious disease that affects the nerves, skin, eyes, as well as the nasal mucosa. *Mycobacterium smegmatis*, a safe and easy to culture alternative to these pathogenic strains of mycobacteria had been utilized as the host cell for the discovery of novel mycobacteriophages reported in this study. A multitude of soil samples were recovered from random sites within Northeast AL. A number of viral isolates had been recovered after the enrichment of multiple soil samples. Current research is now focused on the purification and characterization of each of the mycobacteriophage isolates. Specifically, transmission electron microscopy and DNA isolation (which will be used for whole genome sequencing) of the selected isolate will be utilized for further characterization. This data will hopefully allow for the identification of a potentially therapeutic mycobacteriophage that would be used against the diseases of tuberculosis and/or leprosy.

CURE20 - Three Successive Course Undergraduate Research Experiences (CUREs) implemented at Winthrop University.

Course 2: SEA-PHAGES Bioinformatics

Kristi Westover, Victoria Frost

Winthrop University, Rock Hill, SC

SEA-PHAGES Bioinformatics is the second of a three course undergraduate research experience (CURE) at Winthrop University established as part of the Science Education Alliance (SEA) Program, developed at the Howard Hughes Medical Institute (HHMI). During the first course, SEA-PHAGES Discovery, students focus on isolating and characterizing bacteriophages using standard microbiology, microscopy and molecular techniques. Representative viruses are sequenced at the University of Pittsburgh and the assembled genomes are annotated in the second course. Using DNA Master, Phamerator, and Starterator, along with homology comparisons to databases at HHPred and NCBI, the putative open reading frames are assessed for start site codons and function. Multiple students call each gene allowing for independent assessment of the reading frames. The culminating results include the publication of the annotated genomes at NCBI's GenBank and presentation of the yearlong experience at national and regional conferences. To date, close to 20 genomes have been annotated and published by Winthrop freshmen. The bioinformatics workflow is new to most all students, challenging their preconceptions about typical research projects. It tests their ability to critically assess models and assumptions of molecular biology and their application to viral genomics. By the end of the second course, students are trained to use sequence data, homology comparisons, and phylogenetics to make predictions about viral relationships, host-virus coevolution, and gene function.

P20 - Albendazole induces apoptosis through activation of mitochondrial outer membrane permeabilization in PC3 prostate cancer cells

Jonathan Jansma, Kevin Suh

High Point University, High Point, NC

In the US and many western countries, prostate cancer is the most commonly diagnosed cancer and second leading cause of cancer related death in men. American Cancer Society predicts that there will be 268,490 new cases of prostate cancer in the US in 2022. While treatments such as antiandrogen therapy and orchiectomy have contributed to reducing the fatality of prostate cancer, most prostate cancers relapse and become resistant to hormone manipulation. In the present study, we investigated the role of albendazole in androgen-independent PC3 prostate cancer cells. Albendazole is an antihelminthic drug used for the treatment of a variety of parasitic worm infestations by targeting microtubules which play an important role in cell division. However, albendazole has been shown to exhibit anti-cancer properties recently. When PC3 cells were treated with albendazole, viability was inhibited, and apoptotic cell death was induced in a dose- and time-dependent manner. Apoptosis was verified by detecting the cleavage of poly(ADP-ribose) polymerase and measuring the activity of executioner caspases. Furthermore, we observed increased expression of pro-apoptotic protein Bak which is known to be involved in pore formation on mitochondrial outer membrane. On the other hand, the level of anti-apoptotic protein Bcl-XL was downregulated upon treatment of PC3 cells with the drug. These results indicate that albendazole induces intrinsic apoptosis pathway through the release of cytochrome c into the cytoplasm in PC3 cells. Taken together, these findings suggest that albendazole could be a useful chemotherapeutic agent in treatment of hormone refractory prostate cancer.

CURE21 - Three Sequential Course Undergraduate Research Experiences (CUREs) implemented at Winthrop University.

Course 3: SEA-GENES

Victoria Frost, Kathryn Kohl

Winthrop University, Rock Hill, SC

SEA-GENES (Science Education Alliance-Gene-function Exploration by a Network of Emerging Scientists) is the culminating research course of the SEA Program. As part of the preceding SEA-PHAGES modules, undergraduate students across the world have collectively isolated and annotated thousands of phage genomes. Remarkably, the majority of the genes have no predicted function. In GENES, students return to the bench to build on the discoveries of the PHAGES projects, using a variety of cutting-edge molecular and genetic techniques to explore phage gene function. During this course, expression libraries of individual phage genes are generated, the effects of these genes on bacterial host phenotypes are tested, and genes targeting the host proteome are investigated. It is a challenging course, but familiarity with the cohort, instructors and phage biology is a tremendous advantage. The majority of the class members are sophomores, however, since course scheduling can sometimes interfere with the sequential flow, SEA-PHAGE alums are welcomed and encouraged to rejoin the cohort. Thus, the students contribute a balanced mix of research experience, accompanied by a collection of elementary to more advanced knowledge in the disciplines of molecular biology, microbiology, genetics and bioinformatics. At Winthrop our present phage of interest, Cain, is a cluster K6 temperate bacteriophage with only 30 of its 100 genes hypothesized to have a function. To date, GENES students have demonstrated that 8 of Cain's genes, tested phenotypically, inhibit the growth of the host *Mycobacterium smegmatis* and warrant further investigation. Significantly, publication of this research will highlight all students as co-authors. The CUREs have also seeded a number of individual phage projects, as well as a growing demand for these students by other investigators in the department. Ultimately, the SEA Program makes it possible for undergraduates to receive a set of valuable and genuine research experiences, with impressive outcomes.

P21 - Examining the Pathogenicity of VUS R75Q in Human Gene *CTLA4*

JoAnna LaPoint

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Since the onset of the current global COVID-19 pandemic research scientists and medical professionals have discovered many strange side effects brought on by infections from this novel virus. SARS-CoV-2 has proven to exacerbate pre-existing health conditions in patients across the globe, raising many questions for geneticists and other researchers. It is well documented that viral infections can interact with and affect the genome of an infected organism and studies are beginning to emerge showing that patients have an increased risk of developing other conditions after being infected with COVID-19. Recently, a study by the CDC discovered patient samples exhibit an increase in new diabetes diagnoses within the first 30 days after infection. A link between viral infection and autoimmune disorders is already known. The gene *CTLA4*, which is located at 2q33.2 and has a GERP score of 5.08, codes for cytotoxic T-lymphocyte associated protein 4. This protein is important in immune response to viral infection. Diseases associated with *CTLA4* mutations include, diabetes 1, thyroiditis, and multiple autoimmune disorders. The variant chosen was the variant of unknown significance (VUS) c.224G>A(p.Arg75Gln); a missense mutation at c.224 resulting in the amino acid Arginine being replaced by Glutamine. Using YASARA, a protein model was viewed to observe the location. VUS R75Q was found to be in a folding region which increases the likelihood that this SNP will cause a change in the tertiary structure of one side of the quaternary homodimer. The VUS is predicted to have a high probability of damaging effect through Polyphen2 and SIFT. The RVIS score for this gene is -0.1157 which is in line with generated data indicating that it is likely a pathogenic variant. The results from the research conducted via multiple bioinformatics platforms will be presented along with an MSA.

CURE22 - Using environmental and biological data to teach data analysis skills in an introductory Physics class (CURE)

Lina Merchan Alvarez

Savannah State University, Savannah, GA

As part of the CURE implementation at Savannah State, in several sections of our introductory algebra-based physics class, we explored using current data to discuss kinematics concepts. We estimated growth rates for several systems such the difference in growth rate for the height of an oak tree vs the expansion of its trunk, how fast does a child grow at different times in their life, how fast does the water rise and fall in the ocean, among others. We used spreadsheets to calculate the velocity of the eye of Hurricane Mathew and Dorian as they approached the Coast of Georgia. We learn how to manage data from NOAA to calculate instantaneous velocities and accelerations for the tides in Fort Pulaski and around the US coast. The students learned how to plot the data in Excel and Google Sheets. The implementation coincided with the COVID pandemic, which meant that instead of doing physics experiments in the lab, our students were able to see real systems change over time and use physics to understand their motion.

P22 - Repurposing fenbendazole: new potential as a chemotherapeutic agent against cervical cancer cells

Michaela Cummings, Jonathan Jansma, Kevin Suh

High Point University, High Point, NC

Drug repurposing, also known as drug repositioning or drug reprofiling, is an approach to accelerate the drug discovery process through the identification of a novel clinical use for an existing drug that is approved for another use or withdrawn because of adverse effects. Benzimidazole derivatives such as albendazole and fenbendazole are used for the treatment of a variety of parasitic worm infestations. Recently, these drugs gained considerable attention because of their unexpected effects against cancer. Even though dewormers have greater affinity for helminth tubulin, which polymerizes into long chains that form microtubules, these drugs can target mammalian tubulins. In this study, we found that fenbendazole can inhibit the proliferation of HeLa cervical cancer cells by inducing programmed cell death which was measured in multiple ways. We observed membrane blebbing, nuclear fragmentation, and PARP cleavage which are key characteristics of apoptotic cell death, in HeLa cells treated with fenbendazole. The drug treatment also increased the activity of caspase-3/7 significantly which was measured by utilizing proluminescent caspase substrates. Cells treated with fenbendazole showed less organized microtubules which negatively affects cell division.

P23 - Validation of Homozygous Transparent Transgenic Zebrafish to Study Cardiomyocyte Activity

May Ye Mon[1], Kunal Hotwani[2], Vaani Balyan[2], Logan Ouellette[2], Vishal Arora[3], Surendra Rajpurohit[4]

[1]Georgia Cancer Center, Augusta University, AUGUSTA, GA, [2]Georgia Cancer Center, Augusta University, Augusta, GA, [3]Cardiology Division, Department of Medicine, Medical College of GeorgiaAugusta University, AUGUSTA, GA, [4]Georgia Cancer Center, Medical College of Georgia, Augusta University, Augusta, GA

The zebrafish model has provided an excellent platform to study the genetic and molecular approach of basic and translational cardiac research. Zebrafish heart cells are similar to human heart cells at the molecular level and determine the function of genes that control cardiac function and dysfunction. In zebrafish, myl7 is myosin light chain 7 gene and identified as a regulatory gene of heart orthologs to human MYL7. We have developed transparent transgenic zebrafish cellular phenotype to study annexin-5 activity in the cardiovascular function under normal and in metabolic aberration and pathological circumstances by generating casper/ myl7:RFP; annexin-5:YFP transgenic zebrafish. In vertebrates, including zebrafish, murine and human systems, the in-vivo spatial resolution is limited due to the normal opacification of skin and subdermal structures. For in-vivo imaging the skin transparency is primary requirement and to maintain the transparency, blocking the pigmentation needs to maintain. Blocking of the pigmentation can be maintained by chemical inhibition by block melanization. Chemical inhibitor PTU (1-phenyl 2-thiourea) is adequate to block the pigmentation in pigment epithelium melanization. Chemical inhibition treatment is temporary and possible till the organism treated with the chemical inhibitor agent. Zebrafish casper mutant maintain transparency throughout the life and serve as ideal combination of sensitivity and resolution for in-vivo stem cell analyses and in-vivo imaging. In this study, we established transparent transgenic zebrafish model and establishment of time lapse in-vivo confocal microscopy to study of cellular phenotype/pathologies of the cardiomyocytes to quantify changes in cardiomyocyte morphology and function overtime by comparing control and cardiac injury. Our strategist approach to yield crucial new insights into in-vivo cardiomyocyte imaging by confocal microscopy to observe and track the cell death pattern and cardio inflammatory pathways in cardiomyocyte and develop novel therapeutic approaches to treat cardio inflammatory pathology.

CURE23 - Advances, Challenges and Future Plans of the Small World Initiative CURE at Jacksonville State University

Jenna Ridlen, Richard Watkins, Megan Meade, Jocelyn Moore

Jacksonville State University, Jacksonville, AL

This project represents results of the introduction of the Small World Initiative Course based undergraduate research experience (CURE) to Jacksonville State University (JSU) Biology I laboratories. The Small World Initiative CURE was originally piloted at Yale University from 2012-2013 before being introduced to over 300 schools in over 15 countries by 2019. We joined the initiative in 2021 as student rejoined face-to-face laboratory classes after a year of virtual class instruction in high school and/or college.

We set-up four laboratory sections to investigate the discovery of antibiotics following the World Health Organization's (WHO) prediction of potential premature deaths associated with superbug growth in immunocompromised patients by the year 2050. Students took local soil samples and cultured their own strains of bacteria. Along the way they learned important microbiology and laboratory techniques as well as enhanced scientific communication. This CURE is aimed to increase student engagement in research and matriculation in the face of an enrollment increase at JSU. We will present our SWI start-up challenges, first semester debrief, current setup, and future plans for this program in JSU curriculum.

P24 - A role for the putative Mannose-6-Phosphate domain of Atg27

Hannah Smith[1], Brenna Ivory[1], Meaghan Robinson[1], Veronica Segarra[2]

[1]High Point University, High Point, NC, [2]Interim Chair and Assistant Professor of Biology, High Point University, High Point, NC

While mutations of the C-terminus of Atg27, a transmembrane protein that contributes to cellular self-eating or autophagy, are known to control the localization of the protein throughout the endosomal/vacuolar system, the effects of abrogating its predicted mannose-6-phosphate receptor domain (MRH) remain unknown. We examine the effects of mutating the putative Atg27 MRH on autophagy and Atg27 trafficking.

CURE24 - Biotechnology Applications in the Detection of Genetically Modified Foods

Ernest Ricks, Jr., Jennifer Hurst-Kennedy, Cindy Achat-Mendes, 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. The second 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 and proteins, respectively, in GM foods. This CURE resulted in over 20 campus and regional conference student presentations over the past 4 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. *S*ignificant outcomes of this new lab curriculum include student-initiated hypothesis-driven authentic research projects, troubleshooting and critical thinking as students worked through technical challenges. This CURE proved to be sustainable in a hybrid format through the use of video recorded training, on-line lab meetings, and virtual research conferences.

CURE25 - The course-based undergraduate research experience: A successful integration of research into a genetics class

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[1]Middle Georgia State University, Macon, GA, [2]Middle Georgia State University, Cochran, GA

We developed a semester-long course-based undergraduate research experience (CURE) for a genetics class to build students' knowledge on model organisms and to develop the skills required for genetic research. Students were engaged in three research projects using *Drosophila* (fruit fly) and *Saccharomyces* (yeast) model systems as part of their training. The first project was developed to help students understand the inheritance pattern of a mutant. They developed the hypothesis based on the observable trait in the filial-one (F1) generation and subsequently tested it in filial-two (F2) generations. The second project was developed to show how gene interactions affect inheritance patterns. In this project, yeast mutants with mutations in one of the two genes were crossbred to help students understand gene interactions. The third project, (BLAST), was developed to provide skills required to understand gene annotation in fruit flies. Data from pre- and post-CURE surveys were collected to assess learning outcomes. The four main elements assessed were: 1) Did the CURE course improve student learning outcomes related to genetics? 2) Did the CURE course improve students' learning of the scientific process? 3) Did the CURE have a positive effect on students' interest in science; 4) Did the CURE increase the frequency of students asking questions during the course? We found that 79% of the students perceived the CURE course as a good way of learning the subject, while 92.86% of the students responded very positively to the element of understanding scientific processes. The data from the CURE survey also showed that for 85.71% of students, the CURE had a positive effect on their interest in science. Students will also be more confident practicing scientific thinking in the future. The majority of students thought that maintaining a lab notebook, experimental repetition, and collaboration were important elements of becoming a successful scientist.

P25 - Up-regulation of Osh6 targets an anti-aging membrane trafficking pathway.

Nazneen Begum

University of Arkansas at Little Rock, Little rock, AR

Eukaryotic cells are characterized by their intracellular membrane-bound organelles. The identity and functions of these organelles decline with age. Slowing down such age-dependent decline is critical for the extension of the health span of cells as well as organisms. We previously found that up-regulation of a non-vesicular lipid transporter Osh6 in yeast cells delays the aging of the degradative organelle vacuoles and significantly extends the lifespan. To explore how Osh6 extends the lifespan, here we conducted multiple cell biology analyses of the longevity mutants from the plasma membrane to intracellular organelles. We found that up-regulation of Osh6 delayed the initiation of endocytosis. Since the initiation of endocytosis depends on interactions between actin cables and proteins/lipids on the plasma membrane, we further checked actin cytoskeleton and found that up-regulation of Osh6 enhanced actin polarization and polymerization. Intriguingly, the enhanced actin polarization was accompanied by a delay of the secretion of the plasma membrane H+-ATPase Pma1. Furthermore, up-regulation of Osh6 reroutes a fraction of Pma1 to vacuoles. Moreover, this rerouting was dependent on the vesicle trafficking from the trans-Golgi network (TGN) to the late endosome (LE), the organelle immediately upstream of vacuoles in many trafficking pathways. Since transporting damaged or obsolete proteins such as Pma1 to vacuoles is beneficial for longevity, we propose that the TGN-to-LE trafficking pathway is a pro-longevity pathway targeted by Osh6.

CURE26 - Unlock the CODE: An undergraduate research experience investigating the impact of DNA variations on human health

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[1]Birmingham-Southern College, Birmingham, AL, [2]HudsonAlpha Institute for Biotechnology, Huntsville, AL

Characterizing Our DNA Exceptions (CODE) is a collaborative project developed by HudsonAlpha Institute of Biotechnology (Huntsville, AL) to offer undergraduate faculty and students an opportunity to investigate the impact of human genomic variations using computational methods in biology. Faculty, guided and trained by the HudsonAlpha team, facilitated independent research projects where students predicted the effect of variants of uncertain significance (VUS) on protein structure or function. As part of the initial cohort of participating institutions, Birmingham-Southern College students developed self-directed research projects or took part in a semester-long course to propose molecular mechanisms that connect DNA variations with human health outcomes. These experiences were easily conducted in both in-person and virtual settings, giving faculty and students much needed flexibility during pandemic restrictions. In addition, most software and databases used were freely available, increasing accessibility to authentic research experiences when funding is limited. Students reported increased fluency in computational methods and independent research skills and motivation among other benefits. HudsonAlpha continues to recruit additional participants for this program and additional information will be available from the presenter.

P26 - ATG8 is conserved between Saccharomyces cerevisiae and psychrophilic, polar-collected fungi

Brenna Ivory[1], Hannah Smith[1], Meaghan Robinson[1], Veronica Segarra[2]

[1]High Point University, High Point, NC, [2]Interim Chair and Assistant Professor of Biology, High Point University, High Point, NC

Autophagy is a conserved catabolic process by which eukaryotic cells respond to stress by targeting damaged or unneeded molecules or organelles for sequestration into specialized vesicles known as autophagosomes. Studies of the budding yeast Saccharomyces cerevisiae have revealed various types of stress that can regulate autophagy, including starvation and extreme temperatures. While autophagy has not yet been directly linked with the ability of yeast to survive extreme cold or freeze-thaw stress, upregulation of autophagy has been directly linked to the ability of arctic insects to survive cold temperatures. To begin to examine the conservation of Atg machinery in polar-collected yeast, we focused on Atg8, a small, ubiquitin-like protein that has an important role in autophagy.

P27 - Investigating the Role of *twist1b* During Zebrafish Sclerotome Differentiation into Tendons

Alexia Akhom, Abby Kitakule, Nikki Glenn

Belmont University, Nashville, TN

Zebrafish have proven to be excellent model organisms for observing the development of tissues such as skeletal muscle and bone. Early embryonic development observations help to predict cellular fates and gene functions important in tendon development. Embryonic mesodermal tissue gives rise to musculoskeletal tissue progenitors like axial somites, which can further partition and differentiate into the sclerotome. The sclerotome forms the axial skeleton, including ribs, vertebrae, and tendons.

The Twist gene family plays an important role in embryonic development. Specifically, *twist* genes are essential for somite differentiation. The zebrafish *twist1b* gene is a paralog to the human *TWIST1* gene. Our research focused on *twist1b*, and we aimed to understand its role in the development of the sclerotome in zebrafish embryos. The goal of this study was to manipulate *twist1b* expression in zebrafish embryos to observe its role in sclerotome differentiation using two methods separately: CRISPR-Cas9 mutagenesis and *in situ* hybridization following morpholino knockdown. These two methods alter gene expression in different ways. CRISPR-Cas9 fully removes the gene from the genome, preventing transcription and subsequent processes, while the morpholino sequesters RNA and prevents translation.

This project will provide more insight into the role of *twis1b* in sclerotome development, specifically in tendon progenitors. We hypothesize that the CRISPR-Cas9 mutagenesis will have resulted in a complete *twist1b* knockout strain of zebrafish that can be studied by future students in this lab. Additionally, we hypothesize that *twist1b* plays an important role during tendon development.

P28 - Small molecules that mimic quorum sensing in *Candida albicans* and *Candida parapsilosis* may statistically inhibit biofilm production via competitive inhibition

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Fungal species use quorum sensing as a method of communication to create virulence factors throughout the population. The signaling causes the release of virulence factors an example of which is the formation of biofilm. In fungal species, adhesion through biofilm allows for proliferation of colonies, which leads to a variety of host infections including the common yeast infection from *Candida parapsilosis*. *Candida albicans* also has numerous effects on human life, particularly by creating Candida Endocarditis in the heart, destroying heart valves. Small molecules, composed of an amino acid and a carboxylic acid coupled through a dehydration synthesis, may mimic the natural signaling molecules and prevent coordinated responses through competitive inhibition. A crystal violet assay was used to assess the biofilm inhibition in *Candida parapsilosis* and *Candida albicans* with over 200 novel compounds. Eight inhibitors were found for *Candida albicans* and three were found for *Candida parapsilosis*, each having an inhibition greater than 40. Notably, two of the three inhibitors found for *Candida parapsilosis* included two aromatic rings in their structure, with the third structure containing a long hydrocarbon chain attached to a basic lysine. All of the compound structures for *Candida albicans* contained at least one aromatic ring, with multiple containing two. These bulky structures indicate that the signaling molecules for *Candida parapsilosis* and *Candida albicans* may have a significant amount of steric hindrance or dispersion forces, and are likely similar in structure. This structural analysis is relevant for understanding the mechanism behind biofilm formation, and pairing it with compound screening could lead to novel treatments of fungal infections.

P29 - Determining the Role of *twist1b* and *twist2* in Zebrafish Bone Development

Harshita Indukuri, Nikki Glenn

Belmont University, Nashville, TN

Sclerotome is a transient, mesenchymal tissue seen in embryological development of many segmented animals ranging from millipedes to humans. Although it is known that the sclerotome gives rise to the cellular progenitors of the axial skeleton and the associated tendons and ligaments (Williams 2019), it is unclear how this process occurs. *twist1b (tw1b)* and *twist2 (tw2)* are two genes that are thought to play a role in helping sclerotomal cells decide between becoming bone or muscle. *sox9a* is a gene marker representative of cells undergoing endochondral ossification which forms most of the bones in the body. *col2a1* is a collagen marker of type II collagen found primarily in cartilage preparing to ossify into bone after *sox9a* expression; much of the skeleton is made of cartilage during early development. The hypothesis going into the project was that *tw1b* and *tw2* are integral for skeletal differentiation. The expression of *sox9a* and *col2a1* were analyzed in wild-type zebrafish as well as those with a *tw1b* or *tw2* knockdown morpholino to confirm this theory. These results will provide insight into the genetic pathway of bone development during embryogenesis and how gene expression can be altered to affect bone formation.

P30 - Partners for Agricultural Innovation and Sustainability: An Ongoing Effort to Foster Collaboration in West Alabama and East Mississippi

Caleb Mullins[1], John McCall[1], Lee Stanton[1], Allen Tartt[1], Micky Smith[2], Schuyler Huff[3], Eric Ford[4]

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Through a collaborative effort beginning in 2018, the University of West Alabama (UWA) and the Sumter County, AL Soil and Water Conservation District (SCSWCD) established Project PAIS (Partners Against Invasive Species). The purpose of PAIS, funded by USDA-NIFA, was to provide education on invasive species, with an emphasis on cogongrass (*Imperata cylindrica*) and feral swine (*Sus scrofa*), in addition to outreach activities for farmers, ranchers, and foresters (stakeholders) in the west Alabama region. Through the success of educational and outreach activities, PAIS eradicated approximately five million square feet of cogongrass and over eight hundred feral swine from west Alabama. An additional benefit to the project was growth of student enrollment in conservation and agricultural sciences at UWA. The success of PAIS enabled UWA and SCSWCD to continue these efforts through PAIS 2.0 – Partners for Agricultural Innovation and Sustainability. As a result of the collaborative efforts between UWA and SCSWCD, PAIS 2.0 increased the impacted area by establishing partnerships with Coastal Alabama Community College and East Mississippi Community College to provide area stakeholders with the knowledge, tools, and manpower to combat environmental and economic threats. PAIS 2.0 is continuing to provide education and assistance in the battle against invasive species; as of December 2021 the project had eradicated approximately 1.2 million square feet of cogongrass and over five hundred feral swine from west Alabama. PAIS 2.0 will broaden the scope of the project thematically by aiding stakeholders with issues related to pollinator support, forest management, and soil quality assessment. Preliminary results as of early 2022 indicate that efforts to eradicate troublesome invaders and raise stakeholder awareness of such has resulted in significant positive impacts to the region served.

P31 - Developmental Effects of WIN55,212-2 on Different Stages of Zebrafish Development

Matt McGowin, Nikki Glenn

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The endocannabinoid system is a signaling system present in the nervous system. Endocannabinoids are lipid messengers that behave as retrograde neurotransmitters, most commonly acting on CB1 and CB2 receptors. Endocannabinoids have been shown to have a significant impact on nervous system development. From prior studies, "endocannabinoids and the cannabinoid CB1 receptor [have been shown to be] important for brain development, regulating neural progenitor differentiation and guiding axonal migration and synaptogenesis." Thus, disturbances to the endocannabinoid system during development could lead to improper embryonic development.

Prior studies from our lab suggest that endocannabinoids may have an impact on zebrafish hatching rate and tail length. THC and CBD embryo treatments during gastrulation have been shown to negatively affect hatching rate and significantly shorten/deform the spine (Ahmed et al., 2018). We intend to further investigate the role of CB1 during zebrafish development by treating embryos with the synthetic cannabinoid WIN55,212-2, which functions as an agonist of CB1 and CB2 in humans and in zebrafish.

The purpose of this study is to examine the hatching rate and tail length of zebrafish treated with WIN during different developmental stages in order to further understand the role of endocannabinoid stimulation during pregnancy. Given previous research, we hypothesized that zebrafish treated with WIN would result in shorter tail measurements compared to control groups and that WIN treatment would affect the hatching rate.

P32 - Leopard Population Density Estimate for the Baviaanskloof Hartland, South Africa

Safia Bouderka, Travis Perry

Furman University, Greenville, SC

As the human population expands biodiversity recedes, creating an urgent need to better integrate human development into the living landscape. In the Baviaanskloof region of South Africa, a UNESCO World Heritage Site, several stakeholders, including the Baviaanskloof Agricultural Association (Landbou Vereniging), the NGO Living Lands, and Eastern Cape Parks, are attempting to measure and monitor their biodiversity resources in an effort to develop long-term, sustainable management practices that directly benefit the local community. Leopards (*Panthera pardus*), as apex predators, are a key component of the natural ecosystem and are of special interest to all stakeholders. They are a positive driver of ecotourism and a negative driver of livestock losses in an economically depressed farming community. We estimated leopard density in the farmland/wildland matrix of the Baviaanskloof using 28 remote cameras distributed over 75 Km sq. We used photo data with the R package secr, from the first 60 days of camera deployment, consistent with the recommendations of Panthera, for leopard density studies. We did not use double camera sets and therefore generated dual data sets, one for left side identifications and one for right side. We identified 4 individual adults from both left and right side identifications each, as well as two females with one and two cubs each. Cubs were not included in the population density estimate. For left and right side identifications secr models estimated the adult leopard population density at 0.88 and 1.5 per 100Km sq, respectively, average 1.9/100Km sq. This is consistent with other estimates generated in the region, and reflects the unique physiography of the kloof and the close proximity to a large protected area, the Baviaanskloof Provincial Reserve.

P33 - Determination of novel RERG tumor suppressor interactions

Alanna Pimenta

Mercer University, Macon, GA

Ras-like estrogen regulated growth inhibitor, RERG, is a small GTPase that has been characterized as a tumor suppressor in human breast cancers. Higher RERG expression has been correlated with better prognosis in breast, kidney, colon, lung, liver, and nasopharynx cancer patients. Unlike the founding family member, Ras, which enhances cell survival, differentiation, and growth, RERG has been shown to be growth inhibitory. Despite these promising clinical finding findings, the molecular basis of RERG's actions have yet to be elucidated. Melanoma-associated antigen 12, MAGEA12, was identified as an RERG interacting partner through yeast-two hybrid analysis using a breast cancer cell library. MAGEA12, belongs to the (MAGE-A) family of antigens which are not expressed in adult tissues, however, have high expression in human malignant tumors where it diminishes apoptosis and increases cell proliferation. DNA sub-cloning was used to generate RERG and MAGEA12 constructs for co-expression in eukaryotic cells to confirm this novel interaction. We hypothesize that RERG is able to inhibit the proliferative functions of MAGEA12 and decrease tumor cell proliferation.

P34 - Wildlife Survey of Philmont Scout Ranch, New Mexico, with Population Density Estimates for Mule Deer and Elk

Sidney Angner, Travis Perry

Furman University, Greenville, SC

Philmont Scout Ranch (PSR) in Colfax County, New Mexico is a 140,000 acre property owned and managed by Scouts of America. The Conservation division of PSR actively manages their biological resources including human-wildlife conflict issues and a guided hunting program. In 2018 PSR partnered with Furman University to conduct a large scale and long-term remote camera survey of the ranch's wildlife resources, with a focus on bear, puma, elk, and mule deer. A primary objective was to generate population density estimates using mark-resight models for these four species based on unique ear tags (bear and puma) or unique antler configurations (elk and mule deer). Total elk and mule deer population density estimates were extrapolated from bull/cow/ calf or buck/doe/fawn ratios reported for similar populations. The survey was conducted between May of 2018 and August of 2020 with 25 Cuddeback remote cameras distributed over 100Kmsq at a density of 1 camera per 4Kmsq. Photo data were collected and archived using the program Photogofer. The R package secr was used to generate mark-resight population density estimates. Twenty-three species of mammal plus several avians were recorded during the survey. In descending order, mule deer, elk, black bear, bobcat, gray fox, coyote, rock squirrel, and puma were the most commonly photographed species. Puma and black bear were common and widespread across the study area, however, no puma and only two bears were ear tagged during the study, and thus, population density estimates could not be generated for these species. We identified 7 individual bull elk and estimated the elk population density to be 1.46 bulls, 3.74 cows, and 1.5 calves, or 6.7 elk per 100Kmsq. We identified 6 individual mule deer bucks and estimated the mule deer population density to be 5.49 bucks, 20.33 does, and 10.17 fawns or 35.99 mule deer per 100Kmsq.

P35 - Fluctuating Asymmetry of Bluegill as a Bioindicator of Environmental Stress from Urbanization

Sarah Kerner, Bradley Lamphere

University of Mary Washington, Fredericksburg, VA

Urbanization increases the environmental stress of a stream's ecosystem due to runoff of effluents and excess nutrients, which is important in understanding how humans are impacting the waterways and its organisms. Here it is tested whether fluctuating asymmetry (FA), the random deviations between normally bilateral morphology, could serve as an indicator of urbanization stress in a common fish, the Bluegill (*Lepomis macrochirus*). The hypothesis is that as urbanization increases in a watershed, then the FA increases from stressful living conditions not within optimal tolerance zones causing developmental errors. FA was quantified by comparing 3 photos of the left and right sides of fish then analyzing the data using geometric morphometric software (TPS, SAGE). Urban land use at the 11 sample sites, as determined from ArcGIS Pro, varied between 4.7% and 92.8%. FA at each stream was slightly different at all 11 sites with vectors showing positively correlated loadings in two groups: operculum, pectoral fins, and lips and nostrils, pelvic fins, and eyes. There is a unimodal negative response with peak of FA in intermediate urban use. This could be from higher stress environments killing off individuals who have high FA and leaving behind robust fish with higher tolerance and low FA, which is defined by the differential-mortality hypothesis (Floate and Fox 2000).

P36 - Building and testing species distribution models to locate rare sedge populations in eastern Arkansas

Brendan Kosnik[1], Diana Soteropoulos[1,2], Emily Bellis[1], Travis Marsico[1]

[1]Arkansas State University, Jonesboro, AR, [2]Arkansas Natural Heritage Commission, Little Rock, AR

One challenge in rare species conservation is that species' geographic distributions are often poorly understood because of incomplete knowledge of extant population localities. Verifiable records of rare species occurrences mainly exist in the form of natural history collections, which are important but have significant spatial, temporal, and taxonomic limitations and biases. Thus, these records, on their own, are not sufficient to describe the geographic range and status (i.e., vulnerability to extirpation) of rare species. Species distribution modeling is one approach that can use collections data to predict species potential ranges with relatively high accuracy. Multiple techniques exist for modeling species distributions and several (e.g., Maxent) are well-suited for use with presence-only data, the form of species occurrence data that is generally available from natural history collections. Still, model predictions are only just that: predictions. Model outputs can and should be verified through ground-truthing, in the form of field surveys for target species.

Our project aims to more completely describe the distribution of rare sedges (*Carex*, Cyperaceae) in eastern Arkansas, specifically in the Mississippi Alluvial Plain and Crowley's Ridge ecoregions. *Carex* is a highly diverse genus in temperate ecosystems (especially wetlands); thus, it is important and valuable to study from conservation and biodiversity perspectives. Specifically, we will (1) build species distribution models for species of conservation concern known to occur in this region, (2) conduct field surveys for targeted species based on model predictions of habitat suitability, (3) analyze field data to determine if model predictions of suitability correlate with species presence vs. absence, (4) make conservation recommendations for targeted *Carex* species based on factors limiting species distribution, and (5) provide guidance to conservation practitioners attempting to incorporate species distribution modeling into rare species assessments, especially those involving field surveys to locate unknown populations of target species.

P37 - Building and testing species distribution models to locate rare sedge populations in eastern Arkansas.

Brendan Kosnik[1], Diana Soteropoulos[1,2], Emily Bellis[1], Travis Marsico[1]

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P38 - Discovering, Counting, and Summarizing the National Park Specimens at UCHT

Samantha Doss-Watson[1], Joey Shaw[2]

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The herbarium at the University of Tennessee at Chattanooga (UCHT) consists of ~50k specimens dating from the 19-teens through the present. General use of the collection led curators to notice many specimens from within the boundaries of several National Parks, from the Great Smoky Mountains National Park to Rocky Mountain National Park to Banff National Park in Canada. While UCHT was a lead herbarium for the 2014 SERNEC specimen digitization effort and skeletal label data were transcribed for these specimens, it was not possible at that time to denote them as being from a National Park. In this study, we are searching UCHT for specimens from National Parks and transcribing additional label data as well as ranking the deterioration of these specimens so we may summarize these aspects of UCHT. Initial data from ~25% of the herbarium have revealed over 500 specimens from National Parks. Of them, 43% were only indicated as such in the locality string and 87% are in excellent condition. At this time, we project UCHT to hold ~2000 specimens from National Parks, which are in very good condition.

P39 - Invasive Fig Buttercup: A Community Approach to Stop the Spread

Isabella Hile

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Ficaria verna, commonly known as fig buttercup or lesser celandine, was introduced to the United States as an ornamental and is now invading urban floodplains and riparian habitats throughout the East and Pacific Northwest. It was first reported in North Carolina in 2005 and has rapidly spread throughout the state, primarily from home gardens that spread along urban streams. The plant emerges in the winter and reproduces with bulblets that multiply when physical removal is attempted; therefore, it can outcompete native species and is most effectively treated with herbicides. In 2021, the WakeNature Preserves Partnership created toolkits and educational fliers for parks and public lands staff using materials from the NC Invasive Plant Council. In addition, they used social media to raise public awareness. Citizens were encouraged to document fig buttercup occurrences using iNaturalist, which helped City of Raleigh staff track and treat populations. The main goals for this year are to increase outreach to neighborhoods in Wake County and to more effectively monitor the spread and treatment efforts. Employees at Wake County and Raleigh Parks are increasing their tracking of sightings and treatment using GIS tools to map which areas have been monitored and treated over time so there can be a more accurate treatment timeline. This will also allow staff to better predict where fig buttercup may be spreading to and preemptively treat areas. Conveying the urgency and severity of this plant at this time of the year to more neighborhoods and municipalities is crucial in order to report and treat while it's in flower and before it disappears in May. In summary, we recommend that a multi-level community approach is needed to successfully control fig buttercup.

P40 - Genomic variation in the black-throated green warbler (*Setophaga virens*) suggests divergence in a disjunct Atlantic Coastal Plain population (*S. v. waynei*)

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New World wood warblers (family: Parulidae) have been the focus of many studies that aimed to resolve relationships between species, and these studies have documented well-known species complexes. However, within-species variation in warblers— including named subspecies—is much more subtle and has led to debate over the origin, maintenance, and conservation status of some warbler subspecies. One example is the black-throated green warbler (*Setophaga virens*), a Neotropical-Nearctic migrant that breeds in deciduous and boreal forests in North America. Wayne's black-throated green warbler (*S. v. waynei*) was described over a century ago based on its disjunct distribution on the Atlantic Coastal Plain of the United States combined with morphological and ecological differences from the nominate subspecies. More recently, some authors have questioned whether *S.v. waynei* is a valid taxon. Here, we employ whole-genome resequencing to estimate the genetic distinctiveness among samples collected across the entirety of the *S. virens* breeding range, including from putative *S. v. waynei*. Although we documented low global differentiation ($F_{ST} = 0.027$) across all samples, we observed discrete genetic clustering among *S. v. waynei*. Principal components analysis of

genome-wide differences shows the main axis of variation separates *S. v. waynei* from other samples. *S. v. waynei* is most similar to another isolated population from the Piedmont of North Carolina. Our results suggest a historical north-to-south geographic dispersal in the entire complex. Our results support designation of *S. v. waynei* as a distinct and recognized subspecies worthy of targeted conservation efforts.

P41 - Profiling Coloring Agents in Turmeric Powder

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Turmeric curry powder is widely used as spices in Middle Eastern and Asian countries. One of the active ingredients of Turmeric Powder, curcumin has been widely studied for its role as anti-inflammatory and antioxidant properties. In this study, we are interested in profiling coloring agent present in turmeric powder. The turmeric powder we purchased has very bright color as compared to the regular organic turmeric powder from local supermarket. The bright color in turmeric powder may have link to lead chromate-based dye. We are interested in finding out the active chemical agent that produce the bright color in the turmeric powder. We plan to profile metal ions present in the curry powder by smelting and dissolving the ashes in aqua-regia. The concentration of metal ions dissolved in aqua-regia will be determined using Coupled Plasma-Optical Emission Spectroscopy (ICP-OES) instrument. We are also interested in finding out synthetic dyes that may have link to the bright color in the powder. we plan to extract the dye using solvent-solvent extraction and identify the dyes using liquid chromatography technique.

P42 - What is a population? Assessing genetic structure of federally endangered *Dalea foliosa* in Middle Tennessee

Skyler Fox, Ashley Morris

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Dalea foliosa (leafy prairie clover; Fabacaeae) is a federally endangered, herbaceous perennial and is one of the many rare species associated with the cedar glades region of the southeastern US. *Dalea foliosa* is found in the limestone glades of northwest Alabama and Middle Tennessee and the dolomite prairies of northern Illinois. In partnership with the Tennessee Department of Environment and Conservation (TDEC), the goal of this project was to help define what a population of *D. foliosa* actually is to facilitate the development of management strategies. Therefore, for this project, we focused solely on occurrences from the Cedars of Lebanon complex and the Duck River complex in Middle Tennessee. Our team collected *D. foliosa* leaf material from eight sites in these two complexes, including six from the Cedars of Lebanon complex and two from the Duck River complex. Our data also include a previously unknown occurrence from Lebanon, TN, that was discovered in the late summer of 2021. We used 10 microsatellite loci that were previously developed for the species to genotype collected samples. Data analyses are currently underway. Our results should inform how connected or isolated the occurrences of the species are in this region. Analyzing the population genetic structure of federally endangered *D. foliosa* is an essential step in being able to determine conservation strategies that might include augmenting existing sites, or even establishing new ones through introduction efforts.

P43 - Assessing the Influence of Fire History on Wild American Chestnut (*Castanea dentata*) Populations on Pine Mountain, Kentucky

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Today, the American Chestnut—functionally extinct by 1950, but dominant in eastern US forests until the arrival of C*ryphonectria parasitica* triggered mass mortality—has stagnant or declining populations. Chestnuts tend to live in a juvenile state as emergent stems succumb to blight and new sprouts emerge. Restoration efforts rely on wild native germplasm—though it is often inaccessible. Increased access to sunlight often increases germplasm production. To determine fire management's feasibility as a means to increase germplasm production in wild chestnuts, we investigated fire and land management at two Pine Mountain sites in southeastern Kentucky differing in their fire and land management history. Hi Lewis Pine Barrens State Nature Preserve (SNP) experienced three widespread arson fires (2000-2018) and clearing of aggressive native plants and a prescribed burn (2020) in parts. Bad Branch SNP, with no fire disturbances in decades, served as a control. Sampling chestnuts within thirteen 50m x 4m transects at each site, we measured height, diameter at ankle height, number of stems, blight severity, and canopy openness at each chestnut. We then explored statistical associations between fire history or site and canopy openness, chestnut density, blight status, and stem number. Chestnut density did not vary across fire history or site. Chestnuts in the prescribed burn area experienced more open canopies than chestnuts in arson or control areas. While stem numbers were similar between arson and control areas, chestnuts in prescribed burn areas had many more stems. We found no direct relationship between canopy openness and number of stems, suggesting the influence of other factors related to the prescribed burn and species removal. Both fire histories likely increased blight severity. Although we found flowering trees, data were insufficient to test if fire influenced maturity. We recommend further research into the relationship between canopy openness and stem number as well as maturity.

P44 - Characterization of nuclear microsatellite loci to assess clonal structure in the rare Oconee bells (*Shortia galacifolia* and *Shortia brevistyla*; Diapensiaceae)

Lauren Eberth, Calla Pederson, Ashley Morris

Furman University, Greenville, SC

Shortia galacifolia (Southern Oconee bells) and *S. brevistyla* (Northern Oconee bells) are rare species of herbaceous, evergreen plants endemic to the Carolinas and Georgia. Previously recognized as varieties of *S. galacifolia* (*S. galacifolia var. galacifolia* and *var. brevistyla*), both were raised to species status on the basis of morphology and genetics within the last few years. Both species are found along shaded streambanks and moist coves in certain mountainous areas, with *S. galacifolia* found in several counties in South Carolina, North Carolina, and Georgia, and *S. brevistyla* found only in McDowell County, North Carolina. According to published literature, *S. galacifolia* spreads by seeds (i.e., sexual reproduction) or by stolons or rhizomes (i.e., clonal growth), although no one has yet assessed the relative roles of these two strategies in either species. The goal of this study was to develop novel nuclear microsatellite loci to assess genetic variation and clonal structure in *S. galacifolia* and *S. brevistyla*. We collected leaf material for *S. galacifolia* from multiple sites in Devils Fork State Park, SC, and for *S. brevistyla* from multiple sites in and around Pisgah National Forest, NC. We screened 24 microsatellite loci for utility in this system, and we present preliminary data from nine of those here. While data analyses are still underway, our work should provide the tools needed to better understand the role of clonality in these species, which will provide information essential to making informed conservation decisions in the future.

P45 - Spatial Analysis and Social Network Analysis of Sustainable Farms in Upstate South Carolina

Grace Bartel

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Food is a central part of our lives and therefore its production is necessary, but negative environmental and social externalities associated with production methods need not be. Our research investigates the viability of small sustainable farms across the Upstate region of South Carolina, the biodiversity and ecosystem services on these farms and how their social connections could potentially improve the local food system. We interviewed ten farmers throughout the Upstate of South Carolina who own small-scale sustainable farms to learn about their farming methods and interactions with other farmers and community stakeholders. The farm was toured to determine the ecological scene of the specific farm. Data was also gathered through an online survey and sent to the ten principal farmers and their subsequent connections. This data contributed to the social network analysis which we employed to analyze the impact of network position on the success of a farm. We found that social network connectedness is helpful for the overall success of a farm, especially for very small farms with an income under $75,000. The community support is very influential in their success. We conclude that connecting small farms with each other and with community stakeholders can be very beneficial for their business and with the dissemination of sustainable farming methods. This could create an overall more sustainable local food system by increasing the viability and popularity of sustainable farming. The ecological prioritization on the farms was a factor in their ability to disseminate sustainable farming methods.

P46 - Characterization of nuclear microsatellite loci to assess clonal structure in the federally endangered bunched arrowhead (*Sagittaria fasciculata*; Alismataceae)

Nora Tillmanns, J. Banks Floyd, Ashley Morris

Furman University, Greenville, SC

Sagittaria fasciculata (bunched arrowhead) is a federally endangered, herbaceous perennial known only from Greenville County, South Carolina, and Henderson County, North Carolina. The species inhabits hydrogeologic environments that are significantly threatened by human development and environmental changes. The species is known to reproduce sexually by seed and can spread vegetatively by rhizomes, yet there has been little work to assess the relative roles of these two strategies in this system. The purpose of this study was to develop novel nuclear microsatellite loci to assess clonal structure and genetic variation in *S. fasciculata*. We collected leaf material from several sites in Greenville County, SC, including Furman University, and three state heritage preserves: Bunched Arrowhead, Blackwell, and Belvue Springs. We screened 24 microsatellite loci for utility in this species, and here we present preliminary data for seven of these loci. While data analyses are still underway, our results suggest that clonality varies by site, with at least one site being highly clonal. Evaluating the population structure of *S. fasciculata* will contribute to the existing knowledge of the species and will assist in the development of management strategies. Our work highlights critical baseline information about a rare and understudied species with the intent to establish an awareness for the need for conservation of *S. fasciculata*.

P47 - The impacts of management and local and landscape features on avian occupancy in Upstate SC

Jake Gerardi, Austin Jones

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Given the rates of urban development in the southeastern United States, it is clear that farmland and other managed ecosystems serve as the bridge between landscapes managed for humans and landscapes set aside explicitly for conservation goals. Data however are needed along a gradient of farmland intensity to best align goals in multi-use landscapes. To address this gap, we conducted avian point count surveys in parcels along a gradient of management intensity. To help explain avian occupancy we conducted vegetation sampling at each location, measuring ground cover, tree canopy amount, and plant height. We used the National Land Cover Database (NLCD) to calculate landscape metrics for diversity and evenness at each point. We used AIC model selection and the unmarked package in R to assess which aspects of parcels and landscapes affected bird abundance. Our data suggests that farms in the Upstate can support a variety of avian populations, particularly in managed lands with dedicated natural habitat space. An overall trend for species was an emphasis on landscape diversity. This accounted for both locally, with species like the Field Sparrow and Blue Grosbeak more abundant with taller vegetation, and at the landscape level, with Red-Bellied Woodpecker and Brown Thrasher populations more prevalent at more diverse sites. Moving forward, this data could potentially be the framework for future conservation policies concerning urban expansion and biodiversity changes in managed ecosystems.

P48 - Does human land use and activity affect insect pollinator diversity in fields embedded in an urbanizing land matrix?

Maeve Arthur, Ann Estelle Freyer, Prof. Christopher Paradise

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Insect pollinators provide vital pollination services to both natural and human-dominated ecosystems across the world, but mounting evidence suggests that multiple factors associated with urbanization and human land use are contributing to global pollinator diversity declines. Evidence also suggests that floral diversity could be a key to supporting pollinator diversity. Our goals were to: 1) understand how land use factors in a heterogeneous agricultural/suburban/urban landscape are related to insect pollinator diversity, and 2) make recommendations to inform pollinator conservation efforts. We collected insect pollinator occurrence and flowering plant data using digital macrophotography in timed transect walks through old fields. Fields were in nine protected and semi-protected habitats of different sizes with variable management practices (ranging from conservation easements, county parks, or greenways) in Mecklenburg County, NC, north of a major urban area, Charlotte. We used QGIS and the National Land Cover Database to determine land use patterns within 500 and 1,000m of each site to examine relationships between land use types and insect pollinator diversity and abundance. We also documented turnover of pollinator communities across time as we visited each field 3-4 times in the spring/summer of 2021. We hypothesized that pollinator diversity and abundance would decrease in fragmented and intensely managed habitats and increase with floral diversity. Butterfly abundance increased at sites surrounded by greater proportions of field. Bumble bee abundance increased with surrounding landscape diversity, contrary to our prediction. We also predicted significant turnover of insect communities, which we found, pointing to the importance of repeated sampling of insect communities. Broadly, pollinator taxa respond to different features of the landscape, and the communities change throughout the season, making conservation of all pollinators difficult. We recommend conserving patches of field across a fragmented and urbanizing landscape to benefit both butterfly and bumble bee abundance and prevent pollinator loss.

P49 - Mitigating CO_2 Emissions through Carbon Sequestration: Four Strategies for Storing Carbon in Forests

Ashlyn Crain, David Vandermast

Elon University, Elon, NC

Accurately quantifying carbon sequestration in forests can provide insight into mitigation strategies of human-induced climate change. Planting trees seems an efficient way to reduce atmospheric CO2 and to maximize ecological and aesthetic benefits, but the reality is more complicated. In this study we calculated the carbon budgets of four CO2-reducing strategies: 1) urban forestry projects, 2) afforestation (plantings of trees in non-urban areas), 3) natural regrowth, and 4) preservation of mature old-growth forests. Natural regrowth study sites were found to sequester 72.6 Mg ha-1 of carbon and old-growth forest sites to sequester 59.7 Mg ha-1 of carbon. Natural forests were found to sequester more carbon than sequestered in planted forests, although there are substantial co-benefits to urban plantings. All planted trees have a carbon cost associated with them at the moment they are placed in the ground. Our estimation is that a tree that is grown from seed, watered until it reaches 2.5 cm DBH, and transported to a planting site within 100 miles could have a per-tree cost of 3.13 kg CO2e. Using the CUFR Tree Carbon Calculator, we estimated that planted trees would take between 1-3 years to grow enough to recoup the carbon costs associated with planting them. Factors such as tree density, geographic range, stand age, and tree species were also considered. This study allows for the direct comparison of the benefits of utilizing forests in the mitigation of greenhouse gas effects on climate change.

P50 - Setting Up a Study to Investigate the Impact of Removal of Understory Species on the Soil Bacterial Microbiome of a Longleaf Pine Restoration Site

Isabella Vahle, Paula Jackson, Sean Davis

Kennesaw State University, Kennesaw, GA

The longleaf pine (*Pinus palustris*) ecosystem is one of the most diverse ecosystems on the planet. For thousands of years, this ecosystem was maintained by fires, and its historic land cover spread from the Carolinas all the way to eastern Texas and down through Florida. Today, only 3% of the ecosystem remains and only 0.01% of that is untouched land. This is largely due to fire suppression and heavy harvesting of the longleaf pine's superior timber. Restoration of the longleaf ecosystem has been of interest because of its economic importance and high ecological diversity. In this study, we propose to investigate the effect of the removal of two grass species on the soil bacterial microbiome of the longleaf pine in a restoration site located in the Piedmont region of Georgia. These two grasses are thought to have major effects on the overall maintenance of the ecosystem because they contribute to the spread of forest fires. This helps to clear the understory and make it possible for longleaf pines to dominate the savannah. We have surveyed the vegetation and set up six randomized blocks. Within each block, we have four subplots with the following treatments: 1) control; 2) dominant grass removal; 3) second most dominant grass removal; 4) soil disturbance with no grass species removal. We will present our methodology to study the effect of the removal of the two grass species on the bacterial community of the area under restoration. We hypothesize that the most dominant grass with the highest importance value will have a greater effect on the soil bacterial microbiome composition compared to the next most dominant grass species. Our aim is that results from this project will provide baseline data to help inform and improve restoration practices for the longleaf pine.

P51 - Enhancing marsh restoration by developing best practices for nursery production of *Spartina alterniflora*

Justin Hinson, Heather Sempsrott, Heather Joesting

Georgia Southern University, Savannah, GA

Coastal salt marshes are under threat from rising sea levels and increased erosion, and recent efforts have been put into developing better long-term solutions to combat marsh loss. Living shorelines are a marsh restoration technique that utilizes green infrastructure and native biota to stabilize eroding marsh edges and promote sediment accumulation. Along the East and Gulf Coast of the U.S., the coastal marsh grass *Spartina alterniflora* is often planted due to its critical role in salt marsh growth and maintenance. Prior research indicates the existence of multiple regional ecotypes and suggests that transplanted specimens be collected from no greater than 100 km from the restoration site in order to maximize local adaptation. Furthermore, native stands of *S. alterniflora* exhibit high genetic diversity, and typical methods of clonal propagation may fail to maintain pre-restoration levels of diversity. The aim of this research is to develop optimal seed-based propagation techniques for *S. alterniflora*. Specifically, mature *S. alterniflora* spikelets were collected every two weeks in October and November 2021 from four salt marshes with varying proximity to the ocean. Seeds were placed into one of three storage vessels for cold stratification for at least three months and are currently being tested for viability using both a fluorescent light box and a tetrazolium test, after which germination trials will be conducted to determine optimum temperatures for germination. Preliminary results show significantly more seeds per spikelet at the site furthest from the ocean and a significant effect of collection date, although no clear pattern has yet emerged. The results of this research will contribute to the establishment of a seed propagation protocol for *S. alterniflora* that can be used by native plant nurseries to produce a genetically diverse selection of locally-adapted plants for use and living shoreline projects.

P52 - Game Camera Detection of Songbird Sociality at Artificial Water Sources

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Songbirds often assemble in flocks to reduce the risk of predation, particularly when foraging. In this study we examine the social behavior of Georgia songbirds during two other risky behaviors: drinking and bathing. To view the interactions of birds, we programmed a game camera to take pictures once every minute from sunrise to sunset, and directed it toward an artificial water source. From September 1 to December 15, about 75,000 images were taken. Upon review of the photos, each bird visit was classified into one of three behavioral categories: perch, bathe, or drink. Hourly and daily patterns of visitation were also determined. While 28 species were observed at the bird bath, the focal species in this study were the Brown Thrasher (Toxostoma rufum), Carolina Chickadee (Poecile carolinensis), and the Tufted Titmouse (Baeolophus bicolor). All three species exhibited higher visitation rates in the afternoon compared to morning. Rates of solo visitation were highest for the thrasher (92%), while chickadees (77%) and titmice (68%) were less likely to visit the bird bath alone. Shared heterospecific visits (i.e., with members of other species) were lowest for the thrasher (8%) and higher for titmice (19%) and chickadees (21%). Titmice and chickadees shared the bird bath with a total of 10 and 7 other species, respectively. The titmouse and chickadee are known to associate in mixed species flocks in the winter, and this behavior was observed at the bird bath as well (chi-squared test, $p<0.001$). Drinking and especially bathing are risky behaviors, and therefore songbirds show a tendency to visit water sources in mixed species groups. As other studies have noted, bathing behavior appears to stimulate other birds to bathe and drink.

P53 - Recent high-severity fires promote plant diversity in mixed pine-oak forests of West Virginia

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[1]Marshall University, Huntington, WV, [2]Concord University, Athens, WV

Without periodic fire disturbance, fire-adapted plant communities across the Central Hardwood Forest Region experienced significant changes in forest structure and species composition, most notably a decrease in oak regeneration and herbaceous diversity and an increase in shade-tolerant, fire-sensitive tree species. In this study, we compared the plant community structure of two mixed pine-oak forests with different land management and fire histories in the Cumberland Mountains of southern West Virginia. To determine the relationship between recent fire history and current plant community structure, we made plant community measurements that spatially coincided with fire-scarred pines. Since 1970, there has been one fire at Wall Fork (public land), while six major fires occurred between 1985 and 2017 at Hite Fork (private land). Our results indicate that differences in recent fire history had large effects on plant community structure. Hite Fork's recent high-severity fires resulted in mortality of pole-sized trees, and more open conditions which were more favorable for pine regeneration. In contrast, stands at Wall Fork were characterized by more closed canopy conditions with a higher proportion of shade-tolerant species and little to no pine regeneration. Plant species richness in the herbaceous layer was significantly higher at Hite Fork (mean = 47, $p < 0.01$), particularly for forbs and shrubs, compared to Wall Fork (mean = 36). Non-metric multi-dimensional scaling and PERMANOVA indicated that plant species composition was significantly different between the two sites ($p < 0.01$). Collectively, these results suggest that occasional high-severity fire in mixed pine-oak forests of the Cumberland

Mountains can meet management objectives by reducing shade-tolerant tree abundance, increasing herbaceous diversity and pine regeneration, and generally promoting forest heterogeneity.

P54 - The Bee's Knees: Are Pollinator Visitations Related To Crop Yields In Urban Farms?

Esmeralda Lagunas

Agnes Scott College, Decatur, GA; Chicago Botanic Garden, Glencoe, IL

As urban areas continue to grow and expand outwards, the loss of natural environments, green spaces, and an increase in impervious surfaces causes vast variation of pollinator communities. An estimated 87.5% of plants rely on animal pollination, including several food crops. However, pollinator decline is a trend seen globally, especially due to climate change, yet the full effects of pollinator decline in urban areas, especially in urban farms, is not fully documented, or are varied in their results. This project aims to better understand the effects of urbanization on plant pollinators by taking into consideration three main factors: 1. Impervious surfaces, 2. Floral resources, 3. Pollen Limitation. We used six sites for our study, five in varying states of urbanization throughout the city of Chicago and one at the Chicago Botanic Garden as a more suburban site. We had 10 control and 10 experimental plants each of patty pan squash (cucurbita pepo), and sungold tomatoes (solanum lycopersicum) at each site. The squash acted as a generalist pollinator plant while the sungolds acted as a specialized pollinator plant since it can only be buzz-pollinated by specific bees and other animal pollinators. We self pollinated the experimental plants to observe whether there was any relation to pollinator visitation and crop yield, as well as conducted both individual and broader pollinator observations at the sites to find whether there was a difference in the amount of pollinators and the types of pollinators present. Although our data set was small, we were able to find that both site (0.023) and treatment (p=<0.01) had marginally significant effects on the flower-to-fruit ratio.

P55 - Macroinvertebrate Colonization of a Newly Constructed Stream Channel Restoration

Misty Boatman, Michael Deutsch, Chance Garrett, Tori Hebert, Sam Little, Joseph Miller, Daniel Morrill, Alec Reep, Jackson Renfroe, Dylan Romine, Lauren Smith, Danielle Talbot, Reid Adams

University of Central Arkansas, Conway, AR

Freshwater biodiversity is declining globally at a faster rate than terrestrial and marine systems combined via a multitude of anthropogenic stressors, including habitat fragmentation. Extensive efforts have been implemented to re-establish longitudinal connectivity in streams negatively impacted by barriers, yet there is a general lack of biomonitoring following restorations. In January of 2020, the Nature Conservancy in Arkansas constructed a new stream channel, using Natural Channel Design, to bypass a low-water crossing barrier on a tributary to the Kings River in northwest Arkansas. Our objective was to study initial colonization of the new stream channel by aquatic macroinvertebrates, a critical component in evaluating stream restoration. We sampled across a variety of habitats within the new channel and in a reach just upstream of the restoration 46 days following establishment of connectivity. We identified specimens primarily to the family level and assigned functional feeding groups. Assemblages in the new channel were a subset of macroinvertebrates upstream, and were lower in taxa richness, diversity, and abundances of sensitive taxa. The new channel was dominated by collector/gatherer taxa, such as Perlodidae (early instar) and Chironomidae. Initial colonization of the new stream channel was relatively rapid, since colonizers who were abundant upstream dispersed to the new channel via drifting and fed on basal resources. By comparing macroinvertebrate assemblages following restoration, our study highlights the importance of monitoring to adequately assess impacts on biodiversity.

P56 - Change over time in the concentration of common cations found in the wood of the trees in Elon University Forest

Lindley Longstreet, David Vandermast

Elon University, Elon, NC

Changes in atmospheric chemistry, in particular the acidification of rainwater in recent decades, has the potential to change the concentration of cations in soils and therefore in trees. Changes such as these have been demonstrated in the forests of Europe, and closer to Elon, the forests of Great Smoky Mountains National Park. These changes in cation concentrations can be found in the annual rings of trees and can be traced back many decades because of their long lifespan. In this study, we use increment cores collected from a variety of tree species in Elon University Forest in 2015 to examine changes in cations such as iron (Fe), magnesium (Mg), calcium (Ca), potassium (K), manganese (Mn), and sodium (Na). The results of our study will provide data that will help us understand the role that soil acidification has in changes in the chemistry of North Carolina Piedmont soils and the wood of the trees that grow in them.

P57 - Does vernal pool species richness on rock outcrops follow predictions of Island Biogeography? A case study from 40-acre Rock Heritage Preserve.

Rob Bullard, David Vandermast

Elon University, Elon, NC

The theory of Island Biogeography, proposed by E.O. Wilson and Robert MacArthur in 1967, is one of the most important concepts in conservation biology. Using remote sensing, including images collected from a drone, we examine the relationship between vernal pool size, connectivity, distance from the "mainland" (the forest surrounding the rock outcrop), and species richness in vernal pools on 40-Acre Rock Heritage Preserve in Kershaw, SC. This is an ideal place to test this hypothesis because of its numerous vernal pools of varying sizes, easy access, and the presence of specialists such as *Diamorpha smallii*, *Mononeuria* (*Minuartia*) *uniflora*, *Gratiola amphianthus*, and *Sedum pusillum*. In addition, we examine the roles that pool shape and substrate type have in both species richnesses and co-occurrences of species within pools. We hypothesize that pool size and substrate type have a greater impact on species richness values than does distance from the mainland. We found that there are statistically significant co-occurrences ($p<0.05$) between species that require organic soil and that there are similarly strong co-occurrences between species found in gravelly soil with standing water, but not between these two species pools. Species found in pools with organic soils occur on the mainland, while those in gravelly wet soils do not. Our results will show whether species in pools with organic soils follow patterns of richness predicted by Island Biogeography Theory.

P58 - How do changes in soil microbial communities due to Kudzu invasion influence native plant species?

Robert Kiefer, Raegan Rainey, Benedict Okeke, Claudia Stein

Auburn University Montgomery, Montgomery, AL

Kudzu (*Pueraria montana* var. *lobata*) is one of the fastest growing and most noxious invasive species in the US. Its superior competitive ability is one major reason for its rapid spread. As a member of the legume family (Fabacea), kudzu has a strong impact on the soil environment, changing not only carbon and nitrogen dynamics but very likely also the soil microbial composition. Such alterations to the soil microbial community might hinder the establishment of desired native plant species in restored ecosystems, as many native and rare plant species require specific soil microorganisms for their establishment. We present preliminary results from a greenhouse experiment that tests how soil microbial communities associated with Kudzu influence the growth of 17 plant species native to Black Belt Prairies.

Especially the native legumes produced lower biomass when grown with soil microbial organisms associated with kudzu compared to soil without any live soil microbes. We found weak support for the hypothesis that soil microbial communities from intact native plant communities provide a benefit for native plant establishment. Our next steps are to isolate and identify soil microbes associated with kudzu roots and to assess species-specific effects. Our results indicate that soil microbial communities associated with kudzu inhibit the growth of native legume species and thus can have important implications for the development of restoration strategies.

P59 - Reproductive Biology of Redbreast Sunfish in an Urban Watershed

Hannah Talbert, Peter Sakaris

Georgia Gwinnett College, Lawrenceville, GA

The main goal of our project was to study the reproductive biology of Redbreast Sunfish, *Lepomis auritus*, in a highly impacted urban stream near Georgia Gwinnett College, Lawrenceville, Georgia. Sunfish were collected from the Yellow River Watershed by backpack electrofishing from June 2015 until September 2016. Sunfish were weighed (g), measured (mm TL), and dissected in the laboratory, where otoliths were extracted and gonads were dissected, weighed (g), and stored frozen until workup. After each ovary was thawed, all eggs were counted manually, and the diameter (mm) was measured for a subsample of 10 eggs from each ovary. Egg count ranged from 670 to 2,643 (mean ± SE = 1,355 ± 139), and egg diameter varied from 1.24 to 2.14 mm (mean ± SE = 1.75 ± 0.04). For females with detectable ovaries with eggs, mean GSI (gonadosomatic index) was 5.1 ± 0.6 and ranged from 0.7 to 14.2%. Ages of mature sunfish ranged from one to 6 years, with nearly 40% of the sample comprised of young individuals (1-2 years old). Additionally, we observed a one-year old female that invested significantly in reproduction (GSI = 14.2%, 1,788 eggs). Analysis of female GSI over time indicated that fish likely spawned from April to September, with the biggest spike in GSI occurring between May and July. Examination of egg counts indicated that individual Redbreast Sunfish might spawn more than once during the spawning season. Our results revealed a Redbreast Sunfish population that has likely adapted a strategy for maximizing reproduction in a highly disturbed, urban environment. Redbreast sunfish exhibited early maturation, large investment of energy into reproduction (max GSI of 14%), and a protracted spawning season.

P60 - Seed bank of the invasive species *Ligustrum sinense* (Chinese privet)

Aleya Last, Christy Carter

Wingate University, Wingate, NC

Ligustrum sinense, commonly known as Chinese privet, was originally introduced to the US as an ornamental plant and has rapidly spread across the US. The goal of this study was to determine the effects of the presence of *L. sinense* on the seed bank by comparing the seed density and diversity of one section of a forest uninhabited by *L. sinense* to another nearby section that had extensive *L. sinense* growth. Five 1-m^2 plots were randomly located along a transect in each of the two sections of forest. Five cores were taken from each plot using 5.5 cm d × 10 cm depth soil core on 19 October 2021. Each soil core was stored in a plastic container in a Percival growth chamber at 5.0°C until sieved. Soil was wet sieved through five mesh sizes and seeds were counted and identified. The area of the forest with extensive privet growth contained an average of 177 seeds/m^2, whereas no seeds were found in the seed bank of the non-privet area. Seeds found in the privet area of the forest were not seeds from *L. sinense*. Unlike previous investigations, this study indicated little to no input of *L. sinense* seeds into the seed bank within the area it inhabits. Additionally, the lack of seeds in the area uninhabited by *L. sinense* could be due to the fact that there is no herb or shrub layer in this oak/hickory forest stand. Further investigation is needed to obtain more samples to further verify the findings.

P61 - Joint-Nesting and Cooperation between a Western Kingbird (*Tyrannus verticalis*) and a Hybrid Western Kingbird x Scissor-tailed Flycatcher (*T. forficatus*) in Arkansas

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Joint-nesting is a form of cooperative breeding when multiple adults of the same sex contribute both genetically and parentally to the same clutch. Joint-nesting can often lead to reduced fitness for the adults involved but could be advantageous for species with limited breeding opportunities. This could be especially true for species at the periphery of their ranges, where hybridization may be more likely to occur. However, very little is known about these factors, primarily because joint-nesting involving hybrids is rarely documented. Here, we describe the first documented case of joint-nesting in the genus *Tyrannus.* On June 13, 2021, we located a female Western Kingbird (*Tyrannus verticalis*) and a confirmed banded hybrid Scissor-tailed Flycatcher (*T. forficatus*) x Western Kingbird (*T. verticalis*) joint-incubating a nest in Bald Knob, Arkansas. We monitored the nest until it successfully fledged four young on July 9. We were able to band all four fledglings and both adults and collect blood for genetic analysis. We used whole-genome sequencing and morphology to confirm that the pure Western Kingbird adult was the mother of three of the four offspring and the hybrid adult the mother of the fourth offspring in the clutch. The hybrid female (at least 8 years old) has fledged three young in both 2016 and 2018, indicating that she has lowered her fitness by joint-nesting, while the female Western Kingbird fledged three young, an average clutch size for breeding Western Kingbirds in the area. This event (which is likely very rare) indicates that joint nesting in *Tyrannus* likely leads to reduced fitness for one or more adults involved. More broadly, this may indicate that hybrids can produce viable offspring by joint-nesting when mates are rare, which can reinforce hybridization from both a genotypic and phenotypic scale.

P62 - Analytical Research of Opioid Epidemic Data in Forsyth County

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Research on the opioid epidemic has been conducted nationwide for over a decade, as it is an ongoing national public health concern. The purpose of this project is to determine the effect of prevention and treatment services for opioid use and opioid use disorder in Forsyth County, NC. We hypothesize that there will be a decrease in the number of individuals that use synthetic opioids, as well as a decrease in the number of individuals who experience opioid use disorder after the development of community-wide initiatives by the Forsyth Regional Opioid and Substance Use Team (FROST). We will collaborate with representatives of the Forsyth County Department of Public Health (NC) to collect and analyze de-identified data related to opioid overdose and treatment in Forsyth County, such as the number of Narcan kits used by each agency per month, the number of individuals referred to treatment, the number of individuals who have started medication-assisted treatment (MAT) and the number of hospital Emergency Department visit for opioid overdoses. The preliminary data showed that a heightened number of middle-aged individuals are the main users of synthetic opioids. More information on these individuals has been requested to answer questions regarding the lives of these individuals, as well as what the initial cause of partaking in Opioid usage was. Future research will focus on collecting additional data from a variety of agencies in Forsyth County to determine the effectiveness of the community-wide programs.

P63 - Does local human disturbance affect species richness of mammal communities?

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From changes in their behavior to declines in population size, mammals are influenced by human disturbance. Additionally, in the presence of human disturbance, mammal community composition can change, and species diversity may decrease. At the local scale, human disturbances can be lasting (e.g., the removal of forests creating open and edge habitats) or temporary (e.g., hiking, field maintenance, vehicle traffic). In this study, we investigated whether lasting and temporary human disturbances (THD) at the local scale decrease species richness of mammal communities in Upstate South Carolina. We predicted species richness would be lower in areas with higher THD and in more open habitats. To test our predictions, we collected images using camera traps in various stations across four sites. Each station was classified as forest, open, or edge habitat and given a THD score. The mammal species in each image were identified, and we used the Chao 1 estimator to determine species richness for each station. We found no significant difference in the mean species richness between the high, low, and no THD stations. We also detected no difference in mean species richness between the three habitat types. Overall, local human disturbance does not significantly decrease species richness in mammal communities at our sites. This suggests that the mammal species we observed in Upstate South Carolina are tolerant to this local disturbance. In future studies, we will use GIS to investigate the effects of landscape-level human disturbances on mammal communities.

P64 - How does climate change help the spread of vector borne diseases transmitted by mosquitoes?

Asmiya Kazmin, Jennifer Kovacs

Agnes Scott College, Decatur, GA

Due to climate change, there have been geographic changes in landscape and temperature around the world. Because of this, mosquitoes have found new places to relocate to and live. The shifts in weather patterns and temperature have a huge impact on the spread of vector-borne disease transmitted by mosquitoes. Here we investigate how temperature influences the mosquito population in four cities on the east coast over five years. We compared differences in the biodiversity of mosquito species present in the four locations and analyzed its effect on the spread of vector-borne diseases transmitted by mosquitoes. We used the publicly-accessible NEON database to collect mosquito and temperature data. We used Python to code for an association between the two variables. We found no correlation with temperature and richness nor temperature and population. Our project aims to present a solution to the problem.

P65 - Using citizen science data to assess the impacts of urbanization and predation on lizard species across Tennessee

Eliana Blash, Izzy Hartwig, Haleema Shamsuddin, Emma Van Why, Matt Heard

Belmont University, Nashville, TN

Urbanization poses a significant threat to animals and can drive habitat loss and changes in species interactions. In this study, we evaluated whether we could use citizen science data from iNaturalist to analyze the impact of urbanization on ten lizard species and their exposure to predation across the state of Tennessee. Using this approach, we downloaded occurrence data and photos for our seven species using records from iNaturalist for 2016-2020 (n=990). Using photos from individual observations we then quantified predation risk by looking for lizards with broken tails and injuries. To assess the impacts of urbanization on lizard species, we also looked to see if there were correlations between occurrence records of individuals both impacted by predators and not impacted by predators and impervious surface cover. Using this approach, we determined that our ten different lizard species were affected in different ways by predation risk and urbanization. In addition, our results show that citizen science data and more specifically photo-vouchered occurrence data can be helpful for assessing interspecific interactions and the impacts of urbanization on animals.

P66 - Regulation of Dhurrin Biosynthetic Pathway in *Sorghum halepense* seedlings

Connor Purvis, Jeremy Rentsch, Elizabeth Jones

Francis Marion University, Florence, SC

Sorghum halepense or Johnsongrass is cited as one of the world's most noxious weeds by many accounts. Though it was first brought over to use as a feed for cattle, it is of great use because of its high yields. Death by cyanide poisoning in cattle raised awareness that there were underlying processes in Johnsongrass that were not known. A cyanogenic glucoside dhurrin was found to be the cause of the cyanide buildup in *S. halepense*. Studies have shown that stress and age of *S. halepense* affect the dhurrin production. This study aimed at understanding the correlation between *S. halepense* age and the dhurrin production. This was done by isolating RNA from seedlings of *S. halepense* by week and synthesizing cDNA. That cDNA was then utilized for qPCR to look at the regulation of three genes. CYP71E1 and UGT85B1, in the dhurrin biosynthetic pathway and 18s serving as a housekeeping gene. We hypothesis that dhurrin production is rapidly increased after germination and decreases once the seedling is around 4 weeks old.

P67 - Bat Species Richness and Activity in an Urban and Rural Area in Davidson County, Tennessee

Harrison Williams, Maria Aguirre, Jocelyne Lara-Rojos, Darlene Panvini

Belmont University, Nashville, TN

The occurrence of bats depends on the availability of suitable habitat and food resources, which can vary across the landscape in the transition from urban to rural locations. Bat activity is dependent on multiple factors such as type of environment, population, housing, and even artificial light. Each species of bat uses unique high-frequency calls to echolocate across the landscape. This study recorded bat echolocation calls and identified species to determine if bat species richness differs between an urban and a rural setting. Bat calls were surveyed in one urban park and a rural area of Davidson County, Tennessee using an EchoMeter Touch 2 at dusk, twice per week, during September and October 2021. The locations used were Centennial Park and Belle Forrest. Initial data such as temperature, pressure, moon percentage, decibel, and humidity were all recorded. Then bat observation was done and recorded over an hour and a half. KaleidoscopePro Analysis Software was used to confirm bat species identities. The data suggest slight differences in the occurrence of bat species and a difference in bat activity between the two locations. Seven bat species were recorded at each location, five species at both sites, *Eptesicus fuscus* at the urban site only, and *Myotis austroriparius* at the rural site only. However, bat activity was 70% dissimilar among the two sites. Knowing which bat species occur in each setting provides insight into the habitats that bats rely on and what measures should be taken to preserve their niches. This study also shows us how urbanization might affect the occurrence of different bat species.

P68 - Exploring the Effects of Fertilization and Defoliation on Carbohydrate Remobilization in Northern Red Oak (*Quercus velutina*) and River Birch (*Betula nigra*) Saplings

Joseph Dunlap, Emiley Sorge, Erin Wiley

University of Central Arkansas, Conway, AR

Nonstructural carbohydrates (NSC) play an important role as storage molecules in trees, providing a source of carbon when photosynthesis is limited. Because climate change may increase the frequency of stressors that demand a reliance on NSC remobilization, a better understanding of how storage is regulated is needed to predict how trees will respond. However, there is much debate whether NSC storage is maintained at the expense of growth or if it is passively controlled by sink demands for growth. Defoliation is a common disturbance requiring the remobilization of stored resources. Following defoliation, NSC levels initially decline to support respiration and canopy flush. However, NSC levels usually never reach depletion even though leaf recovery typically does not reach the leaf area of the original canopy. One reason for this could be that canopy recovery is nitrogen not carbon limited. In this study, we investigated how nitrogen fertilization impacted leaf reflush and NSC remobilization in the roots and stems of one year old Northern Red Oak (*Quercus velutina*) and River Birch (*Betula nigra*) saplings following complete defoliation. In early June, trees were completely defoliated and differentially fertilized. Trees were then harvested three and a half weeks later, and the starch and sugar (NSC) concentrations of roots and stems were measured. We discuss how fertilization impacted remobilization and how the difference in NSC levels between the two species relates to their different growth forms (semi-determinate vs indeterminate).

P69 - Morphological and molecular analyses of zoantharians located at the southernmost region of the Caribbean Sea

Samantha Kilian, Chloe Cummins, Stanton Belford

University of Tennessee Southern, Pulaski, TN

Zoantharians are colonial cnidarians that are globally distributed throughout various tropical and subtropical marine ecosystems. Despite their high abundance and vital ecological role in these marine habitats, few studies have accurately identified zoantharians located along the northeastern coast of Trinidad, southern Caribbean Sea. Here, we examine morphological differences *in situ*, such as oral disc size, disc and tentacle color, and number of tentacles, together with molecular analyses. We sequenced the mitochondrial 16S ribosomal DNA (16S rDNA), cytochrome oxidase subunit I (COI), and Internal transcribed spacer (ITS-rDNA) genes of zoantharian polyps collected from this region. Zoantharians were identified as *Zoanthus pulchellus*, *Zoanthus sociatus*, and *Palythoa caribaeorum* using gene markers. Morphological analysis results showed variation in oral disc and tentacle colors from bright to dark green, and blue in *Zoanthus* spp. and brown to green in *Palythoa* spp. Tentacle count ranged from 42-46 in *Zoanthus* spp. and 26-36 in *Palythoa* spp. Oral disc diameter in *Zoanthus* ranged from 5-10 mm, and 10-13 mm in *Palythoa*. Molecular and phylogenetic analyses allowed us to gain a more comprehensive understanding of zoantharian diversity in Trinidad. Both molecular and morphological data provide information regarding zoantharian identification in Trinidad, where it is limited, and further research is necessary to attain knowledge of zoantharian species diversity in this region of the southern Caribbean Sea.

P70 - The interactive effects of heatwaves and defoliation on *Quercus palustris* performance

Benjamin O'Connell, Erin Wiley

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In recent decades, mass forest die-off events around the planet have been observed, often resulting from the interaction of multiple stressors. As many of these stressors—including biotic attacks and heatwaves—are expected to increase in frequency with climate change, a better understanding of how these stressors limit growth and survival, and how multiple stressors interact is needed in order to predict forest responses. Severe defoliation is a common stressor that requires trees to regrow a new canopy to recover, but it is unclear what limits canopy regrowth, including the impacts of co-occurring stressors. In this experiment, we examined how defoliation may impact trees in a warmer world, by comparing experimentally defoliated (DEF) and undefoliated (UNDEF) pin oak (*Quercus palustris*) seedling responses to simulated ambient (AMB) and +10°C heatwave (HW) late spring conditions for 25 days. Impacts were assessed in terms of final biomass and leaf area, gas exchange rates, leaf N concentration, and carbohydrate storage.

Initially, respiration rates were significantly higher across HW treatments, but were near fully acclimated after three weeks. In contrast, photosynthesis remained higher under the HW throughout the experiment. HW trees also had increased leaf [N], which may account for the enhanced photosynthetic rates. DEF trees accumulated significantly less stem and leaf mass but had higher photosynthetic rates than UNDEF trees after leaf regrowth. However, there was no difference in leaf area recovery between temperature treatments, likely due to the similar respiration rates of DEF trees in the AMB and HW treatments. Among DEF trees, percent leaf area recovery and leaf [N] were not related, suggesting that N does not limit leaf regrowth. Overall, our results suggest that tree recovery from spring defoliation will not be negatively impacted by rising temperatures, suggesting more resilience from our forests in the future.

P71 - Effects of Urbanization on Organic Matter Inputs and Food Webs

Sarah Limer, Adelaide Obo, Maitri Patel, Natahlia Robinson, Troy Mutchler

Kennesaw State University, Kennesaw, GA

Urban Stream Syndrome has been causing changes in streams' physical characteristics and water quality for years. These changes in the environmental characteristics of an urbanized stream negatively impact the biological communities present by altering species' habitats and food availability. The purpose of this study was to further understand the effects of urbanization on the supply of organic matter to the food webs of selected streams within north Georgia because of changes in allochthonous organic matter inputs. This study was a comparative analysis between Racoon Creek, Noonday Creek, and Peachtree Creek; three streams along a gradient of land use, from rural to urban, respectively. Each stream was visited in early spring to collect data on organic matter and streamflow. At the point of sampling, Racoon Creek watershed contains 82.5% forest, 3.66% developed space, and 13.84% other. Noonday Creek watershed (upstream of the sampling point) contains 52.8% open-low developed space, 22.13% medium-high developed space, 20.95% forest, and 4.12% other space in the watershed. Peachtree Creek watershed, the largest of the three, contains 52.88% open-low developed space, 29.36% medium-high developed space, 15.97% forest, and 1.79% other in the watershed. Over a 100-meter transect, Racoon Creek had 488.61g/m^2 of organic matter, Noonday Creek had 3.97g/m^2, and Peachtree Creek had 70.41g/m^2. Additionally, stable isotope data for carbon and nitrogen were collected for representative organisms and coarse particulate organic matter at each site. These results suggest that less urbanized, smaller stream locations receive more allochthonous organic matter. The stable isotope values of carbon and nitrogen indicated changes in the food web structures and functions between Racoon and Noonday Creek; this data will be compared to Peachtree creek to examine whether there are additional changes associated with more intense urbanization.

P72 - Characterizing plant biochemical responses to pathogenic stress: a spotlight on red leaf spots

Maggie Salley, Bailey McCormick, Anna Ferraro, Nicole Hughes

High Point University, High Point, NC

Red leaf spots commonly accompany pathogen infection in plants. Yet, the function of red anthocyanins pigments in infected tissues is unknown. We characterized biochemical responses of two plant species, red-tip photinia (*Photinia glabra*) and Indian hawthorn (*Rhaphiolepis indica*), to infection by the pathogenic fungus, *Entomosporium mespili.* We used analytical HPLC and LC-MS to identify and quantify anthocyanins and photopigments in red leaves or tissues (including red expanding leaves, red senescing leaves, and red spots) and green tissues (green areas around red spots, fully-expanded green leaves) of the same plants. Maximum quantum yield efficiency of PSII (F_v/F_m) and xanthophyll cycle pigment ratios was measured as a proxy for sustained high-light stress. DPPH radical scavenging assay assessed low molecular weight activity (LMWA) in red spots versus surrounding green tissues. The major anthocyanins in red tissues of both species were cyanidin-3-*O*-galactoside and cyanidin-3-*O*-arabinoside. Red tissues of photinia also contained small amounts of three additional cyanidin mono-glycosides (cyanidin-3-*O*-glucoside and two unidentified cyanidin-*O*-pentosides); red spots lacked cyanidin-3-*O*-arabinoside. All red tissues had significantly lower chlorophyll and F_v/F_m than green tissues, suggesting increased vulnerability to photo-oxidative stress. Photoprotective carotenoids did not differ between red and green tissues, likely due to small sample size. Antioxidant activity was 1.5-3.4x higher in red spots versus surrounding green tissues; follow up assays with purified anthocyanins suggested anthocyanins were responsible for ca. 1/3 antioxidant activity in red spots. From these results, we predict the function of anthocyanins in red spots is similar to anthocyanins in young and senescing leaves, and this function likely includes photoprotection (i.e. light attenuation and antioxidant defense). We are currently investigating a possible anti-microbial function as well.

P73 - Symbiodiniaceae diversity of zooxanthellate zoantharians at the southern edge of the Caribbean Sea

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Dinoflagellate family Symbiodiniaceae display diverse symbionts, which are found in cnidarians and other marine invertebrates. Current studies continue to investigate these common marine organisms, together with their symbiotic association between cnidarians and invertebrates. Despite their high ecological importance, little research has investigated zoantharian endosymbiont diversity located along the northeastern coast of Toco, Trinidad, southern Caribbean Sea. In this study, zoantharian specimens collected and photographed *in situ* were used to molecularly confirm identification of Symbiodiniaceae diversity found in *Zoanthus* and *Palythoa* spp. We isolated DNA from endosymbionts and used polymerase chain reaction (PCR) of the internal transcribed spacer (ITS 2) gene marker, followed by Denaturing Gradient Gel Electrophoresis (DGGE) to evaluate symbiont diversity. Results showed diverse zooxanthellae found within zoantharians, most notably *Symbiodinium* (formerly clade A) in *Zoanthus pulchellus*, *Z. sociatus*, and *Cladocopium* (formerly clade C) in *Palythoa caribaeorum*. Our goal is to attain a more extensive knowledge on the endosymbiont diversity of zoantharians to better understand its diversity relative to their cnidarian counterparts found in this southernmost region of the Caribbean Sea

P74 - Using the COI barcode to differentiate three species of yellow-faced bees (*Hylaeus* spp., Colletidae)

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Wild pollinators play a vital role in the biodiversity of ecosystems by providing free pollination services that allow flowering plants and crops to reproduce and form fruit. The Mid-Atlantic Region of the US harbors ca. 600 species of wild bees though due to the complexity of their

taxonomy, this diversity is likely underestimated. Sex dimorphism, together with the solitary habitat of most wild bees make bee identification challenging.

In this study, we use the COI barcode to differentiate three species of wild bees from the genus *Hylaeus* (Colletidae): *H. affinis*, *H. modestus*, and *H. illinoisensis*. These three species are very similar morphologically and form a species complex. *Hylaeus* consists of bees that have yellow characteristics on their face, and they pollinate carrots, clover, and other plants in different families like Ericaceae and Lamiaceae. Using 234 sequences from the Barcode of Life Data System (BOLD), we reconstruct a phylogeny using Bayesian inference to assess if the COI barcode could be useful in differentiating taxa within this species complex.

Our phylogeny supports the recognition of the three species. *Hylaeus affinis* and *H. modestus* appear as sister taxa, but *H. illinoisensis* appears more closely related to *H. ornatus*. Furthermore, samples of *H. modestus* appear divided into two subgroups. These might correspond to different morphotypes within *H. modestus.* Sequences with ambiguous determinations ("*H. affinis/modestus*") fall within the *H. modestus* or *H. affinis* groups which may confirm their determination as one taxon or the other. Our study supports the usefulness of the COI barcode to aid in the identification of taxonomically challenging species of wild bees.

P75 - Diversity and abundance of ectoparasites on birds in Northeastern Arkansas

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Parasite biodiversity and conservation is often overlooked due to the obscure lifestyles, cryptic morphology, and insufficient data of many species of parasites. This is especially characteristic of ectoparasites such as bird lice. Most lice have highly specific associations with particular bird species, which is primarily due to the limited dispersal ability of lice. However, the biodiversity and prevalence of bird lice remain relatively understudied, especially in the southern United States. It is also unknown how the presence of other ectoparasites, such as feather mites, effect bird-louse associations. Here, we assessed the diversity and prevalence of lice from birds in eastern Arkansas by focusing on three questions: (1) Is there variation in louse prevalence and abundance among different groups of birds? (2) What are the most common genera of lice associated with birds? (3) How frequently do lice and mites co-occur on bird host? To address these questions, we searched over 600 birds from the Arkansas State University bird collection or from the field. We identified lice to genus and calculated prevalence of lice and mites, and abundance and intensity of lice. Overall, we found 10 different genera of lice, with *Brueelia* being the most prevalent genus from among different bird hosts. Additionally, we found four novel louse-host associations. We found that louse prevalence and abundance vary considerably among different host taxa. For example, birds in the family Turdidae typically have higher parasitic lice prevalence (17.28%) compared to birds in the family Parulidae (7.94%). We also found mite and lice co-occur infrequently relative to the prevalence of only mites or lice. Together, our results provide important insights into the biodiversity and host relationships of avian ectoparasites and contributes to an increasing focus on understanding parasite biodiversity across the globe.

P76 - Survey of Bee Communities in Differently Managed Sites in Central Arkansas

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With increased concern over pollinator decline, it is important to understand the effect of management on pollinator communities. Bees have been consistently shown to be the most effective animal pollinators. Our study was conducted to expand the knowledge base on species presence of bees in Central Arkansas, as well as evaluate the potential benefits the habitat restoration of Northern Bobwhite quail (*Colinus virginianus)* could have on species diversity. Additionally, sampling across multiple seasons offered a more complete picture of the communities present in our differently managed sites. Bees were collected across 3 research sites for 3 sampling seasons (Spring, Summer, Fall) from March to November 2021. Sample sites were a pasture maintained through mowing and cattle grazing, a prairie managed for Northern Bobwhite quail with prescribed burning and replanting of native plants, and a rocky outcrop site managed by prescribed burning. Bees were captured through pan trapping for 24 hour periods plus 1 hour of hand netting per site per day. Across all study sites 832 bees representing 93 species were collected: pasture (348 individuals from 52 species), prairie (313 individuals from 57 species), rocky outcrop (171 individuals from 47 species). Using Shannon's diversity index we found no significant difference in diversity across and between sites (SDI Prairie=1.53±0.20SE, SDI Pasture=1.48±0.17SE, SDI Outcrop=1.51±0.14SE; p=0.97). When comparing community similarity using Sorenson-Dice index, the rocky outcrop and pasture sites had the highest correlation (DSC = 0.57) followed by the prairie and pasture (DSC=0.55) and the rocky outcrop and prairie (DSC=0.50). These results suggest that differences in management of land have a demonstrable effect on the makeup of bee communities present.

P77 - The proboscis' mechanosensory sensitivity to angle of #Manduca sexta#. *Terry L. Newsome*,* Emily Hudgins*, and Joaquin Goyret *University of Tennessee at Martin, Martin, Tennessee.*

Terry Newsome

University of Tennessee at Martin, martin, TN

#Manduca sexta#, is a large crepuscular-nocturnal hawkmoth, that forages for flowers using olfactory and visual stimuli. When hovering at the flower, it relies more on tactile sense of its proboscis to locate concealed nectar. Initially it will tape on the corolla, exploring its surface. Upon detection of specific surface features, such as grooves, it enters a back-and-forth flying pattern (BnF) while dragging its proboscis on the flower's surface attempting to feed. We have previously used the display of BnF to assess the detection of grooves of different size on the flat corollas of surrogate flowers. Here we use the BnF to 1) assess whether the detection of inclined surfaces elicits the BnF and 2) determine the minimum angle eliciting the BnF i.e. angular sensitivity.

P78 - Symbiont Mediated Pathogenesis of Entomopathogenic Nematodes

Elizabeth Wiles, Michelle Thomas

Campbell University, Buies Creek, NC

Entomopathogenic nematodes (EPNs or beneficial nematodes) are roundworms that parasitize insects. EPNs have industrial and agricultural uses as natural biopesticides. EPNs are effective against various species of insect pests, while being harmless to other animals. Pathogenesis of EPNs is largely dependent on their bacterial symbionts, which aid in killing the host, allowing the nematodes to proliferate inside insect cadavers. The EPN, Steinernema carpocapsae, associates with bacteria in the genus Xenorhabdus, which are well studied for their secretion of potent antimicrobial and insecticidal compounds. The goal of this study is to better understand how Xenorhabdus sp. mediate nematode infection and emergence using greater wax moth (Galleria mellonella) larvae as model host insects. S. carpocapsae nematodes will be reared in G. mellonella larvae, and samples will be taken from infected larvae to determine the prevalence of Xenorhabdus throughout the nematode life cycle. This research could provide a better understanding of nematode virulence and how the host environment impacts their life cycle.

P79 - Assessing the foraging habit of two species of long-horned bees, *Melissodes agilis* and *M. trinodis* (Apidae) using metabarcoding

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Sunflower is an important crop in the Great Plains region of North America. It is a source of edible oil, leaves are used as fodder and as source of yellow dye, and the seeds are used for food. European honeybees are used to pollinate sunflower; however, many wild bees are specialized in sunflower pollination and do a better job at it than the generalist honeybee. Unfortunately, wild bees and the plants they pollinate are largely unknown. Our research looks at the foraging preference of two species of long-horned bees that occur across the USA, *Melissodes agilis* and *M. trinodis* (Apidae). There is some taxonomic dispute as to whether these species constitute a single taxon or not, so our study aims to assess if there are differences in their foraging habit. *Melissodes* is a group of ground-burrowers, solitary bees that specialize in sunflower pollination (*Helianthus* spp., Asteraceae). We analyzed the pollen load from 36 bees collected in a sunflower field in Casselton, North Dakota in 2019. DNA was extracted from the pollen and two genes were amplified, ITS2 (nuclear) and trnL (chloroplast), and used to determine the provenance of the pollen. Both species, *Melissodes agilis* and *M. trinodis,* show a clear preference for the sunflower family, Asteraceae, but our data shows they also visited plants in the Fabaceae. Pollen from Brassicaceae was found in *M. agilis* and some pollen from Linaceae was found in *M. trinodis*. Surprisingly, results from TrnL show bryophyte spores as part of the pollen load in both species. Our study indicates differences in the pollen composition collected by these two species and contributes to the knowledge of the foraging habits of wild bees in the USA.

P80 - Helminth Parasite Community Structure of Juvenile Green Sunfish (*Lepomis cyanellus*) in an Urban Stream

Mr. Nicholas Tsangarides, Riccardo Fiorillo

Georgia Gwinnett College, Lawrenceville, GA

Many fresh water streams in metro Atlanta, GA have been disturbed by construction and/or pollution. Tree Creek flows in Gwinnett County, near a busy state highway, adjacent several large housing developments, and our sampling location was near an active construction site. A real hell hole! During unrelated fish sampling in summer 2021, we identified green sunfish, *Lepomis cyanellus,* as the most abundant fish in this section of Tree Creek. Unsurprisingly, this centrarchid is highly tolerant of poor water quality and tends to thrive is highly disturbed habitats. We wanted to characterize the parasite community structure of this host in a highly disturbed habitat. We sampled green sunfish with minnow traps baited with cat food in August, September, November, and December 2021, and we will collect again in early spring 2022. To date we have examined 90 fish hosts from the first 2 sampling periods. We recovered a total of ~1200 worms representing 7 helminth taxa (2 trematode, 2 Cestode, 3 Nematodes). Most of these helminths represent larval stages, with the exception of the trematode *Pisciamphistoma stunkardi* which was recovered as non gravid adults in the intestinal tract of this host and a single *Bothriocephalus sp.* tapeworm. The most prevalent helminth is the metacercaria of the trematode *Posthodiplostomum minimum*, which matures in bird definitive hosts. Nematodes we also abundant as encysted juveniles within the viscera of these hosts. We will report on the prevalence abundance, and mean intensity of these taxa and parasite community indices across collecting periods. See ya!

P81 - The Role of Diet and Density on Adult-Egg Cannibalism in Red Flour Beetles

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Red flour beetles (Tribolium castaneum) complete their entire life cycle in flour, which thus serves multiple functions: habitat, food, and a source of microbiomes, making it an ideal, tractable system. Moreover, these beetles are facultative cannibals in stressful conditions, so stress factors such as insufficient nutrition in diet and over-population were used to induce cannibalistic behavior. Cannibal-victim dynamics occur at various life stages, but adult-egg cannibalism was used to determine whether flour diet and population density alter the beetle gut microbiome and cannibalism rates. Two experiments were performed that manipulated different environmental stressors: host diet and population density. For the first experiment, the role of the host diet was isolated by rearing flour beetles on alternative flour diets varying in nutritional content: (1) whole wheat (high-nutrient), (2) high-gluten flour, (3) teff, and (4) oat (low-nutrient), with the same population size (n=20). For the second experiment, the role of population density was isolated by rearing flour beetles in a range of population sizes (n= 20, 40, 80, and 100) on whole wheat flour. For each experiment, adult-egg cannibalism rates were measured by counting the number of eggs in each sample every two days. For the first experiment examining the role of the host diet in terms of cannibalism, if a low-nutrient diet is more stressful than a high-nutrient diet, it was expected the lowest-nutrient diet (oat flour) would have the most egg victims over time. For the second experiment examining the role of population density in terms of cannibalism, if a high population density is more stressful, the population with the highest density (n=100) was expected to have the most egg victims over time. Our results indicate that stress type and cannibalistic behavior are correlated.

P82 - Demystifying Dendrology: An online preparation course develops a growth mindset and successful strategies for learning tree identification

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Many students taking Dendrology for the first time have not had previous experience with learning plant identification. This can be an early setback in an important course that is required for several undergraduate programs. We developed a four-week, online preparation course to increase student confidence and share successful strategies for learning plant identification. The main focus was on basic vocabulary, use of effective study strategies, and identification of key characteristics within species. Students practiced these skills by learning 30 tree species while utilizing flashcards, guided notes, and our ILEX (Identify-Learn-EXplore) practice tool. We surveyed students at the end of the preparation course and at the end of the main Dendrology course to assess the effectiveness of this approach. Preliminary results from 31 students indicate students reporting that the prep course was "extremely helpful" in understanding and applying botanical knowledge (61%), developing beginning experience with plant identification (61%), and using effective strategies to practice plant identification skills (58%). Exposure to different practice strategies and identification tools in the preparation course helps students develop a growth mindset that enhances their success in Dendrology.

P83 - Evaluation of Developmental Toxicity of Bupivacaine Hydrochloride and Sea Salt Using the Frog Embryo Teratogenesis Assay: Xenopus (FETAX)

Kayla Way, Kabita Kunwar, James Rayburn

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Bupivacaine hydrochloride is used as a long-lasting pharmaceutical local anesthetic to reduce opioid abuse. Sea Salts are mainly comprised of sodium chloride and 0.2 to 10% of other salts and are commonly found in the environment through the use of road deicing salts. The potential teratogenic hazard of Bupivacaine HCl and Sea Salts was evaluated using the Frog Embryo Teratogenesis Assay-Xenopus (FETAX). Embryos of the South African clawed frog, Xenopus *laevis*, were exposed to concentrations of Bupivacaine HCl ranging from 1 mg/L to 100 mg/L. In a separate experiment embryos were exposed to concentrations of Sea Salts ranging from 1 mg/L to 8mg/L. A chemical is accepted as a teratogen when the teratogenic index is over a 1.5 ratio (LC50/EC50). The teratogenic potential of Bupivacaine HCl was based on teratogenic indices over a 96-hour test (LC50/96 and EC50/96) and was roughly 5 overall. The teratogenic potential of Sea Salts was based on the same teratogenic indices as the Bupivacaine HCl and was found to be 0.95 overall. The teratogenic potential of Bupivacaine HCl was of a high index and the teratogenic indices for Sea Salts was considered a low index. Observations throughout the experiments were made for the type and severity of malformation and effects on embryonic growth. These results demonstrate that Bupivacaine HCl would pose a higher teratogenic risk to developing embryos and Sea Salts would pose a lower teratogenic risk. The results of these experiments demonstrated the efficacy of using the FETAX assay to evaluate the developmental toxicology of pharmaceuticals.

P84 - Development and implementation of Coronavirus modules in multiple biology courses to enhance knowledge in genetics, evolution, and diversity, equity, and inclusion

Jennell Talley, Lee Kurtz, Sharon Keller, Indhira De La Rosa

Georgia Gwinnett College, Lawrenceville, GA

Georgia Gwinnett College (GGC) is a four-year, liberal arts school in Lawrenceville, GA that is consistently ranked the most ethnically diverse regional college in the southeast. As such we want to ensure students in our biology program have opportunities to consider how topics in science impact people from different backgrounds. Additionally, program assessments at GGC identified student weaknesses in both genetics and evolution learning outcomes from freshman to seniors. To enhance learning outcomes in these core concepts and increase awareness in topics of diversity, equity, and inclusion (DEI), GGC biology faculty developed modules integrating themed biology content and DEI in courses that all or most biology majors take. The current pandemic has made visible the differences in access to vaccines or medical treatments not only in the United States but many countries around the world and brought the family of viruses known as Coronaviridae to the forefront. Thus, we used Coronaviruses as the module theme and have developed modules in Introductory Biology, Genetics, and Microbiology courses to expose students to different concepts at different academic levels in genetics, evolution, and DEI topics. Our poster will discuss the training we received to develop modules, how we worked to develop each set of modules; how we are assessing content and deepening of knowledge in DEI, as well as in what future courses we will be developing modules. Successes and challenges will also be discussed.

P85 - Froggy Goes To School: Hylid Frogs on an Suburban Campus

Ryan Davenport, Hannah Talbert, Kelly Simpson, Ninknee Kongmanichanh, Riccardo Fiorillo, Christopher Brown

Georgia Gwinnett College, Lawrenceville, GA

Hylid tree frogs are often clinging to windows on the campus of Georgia Gwinnett College, located in Metro Atlanta. Considering the distance to nearby natural habitat patches (wooded areas and retention ponds) and intervening low-quality landscape (parking lots and roads), we asked: (1) What species of Hylid frogs are on campus? (2) Do species show preferences for habitats? (3) Where are they breeding? And (4) how do they move about the area? To answer these questions, passive PVC pipe traps (individuals were able to move freely into and out of traps) were placed in both heavily-developed and forested areas around campus in June 2021 and checked biweekly thereafter. We PIT tagged captured individuals, measured tibia and femur length, and weighed them. We then returned the individuals to the pipe. We have caught three species of frogs on and around campus: green tree frogs (*Hyla cinerea*), Cope's gray tree frog (*Dryophytes chrysocells*), and a single squirrel tree frog *Hyla squirella*. The majority of Hylids found in the heavily-developed areas of campus were *H. cinerea*, while *D. chrysocells* were mainly found in the forested areas. Recaptured frogs rarely travel between locations or between pipes within a location. Many juvenile *H. cinerea* were observed in grass adjacent to a retention pond, but were too small to tag. On the first day below 50° F, a few pipes had multiple frogs, but as winter has progressed, we are no longer capturing frogs in our pipe traps.

P86 - Redesigning a biology curriculum for flexibility leads to increased graduation rates but decreased MFT scores

Emily Prince, Lisa McDonald

Lander University, Greenwood, SC

In 2016, Lander University's biology curriculum was redesigned to align with AAAS's "Vision and Change" document and to improve retention by increasing flexibility within the major. The introductory biology course was stretched to two semesters and "flipped" to focus on student learning and engagement. The number of required courses was reduced, and students chose among several upper-level courses that covered the core competencies. To assess the success of the curriculum revision we compared the 4-year graduation rate and ETS Biology Major Field Test (MFT) scores of cohorts of students matriculating during three different periods: those entirely under the old curriculum (old, 2013), those with the changed upper-level courses but not the revised freshman course (mixed, 2014-1016), and those entirely under the new curriculum (new, 2017). We also looked specifically at students with two or more risk factors for failure (i.e., underrepresented minority, first-generation, low socio-economic status, and female). We found that, while the graduation rate of biology majors was similar in the old and mixed curricula (14.3% and 12.2%, respectively), the graduation rate of students in the new curriculum increased to 25.0% (significantly higher than the mixed curriculum; $p = 0.0243$). The effect was more pronounced for students with ≥ 2 risk factors. The graduation rate was 7.7% under the old and 9.4% under the mixed curricula, but 26.4% under the new curriculum ($p < 0.05$ for both). Overall scores on the MFT decreased from 161.5 ± 10.3 under the old curriculum to 152.5 ± 11.1 and 151.0 ± 8.9 under the mixed and new curricula, respectively ($p < 0.05$ for both). Our findings suggest a trade-off between graduation rates and MFT scores that may result from fewer required upper-level classes preparing majors less for the MFT or from an increasing number of graduates taking the MFT.

P87 - Impacts of Land Cover and Development on Herpetofauna Occupancy

Isabelle Barnes

Furman University, Greenville, SC

Given the ongoing and projected increase in anthropogenic development in the United States, national and global biodiversity are under threat as natural habitats continue to decrease in both size and frequency. However, further data is needed to assess the differing correlations between urbanization consequences and species occupancy to establish conservation efforts and priorities. To address this gap, we conducted an audio-visual analysis of herpetofauna diversity along the Swamp Rabbit Trail in Greenville, South Carolina. We conducted audio recordings along 400m transects of the trail as well as visual assessments via walks and the use of online databases such as iNaturalist. We used anuran call frequency to establish varying levels of occupancy along the trail. Geographic Information Systems (GIS) was utilized to establish land cover and vegetation type as well as proximity to both a water source and development. Preliminary data analysis has focused on species identification of both audio and visual data as well as determination of organisms present at each point along the trail with the goal of establishing correlative relationships between herpetofauna occupancy and varying factors and potential consequences of urbanization. For example, the Cope's Gray Treefrog has been found to have high abundance at most assessed sites, giving insight into urbanization implications based on call frequency and organismal identification as a global species in the study site. Moving forward, this data could potentially be useful in the establishment of future conservation policies and efforts concerning urbanization, forest fragmentation, and biodiversity in natural, particularly forested, ecosystems.

P88 - Remote online open-book open-web versus face-to-face online closed-book closed-web examinations in university science classes

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In the university setting, the examination protocol has been predominantly closed-book. However, as a result of COVID and distance learning, traditional learning methods must be modified. A possible method in response is open-book examinations. Open-book examinations have drawbacks and benefits to a student's learning experience, specifically their study time and performance. We tested the hypothesis that students taking open-book, open-web exams spend less time studying anatomy and physiology compared to students taking closed-book, closed-web exams. Moreover, we tested the exam performance using different types of exam questions including those of knowledge, comprehension, application, analysis, and evaluation types according to Bloom's taxonomy. Students in anatomy and physiology classes were assigned either open-book, open-web or closed-book, closed-web groups at the beginning of the semester. Participants in this study kept a study journal in an Excel format entering the minutes that they spent daily in studying the subject throughout the entire semester. On the day of each examination (three major exams and the final exam), participants emailed the instructor their study journal. At the end of the semester, participants also filled out an online survey answering questions regarding their participation in the study. Study time and exam performance of each period were compared between open-book, open-web and closed-book, closed-web groups. Students' performance in answering different types of questions in exams were analyzed. This study is in-progress, and the results will be shared with the scientific community in the annual meeting of Association of Southeastern Biologists.

P89 - Lavender Essential Oil Reduces Aggression in Male Crown-tail *Betta splendens*

Ashleigh Woods, Holly Boettger-Tong

Wesleyan College, Macon, GA

Lavender essential oil (LEO) is distilled from the plant *Lavender angustifolia* and is commonly used for aromatherapy in humans. Reports claim it treats insomnia, anxiety, depression and more. However there are no scientific studies that support these claims. In recent years, it has been used on some fish species to test its efficacy as an anesthetic during medical procedures and during transport of fish to new locations. This study aimed to investigate the efficacy of LEO as a sedative and its effectiveness at reducing aggression in male crown-tail betta fish (*Betta splendens*). A preliminary study determined that 100µL of LEO was an effective sedative treatment. To determine the effect of this treatment on aggressive behaviors, a pre/post study design was conducted. First, the agonistic behaviors of male crown-tail betta fish were observed, untreated, in response to male veil tail betta fish challengers. Fish were recorded for 3 minutes, and the aggression was measured by the number of times frontal display and caudal swing were exhibited. Next, fish were treated with 100ul of LEO and recorded for 3 minutes, during which time they were exposed to male veil tail betta fish challengers to measure differences, if any, of these same agonistic behaviors in the context of the treatment. Statistical analysis revealed that LEO reduced aggression in male crown-tail betta fish. Further studies to characterize this response are ongoing. As the literature has few reports of LEO effects on *Betta splendens*, this study provides new data on the potential efficacy of an alternative substance which might be useful for anesthetic purposes in fish.

P90 - Biology Booster Shot: Getting our Second Dose to Foster Student Success

Randall Small, Caroline Wienhold

University of Tennessee, Knoxville, TN

We are implementing a 3-pronged approach to improve student success in introductory biology courses at the University of Tennessee. These are large foundational lecture courses for students in Biology, as well as other majors. Ten years ago we restructured the courses to follow Vision and Change (AAAS, 2011), and train faculty in evidence-based teaching. We are now ready to build upon those original efforts. We aim to improve student success by (1) enhancing tutoring and undergraduate TA

involvement; (2) re-aligning learning objectives and pedagogical approaches; and (3) creating a culture of continuous pedagogical reflection and innovation framed within positive psychology.

P91 - Characterization of the glucocorticoid and mineralocorticoid receptors in *Thamnophis sirtalis parietalis*

Rysa Thomas, M. Rockwell Parker

James Madison University, Harrisonburg, VA

Vertebrates experience diverse and unique life-history events, many of which are annual and energetically taxing. Energy is a limiting resource and its careful budgeting is crucial for successful transitions annually and across the lifetime of a species. Glucocorticoids (GCs) primarily promote energy mobilization in metabolic tissues (liver, fat, muscle) through activation of two main receptors, the glucocorticoid receptor (GR) and mineralocorticoid receptor (MR). Species with extreme life histories carefully balance expression of these two receptors to manage their energy allocation as they transition through energetically demanding events like migration. Red-sided garter snakes are an excellent model because they emerge after an eight-month dormancy and engage in a brief-but-explosive breeding event followed by a high-energy migration, all in a non-feeding state. Many vertebrates show suppressed courtship behavior when GCs are high, but this species has circumvented these limitations by uncoupling the hormonal and behavioral response to elevated GCs during mating. Sensitivity to external stressors is suppressed during mating but is restored upon migration to feeding. A physiological mechanism governing this change in sensitivity must exist. We tested the hypothesis that GR and MR work reciprocally to regulate energy budgets in red-sided garter snakes annually. We expect to see sex differences in expression of both receptors and elevated GR expression when circulating GCs are high. MR expression is predicted to be relatively low in spring, thus the two receptors should behave oppositely with MR expression increasing after spring. Results of this study may illuminate the relationship between ectothermic energy budgeting and the physiological stress response.

P92 - Scientific societies fostering inclusivity in the life sciences through engagement of undergraduate scientists

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Scientific societies serve as communities of practice in which scientists develop many of the skills and connections required for the progression of their careers. For example, scientific societies offer a range of opportunities to attend career development programs, gain experience in communicating science, and receive recognition for achievements within their discipline. Programming for undergraduate student members has recently been increasing, both in prevalence and in its range of offerings. The Alliance to Catalyze Change for Equity in STEM Success, ACCESS, a meta-organization seeking equity and inclusivity in life sciences fields, has examined programs and opportunities focused on undergraduates across its member scientific societies to identify common themes, promising practices, and challenges.

P93 - Barriers to Healthcare Access in the Time of COVID-19: Where are we at Dalton State College?

Jacob Hardin, Kimberly Hays

Dalton State College, Dalton, GA

In the United States, access to health insurance has improved for many since the passage of the Affordable Care Act; however, there are still many financial, structural, and perceived barriers in access to quality healthcare, especially among young adults (Luquis & Kensinger, 2017). In 2014, Owens conducted a survey of Dalton State College students to evaluate their health needs and these results served as the basis for the formation of the Ken White Student Health Center on the Dalton State College campus. The stress and economic challenges of the COVID-19 pandemic led us to an interest in exploring the current barriers to healthcare access among Dalton State College students. We accomplished this via an online survey modified from the original survey conducted by Owens (2014). The survey was distributed to 3730 students on February 1st, 2022 through March 1st, 2022 and completed by 284 (7.6%) students. Our results indicated that cost, schedule conflicts, previous negative healthcare experiences, and COVID-19 were the main barriers experienced by responding students.

P95 - Evaluating gene expression changes following exposure of different anti-malarial compounds

Anna Gray, Chris Barton

Belmont University, Nashville, TN

Colorectal cancer has relatively low survival rates. Current treatment options for this cancer still lack efficacy, so there is a demand for new and different drug therapies. There are multiple antimalarial drugs that show evidence of anti-cancer properties, and it has been shown that these molecules can reduce cell viability in colorectal cancer cells. However, the gene expression profiles of cells exposed to these molecules are largely unknown. Here, we analyzed gene expression profiles of multiple stress-related genes following exposure to two different antimalarial drugs, amodiaquine and tafenoquine. Our data suggest a set of altered genes that are common to both drug treatments, as well as some genes that are unique to only one. These data may provide useful as we continue to elucidate the mechanism by which these two drugs negatively

affect the growth of cancer cells.

P96 - A screen to identify force sensitive domains using a *Drosophila* cell-cell signaling platform

Jacob Harman, Paul Langridge

Augusta University, Augusta, GA

Notch receptors are found in all animal life and function in a wide range of intercellular signaling events. The receptor is made up of four parts: ligand/receptor binding extracellular domains, a Negative Regulatory Region (NRR), a transmembrane domain, and an intracellular transcription factor domain. Receptor activation is initiated by proteolytic cleavage of the NRR domain in response to force provided by the Epsin-mediated endocytosis of a ligand bound to the receptor. In this study, multiple chimeric Notch variants were produced in which the NRR was replaced with a potential force sensitive domain from another protein. A small scale screen was then performed using a *Drosophila* force sensing assay to identify domain cleavage in response to force. The screen yielded force sensitive domains from a wide range of sources, which has implications for the biology of the source proteins and a greater understanding of what makes a protein mechanosensitive, together the design of new versions of therapeutically valuable Syn-Notch receptors.

P97 - Tafenoquine reduces the efficacy of multiple chemotherapeutic compounds when used in multiagent therapy.

Hannah Moore, Chris Barton

Belmont University, Nashville, TN

Cancer is a highly adaptive disease that is diagnosed in about a third of people during their lifetime. Drug repositioning is an effective and efficient way to explore treatments for existing drugs. Amodiaquine, an anti-malarial, has been shown to inhibit the growth of cancer cells and the ability to synergize with cellular starvation in melanoma cells. Our lab has shown a second drug, tafenoquine, is effective at blocking the growth of cancer cells. Here, we present data analyzing the ability of tafenoquine to function synergistically with a number of commonly-used chemotherapeutic compounds. These data will guide our future studies as we continue to analyze the role of antimalarial drugs as a part of different cancer therapeutic regimens.

P98 - "East meets West:" Applications of Traditional Chinese Herbal Medicines as a Complementary Therapy in Triple-Negative Breast Cancer Treatments

Katherine Patterson

Florida Gulf Coast University, Fort Myers, FL

Traditional Chinese Medicine is a medical system that evolved from ancient Chinese traditions and philosophies that aim to diagnose, prevent, and treat diseases. Several studies indicate that herbals medicines can be applied to treat triple-negative breast cancer as either a primary cancer treatment or as an adjacent treatment. Through a literature review, this project identified the herbs *astragalus membranaceus*, which can promote the inhibition of proliferation through the EGFR/P13K/AKT cascade, and luteolin, which can reduce metastasis through the epithelial-mesenchymal transition pathway. These characteristics were selected because the key characteristics of triple-negative breast cancer are its highly invasive and very aggressive nature. This research also identified that these herbal medicines could bind to multiple cellular targets to decrease tumor progression and increase tumor sensitivity to chemotherapy. There are currently clinical trials ongoing to investigate the combination of Western and Eastern herbal medicines with implications for cancer therapy.

P99 - Anti-proliferative effects of tafenoquine on various cancer cell types

Rylee Rickett, Chris Barton

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Drug repurposing is the act of using current FDA-approved medications for the treatment of different pathological conditions. Previous research has shown that a number of repurposed drugs are effective at preventing the growth of cancer cells, and some of these molecules are currently being studied in clinical cancer trials. Our laboratory previously found that amodiaquine, a drug typically used for the treatment of malaria, is effective at stopping the growth of cancer cells in culture. Whether other anti-malarial compounds are effective at preventing cancer growth has yet to be determined. Here, we show that an additional anti-malarial drug, tafenoquine, is effective at blocking the growth of multiple cancer cell types. We also show that tafenoquine, like amodiaquine, activates the activity of caspase enzymes. These data suggest that, like amodiaquine, tafenoquine is also activating an apoptotic pathway in cancer cells.

P100 - Structural Similarities in *C. neoformans* Biofilm Accelerators

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Cryptococcus neoformans is a yeast-like species capable of causing life-threatening infections such as cryptococcal meningitis and pneumonia-like illness. Biofilm formation of *C. neoformans* is notoriously known for causing a plethora of issues, from reoccurring infections on medically implanted devices to resistance to antifungal treatments and host defenses. We found molecules similar to quorum sensing signaling molecules that increase biofilm formation in *C. neoformans*. We hypothesized that compounds whose structures are similar to substrates used in bacterial biofilm synthesis pathways could accelerate biofilm production in *C. neoformans*. We tested over 300 novel lead compounds for their ability to accelerate biofilm growth using a crystal violet assay to quantify biofilm production. We found three tyrosine-based accelerators that consistently and significantly accelerated biofilm production in *C. neoformans*. These compounds contain an aromatic ring connected to an electron-donating hydroxyl group, a marker that can search for future accelerators. Investigating the tyrosine-based accelerators can better understand *C. neoformans* biofilm formation, which can then help target specific virulence factors instead of the pathogen itself. Initial growth rate determinations and fungicidal activity indicate biofilm acceleration is not a result of accelerated growth. Future studies will include optimizing the search for accelerators by finding structural comparisons in known accelerators and using these observations to construct a potential substrate involved in the biofilm synthesis pathway of *C. neoformans*.

P101 - Examining the Effects of Anti-Malarial Compounds Against Multiple Cancer Cell Types Grown in Culture

Amanda Long, Lydia Heron-Goar, Libby Godo, Chris Barton

Belmont University, Nashville, TN

Drug repurposing is the process of identifying new uses for existing pharmaceutical compounds. Previous studies have shown that certain antimalarial drugs are effective at stopping the growth of some cancer cell lines. In this study, we tested the effect of three antimalarial drugs on various cancer cell lines. These drugs were effective at decreasing cell viability, but only at high concentrations. These data suggest that these molecules maintain the ability to block the growth of cancer cells in culture, however, the high concentration suggests that these molecules may not be clinically relevant options as cancer therapeutics. Next steps include determining whether or not the antimalarials can be used as an alternative to current chemotherapies, and how the drug is effective against cancer by way of mechanism of action

P102 - Design of sgRNA for CRISPR-Cas9 mediated ablation of the *Danio rerio* Flt-1 receptor.

Maraline Argueta, Holly Boettger-Tong

Wesleyan College, Macon, GA

The formation of new blood vessels from simple vascular structures is a critical part of development. Vascular endothelial growth factor (VEGF) is a key regulator of angiogenesis during embryonic growth; its function is mediated by high affinity binding to two receptor tyrosine kinases, Flt-1 and Flk-1. Disruption of VEGF signaling, whether by genetic or by pharmacological manipulation, has been shown to be deleterious to normal angiogenesis in teleost fish; previous DNA microarray studies from our lab determined that treatment of teleost fish embryos with all-trans retinoic acid, a potent derivative of Vitamin A, resulted in altered expression of both VEGF and Flt-1 mRNA. Retinoids have been reported to be important in regulating endothelial cell differentiation in many vertebrates, but the exact mechanism of these effects and any direct relationships with Flt-1 mediated VEGF signaling have yet to be determined. To better understand this process in *Danio rerio*, CRISPR-Cas9 mediated ablation of Flt-1 will be attempted. Candidate sgRNAs will be identified using CRISPRscan and selected sgRNA DNA templates synthesized via PCR. These candidates will be used for subsequent in vitro transcription reactions, to prepare for induced mutagenesis with Cas9mRNA via zebrafish embryo microinjection.

P103 - Investigating a potential link between hormone therapy and cervical cancer in trans men

Katlin Schultz, Centdrika Hurt

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The trans community consists of a group of individuals whose gender identity or expression differs than that assigned to them at birth. To treat this incongruence, some members of this community choose to seek medical gender affirmation, which may include psychotherapy, hormone treatment therapy, and/or surgical change. Several studies show that trans individuals may be at a higher risk for malignancies due to barriers that prevent them from receiving adequate health care, including gynecology and oncology. While efforts have been made to address risks associated with sexually transmitted infections, use of alcohol and drugs, and limited access to proper screening, a lack of data and research concerning cancer and the effects of long-term hormone therapy in the trans population remains. The goal of this project is to investigate the potential carcinogenic effects of testosterone hormone treatment therapy and how it may be linked to cervical cancer in transmen. To test this, the cytotoxic effects of testosterone on HT-3 and HeLa cervical cancer cells and cell proliferation were analyzed using trypan blue exclusion and CyQuant cell proliferation assays. The presence and differential expression of genes in the cervical cancer cell lines in response to treatment will be determined

via qPCR and signaling pathways affected will be analyzed via western blot. By understanding the effects of testosterone in cervical cancer, we hope to identify and target multiple tumorigenic pathways that may be dysregulated in response to testosterone therapy in the trans population.

P104 - A Systems Biology Approach to Validate Potential Biomarkers for Early Detection and Personalized Therapy for BRCA1-Associated TNBC

Shai Waldrip

Morehouse School of Medicine, Atlanta, GA

Background & significance: Triple-negative breast cancer (TNBC) is the most aggressive subtype of breast cancer that has a high mortality rate in young African-American women (AA). Due to the lack of hormone receptors in TNBC, there are currently no mechanism-based targeted therapies or biomarkers for early detection. It is known that BRCA1 mutation carriers are at a high risk for developing TNBC. Our lab has previously shown BRCA1/1a/1b isoforms to function as tumor suppressors in TNBC. They have found wildtype BRCA1, not the pathogenic mutant BRCA1 proteins found in TNBC, to bind a sole SUMO conjugating enzyme Ubc9, which has been shown to promote proliferation, migration, and metastasis of multiple malignancies, including TNBC. They have also found Ubc9 to be overexpressed in patient-derived BRCA1 mutant TNBC cells and tumor samples. Knockdown of Ubc9 was shown to have decreased migration and anchorage-independent growth of TNBC cells.

Hypothesis: This work is based on the hypothesis that high Ubc9 protein expression seen in patient-derived BRCA1 mutant TNBC cell line HCC1937 should correlate with high UBE2I RNA levels via mRNA sequencing analysis. If true, it will result in the identification of a molecular mechanism-based biomarker and targeted therapy for TNBC.

Results: Our analysis could not detect a significant fold change in UBE2I RNA expression. It could be possible that it has a high turnover rate, which could explain why the fold change was not significant. Using Ingenuity Pathway Analysis, we performed a systems biology pathway analysis and found variations in associated network maps active in both stable cell lines, leading to the discovery of potential downstream targets that could be used for early detection and a mechanism-based targeted therapy for TNBC.

P105 - The Role of Exosomes in Ewing's Sarcoma Cancer Cell Proliferation and Migration

Kaylee Rawlins, Lori Hensley

Jacksonville State University, Jacksonville, AL

Since their discovery in the 1980s, exosomes have been a topic of interest for their potential roles in a variety of biological and pathological conditions. Exosomes have been detected in the microenvironment of cancerous tumors. While much is still not known about their functioning and mechanism of action, it is thought they promote tumorigenesis through several routes such as the regulation of metastasis. Another area of interest with cancer research are cannabinoids which also seem to influence the proliferation of cancer cells. As with exosomes, little is known about the mechanism of action of cannabinoids although it has been proposed that the endocannabinoid system is involved. This study focused on the effects of cancer-secreted exosomes from cannabinoid treated cells in comparison to cancer-secreted exosomes from untreated cancer cells on the proliferation and migration of *in vitro* Ewing's sarcoma cancer cells. The exosomes were used in a series of MTT and scratch wound assays to assess proliferation and migration. The implications of a difference in the cancer cell proliferation and migration as a result of the treatment groups could be indicative of a new direction for future treatment options.

P106 - Evaluation of cytotoxic and apoptotic effects of several regional plant based extracts on human melanoma cancer cell lines.

Nicholas Spader, Luke Guy

Abraham Baldwin Agricultural College, Tifton, GA

The South has always been a place where home remedies and scientific based medicine go hand in hand. Throughout time, natives and other groups have used homemade salves and ointments for what could have potentially been melanoma or other forms of skin cancers. Through literature study, certain plants of interest have been identified. These plants are to be placed under analysis via HNMR, GCMS and IR/UV/Vis spectroscopy techniques to determine existing, or potential novel compounds of interest. Plants were either grown in the greenhouse or collected from local areas. The plants were subjected to different extraction techniques for analysis within the aforementioned spectroscopies. The extracts will then be used in melanoma cancer cell lines, as well as on cultures of various bacteria, and their cytotoxic and antimicrobial viability will be determined through bioassays. The in-vitro bioassays include cell proliferation, cell toxicity, MTT cell growth and migration/invasion assays.

P107 - The Effects Cannabidiol on Ewing's Sarcoma in the Context of Spheroids

Savannah Blackwell, Lori Hensley

Jacksonville State University, Jacksonville, AL

Spheroids enrich *in vitro* cancer cell culture research by providing three-dimensional models that can mimic tumor tissue structure. Spheroids are composed of numerous differing cell lines, and this conglomeration of varying cell types can be used to model cell-cell and cell-matrix interactions. These 3-D models create a similar physiological environment to *in vivo* systems more so than traditional monolayer 2-D cell cultures. This research aimed to examine the effects of cannabinoids on Ewing's sarcoma in the context of spheroids. The spheroids in this project were co-cultures of three different cell lines: Ewing's Sarcoma (A673), human lung fibroblast tissue (WI-38), and a human/mouse hybridoma line (WBC264-9C) to contribute an immune component. The spheroids were cultured in ultra-low binding, round bottom well plates. After treating the spheroids with varying concentrations of cannabidiol, viability was measured with MTS assays. Future directions for this project include investigating differential protein expression within the spheroid tumor system using western blot and ELISA.

P108 - Characterization of Microglia Specific Markers for Identification and Isolation of Pure CNS Microglia

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Microglia, the tissue-resident macrophage of the central nervous system (CNS), play a paramount role in brain health and disease status. As microglia are crucial in multiple aspects of biology, such as in normal brain development/function, immune response, and cancer. We have developed flow cytometry analysis using microglial specific antibodies and fluorescent staining for microglia identification. We describe flow cytometry methods using novel cell surface markers including CX3CR1, Siglec-H and F4/80 to specifically label microglia while avoiding other bone marrow and/or non-CNS derived macrophages and monocytes. We first stained our isolated cells with commonly used markers to identify microglia, CD11b+/CD45-/lo. In our isolated microglial population, we had a very low rate of CD45 positive staining, which was to be expected, as CD45 highly labels blood leukocytes and not CNS leukocytes. Recent studies have highlighted a growing number of issues with using just these markers alone, including lack of microglial specificity. Therefore, we further examined our isolated cells for CX3CR1 expression and found 83% positivity. To confirm high CX3CR1 staining, we performed another microglial cell isolation and stained the cells with just these two markers. This second round of flow cytometry data showed an even higher level of Positivity CX3CR1(92%) and CD11b(57%). Due to variability in the CD11b flow results, we examined cell surface markers more recently identified as microglial specific markers CX3CR1, Siglec-H, and F4/80. Analysis of our isolated microglial population shows these cells are again, highly positive for CX3CR1 (92%). Even more striking is the positivity rate for the marker Siglec-H(98%) and for F4/80(77%). Being able to isolate a largely pure population of microglia could allow for a more comprehensive understanding of their functional dynamics and role in disease mechanisms, advancement of potential biomarkers, and development of novel therapeutic targets to improve prognosis and quality of life in multiple diseases.

P109 - Modification of Tumor Microenvironment by Lung Carcinoma Exosomes

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Cancer uses intercellular communication to induce tumor growth and metastasis. Fibroblasts can become specifically transformed and associated with cancer to aid in the process. Extracellular vesicles, specifically exosomes, contain proteins, RNA, and DNA that are taken up by local cells to affect cellular behavior. Exosomes were isolated from lung carcinoma using total exosome isolation reagent and quantified. These exosomes were used to treat lung fibroblasts and enrich lung carcinoma cells, and the effects of exosomes on cancerous properties, cell viability and cell migration, were studied. An increase of cell viability was found with exosome treatment for both cell lines while migration only increased for enriched lung carcinoma cells. Additionally, mass spectrometry-based proteomics of exosomes isolated from hepatocellular carcinoma was analyzed. Through a survey of differentially expressed proteins between high and low grade hepatocellular carcinomas against normal liver cells, several pathways of interest were identified. Some common motifs in underexpressed genes were the regulations of cell signaling, cell metabolism, and cell death.

P110 - Endothelial tube maintenance in a cell culture model for Myotonic Dystrophy type 1

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Myotonic dystrophy type 1 (DM1) is a multi-systemic disorder that results in severe muscle weakening and wasting. DM1 is caused by expansion of CTG repeats in the 3' untranslated region of the DMPK gene. Muscles require vasculature to supply nutrients and oxygen for muscle maintenance. A previous study involving muscle wasting in a mouse model for DM1, implicated angiogenic genes as contributors to skeletal

muscle wasting. The ultimate goal of this project is to test whether muscle-secreted cytokines (myokines) are involved in communications between skeletal muscles and vasculature to maintain stability of both tissue types. As a baseline analysis, we are testing whether exogenous expression of expanded-CUG repeats in human umbilical vein endothelial cells (HUVECs) will disrupt the maintenance of endothelial tubes. HUVECs were differentiated, followed by transient transfection with plasmid containing DMPK exons 11-15 with 960 CUG repeats (CUG960) or without CUG repeats (CUG0). Transfected and mock-transfected cells were imaged every 3 to 6 hours over 24 hours. Preliminary results indicate that the differentiated CUG960 cells showed degradation of the endothelial tube network, compared with the CUG0 and mock-transfected controls in both tube-length and tube-width. The quantification of endothelial tube width and length using ImageJ software will establish a baseline response of the endothelial tubes to CUG repeat expression. This baseline data will allow us to assess whether expression of expanded CUG repeats affects endothelial tube maintenance, and in additional studies, development of the vasculature. The baseline response will also allow us to compared whether conditioned media from human DM1 myoblast cultures affect endothelial tube maintenance and/or development and provide a comparison for treatments intended to rescue the endothelial tube phenotype.

P111 - Variant of Unknown Significance V71L in Autoimmune Role of CTLA4

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The CDC reported a significant risk of newly diagnosed DM1 in the 30-day period post- SARS-CoV-2 infection. CTLA4, located at 2q33.2, codes for cytotoxic T-lymphocyte protein associated protein 4--an important protein in the immune response to viral illness. This protein functions as a brake to slow down and control the action of the immune system by suppressing excessive T-cell proliferation. Mutations of the CTLA4 gene have been implicated in type 1 diabetes, autoimmune thyroiditis, lupus, celiac, and other autoimmune illnesses. My CTLA4 variant, V71L, is a missense mutation which resulted in amino acid switch from valine to leucine at position 71. YASARA protein mapping was used to visualize and analyze the features of this variation. PolyPhen2, SIFT, CADD, Align, and other analyses, were completed to assess variation pathogenicity. V71L, which previously had an uncertainty as to how it would phenotypically express, was found to be likely pathogenic and probably damaging. These bioinformatic results will be presented along with protein modeling, multiple sequence alignment, and other analysis. https://www.cdc.gov/mmwr/volumes/71/wr/mm7102e2.htm CTLA4 cytotoxic T-lymphocyte associated protein 4 [Homo sapiens (human)] - Gene - NCBI (nih.gov)

P112 - The Effects of Cannabidiol on Ewing's Sarcoma in the Context of Spheroids

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Spheroids enrich *in vitro* cancer cell culture research by providing three-dimensional models that can mimic tumor tissue structure. Spheroids are composed of numerous differing cell lines, and this conglomeration of varying cell types can be used to model cell-cell and cell-matrix interactions. These 3-D models create a similar physiological environment to *in vivo* systems more so than traditional monolayer 2-D cell cultures. This research aimed to examine the effects of cannabinoids on Ewing's Sarcoma in the context of spheroids. The spheroids in this project were co-cultures of three different cell lines: Ewing's sarcoma (A673), human lung fibroblast tissue (WI-38), and a human/mouse hybridoma line (WBC264-9C) to contribute an immune component. The spheroids were cultured in ultra-low binding, round bottom well plates. After treating the spheroids with varying concentrations of cannabidiol, viability was measured with MTS assays. Future directions for this project include investigating differential protein expression within the spheroid tumor system using western blot and ELISA.

P113 - Engineered device in *E. coli* lyses *S. aureus* at physiological fever temperatures

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Multiple strains of a virulent pathogen called Staphylococcus are resistant to antibiotics, including the well-known methicillin resistant Staphylococcus aureus (MRSA). In order to explore a method to treat S. aureus contamination in a clinical setting, we created a device that lyses S. aureus. Three biobrick parts were obtained from the International Genetically Engineered Machine foundation (iGEM). The device consists of a temperature sensitive promoter that is activated in physiological fever temperatures above 37°C. The activation of this device led to the transcription of a gene producing a lysostaphin enzyme that lyses Staphylococcus aureus and a blue chromoprotein gene that visually indicates device activation. The three parts were ligated together using standard 3A assembly, and were transformed into E. coli. The functioning device was then put through several tests to find optimal conditions, which concluded that the lysostaphin activity was increased when the device temperature and concentration were also increased. Additionally, we found that the type of E. coli chassis affects lysing activity.

P114 - Synthesis of Novel Chalcones with N-sulfonamide Moieties and their Antimicrobial Properties.

Chalcones have been of great interest lately, not only due to their synthetic perspective, but due their biological and potential pharmacological activity. Chalcones have been utilized for thousands of years through the use of plants and herbs to treat medical disorders, such as antihypertensive, anti-retroviral, anti-inflammatory, anti-fungal, anti-oxidant, and anti-bacterial properties. Drug resistance and the increase of infectious diseases is one a major concern today. There is an increase in the demand for the discovery of new drugs with potent anti-microbial activity, particularly against resistance strains. Recently, there have been reports that chalcones have anti-microbial properties. Reports have shown that derivatives of chalcones, in particular, ring fused chalcones, have been shown to have antimicrobial activity. In particular, 3-(carboxylalkyl) rhodanine showed high antimicrobial properties against both *Staphylacocus aureus* and methicillin resistant *S. Aureus*. Chalcones were determined to be enhancers of antimicrobial agents in the treatment of oral microbial infections. Today sulfonamide derivatives have been shown to have anti-HIV, anticancer, antimicrobial, and hypogylcemic biological activity. Currently, thousands of derivatives have been synthesized and have shown varying pharmacological properties. The biological activity is due to the main structure where $R^{'}$ maybe hydrogen, alkyl, aryl, or hetero aryl, etc. It is the lipophilicity of the amino group that demonstrates the largest effect in protein binding. Numerous reports have shown the antimicrobial properties activity of chalcones and sulfonamides. Sulfonamides, in particular, N-sulfonamide derivatives have been reported to demonstrate antibacterial properties; however, there is little data on derivatives of chalcones with N-sulfonamide moieties to test their anti-microbial properties. The major aim of this project is to synthesize chalcones with N-substituted sulfonamide moieties to test broad-spectrum antimicrobial efficacy.

P115 - Antimicrobial characterization of *Odontotaenius disjunctus* frass using the Kirby Bauer assay

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As the numbers of resistant bacteria increase, alternative sources of antibiotics are being explored, some derived from organisms whose environmental challenges required the evolution of antimicrobial protections. One such organism, *Odontotaenius disjunctus,* has evolved a unique way of combating microbial challenges through its production of frass (fecal material). Previous studies have indicated that frass exhibits antimicrobial activity, likely derived from the association of this passalid beetle with actinomycetes (Pessotti et al., 2021). However, the spectrum of antimicrobial activity of *O disjunctus* frass has yet to be examined. This study is designed to test the antimicrobial properties of *O disjunctus* frass using the Kirby Bauer assay. Determination of the relative potency of *O disjunctus* frass in inhibiting microbial growth is an important first step in determining its potential utility for further study as a novel antibiotic source. Furthering our understanding of new sources of antimicrobials is vital to developing new types of treatments which can combat the rise of resistant strains of bacteria.

P117 - The effects of polyunsaturated fatty acids in the presence of piscidins on *Vibrio cholerae*

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Piscidins are fish antimicrobial peptides important for first line defense against microbes. These innate immune effectors adopt metalated and nonmetalated forms, although it is unknown how and when each isoform is produced. Piscidin 1 (P1) exhibits membrane disruptive properties, while piscidin 3 (P3) targets DNA, and metalation with copper (Cu2+) improves their antimicrobial activity in vitro. Vibrio cholerae is a gram-negative marine bacterium responsible for cholera, the acute gastrointestinal infection that threatens millions each year, especially in developing countries without access to clean water. Vibrio cholerae is known to utilizes exogenous polyunsaturated fatty acids (PUFAs) to remodel its membrane phospholipids. To examine the impact of PUFAs on piscidin-mediated membrane permeability and antimicrobial susceptibility, we performed dye uptake and minimum inhibitory concentration (MIC) assays with arachidonic (20:4) and docosahexaenoic (22:6) acids. In general, addition of each piscidin counteracts the PUFA-mediated lowering of membrane permeability when measured with the hydrophobic dye crystal violet. Thus, the piscidins are creating bacterial vulnerability despite the membrane-strengthening effects of PUFA incorporation into phospholipids. Concomitantly, the PUFA-induced changes to piscidin MIC mostly correlated with the effects on permeability. Collectively, the data highlights antimicrobial susceptibility differences based on piscidin isoform, while also demonstrating the significant effects of piscidins on membrane permeability.

P118 - Polyunsaturated fatty acids affect membrane permeability and antimicrobial activity of polymyxin B and colistin on *Vibrio cholerae*

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In recent years, public health officials have faced a great challenge with regard to antibiotic resistance. *Vibrio cholerae*, a gram-negative bacterium that normally resides in aquatic environments, is capable of adjusting its membrane phospholipid composition through the uptake and assimilation of exogenous polyunsaturated fatty acids (PUFAs). The purpose of this study was to measure PUFA-mediated changes in the membrane permeability and antibiotic resistance of *Vibrio cholerae*. Three physiologically relevant PUFAs were used: linoleic acid [18:2], arachidonic acid [20:4], and docosahexaenoic acid [22:6]). Bacterial membrane permeability was measured using a crystal violet assay with each PUFA resulting in at least a 10% change in uptake of the dye. When the cationic cyclic peptides polymyxin B (PMB) and colistin were administered at subinhibitory concentrations, PUFA-specific permeability trends were observed. The availability of PUFAs caused significant changes to the minimum inhibitory concentrations (MICs) of PMB and colistin. Strikingly, each peptide was found to decrease the MIC by at least 4-fold. Not only do PUFAs alter bacterial permeability, but they also induce vulnerability to PMB and colistin in *V. cholerae*, perhaps suggesting synergistic potential in control and prevention of pathogens.

P119 - Antibiotic resistance in Salmonella isolated from poultry environments

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Salmonella enterica is a bacterial foodborne pathogen that causes an estimated 1.3 million cases of illness each year throughout the United States and outbreaks are often linked to poultry. Salmonella is composed of over 2,600 serovars, some of which are more commonly associated with human illness. Serovars are defined by their cell-surface O and H antigens, and serovars with the same serogroup share the same O antigen. Environmental bootsock samples were collected from various commercial poultry broiler houses in the Southeast. Four complexes were visited; each complex had five farms, and four houses were sampled with duplicate bootsocks within each farm, totaling 80 houses and 160 samples in this study. We hypothesized that different serovars would exhibit different patterns of antimicrobial resistance. Therefore, the goal of this study was to investigate Salmonella prevalence and to determine the serogroup of isolates recovered and assess patterns of antimicrobial resistance. Salmonella isolates were serogrouped using commercial O antigen serum and then tested against 11 antibiotics using the Kirby-Bauer disk diffusion assay. Antibiotics chosen for this study represent a variety of different classes, reflecting agricultural and industry practices. The overall prevalence of Salmonella across 80 houses was 76%. A total of 122 isolates were serogrouped, and we identified four different serogroups of 12 different serovars. Serogroup C2 was the most common. Based on the Kirby-Bauer assay, the samples were most frequently resistant to tetracyclines and aminoglycosides. In addition, 6% of isolates exhibited multi drug resistance, being resistant to three or more classes of antibiotics. Understanding antibiotic resistance in Salmonella is key to being able to develop effective Salmonella controls in poultry production and to also inform public health practices.

P120 - *In vitro* Antimicrobial Effectiveness of Essential Oils on *Streptococcus mutans*

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Streptococcus mutans is known as the primary agent in the formation of dental caries. Insoluble glucans synthesized by *S. mutans* promote surface adherence and aggregation of bacteria on tooth surfaces. The accumulation of *S. mutans* along tooth surfaces generates a biofilm that must be destroyed in order to prevent the formation of dental caries. Ingredients such as chlorhexidine, cetylpyridinium chloride, and fluoride are common chemicals used in commercial mouthwashes to limit biofilm formation of *Streptococcus mutans* and hence, dental caries. However, prolonged use of these commercial agents may lead to darkening of tooth enamel and, in some cases, faster buildup of tooth calculus. Recent research has demonstrated that essential oils not only display antimicrobial properties, but are also beneficial and safe when applied topically to epithelial surfaces. Essential oils have been shown to disrupt bacterial membranes and enzyme activity in various bacteria, but their effectiveness in inhibiting bacteria responsible for the formation of dental caries has not been extensively studied. The goal of this study was to evaluate the antimicrobial effects of essential oils, specifically from *Thymus vulgaris*, *Eucalyptus globulus*, *Melaleuca alternifolia*, *Mentha spicata*, and *Gauithena procmbens,* on growth of *S. mutants* using the *in vitro* disc diffusion method.

P121 - Green Streamers in Hot Spring Effluents at the Boundaries of Photosynthesis

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In the course of decades of studying cyanobacterial mat communities of alkaline siliceous hot springs in Yellowstone National Park scientists have noted the presence of green-colored streamers above the otherwise flat mats formed by Cyanobacteria. These occur in the effluent channels just after the source-pool water begins to flow down effluent channels, where temperatures are on the order of 65-73°C, the upper limit of photosynthesis. Although other three-dimensional structures are formed in cooler downstream effluents by filamentous Cyanobacteria (*Leptolyngbya*), these organisms are not found at temperatures where green streamers occur. Source pools might provide energy sources for chemosynthetic streamer forming organisms where source pool temperatures are below or slightly above the upper temperature limit of *Synechococcus* Cyanobacteria mats. Hence, there may be ecological niches for both chemosynthetic streamer organisms and *Synechococcus*, and the green streamers result from the colonization of the former by the latter organisms. Here were analyze the microbial diversity along effluents of multiple hot springs in Yellowstone National Park that contain green streamers, including the green streamers themselves. *Synechococcus* that colonize the streamers are evolutionarily divergent from *Synechococcus* in the nearby microbial mat. Additionally, the streamers contained unexpected microbial diversity, including multiple unknown lineages in high abundance. This research is the first molecular analysis of microbial communities within the green streamers in hot spring effluents at the boundaries of photosynthesis.

P122 - Testing Various Collection Methods for Freshwater Microbial Environmental Metabarcoding

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The purpose of this study was to determine if various sampling methods would differ in their ability to collect freshwater microbes from karst springs for environmental DNA metabarcoding. We used a number of different methods to determine the diversity of microbes in a karst spring in Scott County, VA (Mill Creek Springs). 1 - Water was scooped and filtered, 2 - sediment was collected, 3 - pebbles were collected for biofilm analysis, 4 - glass slides were immersed in a periphytometer, and 5 - glass beads were immersed within tea strainers, sink strainers of various sizes, and polyester bags. Glass slides and beads were left in the spring for 1 week and then collected. Filtered water, sediment, and pebbles were collected when the slides and beads were removed. DNA was extracted using Qiagen's Power Water kit, the 16S and 18S rDNA amplicons were produced using "universal" primers ,and they were sequenced using Illumina MiSeq technology. Amplicons were paired, denoised, and analyzed using QIIME2. All methods retrieved microbes from the spring water for both prokaryotic (16S) and eukaryotic (18S) microbes. The glass beads enclosed in polyester bags provided the greatest alpha-diversity, closely followed by filtered water. Despite the noticeable difference, there was no significant alpha-diversity difference from any other method (Kruskal-Wallis).

. Beta-diversity analyses suggested the glass beads in polyester bags collected a similar array of microbes as filtered water but these were not significantly different (PERMANOVA) from other collection methods. This study suggests that planktonic microbes can be collected from freshwater using glass beads enclosed in polyester bags at a rate and diversity similar to retrieving and filtering liters of water. This study requires more replicates but the glass bead submersion shows promise and is much less labor intensive than the more common method of filtering liters of water.

P123 - Evolution of a Microbial Fossil

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Deep subsurface microorganisms are now estimated to constitute ~10% of our planet's total biomass and are found to contain a large fraction of uncharacterized biological diversity. Many of these microorganisms have access to extremely limited energy sources, resulting in estimated generation times that exceed decades. "Candidatus Desulforudis audaxviator" (CDA) is an uncultured lineage of the bacterial phylum Firmicutes that was originally discovered in deep rock fracture fluids in South Africa. Recently, it was shown that 136 partial CDA single amplified genomes from the three continents, a complete genome from of an isolate from Eurasia, and metagenome-assembled genomes from Africa and Eurasia shared >99.2% average nucleotide identity, low frequency of single nucleotide polymorphisms, and near-perfectly conserved prophages and CRISPR regions. It was concluded that the analyzed CDA populations underwent only minimal evolution since their physical separation, potentially as far back as the breakup of Pangea between 165 and 55 Ma ago. CDA presents a stark contrast to the current model organisms in microbial evolutionary studies, which are found to develop adaptive traits over ~109-fold shorter periods of time. In this study we identified 14 additional single amplified genomes from California and South Africa that contained near-identical 16S rRNA and between 90-95% average nucleotide identify compared to the parent population. The additional CDA formed distinct, closely related evolutionary clusters. The genomes contained unique, site-specific proteins that were related to the geochemistry of the specific sites and contained signatures of positive selection. Here we show the evolution of distinct subsurface CDA species populations that likely diverged at some point in the past 55 Ma from the largely conserved parental population that showed only minimal evolution.

P124 - The long-term effects of stream restoration on aquatic macroinvertebrates in a second-order stream in West Tennessee.

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Stream channelization is the process of removing natural meanders of a stream to improve navigation and to increase drainage. The process of stream straightening is known to cause head-cutting, valley plug formation, and a reduction in the variability of microhabitat types available to aquatic organisms. In West Tennessee, most rivers and streams have been extensively channelized. Because of the known adverse effects of channelization, stream restructuring projects have been implemented by the West Tennessee River Basin Authority (WTRBA) to restore the natural sinuosity to sections of heavily straightened streams of West Tennessee. The stream restructuring projects have been successful in lessening problems associated with excessive sediment load and transport at project sites. However, little is known regarding the effects of stream restructuring on aquatic macroinvertebrates in these systems. In 2015, shortly after restoration was completed at one of the sites (Town Creek in Henry Co., TN), aquatic macroinvertebrates were collected to examine the initial response of these organisms to stream restoration. The current project was intended to examine longer-term effects of stream restoration on aquatic macroinvertebrates by sampling the Town Creek site after six years of habitat recovery. In September of 2021, we sampled aquatic macroinvertebrates along three transects within the restored section, and along three transects in an upstream, channelized section. As in the 2015 study, we used kick-net sampling to collect aquatic macroinvertebrates from restored and channelized reaches. Upon collection, all specimens were preserved in 70 % ethyl alcohol and returned to the laboratory at UTM for identification and enumeration. Specimens were identified to the lowest taxonomic category possible (genus for most). We determined overall density of organisms, taxa richness, taxa diversity, and community structure of aquatic macroinvertebrates and compared our results to information reported from the 2015 study.

P125 - A Cross-Comparative Evaluation of Structural Properties Associated With Novel Compounds and the Corresponding Ability to Decrease Biofilm Quantity in Gram-Positive Bacteria

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A database of 280+ compounds tested for biofilm inhibition in several bacterial species were analyzed with MySQL Workbench to query amongst multiple criteria. Compounds were synthesized by amide coupling reactions between amino acids and simple carboxylic acids, and assayed by several iterations of Crystal Violet Assays to quantify effects on biofilm production. Tukey-Kramer HSD pairwise comparisons and Means/ANOVA statistical tests are employed to test for statistical significance. To evaluate which, if any, structural attributes may generate statistically significant reductions in biofilm, full profiles were created for each compound. These outlines consist of different factors relating to the compounds' biochemical configuration, ranging from the polarity of the amino acid to the number of substituents present on the aromatic ring, totaling 16 unique parameters. Respective determinations were made based on the compounds' activity level as well as the statistical significance at the 0.05 level. After thorough evaluation amongst *Bacillus subtilis, Staphylococcus aureus,* and *Streptococcus mutans* species, it was recognized that more than half of the statistically significant inhibitors possessed a carboxylic acid greater than 200 grams per molecule; a halogen; an aromatic ring; greater than two substituents on the aromatic ring (and at least one in the meta position); did not contain hydroxyl nor nitro groups; and had the aromatic ring in the gamma position relative to a carbonyl group of the carboxylic acid. Several features were additionally noticed upon the evaluation of individual bacterial species, as well as when compared against compounds that accelerated biofilm production. Overall, it is anticipated that this analysis will guide designs in the future, as well as the enhance the understanding of different bacterial species' responses.

P126 - Molecular identification of rock-boring sea urchins (Echinometra: Echinoidea) located at the edge of the Caribbean Sea

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The rock-boring sea urchin *Echinometra lucunter* is found in much of the Caribbean Sea and is widely distributed in the Atlantic Ocean. These echinoderms can be found throughout the intertidal zone along the northeastern coast of Trinidad, where both red and black color morphs are common. Sequencing of the mitochondrial cytochrome *c* oxidase subunit 1 (*COI*) gene in sea urchins collected from three sites in northeastern Trinidad confirms the identity of both color morphs as *Echinometra lucunter*, with red and black individuals sharing common haplotypes. An apparent restriction to gene flow between Caribbean and Atlantic populations of *E. lucunter* has been reported, as single-nucleotide polymorphisms (SNPs) found near the 3′ end of the *COI* gene are unique to each population. Comparison of these previously reported *COI* sequences with those of *E. lucunter* collected in Trinidad, at the southernmost part of the Caribbean Sea, reveals SNPs that are either unique or else shared only with those from other Caribbean locations. Furthermore, the haplotypes of sea urchins collected at Big Pine Key, Florida, just north of the Caribbean Sea, also match the Caribbean-specific sequences. Together, these observations support the earlier conclusion of restricted gene flow, and extend the range of the Caribbean population of *E. lucunter* that has been characterized by sequencing a mitochondrial gene. The sea urchins at the southernmost edge of the population are part of a fringing coral reef community along the north coast of Trinidad. Our molecular characterization of these organisms is part of an ongoing study of the biodiversity of this unprotected and environmentally threatened habitat.

P127 - The Louisiana Freshwater Sponge Project: Examining Changes in Species Diversity through a Comparison of two Ecological Studies

Kenzie Cooke, Abhi Mehrotra, Mary Miller

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Began in 2018, the Louisiana Freshwater Sponge Project (LFSP) is a longitudinal study focused on describing the diversity of freshwater sponge species in Louisiana water systems. While very understudied, freshwater sponges have been reported to be environmental health indicators. Tracking any change in species diversity over time may provide a picture of the health of an ecosystem and the impact of those environmental factors on freshwater sponges. The LFSP ecological survey is designed to compare the current freshwater sponge diversity with the documented 1969 freshwater sponge diversity. Thus far, LFSP has resurveyed over 50 of the original sites included in the previous survey. In a select few areas, we have observed an increase in diversity, but overall, we have recorded a decline. The most prevalent species are *Trochospongilla horrida* and *Eunapius fragilis* which is consistent with the previous study. In addition to comparing previous water systems, we have expanded the study to include 90 new sites and have identified over 500 samples.

P128 - Influence of Nutrient Contamination on Macroinvertebrate Communities in two Tidal Freshwater Creeks

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Freshwater ecosystems are some of the most biodiverse on the planet, but they are threatened due to human actions resulting in habitat loss, pollution, and nutrient runoff. Macroinvertebrates can be used to measure the health of a freshwater system because different taxa have different tolerances to pollutants. However, the relationship between nutrient runoff and macroinvertebrates remains understudied. Accokeek Creek and Aquia Creek are two tidal freshwater streams in Stafford, VA. Accokeek Creeks drains a watershed containing the Crow's Nest Natural Area Preserve and minimal development. Aquia Creek's watershed is largely suburban. The objectives of this study are a) to examine differences in macroinvertebrate diversity and sensitive taxa presence between Accokeek and Aquia Creeks and b) to investigate the relationship between nutrient concentration and macroinvertebrate community assemblage. Because we expect nutrient levels to be higher in Aquia Creek, we hypothesize that Accokeek Creek will have higher macroinvertebrate biodiversity than Aquia Creek. In late spring 2021, three macroinvertebrate samples were taken from six Accokeek sites and four Aquia sites. Two water samples and one sediment sample were collected from each Accokeek and Aquia site for nitrogen and phosphorus testing. Preliminary data suggests richness is higher in Accokeek Creek (12 taxa) compared Aquia Creek (10 taxa). The most common taxon across both creeks is Oligochaeta. Accokeek also has a lower median phosphate concentration (0.055 mg/L) than Aquia (0.150 mg/L, p=0.006, n=7) which supports our hypothesis. The results of this study will further our understanding of how nutrient runoff affects tidal freshwater benthic communities.

P129 - A Comparison of Estuarine Nekton Communities Collected by Three Different Gear Types

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Biological sampling in aquatic habitats presents many challenges. One challenge is determining which sampling gear type will most accurately assess the local aquatic community. For sampling nekton (aquatic animals that can swim and move independently), difficulties can arise from several different factors. One issue faced in the Pontchartrain Estuary is that the muddy substrate makes two-person beach seine sampling nearly impossible. We sampled nekton communities monthly using three non-beach seine gear types (cast nets, minnow traps, and crab traps) from January to August 2021. Sampling occurred at the University of New Orleans Coastal Education and Research Facility located on Chef Menteur Pass, one of two natural passes between Lake Borgne and Lake Pontchartrain. Chef Menteur Pass is an important migratory corridor for estuarine species such as blue crabs (*Callinectes sapidus),* brown shrimp, (*Farfantepenaeus aztecus)*, white shrimp (*Litopenaeus setiferus)*, and resident and estuarine dependent fish species. Significant differences in species composition occurred among all three gear types, (ANOSIM, $p < 0.01$), indicating each gear type sampled a different subset of the local nekton community. Our results suggest that using a single method alone will be unsuccessful in accurately assessing the entire nekton community.

P130 - Two Species of Aquatic Snails*, Physella acuta* and *Lymnaea auricularia* Differ in Their Susceptibility to Ammonium Phosphate

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Previous research has shown that chemicals present in most common fertilizers have negative effects on the health of aquatic organisms. Ammonium phosphate, one of the most prevalent of these ingredients, has a detrimental effect on the health of common aquatic snails as measured by differences in feeding behavior. Feeding behavior is a biological indicator commonly used to measure the effects of environmental toxicants on snails which includes the ability of snails to locate and consume food. In this study, feeding behavior was used to study the effect of ammonium phosphate on two species of common aquatic snails, *Physella acuta* and *Lymnaea auricularia*. *Physella acuta* and *Lymnaea auricularia* were exposed to varying concentrations of ammonium phosphate (0.05 mg/L - 40 mg/L) over different periods of time. After exposure to ammonium phosphate, feeding behavior was assessed by analyzing the number of snails in a feeding area and the number of snails actively feeding. Statistical analysis using a single factor ANOVA demonstrated that at lower concentrations of ammonium phosphate (0.05 mg/L - 3 mg/L) *Physella acuta* showed significant changes in feeding behavior after 24 hours of exposure continuing up to 6 days post-exposure. On the other hand, *Lymnaea auricularia* showed significant changes in feeding behavior at higher concentrations of ammonium phosphate (6 mg/L - 40 mg/L) especially at the fourth day post-exposure time point. This study indicates that not only does ammonium phosphate exposure negatively impact the well-being of snails, but also that different common species of aquatic snails differ in their respective susceptibilities to this environmental toxicant.

P131 - Relationships between watershed-scale and microhabitat-scale land cover measurements with stream habitat quality, stream sediment composition, and fish abundance and diversity in the South Carolina Piedmont

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Prior research we have conducted has suggested that rural Piedmont streams in South Carolina often possess lower diversity and greater homogeneity of fish populations than would be expected for streams with minimal urban impacts. One possible explanation for these observations relates to current land use. As such, our project focused on an examination of stream riparian zones at an extremely localized, microhabitat level to see whether they can better explain, as compared to large-scale land cover, the distribution patterns of stream fishes here in the SC Piedmont. We were also interested in relationships between microhabitat level measurements with those watershed-scale land covers and measures of habitat and sediment quality. Watershed-level land cover data was calculated using StreamStats, WMS, and ArcMap for 12 sites varying in the percent of developed land from 4-63%. At each site we took riparian measurements in two randomly determined quadrats, including canopy cover, ground cover and number of trees and shrubs, and collected a stream sediment sample for grain size analysis. Stream habitat quality was assessed using the quality habitat evaluation index (QHEI). Preliminary results show that increased development and impervious surface in the watershed was significantly negatively correlated with riparian and instream canopy cover, and was associated with larger and less poorly sorted stream sediments. Sites with higher QHEI scores were positively correlated with increasing size of riparian vegetation. Interestingly, sites with greater riparian and instream canopy cover and tree/shrub numbers were associated with smaller, more poorly sorted stream sediments that skewed toward finer particle sizes. So, while some microhabitat variables are associated with watershed-scale land covers, many are not, suggesting microhabitat-level stream characteristics may turn out to be important in explaining distribution patterns of stream fishes.

P132 - Evaluation of a Modified Index of Biotic Integrity (IBI) for Alabama Headwater Streams

Mark Meade, Cade Capron, Aden Kraft, Hannah Lafiosca, Connors Landwehr, William Middleton, Madison Mitchell, Deanna Palermo, Kevin Roberts, Caroline Teal

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An index of biotic integrity (IBI) is a rapid bioassessment protocol (RBP) used by environmental scientists to evaluate an aquatic system based upon population demographics of a given species. Fishes, invertebrates, and plants are the three main organisms typically used in any IBI survey. IBI metrics have been developed for Alabama's ridge and valley physiographic regions, however many headwater streams often score poorly based upon organismal composition alone. Here we evaluate a new IBI metric which includes fishes, amphibians and crayfishes in headwater stream assessments. Our aim was to determine if a new IBI metric might better reflect the quality of headwater streams. Six headwater streams in the ridge and valley physiographic regions of north-central Alabama associated with the Black Warrior, Cahaba, and Coosa River systems were surveyed during the BSC January Exploratory Term (2022). We modified two of the metrics used in scoring (i.e., number of native species, number of overall species) to include amphibians and crayfishes encountered. A total of 1,160 fish (28 species) were captured, identified, and released on site. Using traditional metrics, IBI scores were poor to very poor at all sites except for South Fork Terrapin creek which scored fair. At total of three amphibian and four crayfish species were observed at the sites. Incorporating amphibian and crayfish species to IBI calculations did not alter score evaluations for most sites. Scores for each site before and after modification were: 24/24 Watkins Brook, 28/30 Five Mile Creek, 32/32 Middle Black Creek, 24/26 Cane Creek, 22/22 Beaver Creek, and 42/44 South Fork Terrapin Creek. South Fork Terrapin creek was the only site that improved in evaluation after including amphibian and crayfish species to the metric. Overall, the addition of native crayfish and amphibian species to IBI metrics did not substantially influence stream evaluations.

P133 - The utility of grass shrimp embryos in the evaluation of the dyes methylene blue and orange G.

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This experiment was formed to determine the effects of Methylene Blue and Orange G on the eggs of *Palaemontes pugio (Grass Shrimp).* We extracted the eggs from already gravid female shrimps we acquired in the marshlands from Dauphin Island and submerged the eggs into varying levels of concentrations of Methylene Blue and Orange G. Three experiments were conducted where the eggs were separated into well plates (24 wells per plate) with each plate containing a concentration of dye. We observed the eggs hatch, the coloration of the hatchlings, and mortality rates within the span of a week per experiment. The hypothesis anticipated the higher concentrations of Orange G and Methylene Blue would be more or less toxic to the hatchlings. Our results showed that Methylene Blue was more toxic than Orange G in their respective mL concentrations. These results show the utility of using the Grass Shrimp embryos for assessing the toxicity of chemicals such as Methylene Blue and Orange G.

P134 - Diversity and Abundance of Early Life History Stages of Estuarine Fishes Associated with Benthic Algae

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Patterns of diversity and abundance of larval and post-metamorphic stages of fishes were studied in shallow algal beds in the Charleston Harbor estuary. These habitats are dominated by an invasive red alga, *Gracilaria vermiculophylla,* although the degree to which these structures support small fishes is unknown. Summer interns participated in the project from June to August of 2017 and 2018 with the goal of determining patterns of association of these fishes with algal beds of either dense or sparse coverage. Samples were obtained by a fine-mesh beach seine (4.57 m in length with 1.6 mm mesh) hauled along a 15 m transect. All fishes captured were preserved then later identified by visual means to the lowest taxonomic level possible. In 2017 a total of 3,305 specimens were caught, representing 25 species, and in 2018 1,088 specimens were caught and accounted for 27 species. The ten most common species were, in descending rank of abundance: *Menidia menidia*, *Anchoa mitchilli*, *Fundulus majalis, Syngnathus* sp., *Mugil curema, Bairdiella chrysoura, Eucinostomus* sp., *Micropogonias undulatus, Trachinotus carolinus* and *Symphurus plagiusa*. Significant differences with respect to occurrence of these species were found between the sparse and dense habitats, although major differences in pattern between 2017 and 2018 were observed. Calculation of Simpson's Diversity Index shows that in 2017 diversity was highest in the sparse algal beds, whereas in 2018 it was higher for the dense beds. Substantial differences in abundance patterns were also observed

between these two sampling seasons. These somewhat conflicting results could be due to a number of factors that include interannual variation in water temperature, timing of the appearance of young-of-the-year, seasonal variation in suspended and attached forage organisms, and sample size. The project will continue and with modifications of some design components.

P135 - Recovery efforts of Chrosomus cumberlandensis under the Endangered Species Act

Kelly Simpson

Georgia Gwinnett College, Lawrenceville, GA

Despite stringent protective regulations and conservation efforts, Chrosomus cumberlandensis appears to have a significant population decrease. Though it has been a critically threatened species previously, the existing protections are inadequate to preserve its habitat and the habitats of its co-occuring species. Chrosomus cumberlandensis should be uplisted to an endangered species and mining and development near its historical range should be banned immediately to prevent extinction.

P136 - Ten years after: Long term effects of a stream restoration project on benthic communities

Elizabeth Dobbins

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Urban and suburban streams are degraded by thermal, chemical, and mechanical stressors. Shades Creek, located in the Cahaba River watershed in north central Alabama, has headwaters impacted by light industry, residential run off, and channelization. Much attention has been paid to attempts to rehabilitate and restore damaged streams. In November 2010, ten rock vanes were installed in a 330 m section of Shades Creek to reduce erosion and trap sediment. It was predicted that there would be supplemental benefits including improving water quality and habitat downstream of the vanes and that these benefits would accrue over time. Using EPA rapid bioassessment protocols, macroinvertebrates 100 m downstream of the rock vanes were sampled prior to construction then one-, four-, and ten-years post-construction. There was a persistent improvement in community structure over time, including an increase in sensitive Ephemeroptera, Plecoptera, and Tricoptera (EPT) taxa and a decrease in Chironomid taxa. These results suggest a persistent local benefit to macroinvertebrate communities downstream from the installed vanes.

P137 - Extended development in a terrestrially-nesting salamander is associated with larger hatchling size relative to aquatic congeners

Dr. Rebecca Hale, PhD, Kimberly Treadaway

University of North Carolina Asheville, Asheville, NC

Breeding ecology varies widely across the salamander genus *Ambystoma*. Most species breed in winter or early spring and deposit eggs in masses, submerged in water of ponds. However, a few species have shifted to fall breeding, arriving at ponds months earlier than their competitors. Some lay eggs loose in soil of dry pond beds prior to winter rains, and one has shifted to breeding in flowing streams. Further, while most species leave ponds after laying eggs, one stays and cares for young until hatching. This variation not only is associated with variation in the behavior of these species, but may also have consequences for the developing embryos. We present the results of a study that builds on previous work of ours in this genus, comparing embryonic development between three species that vary in seasonality, location of egg deposition, and parental care. Our goal was to identify the effects of breeding early (in the fall) and laying eggs terrestrially on embryonic developmental rate and life histories. We found that marbled salamander (*Ambystoma opacum*), a terrestrial-laying and care-providing species, exhibits prolonged embryonic development and larger size at hatching relative to two aquatic-laying, non-parental species: ringed (*A. cingulatum*) and spotted (*A. maculatum*) salamanders. We suggest that laying eggs terrestrially relaxes selection for rapid development. Embryos must wait for ponds to fill before they can hatch, which may be considerably longer than the typical time to hatching in aquatic-laying species. By using that time to extend development, marbled salamander embryos grow to a larger size under the protection of their caring mothers. When they hatch, they are larger than their congeners, and larval size may be associated with larval survival, as it is in many amphibian species.

P138 - Pollinator visitation rates on Schweinitz's sunflower *(Helianthus schweinitzii)* vary by site and temperature

Hal Ridgeway, Prof. Christopher Paradise

Davidson College, Davidson, NC

Habitat loss and the effects of human development are major threats to pollinator diversity. Pollinator declines will affect plant/pollinator interactions, as many plant species rely on pollinators to sustain their populations. Schweinitz's sunflower *(Helianthus schweinitzii)* is recognized as a federally endangered species and is endemic to the Piedmont regions of North and South Carolina. Several factors are thought to have contributed to the decline of this flowering plant, including predation by white-tailed deer, mowing, and reduction of insect pollinator abundance. In *H. schweinitzii* populations in protected areas, the effectiveness and frequency of pollinator visits may contribute to continual decline or

prevent extensive regrowth of populations. In this preliminary study, part of a larger study on the ecology and demography of *H. schweinitzii* populations in Mecklenburg County, NC, we document the variety of insect pollinator species found to visit *H. schweinitzii* during one flowering season. We also evaluated how pollinator visitation rates at *H. schweinitzii* populations varied between different sites and at different temperatures. The sites utilized for this project were at Latta Plantation Park and McCoy Road, both in Mecklenburg County, NC. These patches, and the *H. schweinitzii* populations therein, are monitored by the Catawba Land Conservancy and Mecklenburg County Parks and Recreation Department. Pollinator visits were recorded using sight identification and macrophotography during timed observations to identify insect species in the least invasive way and protect this endangered sunflower. We found nine pollinator species across sites, but that species assemblages varied between *H. schweinitzii* populations. The rates of visitation also varied between these sites, as sites which experienced prolonged sunlight were found to be have more insect pollinator visits. In part, this adds to our understanding of why *H. schweinitzii* populations are in decline, as plant-pollinator interactions are crucial for the survival of this species.

P139 - Pilot Study: Surveying Medium and Large Mammals at the Newly Formed Cahaba Biodiversity Center

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The Cahaba Biodiversity Center (CBC) is a newly established conservation easement located on 2,100 acres in central Alabama. The purpose of the easement is to provide research and educational opportunities for faculty, students, and collaborators of the University of West Alabama, encompassing botanical, zoological, archeological, and water and land management designs. This pilot study is the first stage of a four-part research project designed to systematically identify the small to large terrestrial mammals present on the property across seasons and dominant stand types, and relative to ongoing land management activities (prescribed fire and logging). In order to capture the full range of mammals, survey methods will eventually include baited and unbaited game cameras, track plate boxes, scat and track surveys, and habitat and forage surveys. Initial survey efforts include only unbaited game cameras in order to evaluate future permanent and/or baited camera and track plate locations. In January 2022, 25 Browning Strike Force Pro XD game cameras were randomly positioned within 5 stand types (deciduous, evergreen, mixed evergreen/deciduous, mixed shrubland, and riparian) on three set types: game trail, internal stand, or stand edge. Cameras were attached to a tree or stake 30 cm above the ground and set to video (3 sec, IR motion detect), and will remain active through at least April. Preliminary data has detected 6 mammal species, and further seasonal data is expected to increase the known diversity and distribution of species on the property. Furthermore, these surveys may supplement efforts conducted by the Alabama Department of Conservation of Natural Resources to determine the distribution of species of interest, including eastern spotted skunks (*Spilogale putorius*) and long-tailed weasels (*Mustela frenata*), if they are detected.

P140 - NEON: Open data expanding small mammal and tick pathogen research

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The National Ecological Observatory Network (NEON) is a continental-scale ecological observation facility sponsored by the National Science Foundation. NEON collects data at 81 sites within 20 Domain ecoregions across the United States. NEON provides these data free of charge to help address many research and education questions including about the impacts of climate change, land use change and invasive species on natural resources and biodiversity. These data can support your research as well as numerous student-centered activities in your classroom. Over 180 data products, ranging from small mammal pathology to lidar remote sensing, can be accessed from the NEON data portal. Starting in 2021 NEON is implementing a rodent pathology plan that will allow researchers to explore the relationships between small mammal populations, tick populations, and the pathogens they host. The NEON data portal is one of few data repositories that will allow these types of cross-system comparisons. This poster will provide an overview of NEON, as well as the small mammal population, tick population, and pathogen data. Additionally, the poster will highlight some preliminary trends emerging from those data products within some of NEON's southeastern Domains.

P142 - Long-term dynamics of a flower-pollinating longhorned beetle community

Paul Gier

Huntingdon College, Montgomery, AL

Studies of the community structure of longhorned beetles (family Cerambycidae) are hindered by the cryptic nature of most species, but the mostly diurnal flower-pollinating subfamily Lepturinae are an exception. Since 2007 I have made annual surveys of a community of 22 Cerambycids (mostly Lepturines) visiting the flowers of *Hydrangea quercifolia* in the Talladega Mountains of Alabama. The brief window of peak blooming allows for efficient and consistent sampling. Species richness has remained consistent but two measures of diversity (Shannon Index and Evenness) have declined since 2017. This is due partly to one species (*Strangalepta abbreviata*) rising in dominance from <20% to almost 50% of a typical sample. This change coincided with a fire event in 2017 that may have changed the availability of dead wood, which these beetles use as a larval food source.

P143 - A Honking Hot World

Katie Bailey

Agnes Scott College, Decatur, GA

Have you ever looked up to the morning sky and seen it darken with a passing flock of honking wild geese? When we were little we were taught that as our countries get colder and the south stays nice and hot that the geese would migrate every winter like clockwork. This is no longer the case. Scientists hypothesize that climate change is affecting the migration route and timing of migratory birds. My mentor and I were interested in studying the effects of these warmer temperatures on migratory bird behavior with our research. Specifically, We investigated whether rising temperatures were causing migratory ducks to begin their migrations earlier in the year which in turn shortens their reproduction cycle. Using wood duck observation data from 2015-2020 in the State of Texas We documented a trend of the ducks arriving earlier in the spring in progressive years. We predict this trend will correlate with the warmer temperatures. Using this data we focused on the time of year the ducks are seen, the average temperature of the season, and the number of birds observed at a time. We then used previously published data, to get a consistent average for the birds' usual behaviors and their reproduction cycle. Overall, we discovered that global climate change has the potential to reshape vital migration patterns which in turn throws off the food chains of each location along their migration route. This research will allow us to better understand how one species of waterfowl may be affected and then allow us to predict potential patterns for a wide array of other bird species.

P144 - Interactive Effects of Puma Activity and Habitat Characteristics on Mesocarnivore Community Structure

Zach Buddie, Travis Perry

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We investigated the relationship between puma (*Puma concolor*) activity and mesocarnivore community structure, as determined by principal components analysis, and whether or not habitat characteristics modify this relationship. The study area was 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 2009 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, as was the structure of the mesocarnivore community, which was then characterized using principal component analyses. 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 0.9. 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 change in the mesocarnivore community structure ($p<0.004$). However, this relationship is significantly modified, reversed actually, in riparian habitats ($p<0.004$). Puma activity alters the structure of the mesocarnivore community 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 structure of the mesocarnivore community.

P145 - Functional Characteristics of the Whispered Low Chip Call Harmonics of the Chinese Blue-breasted Quail Chick (*Coturnix chinensis*).

Edward Mills

Wingate University, Wingate, NC

Chinese Blue-breasted Quail chicks produce several low amplitude (dB) calls, and one of these is the whispered low chip call. This low frequency, one-syllable signal (2908.23 Hz) is relatively short (0.08 sec) and includes two harmonics (6002.78 Hz, 14572.73 Hz) above the main call. This call has not been recorded from adults, only from juveniles. One probable function of whispered calls (low amplitude) produced by juvenile birds is to communicate with conspecifics without attracting the attention of potential predators. Juvenile birds in nonflight plumage are especially vulnerable to predators and often use whispered calls to communicate with their parents and siblings. Contact calls are important for maintaining family cohesion among precocial birds that are active soon after hatching. In order for it to deteriorate over active space but still reach close-proximity receivers, the main low chip signal (82.9 dB), as well as its harmonics (60.49, 51.59 dB), are produced at low amplitude. Seven spectral measures of the harmonics were analyzed: call length (sec), average and maximum power (dB), as well as call frequencies (high, low, center, width, Hz). The high harmonic has a significantly longer call length than the low harmonic. The high harmonic also has a significantly higher maximum frequency (top), center frequency, high frequency, and low frequency (bottom) than the low harmonic. The high harmonic is a narrower signal, with a significantly lower frequency width than low harmonic. These spectral features are consistent with the hypothesis that *C. chinensis* chicks use the low chip call and its harmonics as a low amplitude (dB), whispered call to maintain family cohesion without attracting unwanted attention.

P146 - Niche Modeling with Texas Brown Tarantulas (*Aphonopelma hentzi*)

Samantha Ethier, Christian George

High Point University, High Point, NC

The Texas brown tarantula (*Aphonopelma hentzi)* exhibits features in its physiology and preferred habitat that could be impacted by climate change. In order to determine if these features heavily impact its ecological range and if the range is affected by any other factors could be impacted, the range was plotted in the form of a niche model using Maxent after being formatted in ArcGIS. The Jackknife test of variable importance was then used to ascertain the greatest contributing factors necessary for occurrence. These factors were then assessed to determine whether they may be impacted by climate change. The top five greatest contributing factors included winter temperature, 90th percentile consecutive dry days, the number of wetting rain days in June, percent clay in the soil, and winter precipitation. It can be inferred from these factors that the ecological range of the Texas brown tarantula will not only be affected by climate change, but will increase and spread farther north of the equator due to its effects.

P147 - The Complete Mitochondrial Genome of *Aneides aeneus* (Green Salamander)

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Our goal was to sequence the mitochondrial genome of the green salamander (*Aneides aeneus*). This rare species is an obligate rock outcrop species that spends substantial amounts of time in rock crevices across the mid to southern Appalachian Mountains. This sequence was produced to increase the genome-level resources available for this species which could aid in remote identification procedures like environmental barcoding. Tissue (autonomic tail fragments) was collected from wild specimens encountered in southwestern Virginia. Total DNA was extracted using a commercial mini prep kit. PCR amplification was performed based on homology to other *Aneides* mitochondrial genomes and amplified fragments were sequenced using Sanger sequencing technology. A whole genome sequence was also procured with Illumina MiSeq technology. The entire genome was assembled with fragments produced using these two technologies. The completed mitochondrial genome was circular with 18008 base pairs. There were 14 protein coding genes, 22 tRNAs, and both large and small ribosoml RNAs. It had gene synteny and repetitive sequences consistent with closely related species. Two genes, *cox3* and *nad4*, lacked stop codons, suggesting they are constructed post-tanscriptionally by the addition of poly-A tails. Phylogenetic analysis using whole chromosome alignments confirmed *A. aeneus* belongs within the *Aneides* clade and is ancestral to two species endemic to the North American west coast, *A. hardii* and *A. flavipunctatus*.

P148 - Abundance, Diversity, and Analysis of Ecologically Important Traits of Southern Appalachian Bumble Bees

Breana Cook[1], Paul Super[2], Sam Droege[3], Brooke Reutinger[1], Rutuja Rothe[1], Ally Nisbet[1], Jennifer Geib[1]

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Bumble bees are important pollinators that are responsible for the vitality of native plant communities worldwide, and many species have shown population declines in the past twenty years. Despite increased awareness of their plight, scientists are still working to learn basic aspects of their biology. My project objective is to understand which environmental factors influence biometrics of ecologically important traits, such as body size and tongue-length, for bumble bees in the Southern Appalachians. I hypothesize that biometrics of these important traits will vary significantly with elevation, latitude, and floral availability, and specifically will be inversely related to higher elevations, northern latitudes, and decreased floral resources due to increased energy expenditures needed in these environments. Samples were collected during a Citizen Science Pollinator Inventory that was coordinated in 2019 along the entire length of the Blue Ridge Parkway, NC and VA, in partnership with the National Park Service. Sixty survey sites were randomly selected along the BRPW. Foraging bees were captured using passive traps that were fluorescently painted to mimic flowers. Trait biometrics have implications for a number of aspects of bee's life histories. For example, the larger the bee body size, the longer foraging trips an individual bumble bee can take. Bee foraging distance is directly related to population dynamics, genetics, and life history. Consequences of disturbed foraging distance include reduced pollination for plants, predation, parasitism, nutrient transfer, and seed dispersal. Tongue-length indicates dietary preference, as individuals with longer tongues can access different floral resources. Bumble bee tongue lengths have shown evolutionary sensitivity to abundance of floral resources, with fewer resources resulting in shorter tongues and a more generalized foraging niche. Without having diverse physical traits within bumble bee populations, flower abundance and diversity are at risk of declining. My study examines how the environment influences bumble bee biometrics.

P149 - Preliminary effects of methylene blue on xenopus embryos using FETAX (Frog Embryo Teratogenesis Assay: Xenopus)

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Methylene blue is a compound consisting of dark green crystals or crystalline powder, which gives out a deep blue color in solutions with water or alcohol. Its most common uses are as bacteriologic stain and indicator. It has often been used to treat methemoglobin and is often considered to be a safe drug when used in moderate dose of <2 mg. On recent studies methylene blue has found to cause severe central nervous system toxicity with other results such a nitrogen and ammonia poisoning. To understand the harmful developmental effects of Methylene blue, Xenopus frog embryos under lab conditions were exposed to a range of methylene blue concentrations. For the experiment fertilized embryos were sorted and allowed to develop in methylene blue solutions made by-dissolving solid methylene blue in FETAX solution. FETAX (frog embryo teratogenesis

assay -Xenopus) is a 96-hour test that uses South African clawed frog (Xenopus laevis) in their early developmental stage of embryo to measure the potential of substances to cause mortality, malformation, and growth inhibition in developing embryos. The experiment setup was to expose the embryos to methylene blue concentration ranging from 0-100 mg/ L with 4 sets of control for each trial. Control consisted of Xenopus embryos kept in only FETAX solutions. The results indicate and LC50 (mortality) of approximately 6% and EC50 (malformation) of 2.7%. Abnormalities were observed in abdominal, notochord, gut, eye, brain and many other body structures including conditions such as edema, hemorrhage and blisters. The results suggested that methylene blue has slight teratogenic effects.

P150 - Viral Spillover from Honeybee Apiaries in Native Solitary Bee Populations

Matthew Johnson, Jennifer Geib

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Over the past 20 years native bee populations have been on the decline. One potential class of stressors affecting native bee populations include novel pathogens that originate from commercial colonies of *Apis mellifera* (honey bees). Recent studies documenting honey bee virus spill over into native bee populations have generally been limited to eusocial species, e.g. bumble bees. This study seeks to determine the degree to which native solitary bees are infected by common diseases carried by commercial honeybee populations: Kashmir Bee Virus (KBV), Israili Acute Paralysis Virus (IAPV) and Deformed Wing Virus (DWV). I will collect native solitary bees within and outside of the foraging range of managed *Apis mellifera* apiaries and quantify infection rates by KBV, IAPV, and/or DWV. Samples will be tested using RT-PCR with oligo primers specific to each virus. The amplified DNA will be separated by size via gel electrophoresis and identified by base pair length. I hypothesize that distance plays a role in the intensity of viral spillover from managed honeybees to native solitary bee species. Furthermore, I predict that native solitary bees within the foraging range of *Apis mellifera* will be infected with KBV, IAPV, and DWV more frequently than those outside the foraging range. Native solitary bee species are critical pollinators for the plants indigenous to the area, making them an important component of healthy native ecosystems. Understanding how honeybee viral spillover affects our solitary bees is a key piece of information that can be used to help implement strategies to prevent apiaries from passively infecting solitary bee species and maintain our indigenous wildlife.

P151 - Developing a Predictive Geospatial Habitat Model for Green Salamanders (*Aneides aeneus*) in East Tennessee.

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Green Salamanders (Aneides aeneus; Cope and Packard, 1881) are a secretive and cryptic species of salamander that can be relatively difficult to detect, due to their occupation of arboreal habitats. As a result, their populations are not well studied in Tennessee. The incorporation of geospatial tools is critical in developing models that can be used to predict undocumented locations in Tennessee and elsewhere. Determining prime habitat by identifying key variables for the species could offer insight on their status in the state and the aid in identifying the various threats that these populations face. The objectives of this study are to: locate potential populations of A. aeneus in Tennessee, to better understand and recognize the habitat variables that are necessary for the species to be present, to acknowledge suitable habitat that may be uninhabited by the species, and to potentially gain insight for future studies on their patchy distributions. Sites deemed to have high habitat specificity and increased probability of occupancy will be assessed and a habitat structure analysis will be conducted using various data sets. Paired Logistic Regression, Maxent, Circuitscape, and Akaike's Information Criteria will be used to evaluate model performance in the real-world. In closing, integrating geospatial tools for measuring and monitoring rare biodiversity is necessary to develop adaptive conservation and management strategies.

P152 - **Diversity, Abundance, and Foraging Habitat Preferences of Solitary Bees on the Blue Ridge Parkway**

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Habitat loss through fragmentation and urbanization are key threats facing bee populations worldwide. In the last two decades, it has been documented that populations of many bee species have been declining. However, most data on bee declines originates from eusocial bee species, particularly bumble bees (*Bombus* sp.); the status of most solitary bee populations is unknown despite comprising a vast majority of bee species. Like social bees, solitary bees contribute integral pollination services to agricultural and native ecosystems, yet, key aspects of their life history and ecology remain unknown. To address these gaps in knowledge for species in the southern Appalachians, I will quantify solitary bee abundance and diversity along the entire length of the Blue Ridge Parkway, using bees samples collected by students and citizen scientists in a 2019 survey. I will then develop occupancy models in R software (unmarked package) to investigate habitat preferences of ecologically important solitary bee species and estimate their detectability. I predict that environmental covariates such as elevation, temperature, and availability of bee preferred floral resources will be usable for predicting the true presence and absence of bees at each site. In conservation and management as well as everyday life, bees are often viewed as monolithic with all species being treated the same, whereas in reality different families of solitary bees have different life histories that vary greatly especially when and compared to social families of bees. Understanding the needs of solitary bees is essential for land managers to allow them to have a better understanding of what types of patches need to be conserved.

P153 - The Preliminary developmental effects of microbeads on developing embryos of *Xenopus Laevis*

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Microbeads are the tiny pieces of polyethylene plastic added to health and beauty products. It is used as exfoliating and polishing agents in cosmetics like sunscreen, lotions, deodorants, makeup products, toothpastes, and blood flow determination tests. The effects of the concentration of the microbeads, Fluospheres™ polystyrene, 10μm, was determined by using the Frog Embryo Teratogenesis Assay- Xenopus (FETAX). The early stage of South African clawed frog, Xenopus laevis, were exposed to the concentrations of the microplastics with FETAX solution for 4 days from small cell blastula to a free-living tadpole. The small fraction of microbeads was mixed with 20 mL of FETAX solution to make different concentration microbeads solution. Four different test solutions were used in two set of plastic petri dishes of 10 embryos. The control groups consisted of 4 plastic petri dishes of 10 embryos each with 8 mL FETAX solution without microbeads solution. Dead embryos were removed after every 24 hours, and solutions were renewed. The mortality, malformation and length of tadpole were recorded for all petri dishes at the end of 4 days. The results show that higher the concentration of the microplastics, more likely to increase the mortality of the tadpole. The 96-hr LC50 and 96-hr EC50 of approximately 1866.500 and 931.493 microbeads per ml respectively.

P154 - Examination of False Oleander Scale (*Pseudaulacaspis cockerelli*) Infestation on *Magnolia grandiflora* Across Habitat Types

Ellen Goza, Michele Guidone

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The range of the southern magnolia, *Magnolia grandiflora,* includes the coastal forests of Georgia; it is also a commonly cultivated ornamental. It attracts many insect pests including the scale *Pseudaulacaspis cockerelli*. While methods to control *P. cockerelli* have been studied, little is known about its abundance and impact within forests. The purpose of our research was to determine if the severity of scale infestations differs between landscaped settings and a semi-natural habitat. We hypothesized that trees in a semi-natural habitat would exhibit greater resilience against infestations when compared to those in landscaped settings. To test this hypothesis, we examined magnolias in both settings located on the Georgia Southern University Armstrong Campus. We measured tree height, diameter, presence/absence of scale, and infestation severity, which was determined by estimating insect percent cover on leaf tissue and the percentage of leaves experiencing a sparse, moderate, or dense scale infestation. In contrast to our hypothesis, infestation estimates indicated no significant difference between habitats. However, greater variation in scale infestation was observed among trees in the semi-natural habitat. Further research is needed to determine whether this difference may be linked to environmental heterogeneity and/or genetic diversity.

P155 - A comparison of amphibian diversity among high-elevation wetlands in the Cumberland Mountains Physiographic Province

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High-elevation wetlands hold high conservation priority in the Cumberland Mountains Physiographic Province due to their relative rarity, with little knowledge in the literature related to how amphibians use these high-elevation habitats and to what degree individual species rely upon them during reproductive phases of their life histories. Therefore, forest and wildlife managers have no pre-existing data to use when designing appropriate management guidelines for habitats associated with these wetlands. We sampled a collection of high-elevation wetlands across Pine and Cumberland Mountains in southwest Virginia, USA to address gaps in knowledge about these habitats and their use by amphibians. We specifically inventoried the amphibian diversity at five wetlands using a mixture of visual encounter and auditory surveys. We used standardized, time-constrained visual encounter surveys to inventory the amphibian taxa at each site that consisted of searches of all available cover objects within a 10 meter buffer of the wetland margin. We also used automated digital recorders to record auditory call data from anuran taxa. We encountered 17 total amphibian species (eight anuran and nine salamander species) across these sites, recording numerous occurrences of some species, such as Mud Salamanders (*Pseudotriton montanus*), that have previously been assumed to be absent from high-elevation wetlands in the Appalachian region. Statistical analyses further indicated high turnover in amphibian biodiversity between sites. Our results indicate that these wetlands should be of high conservation concern since they are not redundant in terms of their biodiversity and should be given priority in regional habitat management efforts.

P156 - Syrphid Fly Inventory Along the Blue Ridge Parkway

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Flies of the family Syrphidae are a widespread and diverse group of dipterans consisting of over 6000 species worldwide. Although most of the buzz surrounds bees, syrphid flies are thought to be equally important pollinators of native plants. Additionally, the larval stages of many species are predatory towards common plant pests such as aphids, making them promising biological control agents in both natural and agricultural settings. Despite the dual ecosystem services offered by their holometabolous lifestyle, few studies exploring syrphid distribution and diversity

have been conducted within the United States. Prior to 2019, there were no documented records of syrphid flies along the Blue Ridge Parkway, a major unit of the National Parks System. In order to determine the diversity of species present in this region, a citizen scientist inventory collected Syrphid Flies through passive trapping (2019, 2020) as well as active netting efforts (2021) at 64 sites alongside the Blue Ridge Parkway in North Carolina and Virginia. Field sites were generally characterized by meadows with abundant floral resources ranging from high points to wetlands. Samples ($N = 1000$) were euthanized on site and frozen before being pinned and identified. Collections yielded over sixty syrphid species total with a range of 3 - 12 species per site. As many native pollinators begin to experience declines in abundance, a heightened focus on the conservation of syrphid flies may prove beneficial in managing natural, recreational, and agricultural assets. The data collected by this project serves as a valuable baseline for future monitoring and studies of an extremely undervalued species.

P157 - Green Salamander, *Aneides aeneus*, Abundance and Proximity to Hiking Trails in the Greater Chattanooga Area

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Many people are attracted to the Greater Chattanooga Metropolitan Area because of the quality and quantity of outdoor recreation that is available to the public. Unfortunately, the popularity of outdoor recreation can increase the negative effects on the environment. Hiking trails can alter the landscape and influence wildlife behavior and relative abundance. Salamanders are sensitive to environmental disturbances due to their complex life cycle that often require upland and wetland habitats in juxtaposition. We aim to assess the effects of hiking trails on Green Salamander (*Aneides aeneus;* Cope and Packard, 1881) relative abundance by evaluating the various metrics encompassing usage, style, soil type, construction, and typology; and make recommendations on best management practices. Our areas of study will be The Tennessee River Gorge and Enterprise South Nature Park. We will search for *A. aeneus* at predetermined intervals along each trail using 100m transects and a randomized blocks design. Habitat will be measured with both known and random points Habitat metrics will be recorded along with other geospatial data. Data will be analyzed using ArcPro GIS, SAS and SPSS. Data will be statistically analyzed using paired logistic regression and tested for normality. The conservation implications of this study are many and the results of this study will better inform practitioners to make wise land use decisions.

P158 - Distribution and ecology of the Genus *Asclepias* (Apocynaceae) in Mississippi based on direct examination of herbarium specimens, field work, SERNEC, and iNaturalist.

Michael Wayne Morris[1], Heather Sullivan[2]

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Asclepias Linnaeus is a genus of approximately 120 species in the Apocynaceae. This genus is especially diverse across North America, and there are 16 Asclepias species in Mississippi: A. amplexicaulis, A. hirtella, A. humistrata, A. lanceolata, A. longifolia, A. michauxii, A. obovata, A. perennis, A. purpurascens, A. rubra, A. syriaca, A. tuberosa, A. variegata, A. verticillata, A. viridiflora, and A. viridis. The genus as a whole is present in a wide variety of habitats in Mississippi, ranging from coastal savannas and bogs, to xeric fire-prone longleaf pine forests on sandhills, to prairies and interior flatwoods, to alluvial swamp and bottomland hardwood forests, to mesic and dry-mesic hardwood forests and openings on ravine slopes, bluffs, and ridges. Two species, A. hirtella and A. purpurascens, are of conservation concern. Asclepias humistrata and A. rubra are also monitored by the Mississippi Natural Heritage Program. From November, 2016 through October, 2021, Asclepias specimens in the following herbaria were examined at their respective locations: University of Mississippi (MISS), Mississippi State University (MISSA), University of Southern Mississippi (USMS), Delta State University (DSC), Institute for Botanical Exploration (IBE), Mississippi Museum of Natural Science (MMNS), and the Southern Weed Science Laboratory (SWSL). In 2021, specimens in herbaria outside of Mississippi were examined online through SERNEC, and digital images of Asclepias species in Mississippi were analyzed on iNaturalist. Information on the distribution and habitats of the native Mississippi species will be presented. This research was partially supported by a Troy University Faculty Development Grant, by National Science Foundation grant DBI-1203687, and by the Mississippi Museum of Natural Science Foundation.

P159 - Plant community composition of six Lower Mississippi River islands

Grace McCartha[1], Caitlyn Sims[1], Brendan Kosnik[1], J. Richard Abbott[2], Mathew Jones[1], Ben Benton[1], Scott Mangan[1], Travis Marsico[1]

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The Lower Mississippi River (LMR) contains unique islands that are isolated from the mainland for all or most of the year. These islands experience intense flood regimes that result in the receipt of a constant supply of organic materials from upstream, such as sediment and seeds. Moreover, the islands are some of the last remaining floodplain habitats in the Delta region, and surveying their botanical biodiversity is the first step to learning more about plant community structure and ecosystem function in the Mississippi River. From June 2020 through December 2021, we conducted a flora of six LMR islands from Helena-West Helena, Arkansas, to south of Greenville, Mississippi. More than 1,900 plant specimens were collected for a total of at least 472 species across all six islands. We found 14 species that are putative state records (never before recorded in the state) in Arkansas and three in Mississippi. The six islands span four counties and of the three Arkansas counties, approximately 106 species were found that are county records. From mid-July to late-August 2021, we surveyed plant community composition in 59 100-m^2 plots on these six islands following Carolina Vegetation Survey protocol. These plots were established across a range of elevations and habitat types (e.g., sand dunes, swamps, mesic forests). Data are being analyzed to relate abiotic factors (elevation, soil, proximity to tributary confluences, island size, island age, latitude) to plant communities on LMR islands to understand species distribution patterns in these seasonally flood-disturbed habitats.

P160 - Distribution and ecology of the Genus *Ilex* (Aquifoliaceae) in Mississippi based on direct examination of herbarium specimens, field work, SERNEC, and iNaturalist.

Michael Wayne Morris[1], Heather Sullivan[2]

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Approximately 400 species comprise the cosmopolitan genus *Ilex* Linnaeus in the Aquifoliaceae. *Ilex* species are especially well-represented in tropical and temperate regions of the Americas and Asia. In Mississippi, there are 11 native and one introduced *Ilex* species that have been documented: *I. ambigua, I amelanchier, I. cassine, I. coriacea, I. cornuta, I. decidua, I. glabra, I. longipes, I. myrtifolia, I. opaca, I. verticillata,* and *I. vomitoria*. Some of these species, such as *I. decidua* and *I. opaca,* are widespread across Mississippi. *Ilex coriacea* and *I. glabra,* both primarily characteristic of acidic wetlands, and *I. vomitoria,* typically of upland sites, are common in the southern half of the state. The latter species appears to be expanding its range northward. Two species, *I. amelanchier* and *I. cassine,* are of conservation concern and are restricted to wetlands in extreme southern Mississippi. *Ilex myrtifolia,* associated with pond cypress depressions and adjacent bay swamps, is also monitored by the Mississippi Natural Heritage Program. *Ilex cornuta,* native to Asia, is a naturalized part of the flora. From November, 2016 through October, 2021, *Ilex* specimens in the following herbaria were examined at their respective locations: University of Mississippi (MISS), Mississippi State University (MISSA), University of Southern Mississippi (USMS), Delta State University (DSC), Institute for Botanical Exploration (IBE), Mississippi Museum of Natural Science (MMNS), and the Southern Weed Science Laboratory (SWSL). In 2021, specimens in herbaria outside of Mississippi were examined online through SERNEC, and digital images of *Ilex* species in Mississippi were analyzed on iNaturalist. Information on the distribution and habitats of *Ilex* species in Mississippi will be presented. This research was partially supported by a Troy University Faculty Development Grant, by National Science Foundation grant DBI-1203687, and by the Mississippi Museum of Natural Science Foundation.

P161 - Influence of seasonal flooding on plant reproductive phenology on Buck Island Wildlife Management Area, a Lower Mississippi River island

Caitlyn Sims, Grace McCartha, Brendan Kosnik, Mathew Jones, Ben Benton, Scott Mangan, Travis Marsico

Arkansas State University, Jonesboro, AR

Plant reproductive phenology is sensitive to environmental factors such as temperature, precipitation, soil moisture, nutrient availability, light duration, and flooding. The influence of flooding on reproductive fitness is understudied in temperate systems. The Mississippi River experiences an annual flood cycle and islands in the Lower Mississippi River are subjected to higher river levels in the winter and spring, which may inundate entire islands or leave only the highest island elevations unflooded. We hypothesize that (1) plants at lower elevations that experience longer periods of flooding have later average peak flowering and fruiting periods compared to plants at higher elevations and (2) plants at higher elevations produce more fruits than plants at lower elevations (i.e., have higher fecundity) due to a longer reproductive season. In spring, summer, and fall 2021, seven native, herbaceous dicot species were monitored on Buck Island Wildlife Management Area, outside of Helena-West Helena, Arkansas. Patches were established throughout the elevation gradient of the island and in areas of the same habitat type and elevation. The number of reproductive structures in a phenophase (e.g., flower buds, open flowers, developing fruits) were counted twice per week on individually marked and tracked plants, and mature fruits were collected for all tracked individuals. By the end of data collection, 523 individual plants were tracked in 64 habitat patches ranging in elevation from 45-57 m. During the 245-day field season, the three annual plant species were found in wider elevation ranges than the three perennial species. Analyses are being conducted to determine if peak reproductive phenology and plant fecundity are correlated with island elevation.

P162 - The role of foliar anthocyanins in mitigating winter herbivory and high-light stress in cranefly orchid, *Tipularia discolor*

Emily Gonzalez, Trinity Erjo, Corinne Gumpman, Nicole Hughes

High Point University, High Point, NC

Cranefly orchid (*Tipularia discolor)* is a terrestrial orchid native to the eastern United States. Each plant produces a single wintergreen leaf in autumn, which persists until spring. Upper (adaxial) surfaces of leaves may be solid green or purple, with purple and/or white spots. Lower (abaxial) surfaces are usually dark purple, but individuals with light green abaxial surfaces occur as well. The objective of this study was to test potential adaptive functions of these anthocyanin patterns. The most common folivores targeting *Tipularia* during winter are deer. To test the hypothesis that adaxial purple coloration and spots reduce herbivory (through camouflage, aposematism, or dazzle effects), we conducted herbivory choice assays using motion-sensing cameras in the field, and pre- vs. post winter surveys at four sites in the piedmont of North Carolina. A photoprotective function of abaxial anthocyanins was assessed by comparing quantum yield efficiency of PSII of leaves with dark purple, light purple, or green abaxial leaf surfaces during exposure to high light stress. At all four field sites, the most common morphotype at the beginning of winter was purple-spotted, while solid purple was the least. Preliminary data collected during 2019-2020 field season showed that purple-leaf morphotypes incurred the least herbivory (43% survivorship) during winter, while green and purple spotted morphotypes were

similarly browsed (22-25% survivorship). We are currently collecting data at three additional field sites. Deer herbivory choice experiments are also presently underway. Light-stress experiments showed that adaxially-purple morphotypes incurred significantly less photo-oxidative stress following sustained (2h) high-light exposure compared to green leaves with low, medium, and high abaxial anthocyanin; however, our experiment could not clearly resolve differences between abaxial morphotypes, and is currently being repeated. These preliminary results suggest that that deer herbivory may be a significant driver of natural selection for adaxial leaf color patterns in this species.

P163 - The influences of soil on plant communities on six Lower Mississippi River islands

Mathew Jones, Grace McCartha, Caitlyn Sims, Brendan Kosnik, Ben Benton, Scott Mangan, Travis Marsico

Arkansas State University, Jonesboro, AR

Mississippi River islands are fascinating botanically because they have periods of flooding that influence plant species dispersal and persistence. Flood duration varies with elevation on islands, but the effects of flood duration on plant communities and soils remain understudied. Increases in inundation are known to have positive effects on soil nutrient cycling in alluvial soils. Our objectives were to investigate soil abiotic properties at different elevations of six Lower Mississippi River islands to determine whether river hydrology is related to soil properties of these islands. We hypothesized that soil texture and nutrients are related to elevation (a proxy for inundation or flood period) and variation in plant species richness and compositional similarity on Mississippi River islands. Specifically, we predicted that soils vary in their physical and chemical make-up among different elevations, and this influences species richness and abundance because of varying water holding capacity and nutrient levels. Fifty-nine 100m^2 plots were sampled for plant diversity and soils across six Mississippi River islands at three elevation classes. A composite soil sample was taken within each plot and was analyzed for nutrients, percent moisture, and texture. Most plots had alkaline soils due to an abundance of calcium. Calcium and all other nutrients show a direct correlation with soil texture, increasing as percent sand decreases. Four of the six islands show a significant positive correlation between elevation and percent of sand. Though soil texture is strongly correlated with nutrients, and texture correlates with elevation, vascular plant species richness has no relation with elevation or soil texture or nutrients. Additional investigation of plant community compositional patterns will be discussed.

P164 - A Proposal for Studying the Effects of Warming and Precipitation Treatments on Several Common Moss Species of the Southern Appalachian Mountains

Leigha Henson, Howard Neufeld

Appalachian State University, Boone, NC

Bryophytes often function as keystone species and bioindicators of forest integrity. Because mosses are sensitive to changes in atmospheric conditions and exhibit variation in their responses, they may influence ecosystem functioning out of proportion to their biomass. There are indications that climate change is beginning in the Southern Appalachian Mountains (SAM) with potentially unknown effects on this plant group. However, there have been no studies of moss ecophysiology and changes in bryophyte community structure and their responses to climate change in this region. I propose to investigate ecophysiological responses of six SAM moss species, three from open habitats and three from forest understories, to warming and changes in precipitation amount and timing using mesocosms. Higher temperatures may negatively impact photosynthesis (A) due to quicker desiccation while stimulating A during colder times of the year. Respiration may increase with elevated temperatures, leading to lower net carbon assimilation. Predicted increases in precipitation stochasticity may negatively impact A because they extend periods of desiccation, while deluges followed by drought could reduce the time available for mosses to photosynthesize, again leading to annual growth reductions. I propose to measure field gas exchange following rainfall events and during dry periods, in both summer and winter. I will also measure moisture, light, temperature, and CO2 response curves of mosses in the mesocosms. Stable carbon isotope ratios will be analyzed to indicate any changes in water use efficiency. I will also measure chlorophyll and carotenoid contents to assess the integrity of photosystem II. Changes in moss community composition, structure, or functioning may influence ecosystem resource and trophic dynamics. The results of this study should provide insight into the ecophysiological responses of Southern Appalachian mosses to predicted changes in the climate and help us to understand how these nonvascular plants may affect ecosystem functioning in the future.

P165 - Reassessment of Species Boundaries and Phylogenetic Relationships in the *Desmodium ciliare* complex (Fabaceae) Using Morphological and DNA Data

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Desmodium (Beggar's 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, beggar's 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 uncinate pubescent (with hooked

hairs), pilose (sometimes with uncinate 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 an analysis of nuclear ITS DNA were utilized. DNA data will be analyzed by both parsimony and Maximum Likelihood methodologies. Preliminary data has shown several sites of single nucleotide polymorphisms between members of the complex and morphological differences in leaf sizes and stem and leaf hair characteristics. 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.

P166 - The Effect of Defoliation and Heatwaves on Stomatal Density

Kai Johns, Benjamin O'Connell, Erin Wiley

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Stomata are little pores on the epidermis of leaves and other organs that regulate CO_2 uptake and H_2O loss. Stomatal density can be affected by the environmental conditions during leaf development, and this can influence the rate of gas exchange between the plant and the environment. However, we do not currently know how defoliation influences stomatal density. Therefore, in two separate experiments, we tested how defoliation and leaf size affect stomatal density in green ash (*Fraxinus pennsylvanica*), and how defoliation and temperature affect stomatal density of pin oak (*Quercus palustris*). In the first experiment, we defoliated mature, field-grown, green ash trees in early June 2020 and allowed them to regrow their leaves for 5 weeks. Stomatal density of the new leaflets was compared with that of leaflets from undefoliated trees (n=6 per treatment). However, reflush leaves produced after defoliation develop later in the summer under warmer temperatures, and the higher temperatures alone could also influence stomatal density. Therefore, to disentangle the impacts of temperatures and defoliation, 2-yr old, potted pin oak saplings were subjected to four treatments in May 2021: heat wave and defoliation, heat wave and no defoliation, ambient temperatures and defoliation, ambient temperatures and no defoliation. Stomatal density of new leaves produced in each treatment was then compared (n=6 per treatment). We found that defoliation significantly increased stomatal density in green ash trees, which may increase the rate of photosynthesis, allowing trees to make up for lost carbohydrates used in the regrowth of the leaves. While defoliation often reduces the size of leaves, we found that leaf size was not significantly related to stomatal density in ash. We discuss how changes in stomatal density following defoliation may be affected by a combination of changes in carbon demand, higher temperature during growth, and alterations in leaf size.

P167 - Evidence of cryptic hybridization between divergent lineages of temperate bamboos in the genus *Pleioblastus* (Poaceae)

Morgan Brown, Jimmy Triplett

Jacksonville State University, Jacksonville, AL

Japanese river bamboo (*Pleioblastus simonii*, kawadake) is an ecologically important species of temperate bamboo native to Japan. This species is widely known and historically important in Japanese rural farm life. Based on morphological data, Japanese river bamboo is recognized as a major lineage in genus *Pleioblastus* (section *Medakea*). However, recent studies suggest that Japanese river bamboo may be a species resulting from previously undetected hybridization (also known as cryptic hybridization). Bamboos in *Pleioblastus* exhibit overlapping variation in leaf and stem characteristics, making them hard to identify on the basis of morphology alone (a common problem in plant taxonomy). Cryptic hybridization is a potential explanation for this problem. The role of hybridization in natural plant populations has been studied since the 1950s, however little is known about this phenomenon in the evolution of bamboos. The objective of this study is to analyze molecular data (AFLP and nDNA) to test the hypothesis that *P. simonii* is a cryptic hybrid. Current data provide compelling yet conditional evidence in support of this hypothesis, while also suggesting that ongoing introgression and diversification has obscured that ancestry. We will discuss various analytical techniques from population genetics and phylogenetics that are being used to shed light on this problem. Results of this study provide an example of reticulate evolution in the origin of plant diversity and help reveal why molecular data is an important tool for taxonomic identification.

P169 - Revealing cryptic species in the Japanese Nezasa bamboos (*Pleioblastus* section *Nezasa*, Poaceae) using AFLP markers

Ryan Long[1], Jimmy Triplett[2]

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The genus Pleioblastus is a complex group of Southeast Asian temperate bamboos with 7-21 species, depending on the taxonomic authority. We hypothesize that the taxonomic complexity of the group is due to previously undetected occurrences of hybridization and subsequent backcrossing between filial and parental lineages, creating one or more cryptic hybrids. This is supported by recent research on the temperate bamboos that reveal hybrids at generic and intergeneric levels. This poses the question of where to draw the distinction between species' designations within Pleioblastus. The objective of the current study is to test the hypothesis that Pleioblastus section Nezasa is a mix of parental and hybrid lineages using data from AFLP markers and a combination of tree-building (PAUP) and genotypic assignment analyses (STRUCTURE, NEWHYBRIDS). This is critical to understanding the taxonomy of this group and may have implications in conservation due to hybridization-induced extinction. The current data support the hypothesis that hybridization has had an important role in the evolution of Pleioblastus section Nezasa, and highlight two major lineages (Nezasa I and Nezasa II) and hybrids between these lineages.

P170 - Exploring the correlation between anthocyanins in autumn leaves and seasonal leaf N, leaf mass per unit area, and phenolics

Sarah Smith, Cynthia-Mae Hunt, Corinne Gumpman, Nicole Hughes

High Point University, High Point, NC

The functional significance of autumn leaf coloration is an issue currently debated by plant physiologists and evolutionary biologists. Plant physiologists argue that red anthocyanin pigments evolved in trees adapted to cold and bright conditions in autumn, and function in photoprotection, while evolutionary biologists argue that red coloration coevolved as a signal to insects choosing host trees during autumn (e.g. aphids) that the tree is poor in quality. In a recent paper we argued that N-deficiency (known to induce leaf reddening in many species) should simultaneously increase the need for photoprotection *and* render leaves low-quality to insects, making both hypotheses simultaneously viable. However, so far the inverse relationship between leaf N and autumn reddening has only been demonstrated in maples. The objective of this study was to use populations of trees (5 species representing 3 orders) exhibiting varying degrees of reddening, to test the hypothesis that individuals with redder leaves have lower leaf N. Species studied included *Quercus phellos, Quercus nuttallii, Ulmus americana, Parrotia persica*, and *Pistacia chinensis*. For each species, at least 10 established individuals in sun- exposed parking lots were sampled, in various locations around the Piedmont of North Carolina. Additionally, we measured other plant defenses known to increase under N-deficiency, including carbon-based defenses (phenolics) and leaf mass per unit area. Data collection is currently underway.

P171 - Curatorial Internship with the Furman University Natural History Collections

Jack O'Brien, Ashley Morris

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The Furman Natural History Collections (FUNHC) are housed in the Charles H. Townes Science Center on the Furman University campus. The collections include invertebrates (primarily insects), small vertebrates (reptiles, amphibians, and small mammals), and plants. In Summer 2021, we created a new undergraduate internship position through which I gained experience in collections management, primarily in the herbarium (FUGR) and small vertebrate collections. We worked with herbarium staff from Clemson University (CLEM) to learn the flat specimen digitization workflow for the SC contingent of the SERNEC effort (Southeast Regional Network of Expertise and Collection). Approximately 4,000 specimens from FUGR were barcoded, skeletally databased, and imaged. In the vertebrate collections, ethanol was replaced with fresh solution and jar lids replaced according to color coding and apparent desiccation importance for over a hundred specimens. Collections were highlighted on social media throughout the summer, which drew the attention of donors wanting to contribute their lifes' work. One such donation included several dozen ancient shark and whale fossil specimens. Finally, I assisted Digital Specialists in the James B. Duke Library at Furman to digitize a collection of several hundred 35mm slide photographs (landscapes, plants and people in the Western US) taken by the late Dr. Catherine Keever. These photos are part of an ongoing tribute project in her honor called The Catherine Keever Project. While much more work is needed to raise the profile of collections both on and off campus, great strides through word of mouth, educational, and digital engagements have improved recognition of our collections among faculty and students within the university.

P172 - Quantifying differences in plant community composition and soil nutrients between pimple mounds and matrix of a remnant prairie

Ben Benton, Brendan Kosnik, Grace McCartha, Caitlyn Sims, Travis Marsico, Scott Mangan

Arkansas State University, Jonesboro, AR

Understanding how high-quality plant communities assemble is crucial for effective restoration of disturbed prairie ecosystems. Several mechanisms contribute to the maintenance of diverse prairies, but how the relative importance of these mechanisms may change across spatial scales remains largely unexplored. Prairie pimple mounds provide an ideal system to study the relative importance of below-ground biotic and abiotic factors to the assembly of prairie plant communities, largely due to the unique plant communities of pimple mounds and distinct topographical changes over a small spatial scale. This study aims to determine plant species composition and regulatory mechanisms of pimple mounds in Cherokee Prairie Natural Area, one of the largest intact Arkansas River Valley Ecoregion prairies. In a recent field study, we found that both plant communities and soil nutrient profiles of the mounds were distinct from adjacent prairie matrix. While there was some overlap in species present, the dominant ground cover changed in the transition from prairie matrix to mound. We also found mound soil had higher levels of available macronutrients such as phosphorus and calcium relative to prairie matrix soil. These data will be used to inform the design of a reciprocal transplant greenhouse experiment to determine how physical and chemical soil characteristics interact with microbial communities to influence plant community assemblage.

P173 - Distribution and ecology of the Genus *Hypericum* (Hypericaceae) in Mississippi based on direct examination of herbarium specimens, field work, SERNEC, and iNaturalist.

Michael Wayne Morris[1], Heather Sullivan[2]

[1]Troy University, Troy, AL, [2]Mississippi Dept. of Wildlife, Fisheries, and Parks, Jackson, MS

An estimated 420 species have been recognized in the genus *Hypericum* A. L. de Jussieu in the Hypericaceae. *Hypericum* species are present on every continent except Antarctica. In Mississippi, 23 native and one introduced *Hypericum* species have been documented: *H. brachyphyllum, H. canadense, H. cistifolium, H. crux-andreae, H. drummondii, H. fasciculatum, H. frondosum, H. galioides, H. gentianoides, H. gymnanthum, H. hypericoides, H. lobocarpum, H. mutilum, H. myrtifolium, H. nudiflorum, H. perforatum, H. prolificum, H. pseudomaculatum, H. punctatum, H. setosum, H. sphaerocarpum, H. stragulum, H. suffruticosum,* and *H. virgatum.* Both *H. canadense* and *H. myrtifolium* are on the state tracking list, and *H. fasciculatum, H. nudiflorum,* and *H. pseudomaculatum* are on the state watch list. Habitats supporting populations of native *Hypericum* species include pond cypress swamps and marshes, frequently burned savannas and pitcher plant bogs, rich deciduous woodlands and adjacent meadows, prairies and chalk outcrops, and dry pinelands and sandhills. From November, 2016 through October, 2021, *Hypericum* specimens in the following herbaria were examined at their respective locations: University of Mississippi (MISS), Mississippi State University (MISSA), University of Southern Mississippi (USMS), Delta State University (DSC), Institute for Botanical Exploration (IBE), Mississippi Museum of Natural Science (MMNS), and the Southern Weed Science Laboratory (SWSL). In 2021, specimens in herbaria outside of Mississippi were examined online through SERNEC, and digital images of *Hypericum* species in Mississippi were analyzed on iNaturalist. Information on the distribution and habitats of *Hypericum* species in Mississippi will be presented. This research was partially supported by a Troy University Faculty Development Grant, by National Science Foundation grant DBI-1203687, and by the Mississippi Museum of Natural Science Foundation.

P174 - A comparative analysis of the trade-offs between tree carbon storage and beef production in temperate and tropical pasturelands

Bela Starinchak, Heather Griscom

James Madison University, Harrisonburg, VA

Restoration is the most effective natural climate solution, with the potential to sequester 37% of the carbon dioxide (CO2) needed to reach the mitigation goal outlined in the Paris climate agreement. Nevertheless, novel restoration efforts must be implemented before this potential can be maximized. Cattle pastures offer an underutilized opportunity to increase global restoration efforts and carbon storage potential through the adoption of agroforestry management strategies. Yet, the impact of increased tree carbon on cattle production is not well documented across differing regions and as a result, farmer adoption of such strategies remains low. Furthermore, traditional carbon accounting methods are likely not as accurate in these systems, due to the detailed integration of environmental components and regional variation in land management techniques. As such, the aims of this study are (i) to evaluate the impact of carbon storage in the form of increased tree cover on the amount of cattle per hectare a pasture can sustain in both temperate and tropical ecosystems, (ii) to determine the error in remotely calculated carbon estimates for pastoral landscapes using in-situ measurements, and (iii) to further the understanding of farmers' rationale for planting/conserving or removing trees in their pastures and to identify barriers to enrolling in programs that provide aid for incorporating trees into cattle production systems. To accomplish these goals, a specific carbon accounting protocol was developed for cattle pastures that verifies remote tree group classification through ground-truthing carbon estimates in Rockingham County, Virginia, USA, and the Los Santos province in Panama. By clarifying the relationship between tree carbon and cattle production with a specialized carbon accounting protocol, as well as by improving the understanding of farmer motivations, the development of more specific and thorough guidance for tree integration and carbon accounting in these systems will be possible.

P175 - Distribution and ecology of the Genus *Polygala* (Polygalaceae) in Mississippi based on direct examination of herbarium specimens, field work, SERNEC, and iNaturalist.

Michael Wayne Morris[1], Heather Sullivan[2]

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Polygala Linnaeus includes approximately 400 species in the Polygalaceae, and the genus is widespread on a global scale. In Mississippi, 20 *Polygala* species have been recorded: *P. ambigua, P. appendiculata, P. balduinii, P. boykinii, P. brevifolia, P. chapmanii, P. crenata, P. cruciata, P. curtissii, P. cymosa, P. hookeri, P. incarnata, P. leptostachys, P. lutea, P. mariana, P. nana, P. polygama, P. ramosa, P. sanguinea,* and *P. verticillata.* Habitats for the genus as a whole range from swales on coastal barrier islands, to pond cypress depressions, bogs, flatwoods, and pine savannas, to chalk outcrops in prairies, and to sandhills and upland pine-hardwood forests and adjacent clearings and old fields. Eight species, *P. ambigua, P. appendiculata, P. balduinii, P. chapmanii, P. crenata, P. curtissii, P. hookeri,* and *P. leptostachys,* are of conservation concern; and *P. boykinii, P. brevifolia,* and *P. verticillata* are on the state watch list. From November, 2016 through October, 2021, *Polygala* specimens in the following herbaria were examined at their respective locations: University of Mississippi (MISS), Mississippi State University (MISSA), University of Southern Mississippi (USMS), Delta State University (DSC), Institute for Botanical Exploration (IBE), Mississippi Museum of Natural Science (MMNS), and the Southern Weed Science Laboratory (SWSL). In 2021, specimens in herbaria outside of Mississippi were examined online through SERNEC, and digital images of *Polygala* species in Mississippi were analyzed on iNaturalist. Information on the distribution and habitats of *Polygala* species in Mississippi will be presented. This research was partially supported by a Troy University Faculty Development Grant, by National Science Foundation grant DBI-1203687, and by the Mississippi Museum of Natural Science Foundation.

P176 - Blacks Run: A Novel Approach to Assessing Urban Stream Restoration

Julia Portmann, Shannon Gillen, Bela Starinchak, Heather Griscom

James Madison University, Harrisonburg, VA

Urbanization has drastically changed natural landscapes. As urban spaces increase, tree cover decreases with wildlife habitat, while hampering natural ecosystem functioning. This study presents a unique approach to assessing urban restoration by sampling bird diversity, aquatic macroinvertebrates (Hilsenhoff Biotic Index (HBI) and abundance), and tree carbon storage along Blacks Run, in Harrisonburg, Virginia. Simple and multiple linear regressions were conducted with explanatory variables including time since restoration, distance to urban core, impervious cover, and road density. The best predictors of bird diversity were time since restoration, percent impervious cover, and distance from the urban core (R^2=0.924, p=0.045). Bird abundance and bird richness were best predicted by time since restoration, percent impervious cover, road density, and distance from urban core (R^2=0.9991, p=0.0202; R^2=0.9985, p=0.026, respectively). The HBI was significantly predicted by the percent tree and forest cover with distance to urban core (R^2=0.908, p=0.013), while invertebrate abundance was best predicted by percent impervious, time since restoration, and distance to urban core together (R^2=0.986, p=0.008). Total tree carbon significantly increased as the distance to the urban core increased (R^2=0.823, p=0.012). Overall, distance to urban core was highlighted as one of the most important variables for predicting restoration success. Other factors such as increasing tree cover and reducing impervious surfaces around streams will also have meaningful impacts on improving urban habitat. By assessing restoration progress using both taxonomic diversity and environmental characteristics, a more thorough understanding of the efficacy of restoration projects is possible. Future research on urban green spaces adopting this multi-taxa approach will help inform best practices for restoration implementation and monitoring.

P177 - The Effect of Past Augmentation on the Fitness of the Federally Endangered Southern Appalachian Endemic *Geum radiatum* Michx.

Morgan Gaglianese-Woody, Matt C. Estep

Appalachian State University, Boone, NC

Geum radiatum Michx., or spreading avens, is a federally endangered perennial in Rosaceae. It inhabits high-elevation rock outcrops, spreading along a rhizome within rock cracks and crevices. The long-lived hexaploid is confined to fifteen fragmented locations above 1500 meters along the North Carolina and Tennessee border. Previous studies have concluded that it is vulnerable to various disturbances due to its small range, fragmented populations, and life history, and is threatened by extinction within the next several decades. There is therefore a dire need for integrative conservation management strategies that consider genetic factors. Using genotyping technology and a long-term demographic dataset, we will quantify the effect of a past augmentation on the fitness of admixed generations within the Roan Mountain metapopulation. The aim of this study is to determine if a genetic rescue occurred and help ascertain if genetic rescue is a viable management strategy for G. radiatum and long-lived perennials alike.

P178 - Predictive niche modeling for the identification of cotton, corn, and grape pathogens of greatest concern in Texas

Christopher Randle[1], Laura Bianchi[1], Austin Brenek[2], Jesus Castillo[1], Nicholas Galle[1], Kayla Hankins[1], Kenneth Nobleza[1], Nicholas Reger[1], Justin Williams[1]

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As a border state experiencing both heavy traffic in foreign imports and serving as the nation's second-leading agricultural producer, Texas is particularly vulnerable to invasive crop pests and pathogens. Further, as a large state experiencing extreme north-to-south and east-to-west variation in climate, soils, and vegetative cover, Texas potentially provides a wide range of suitable habitat in which crop pathogens and pests could persist, and from which they could be transported to the croplands of neighboring states. Corn, cotton, and emergent viniculture are identified as leading areas of agricultural concern in the state of Texas. Ecological niche models allow prediction of habitats suitable for pest and pathogen persistence in Texas given occurrence and bioclimatic data from their native range. In this study, MaxEnt, Boosted Regression Trees, and Ensemble models were used to project areas of Texas in which habitats are suitable for colonization by non-native pests and pathogens of corn, cotton, and grapes to 1) identify global hotspots from which pests and pathogens are most likely to be transported to Texas, 2) rank pests and pathogens from greatest to least concern for persistence in Texas croplands and natural habitats, and 3) identify areas of Texas most likely to serve as suitable habitat to dangerous pests and pathogens. Europe, southeast Asia, and southeast Brazil harbor habitats most suitable for persistence of species of greatest concern in Texas. Generally speaking, nearly all of Texas is suitable to harbor at least one pest species with *Diabrotica speciosa* (cucurbit beetle), *Lobesia botrana* (European grape-vine moth), *Spodoptera littoralis* (African cotton leafworm) and *Anthonomus grandis* (Boll Weevil) potentially occupying the largest suitable area in Texas, with greatest habitat suitability along the gulf coast along and its river drainages, and a decline in suitability from east to west.

P179 - Cross amplification of genetic markers from economically significant *Allium* species for use in genetic diversity studies of the native onion, *Allium tricoccum.*

Alexandra DelTurco[1], Jen Rhode Ward[2], Matt C. Estep[1]

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

Allium tricoccum Ait. is a herbaceous perennial most commonly known as Ramps. Ramps are native to eastern North America and have long been harvested by Indigenous American cultures. In recent years, Ramps have become a highly prized forage, with festivals celebrating the coming of spring often accompanied by Ramp eating contests. Although not a rare plant, the species' growing popularity has led to overharvesting and population declines throughout its native range. In order to better understand the current genetic diversity of Ramps and plan for sustainable harvesting into the future, a set of polymorphic genetic markers are needed. The purpose of this project is to cross-amplify 25 microsatellite markers from economically significant *Allium* species, such as *A. fistulosum* (Bunching onion), *A. cepa* (Common onion), and *A. sativum* (Garlic). This work will provide tools for population genetic studies of *Allium tricoccum* and can inform conservation management decisions.

P180 - Wildfires and Soil Microbe Biodiversity

Tori Gyorey, Jennifer Kovacs

Agnes Scott College, Decatur, GA

As global climate change creates warmer and drier conditions, the number of wildfires can increase, this can have far-reaching impacts on the organisms within these ecosystems. In addition to affecting the animals and plants within these ecosystems, fires can also affect soil microbial community composition. In 2016 there was the Chimney Tops 2 Fire near Gatlinburg, Tennessee that burned through most of the Great Smoky Mountains National Park. Prior to the fire, a long-term ecological study was established through the NSF National Ecological Observatory Network project that among other things documented soil microbial community composition at multiple plots throughout the park, which continued after the fires. We used a portion of this data to study the association between the biodiversity of soil microbes and fire. We compared the soil microbial community in soil samples before fire and after on research plots that burned through programming language Python. We predicted that the presence of the wildfire would cause soil microbe biodiversity to decrease. We were also interested in looking at how burn severity might impact the biodiversity of soil microbial communities. Soil microorganisms are essential to fertilizing the soil, cycling nutrients, and decomposing organic matter, so changes in soil microbial biodiversity can negatively impact its environment and make it more difficult to recover from natural disasters. Therefore, it is important for us to evaluate the impacts of wildfires on soil microbial communities to predict and potentially mitigate a huge loss of microbial diversity that allows that environment to thrive.

P181 - Chromosome number and ploidy levels of Virginia spiraea, and implications for conservation of this threatened species

Keegan Jenkins[1], Jen Rhode Ward[2], Matt C. Estep[1]

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Spiraea virginiana Britton (Rosaceae) is a federally-listed rare, clonal shrub that inhabits riparian zones within the Tennessee and Ohio River drainages. The species requires periodic geophysical disturbances, usually in the form of flooding, to remove competition from woody shrubs and to facilitate dispersal of ramets. Sexual reproduction has not been observed under field conditions, and controlled matings result in low seed production and/or viability. Determining the role of chromosome segregation is an important step towards understanding barriers to sexual reproductive barriers experienced by this species, possibly allowing shifts in restoration approaches. Cytogenetic investigations were carried out on a series of Virginia spiraea individuals, propagated asexually from field-grown progenitors. Inflorescences were collected a few days before anthesis and preserved in Carnoy's fixative. Chromosome squashes were prepared using acetocarmine to visualize chromosomes during meiosis. This study aimed to verify published chromosome numbers and identify any chromosome abnormalities visible during meiosis that might be a contributing factor to sexual reproductive barriers within this species.

BBB Talks

BBB Talk 1 - Novel Lead Compounds demonstrating anti-biofilm properties in *Staphylococcus aureus* may act as Nor-A efflux pump inhibitors.

Abdulraheem Kaimari

Mercer University, Macon, GA

Numerous studies have shown that bacteria quantify their density and collectively carry out a certain response with a communication mechanism known as quorum sensing. Biofilms are a type of virulence factor that forms once a bacterial quorum is reached within the host, preventing the host's immune system from detecting and ultimately eradicating these pathogenic bacteria. Efflux pumps may also be involved in biofilm production. These pumps are transport proteins that are responsible for the extrusion of various substances, including toxins, quorum sensing molecules, and biofilm components. The increased activity of efflux pumps has allowed antibiotic-resistant bacteria to increase their survival rates. This study tests certain drugs that were designed to resemble quorum sensing signaling molecules to inhibit biofilm formation. Since these drugs also have structural homology with known Nor-A efflux pump inhibitors (EPI) in *S. aureus,* we tested their activity on this pump. Fourteen of our previously synthesized drugs share this structural homology, with three of them revealing significant biofilm reduction in SA-1199 (wildtype) and SA-1199B (Nor-A overexpressor) but not in SA-K1758 (Nor-A knockout). This indicates that the drugs function in targeting the Nor-A pump rather than as competitive inhibitors at the receptor sites of the *S. aureus.* The conjugated aromatic ring with alternating electron-withdrawing and donating groups on the ortho and para positions appear to affect the inhibitory characteristics of these drugs. Developing a cocktail of drugs that curtail quorum sensing and inhibit efflux pump activity can maximize biofilm inhibition in *S. aureus*.

BBB Talk 2 - The harder they fall: Measuring the decline of a green ash swamp forest due to emerald ash borer damage in North Carolina

Arilyn Lynch, Emma Halstead

Catawba College, Salisbury, NC

The Emerald Ash Borer (EAB) is an invasive species to the central piedmont of North Carolina. Our goal is to measure the decline and patterns of change in a Green Ash (*Fraxinus pennsylvanica*) dominated swamp forest in the Catawba College Fred Stanback Jr. Ecological Preserve (FSJEP). In the fall of 2019 we established six, 200 m^2 plots using a nested plot design to measure changes in the canopy, sapling, and herbaceous vegetation. We resampled the plots in fall 2020 and 2021. Our data indicated low diversity in the tree canopy, tree importance values in descending order, green ash, sweet gum (*Liquidambar styraciflua*), red maple (*Acer rubrum*), black willow (*Salix nigra*), American elm (*Ulmus americana*), and the American Sycamore (*Platanus occidentalis*). In Fall of 2019, 2020, and 2021, green ash trees were visibly showing signs of EAB infection. In Fall 2019 no ash trees were standing dead and 11% and 37% of the original ash trees were dead in fall 2020 and 2021, respectively. The importance value of the green ash trees declined from 2019 (IV = 1.62) to 2021 (IV = 1.56). Canopy coverage declined strikingly from 73.1% to 18.5% from fall 2020 to fall 2021. Successional trends based on canopy mortality and sapling dynamics will be presented. Finally, we used a fixed-wing drone with a multispectral sensor to collect baseline data to evaluate change in vegetation in the Fall of 2021.

BBB Talk 3 - Investigating Dietary and Microbial Community Variation between Urban and Rural Coyote (Canis latrans) Populations

Candace Swepson

Catawba College, Salisbury, NC

Human populations continue to expand their ecological footprint resulting in habitat loss and change for wildlife species. In Rowan County, NC and around the USA, populations of *Canis latrans* (Coyote) habitat are shared closely with humans. For omnivores such as *C. latrans*, human activity may result in alteration of their prey and plant food availability. This study seeks to investigate the urban-rural gradient on *C. latrans* diet. We collected scat samples across an urban-rural gradient and 1) conducted a stable isotope analysis to compare the δ13C and δ15N signatures, 2) investigated microbial communities using differential and selective media, and 3) analyzed the contents via 18S rDNA barcoding and 16S rDNA barcoding to estimate diet and microbial communities. Differences in the prey choice through isotope signatures, barcoding analysis and microbial content of *C. latrans* scat between the urban and rural environments will be presented to further understand variation in coyote diet across an urban-rural gradient.

BBB Talk 4 - Investigating the Peroxidation-Associated Mechanism of Artemisinin-heme Adducts in a Yeast Model System

Morgan Pearson, Everette Rhymer

Catawba College, Salisbury, NC

Abstract:

Artemisinin continues to be the most promising antimalarial treatment in human populations, due to its ability to rapidly kill *Plasmodium* parasites with lower required concentrations. Currently, artemisinin and its derivatives are used in combination therapies, to help stave off parasite pharmacokinetic resistance. Chemically, artemisinin is a naturally occurring sesquiterpene lactone, containing an endoperoxide pharmacophore. Heme iron-mediated cleavage of the endoperoxide within the parasite digestive vacuole is hypothesized to generate cytotoxic metabolites capable of alkylating heme and damaging cellular macromolecules, such as proteins; however, the exact mechanism by which artemisinin exerts its antimalarial activity is still disputed. Our laboratory has demonstrated a previous connection between artemisinin-heme adduct formation and peroxidation of neutral lipids, suggesting a mechanism by which artemisinin activation leads to cellular oxidative peroxidation and death. To further address the question of artemisinin toxicity mechanisms within the malaria parasite, we have adapted our *in vitro* assay to a yeast model system that serves to investigate the heme-mediated ability of artemisinin to induce cellular toxicity via lipid peroxidation. Specifically, we hypothesize in a heme-enriched environment, that simulates malaria parasites, artemisinin will form heme adducts that will in-turn initiate lipid peroxidation cascades and induce apoptosis in yeast cells, as demonstrated through cell viability and peroxidation detection assays.

BBB Talk 5 - Atypical Magnesium Requirement of a Rare Plant Species, *Pediomelum piedmontanum*

Matthew Zimmerman

Augusta University, Augusta, GA

Pediomelum piedmontanum, (Dixie Mt. Breadroot), is a recently discovered rare legume species. Only three populations are known, one found on serpentine soil in Georgia (S1) and the others on phyllite soil in South Carolina. Both soil types contain elevated concentrations of magnesium (Mg) as well as other heavy metals. In previous experiments, propagation of *P. piedmontanum* was unsuccessful in potting soil, in which plants displayed symptoms of Mg and nitrogen (N) deficiencies, ultimately leading to high mortality. Since these populations are adapted to Mg rich soil, it was hypothesized that survival rate and growth of seedlings would be greater in Mg enriched soil than in unenriched potting soil. To test this hypothesis, seedlings from one of the phyllite population and the serpentine population were transplanted into one of the following soil enrichments: 50µM $MgSO_4$, 100µM $MgSO_4$, or unenriched controls. The results showed that seedlings in magnesium enrichments displayed higher survival rate and mean shoot growth than the controls. Atypical Mg requirements are noted in literature for some plant species adapted to serpentine, but this is a unique discovery for a population adapted to phyllite. We also hypothesized that *P. piedmontanum*, like many legumes, depends on symbiotic relationships with N-fixing bacteria. This hypothesis was tested by incorporating a rhizobia mix. However, no root nodules were observed when rhizobia were introduced. Overall, these experiments provide greater insight into the atypical nutrient requirements and other adaptations of this rare and unique plant species.

BBB Talk 6 - Reproductive effects of BPA and BPA derivatives in *Daphnia pulex*

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 examined the effects of BPA, and BPAF in varying concentrations on the reproduction rates and age of sexual maturity. Due to the estrogenic effects of BPA and BPA derivatives, our results indicated that the reproduction rates were substantially affected in *D. pulex.* As such, we found that BPA and BPAF exposure led to earlier sexual maturity, larger brood size, and interrupted reproductive cycles. Our findings could highlight possible consequences of BPA and BPAF exposure on *D. pulex* populations, freshwater ecosystems, and human health.

BBB Talk 7 - Neutrophil Fungal Clearance and Inflammation in SARS-CoV-2 Lung Microenvironment

Claire Gallion

Birmingham-Southern College, Birmingham, AL

To study the effects of SARS-CoV-2 infection on fungal clearance by neutrophils, we optimized a fungal killing assay to test whether lung microenvironment alterations occurring in severe viral infection impact neutrophils' ability to kill *A. fumigatus*. We also incubated neutrophils with varying concentrations of key cytokines (RANTES, IL-8, IFN-ß, ENA-78, and GMCSF) present in bronchoalveolar lavage samples from severe COVID-19 patients, then measured these neutrophils' clearance of *A. fumigatus*. Ratios of 100,000 conidia to 250,000 neutrophils over a 10-hour incubation period show approximately 50% less fungi compared to controls without neutrophils. Cytokine assay results show a

significant increase in neutrophil fungal killing when RANTES and IL-8 are added. No significant difference in fungal killing was observed for IFN-ß, ENA-78, or GMCSF. Further investigation into the effects of cytokine elevation during COVID-19 on the innate immune system's fungal clearance is warranted.

BBB Talk 8 - Occurrence of Kanamycin-Resistant Bacteria Along an Urban Hiking Trail in Nashville, Tennessee

Liz Bleyer, Grace Hawkins, Ashlynn Sherwood

Belmont University, Nashville, TN

Increased use of antibiotics in humans and animals has contributed to a rise in antibiotic resistance, undermining the efficacy of antibiotic treatments. This study examines the relationship between antibiotic resistant bacteria in the soil microbiome and human activity. Bacteria resistant to kanamycin were isolated from soil samples collected at twelve sites located various distances from a hiking trail in Nashville, Tennessee in September 2021. Antibiotic resistant bacteria were found in most all locations. Bacterial colonies were quantified and identified through PCR amplification and DNA barcoding. The diversity and abundance of kanamycin-resistant bacteria was greatest at the farthest point away from human activity. Sequence alignments were compared among bacteria found at multiple locations. The diversity and characterization of the bacteria provided additional insight on soil health and the distribution of the bacteria at the site. Future research should focus on investigating other factors that may contribute to differences in abundance and diversity of kanamycin-resistant bacteria, such as water flow, animal presence, and the occurrence of kanamycin-resistant bacteria in guts of soil invertebrates. This research contributes to the general understanding of how human activity relates to antibiotic resistance in the soil microbiome.

BBB Talk 9 - Identification of a Novel Protein Interaction that Elucidates the Mechanism of Idiopathic Recurrent Miscarriages in Women with NLRP2 and NLRP7 Mutations

Nayeon Son

Missouri State University, Springfield, MO

Mutations in NLRP2 and NLRP7 genes result in genetic maternal imprinting disorders. These genes have been identified to be maternal effect genes regulating early embryo development in idiopathic recurrent miscarriage. Previous research suggests that NLRP2 and NLRP7 regulate DNA methylation and immune signaling through inflammasome formation. However, the exact mechanisms underlying recurrent miscarriages are not known. In this study, we report a novel protein interaction of Human proliferation-associated 2G4 (PA2G4, aka: EBP1) with NLRP2 and NLRP7 through an unbiased yeast 2-hybrid screen of a human HeLa cell cDNA library. Protein interactions were confirmed by co-immunoprecipitation, confocal microscopy, and FRET analysis. Furthermore, global DNA methylation decreased in cells that overexpressed NLRP2/7 and EBP1. Our results further support the role for NLRP2/7 in regulating DNA methylation as a mechanism for recurrent miscarriages. Since EBP1 is implicated in apoptosis, cell proliferation, and differentiation, our discovery significantly advances our understanding of NLR biology and helps to explain the cellular pathways involved in idiopathic recurrent miscarriages.

BBB Talk 10 - Trematode Diversity in Molluscan Hosts in Northwest Louisiana

Kasey Moore, Sarah Sargent, Joshua Shelton, Cynthia Doffitt

Northwestern State University, Natchitoches, LA

Trematodes are parasitic flatworms with specific and complex life cycles, involving a molluscan host and one or two vertebrates, commonly a piscine host and an avian or mammalian host. The obligate nature of these parasites, and the ease of sampling from intermediate molluscan hosts, makes larval trematodes a promising bioindicator of vertebrate host species diversity within an ecosystem. Ultimately, this research aims to identify trematodes that infect local mollusk populations and examine their potential as vertebrate biodiversity indicators. In September and October 2021, 458 aquatic snails were collected from the Natchitoches National Fish Hatchery (Natchitoches, LA) production ponds containing either *Ictalurus punctatus* (channel catfish) or *Esox niger* (pickerel). Snails were subdivided into pools of approximately 10 individuals and housed in enclosures containing sterilized spring water. Snails were observed for 14 days to detect infected individuals, indicated by the release of cercariae (juvenile trematodes) into the surrounding water. Overall, 3.06% (14/458) of snails were found to be infected. These infected snails were housed individually in 10-mL sterilized spring water. Average daily cercariae counts were estimated by sampling 1-mL of the water in 0.1-mL aliquots from each enclosure each day over a total of seven days. Average cercariae released from each snail ranged from 244.6 to 5715 cercariae/mL/day. Subsamples of these cercariae were preserved for genetic sequencing and morphological identification. Of the cercariae collected, three morphologically distinct types were observed. Identification of larval trematode species is ongoing. This study will lead to further investigations involving infection studies, and/or vertebrate host surveys.

BBB Talk 11 - The Patent Pending HEFY Assay: A Novel Assay for Biofilm Inhibition in *Bacillus subtilis* and *Staphylococcus aureus*

Evan Floyd, Natalie Yaeger

Mercer University, Macon, GA

With the rise in the number of antibiotic-resistant strains of bacteria, an alternative approach to antimicrobial drugs is needed. Biofilm inhibition is one of the new alternative approaches to combat these antibiotic-resistant strains. The HEFY assay is an inexpensive, undergraduate accessible, and expedient way to quantify biofilm production. This assay uses 3D printed modified Petri dishes to analyze biofilm production in Congo Red using Image J, a free NIH-developed software. Two of our biofilm inhibitors, Tyrosine-trans-4-hydroxycinnamic acid (Tyr 64) and Glycine-trans-cinnamic acid (Gly-16), show consistent, quantifiable biofilm inhibition in the HEFY assay of 41.5 and 34.4 percent respectively within *Bacillus subtilis*. Preliminary results also show promise for the application of the HEFY assay with *Staphylococcus aureus*, with Tryptophan-4-phenolbuteric acid (Trp-37) and Tryptophan-trans-3,5-dibromo-4-methoxylcinnamic acid (Trp-69) showing 7.98 and 14.46 percent inhibition respectively. The consistency in replica testing within *Bacillus subtilis* surpasses the consistency in standard crystal violet assays. This assay could easily be adopted for quantifying biofilm in other bacterial and fungal pathogens.

BBB Posters

BBB1 - Does Genetic Deletion of p65 Alter Microglia Phenotype?

Ashley Koch

Augusta University, Augusta, GA

A glioblastoma (GBM) is a grade IV aggressive brain tumor that currently has no known cure. Part of GBM's aggressiveness results from the tumor's microenvironment being heterogeneous, which means it consists of a variety of cells that are recruited to the tumor. Macrophages are associated with many solid tumors and are often found in large numbers, which correlates with poor prognosis. Microglia, which are a type of macrophage specific to the central nervous system are one of the types of non-cancerous cells that make up the GBM tumor microenvironment and tend to be recruited to the tumor quickly. In early stages, microglia mostly have an M1 phenotype, which targets cancer cells, but as the tumor progresses, microglia tend to have an M2 phenotype, which is cancer promoting. The canonical nuclear factor-kappaB (NF-κB) signaling pathway has been implicated in the M1 to M2 phenotype transition. Our lab has generated a microglia specific mouse model that should lack the NF-κB transcription factor called RelA (or p65) in brain microglia. It is hypothesized that p65 deletion in microglia would inhibit the canonical NF-κB pathway from successfully making the M1 to M2 switch, which could potentially make treating GBM tumors more effective. Various primer combinations have been tested with harvested microglia cells from our animal model to determine genetic deletion of p65 via polymerase chain reaction and western blotting has been performed to determine p65 deletion at the protein level. To further explore our hypothesis, a variety of M1 and M2 markers will be used to determine gene expression levels via real-time PCR in control microglia and microglia lacking p65. Ultimately, control and p65 knockout microglial cells will be cultured with GBM tumor cells to observe how potentially altering microglial phenotype influences the aggressiveness of GBM.

BBB2 - Acute Effects of Thyroid Suppression on Maternal Behavior in a Rat Model

Sarah Monteiro, Joshua Thorpe

Mercer University, Macon, GA

Thyroid hormones play a crucial role in the development of the nervous system and its functions in adults. Thyroid-stimulating hormone (TSH) prompts the thyroid to utilize iodine to produce triiodothyronine (T3) and thyroxine (T4). These two hormones are important in metabolic processes, regulating body temperature, and maintaining adult brain function. Hypothyroidism results when the thyroid gland cannot produce enough T3 and T4. Approximately 0.5% of pregnant women have untreated hypothyroidism in the United States, but this can be much higher in other countries. In previous studies of hypothyroidism in developing rodents, results showed long-lasting effects of prenatal and early postnatal hypothyroidism where pups' later maternal behaviors as adults were impaired. Additionally, hypothyroidism during early postnatal development has significant effects on other behaviors, such as anxiety and social interactions with siblings. However, some of these long-lasting behavioral effects may be mediated by changes in the maternal behavior pups receive during the period of hypothyroidism. In our current study, we induced hypothyroidism beginning on the day the dams gave birth until pups were 23 days old via methimazole administration in drinking water (0.025%). This method consistently reduces thyroid hormone production. Then, we observed maternal behavior by measuring pup retrieval, as well as the time spent nursing, licking, carrying, and grooming pups. We are currently conducting behavioral testing and scoring these behaviors for analysis, and we hypothesize that dams will have impaired maternal behavior while experiencing hypothyroidism, which will affect the pups' development. If there is no effect of hypothyroidism on maternal behavior, then long-lasting effects on offspring behavior may be due to direct changes in neural circuits during development and independent of maternal behavior received. However, if we do find that maternal behavior is altered, then hypothyroidism may alter offspring neural circuitry through changes in maternal behavior.

BBB3 - Genetically Modified Bacteriophage-Microplastics Complex Formation for Potential Solution of Microplastic Pollution

Aubrey Stewart, Lauren Locke

Troy University, Troy, AL

The rapid increase of microplastics (MPs) in water has become a global environmental concern and a potential risk to human health. We propose to develop a new method to remove microplastics from water using genetically engineered M13 bacteriophages. M13 phages with high affinity to polyethylene (one of the most used plastics) will be selected from a phage library in biopanning method. The novel peptide sequence of the selected phage (pIII coat protein) will be displayed on the major coat proteins (pVIII) of the phage via phage display method. The novel peptide-displaying phages can form a complex with MPs in water. The phage-MPs complexes can be easily separated via centrifugation and an additional PE pipe filtration. As a first step, we are now preparing to monitor how WT-phage interacts with MPs as our control group data. We expect our result will guide us a new approach for solving microplastic pollution problems efficiently.

BBB5 - Environmental Mercury in High Rock Lake, North Carolina

Isobel Verbrugge, Joe Poston

Catawba College, Salisbury, NC

Environmental mercury can come from anthropogenic sources or from natural sources. High Rock Lake in central North Carolina has elevated mercury due to two anthropogenic point sources: a former battery factory and ash ponds from a former coal power plant. In previous work, sediment sampled from six locations downstream of the point sources had almost twice as much mercury as sediment from six locations upstream of point sources. This difference was not statistically significant, perhaps due to low statistical power. Thus, further analysis of High Rock Lake is needed. We will report results from an ongoing project in which we are analyzing sediment from twenty locations upstream of point sources for mercury, and twenty locations downstream of point sources. In addition to reporting the spatial variation in environmental mercury, we will discuss the implications of the levels of mercury we document.

BBB4 - Phenol-Sulfuric Acid Colorimetry for Quantifying Biofilm

Derrick Buie, Ebony Lumas, Kathryn Howe

Mercer University, Macon, GA

The formation and inhibition of biofilm production in pathogenic microbes has become an extremely important subject of research. This work focuses on the methods used to quantify biofilm. The crystal violet assay is an effective, cost-efficient, and time-efficient assay that undergraduate students can use to quantify biofilm. Additional assays used to confirm crystal violet results often require expensive equipment or are time-consuming, thus not feasible for an undergraduate classroom. A Phenol-Sulfuric acid method developed by Dubois was modified for accessibility, tested with biofilm inhibitors, and shown to be feasible and effective in an undergraduate classroom setting. Log phase bacteria were plated, grown, pelleted and the supernatant containing biofilm was removed and stained with a phenol/sulfuric acid mixture in 96-well plates. The modified assay was successfully able to identify a statistical difference between the DMSO control and the inhibitor/accelerator tested in *Bacillus subtilis*; moreover, the results support findings with crystal violet. The data collected suggest that the modified Phenol-sulfuric method can effectively quantify biofilm while being feasible for use in an undergraduate setting. Moving forward, the assay will be done in *S.aureus* and *P.aerguinosa* to determine the assay's effectiveness with additional bacterial species.

BBB6 - Effects of long-term storage on crude fat content of *Q. palustris* and *Q. alba* acorns

Cheyenne Villarosa[1], Sabrina Volponi[1,2]

[1]Bridgewater College, Bridgewater, VA, [2]University of Notre Dame, Notre Dame, IN

Quercus palustris and Quercus alba acorns are a primary component in many wild animal diets, particularly during preparation for winter. As such, they provide a natural, easily gathered food staple for wildlife recovering in rehabilitation facilities. We examined whether collection and temperature-controlled storage methods differentially affect the nutritional deterioration of crude fat in acorns to assess both caching by wildlife and to provide recommendations to rehabilitators. We collected acorns from Q. palustris in 2020 (N=8) and Q. alba in 2017 (N=11) in Bridgewater, VA, USA. Acorns were dried for 7 days using a fan or for 30 minutes in an oven at 93°C and then stored at room temperature hanging in onion bags, in the refrigerator, or in the freezer. We assayed fat content from all trees immediately after collection (baseline) and compared fat content after one month and six months of storage for both species and after 2 years of storage for Q. alba only. Storage at 4°C (refrigerator) resulted in germination of some Q. alba acorns and mold growth in both species. Although acorns from Q. palustris had significantly more fat than Q. alba acorns, individual trees varied widely, with greater variation among Q palustris. On average, drying, storage, and combination treatments resulted in greater losses in fat compared to baseline for Q. alba than Q. palustris, but not significantly. Our results suggest that acorns cached by species like squirrels (Sciurus sp.) do not vary significantly in fat content when recovered months later compared to acorns consumed directly from the trees. We recommend wildlife rehabilitators store acorns either in the freezer or at room temperature depending on their storage capabilities.

BBB7 - The Microbial Odyssey: Investigating the viability of commercial probiotics under physiological conditions

Kagan Hall

Catawba College, Salisbury, NC

The human gut microbiome is a complex and incredibly important part of the human body. The human microbiome plays a crucial role in maintaining the body's immune system, preventing gut permeability, and the metabolism of nutrients. As important as these are, it is equally important to maintain these bacterial populations. Our body has several non-specific defenses, such as digestive enzymes and stomach acid, that help protect against potential pathogens. Our goal is to test the viability of commercial probiotic sources after exposure to physiological conditions. Our initial results suggest that probiotic growth may be significantly inhibited by the conditions found in the human body, as demonstrated by our experiments using simulated gastric juice. These initial studies indicated limited growth of probiotic species from Activia yogurt after exposure to simulated gastric juices. We have expanded the experiment to include kefir and kombucha beverages. These fermented beverages have additional probiotic strains, such as *Bacillus coagulans*, that may be able to withstand the gastric conditions of the human gut microbiome. We will use Gram staining, selective media, and 16S ribosomal RNA sequencing to identify isolated bacterial species. We expect there to be an overall decline in probiotic viability in response to gastric exposure. This could limit the efficacy of commercial probiotic sources.

BBB8 - Local geographic variation in the secondary metabolites of *Usnea strigosa*

Ayla Edmiston, Lisa McDonald

Lander University, Greenwood, SC

Although the most common secondary chemicals of the lichen species *Usnea strigosa* have been described in different regions throughout the range of the taxon, very little work has been completed to describe local geographic variation in its secondary chemistry. In this study, we examined local geographic variation in the suite of secondary chemicals produced by *U. strigosa* by identifying and comparing the secondary metabolites of samples collected from 12 sites across Greenwood, South Carolina. Potential secondary metabolites of *U. strigosa* were identified using thin-layer chromatography. We predicted that the chemical variation we detected in the suite of chemicals produced by *U. strigosa* would be better explained by local geographic differences than by individual variation among lichen samples. Although individual lichen samples showed small differences in their secondary chemistry, we found significant local variation between collection sites (ANOSIM, $p = .001$) and visualized these differences using NMDS plots. Further research in this system will include identifying the specific secondary chemicals that are ubiquitous in *U. strigosa* and those that are responsible for the local variation we observed.

BBB9 - Investigation of temporal variation in secondary metabolites of *Usnea strigosa*

Carley Cannon, Lisa McDonald

Lander University, Greenwood, SC

The basic chemical composition of common lichens is often well known because it is required for the successful identification of lichen taxa; however, the ecological roles of the secondary metabolites produced by lichens are just starting to be investigated. In this study, we examined temporal variation in secondary chemistry for a lichen common to our region, *Usnea strigosa*. Between August and November, we collected 10 *U. strigosa* samples each week from downed limbs in a single population, and we used thin-layer chromatography to identify potential secondary compounds. In order to quantify changes in chemistry over time, we used ANOSIM which allowed us to detect differences between collection weeks. We then visualized our data using NMDS. We found what initially appeared to be temporal differences in secondary chemistry ($p = .001$). However, upon inspection of our NMDS plots, we found that the four groups identified in our ordination did not only differ temporally but also spatially (at the level of substrate or microscale). After removing the weeks in which samples were collected from different substrates (trees), we analyzed the remaining data (approximately 9 weeks of samples). In the subsequent NMDS plot, the samples were all part of the same group showing no obvious temporal variation in secondary chemistry. Upcoming research will include a description of substrate-level differences in chemistry and collection of additional lichen samples from the collection area that did not appear to show temporal variation.

BBB10 - Novel Lead Compounds inhibiting *Vibrio fischeri's* biofilm formation

Sophia Guo, Kathryn Howe, Daniel Mendoza, Brenton Puckett

Mercer University, Macon, GA

Studies have discovered that bacteria, such as *Vibrio fischeri,* communicate with their interspecies and intraspecies neighbors through quorum sensing; the ability to detect population density and respond with the release of signaling molecules. When population density exceeds a threshold, the resultant signals lead to responses such as biofilm production. Consequently, the production of this extracellular polymeric substance protects the pathogenic bacteria from the immune system's mechanism of eradication. Certain drug compounds have the potential to reduce or inhibit biofilm production in *Vibrio fischeri* by mimicking chemical messengers and blocking their quorum-sensing ligand-receptor sites. Several hundred novel-drug compounds were tested against this species and one of those drugs, Tyrosine-69-ether, showed statistically significant biofilm inhibition with a crystal violet assay. Biofilm inhibition averaged 60.6%, growth curves demonstrated no bacteriostatic activity with doubling time measurements, and use-dilution assays suggested no bactericidal properties of the signaling molecules. The inhibitor was formed through dehydration synthesis of a tyrosine derivative and a conjugated benzene ring with multiple electron-withdrawing functional groups. Other compounds with similar structure to Tyrosine-69-ether were tested, but showed no significant inhibition, pointing to important features in the drug that are most likely responsible for the inhibition. Future studies will include testing inhibition with compounds that have an ether group attached to an aromatic ring.

BBB11 - Heads up: The effects of age, sex, and group size on vigilance in white-tailed deer

Zachrey Swartzentruber, Elisabeth Howansky, Chandler Russian, Lisa McDonald, Emily Prince

Lander University, Greenwood, SC

In response to the threat of predators, white-tailed deer (*Odocoileus virginianus*) alter their behavior to increase survival. One such behavior, vigilance, is costly but can increase fitness and help avoid predation. Our past research found that solo deer are more vigilant in open habitats and in areas with temporary human disturbance (THD). In this study, we tested whether group size, age, or sex affected vigilance. We also investigated whether group vigilance varied with habitat type or THD. We collected data from images captured by camera traps in Upstate South

Carolina. Each observed deer was labeled vigilant if their head was higher than their back and not vigilant if their head was lower than their back. We hypothesized that adult deer would be more vigilant than juvenile deer and that females would be more vigilant than males. We also hypothesized that groups would be more vigilant than solo deer. Finally, we hypothesized that in groups, vigilance would be higher in more open habitats and in habitats with higher THD. In contrast to our hypotheses, we found that juvenile deer were significantly more vigilant than adult deer, and that males were significantly more vigilant than females. As predicted, we found that groups of deer were significantly more vigilant than solo deer. Habitat type had no significant effect on the vigilance of groups; however, groups were significantly more vigilant in areas with high THD than in areas with low THD. Our results suggest that deer in groups may be less vulnerable to predation because they are more vigilant than solo deer. Furthermore, the benefits of vigilance may outweigh the costs for juveniles, as well as for males. Overall, vigilance in white-tailed deer is complex and influenced by many different environmental and demographic factors.

BBB12 - Predation risk affects group formation of mammals in Upstate South Carolina

Elisabeth Howansky, Zachrey Swartzentruber, Emily Prince, Lisa McDonald

Lander University, Greenwood, SC

Mammals may form groups to access resources, care for offspring, and avoid predation. We hypothesize that in Upstate South Carolina predation is a driving force for group formation. Consequently, we expect groups will be more common in vulnerable prey species than they will be in mammals with lower predation risk. We predict mammals will also be more likely to form groups in open habitats where they are visible to predators. Finally, because temporary human disturbance (THD) has been observed to have a similar effect on mammals as predation, we predict that group formation will be more common when human disturbance is high. To test these hypotheses, we collected data using camera traps at sites with varying levels of human disturbance that include forest, edge, and open habitats. The photos captured were labeled by species and number of individuals. We used a Fisher's exact test to analyze the data collected from the images within each category (predation risk, habitat openness, THD). Groups were most frequently formed in mammals with the highest predation risk ($p<0.0001$), but mammals with medium to low predation risk were not significantly different in their group formation. Group formation was most common in open habitats and least common in forested habitats ($p<0.0001$). Any amount of human disturbance also caused group formation to be more common ($p<0.0001$). As predicted, groups are formed most often in prey species, in open habitats, and in areas with any human disturbance. Our results support the hypothesis that mammals form groups in response to the threat of predation.

BBB13 - Antibiotic Effectiveness of 5-Hydroxymethylfurfural Against Wound-Isolated Bacteria

Chase Bolding

Birmingham Southern College, Birmingham, AL

5-hydroxymethylfurfural – HMF – is a furanic compound formed during the Maillard reaction from the reduction of sugars in a heated and acidic environment. It has been shown to be a neo-forming contaminant with antioxidative, anti-allergic, anti-inflammatory, anti-hypoxic, anti-sickling, and anti-hyperuricemic effects. There is currently little study on the potential for HMF derived from a sustainable sugar source, such as honey, to be used against a variety of pathogenic bacteria. However, it is worthwhile to study potential alternatives to standard antibiotics due to increasing resistivity among pathogenic bacteria to modern antibiotic treatments. Honey has been used historically for treatment of wounds, and a basis for effectiveness has been described as a darker color and more pungent smell – end products of the Maillard reaction. Artificially manufactured honey as a sugar source with known HMF concentrations, determined quantitatively by the White Method, was utilized against 4 bacterial isolates. Kirby-Bauer assays and minimum inhibitory concentration assay techniques demonstrated the extent of antibiotic effectiveness of HMF against Streptococcus pseudintermedius, Pseudomonas aeruginosa, Bacillus mycoides, and Salmonella enterica. HMF showed a minimum bactericidal concentration of 30 µg/mL and inhibitory concentration of 20 µg/mL for all four selected bacteria as well as an average inhibition zone of 30 mm. HMF displays promising effectiveness against various kinds of bacteria, and greater study should be prioritized.

BBB14 - Evaluating Larvicidal Efficacy of Plant-based Extracts on *Culex* and *Aedes* Mosquito Vectors.

Everette Rhymer, Morgan Pearson

Catawba College, Salisbury, NC

The natural herb *Artemisia annua,* from which the highly effective antimalarial Artemisinin is derived, has demonstrated significant larvicidal effects on a variety of mosquito vectors involved in disease transmission. Although several mosquito species fulfill important ecological functions by serving as food sources and floral pollinators, controlling populations of those that harbor and transmit pathogens are of concern, especially in light of global climate change. As with antibiotics and other chemotherapeutics, insecticide resistance is a problem in mosquito vector population control. Furthermore, widely used synthetic insecticides may have detrimental effects on natural ecosystems and the overall health of untargeted species. The use of natural plant extract alternatives in larvicidal control offers the ability to reduce mosquito populations with a compound that is biodegradable, target-specific and less likely to develop resistance amongst mosquitoes. The Fred Stanback Jr. Ecological Preserve (FSJEP) at Catawba College is a highly diverse and species-rich habitat that is home to over 30 mosquito species, some of which are known vectors of infectious agents such as West Nile virus and Eastern Equine Encephalitis. Our previous efforts targeting *Culex restuans* from the Catawba College ecological preserve demonstrated significant larvicidal activity in extracts from *Poncirus trifoliata* fruit peel. To expand our knowledge of potential plant-based larvicidals in our own ecological preserve, extracts of herbaceous plants within *Artemisia, Piper*, and other genera will be evaluated for larvicidal activity against larval populations of *Aedes canadensis canadensis* and *Culex restuans*.

BBB15 - Better Filtration Design for Heavy Metals Palladium, Cadmium, and Chromium

Dalton Sharp, Kayla Janes

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. Few of those heavy metals are Palladium, Cadmium, and Chromium. These heavy metals are known for being extremely toxic and carcinogenic to humans. These heavy metals have been exceedingly prevalent in battery factories, car factories, pesticides, and in pharmaceutical labs. Our research is focused on the removal of Palladium, Cadmium, and Chromium ions using Diatomaceous Earth (DE) silica from the metal ions containing water samples and comparing the results with conventional activated charcoal as the filtration material. Previous findings from other research have shown that silica nanoparticles are effective in the removal of the heavy metal 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 the metal ions by ion-dipole interaction, which facilitates removing the ions from water. To determine the concentration of the metal 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 the metal ions up to 540 - 560 ppm (mg of $Pd2+/L$). We found that the filtration ability of the DE system was enhanced when DE was mixed with activated charcoal for the filtration of the metal ions from water.

BBB16 - Examining the toxicological and molecular effects of BPA on Sf9 insect cells

Kasey McLamb

Catawba College, Salisbury, NC

Bisphenol A (BPA) is an industrial chemical commonly used in the manufacturing of plastic products, including water bottles. This creates the potential for harmful chemicals to leach into food and drinking water. Previous studies have demonstrated potential molecular consequences of BPA, including single- and double-strand DNA breaks, DNA methylation, and the initiation of apoptosis. In order to gain a better understanding of possible genetic repercussions, our research project will observe the impact of BPA on Sf9 cells. The Sf9 insect cell line is derived from ovarian tissue in *Spodoptera frugiperda* pupae, a species of invasive moth. Previous research reveals that Sf9 cells are commonly used in gene expression experimentation, as well as the development of biopesticides. Sf9 cells are also good models for testing the cell and molecular effects of environmental pollutants. Therefore, in our research project, Sf9 cells will be exposed to various concentrations of BPA. We will examine the effects of BPA on cell viability using a Trypan blue assay. Furthermore, we plan to use genetic markers and a Comet assay to measure the extent of DNA damage in Sf9 cells exposed to BPA. The results of this research could highlight the potential adverse toxicological and genetic consequences of BPA exposure in aquatic insects, as well as other eukaryotic organisms, like humans.

BBB17 - Using biofertilizers to enhance traditional fertilization methods

Andrea Rivera, T. J. Davenport

Augusta University, Augusta, GA

Soil fertilization and management are critical to achieve and maintain high crop yield and quality. As farming practices have evolved, growing evidence suggests that the use of synthetic fertilizer has the potential to contribute to soil erosion and the eutrophication of waterways. The goal of this research was to determine if a discernible difference in plant growth may be observed when wheat seedlings are treated with traditional fertilizer methods versus biofertilizers. In particular, we are investigating the effects of farm soil enrichment with arbuscular mycorrhizal fungi (AMF), a root symbiont that significantly increases water and nutrient uptake in natural, undisturbed soils. In order to determine what fertilization method confers the greatest benefit to crop growth, an experiment was designed to expose wheat seedlings to different farm soil fertilizer enrichments. The experimental design included a control farm soil and five soil enrichment groups: manure only, AMF only, Miracle Gro™ fertilizer only, manure + AMF, and Miracle Gro™ fertilizer + AMF. Each variable group contained six 10cm pots with five replicate seedlings/pot, for a total of 30 plants/group. After 8 weeks, plants were harvested and analyzed for fresh and dry biomasses. The average shoot biomass (fresh and dry) was the greatest in both the AMF only enrichment and fertilizer only enrichment compared to the control and other enrichments. The average root biomass (fresh and dry) was the greatest in the fertilizer enrichment only and the fertilizer + AMF enrichment. In conclusion, the AMF enrichment appears to be as efficient as traditional Miracle Gro™ for increasing wheat biomass and may be a natural alternative to compost and synthetic fertilizers.

BBB19 - Soil Sleuths: Characterization of Antimicrobial Compounds from Soil-Dwelling Bacteria

Jacob Hiatt, Will Roque, Hunter Sjobom, Jalen Garner, Amanda Rushing

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 successfully 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 infections. In fact, a recent analysis reports that antibiotic resistant infection was the third leading cause of death in 2019. Alarmingly, the research and development of novel antimicrobial therapeutics has slowed significantly, due largely to the idea that antimicrobial development is not a financially lucrative pursuit. As the antibiotic resistance crisis continues to grow, it is imperative that new and effective antimicrobial metabolites are identified. Here, bacteria from soil samples were isolated and grown in culture to screen their ability to produce antimicrobial activity against ESKAPE relative strains, which are bacterial species that share significant similarities with prominent antibiotic resistant organisms. So far, two antimicrobial-producing bacterial isolates have been identified and work has been done to extract the compound for analysis and tentative characterization by untargeted liquid chromatography - mass spectrometry. Concurrently, 16S rRNA sequencing is underway for genus level identification of these isolates, with the goal of performing random and/or site-directed mutagenesis screening to begin identifying the gene(s) responsible for the observed activity.

BBB18 - Exploring protein isolation and quantification of APL-1 in *C. elegans*

Hannah Lindmeier

Tau Delta Kappa, Tifton, GA

Alzheimer's disease (AD) is associated with the gradual loss of neurons and synaptic connections within the brain. Accumulation of neurofibrillary tangles and amyloid plaques are the major hallmarks of the disease post-mortem in humans. Amyloid Precursor Protein (APP) is a major contributor in the progression of AD due to abnormal cleavage producing accumulation of Aβ peptides. A mutant strain of *Caenorhabditis elegans* exists that overexpresses a protein, amyloid precursor-like protein-1 (APL-1), similar to human APP which is linked to early-onset Alzheimer's disease. The ynIs-79 mutant of *C. elegans* overexpresses APL-1 in ventral chord neurons which causes molting defects, motor disorder, and disrupts development from larval stages to adult. *Ginkgo biloba* extract (GBE) is a popular herbal supplement which may delay or improve the memory problems associated with AD, and we have previously shown that GBE decreases the response of the mutant nematodes to a non-threatening stimulus. We hypothesize that the individual flavonoids in GBE are likely positive contributing factors because of known protective roles in preventing oxidative stress. In order to determine whether antioxidants found in GBE downregulate accumulation of APL-1, we are quantifying the protein through a protein isolation and Western blot procedure. Our ultimate goal is to compare levels between mutant and control nematodes exposed to antioxidant compounds. We have optimized total protein isolation and run several trials of separation by gel electrophoresis using egg albumin, *C. elegans* protein samples along with positive and negative controls. The next step is to optimize use of stain free gel technology and identify APL-1 using an antibody targeted to human amyloid precursor protein.

ASB Special Events

Field Trips

A Botanical Tour of Camp Robinson Special Use Area (AR Game and Fish) with Dwayne Estes, Director of the Southeastern Grassland Initiative and Professor of Biology at Austin Peay Univ., TN

Dwayne Estes

Austin Peay State University

Join Dwayne Estes, director of the Southeastern Grasslands Initiative and Professor and Herberiam Curator at Austin Peay University in Tennessee for a tour of the Camp Robinson Special Use Area near Conway, Arkansas. Dwayne is an expert in plant communities of the United States, with a special love for grasslands of the southeast. Originally part of the nearby National Guard training center, Camp Robinson SUA was deeded to the Arkansas Game and Fish after World War II. It includes a variety of upland and bottomland habitats, including grasslands, oak savanna, upland oak/hickory forest and bottomland hardwood forest. The area is known for its diversity of wildlife, including many birds of interest, bear, bobcat, and even American alligators. The diversity of habitats in a relatively small area is a highlight of this trip.

Lorrance Creek Aquatic Biology with Dustin Lynch, Arkansas Natural Heritage Commission

Dustin Lynch

Arkansas Natural Heritage Commission

Join ANHC's Dustin Lynch for a visit to Lorance Creek Natural Area, south of downtown Little Rock. The natural area is accessible via an elevated boardwalk that takes you through a typical shallow water bald cypress/tupelo swamp. There is also a universally accessible paved trail on higher ground. The greater part of the natural area includes a mosaic of ecosystems including beaver ponds, upland pine and hardwood forests, open water and sandy washes. Numerous streams, seeps, and springs support a rich community of plants and animals. The boardwalk experience at Lorance is sure to please those who want to experience the sites and sounds of swamp life. Your guide will be Arkansas Natural Heritage Commission's Dustin Lynch, an expert in aquatic ecology who knows Lorance Creek well. Join Dustin for an up-close look at aquatic biology in Arkansas

Cove Creek Natural Area--Bluff, Stream, Restoration, and Arkansas Endemic Plant

Travis Marsico, Benjamin Benton, Kunsiri Grubbs

Arkansas State University, Winthrop University

The Cove Creek field trip is a 1/2 day trip including a hike in one of Arkansas's natural areas. Participants will learn about the Arkansas River Valley region, sandstone glades and woodlands, restoration practices, and have a chance to see an Arkansas endemic plant species. We will discuss the unusual patterns of plant biogeography in the Interior Highlands region. This field trip is sponsored in part by the Southern Appalachian Botanical Society (SABS).

Gillam Park Birding and More with Audubon Arkansas

John Young, Jennifer Ogle

Audubon Arkansas, University of Arkansas Herbarium

Gillam Park is a 400 acre, largely wooded site in southeast Little Rock. The park is managed as a natural area by Audubon Arkansas, whose Little Rock Center is found nearby. Gillam Park is home to one of the few exposed igneous rock formations of nepheline syenite in the world, creating several glade communities. Other plant communities include upland and bottomland hardwood forests, open water, and other wetlands. The Park is a popular place for local birders and its proximity to the Audubon Arkansas Center provides additional opportunities to explore. The center has several additional trails as well as gardens and constructed glades. Join Jonathan Young, Audubon Arkansas Field Project Manager for a tour of Gillam Park and its unique ecology and geology.

Middle Fork Barrens Natural Area with Theo Witsell, Arkansas Natural Heritage Commission

Theo Witsell

Arkansas Natural Heritage Commission

Gillam Park is a 400 acre, largely wooded site in southeast Little Rock. The park is managed as a natural area by Audubon Arkansas, whose Little Rock Center is found nearby. Gillam Park is home to one of the few exposed igneous rock formations of nepheline syenite in the world, creating several glade communities. Other plant communities include upland and bottomland hardwood forests, open water, and other wetlands. The Park is a popular place for local birders and its proximity to the Audubon Arkansas Center provides additional opportunities to explore. The center has several additional trails as well as gardens and constructed glades. Join Jonathan Young, Audubon Arkansas Field Project Manager for a tour of Gillam Park and its unique ecology and geology.

Workshops

Workshop: Hitting the ground running with your graduate school applications

Erika Moore, University of Memphis

Chinyere Knight, Tuskegee University

Heather Joesting, Georgia Southern University

Chris Havran, Campbell University

David Giles, University of Tennessee Chattanooga

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

This workshop has been designed to better prepare our undergraduate student members to apply to graduate school. Through dynamic discussion with more experienced ASB member panelists and short exercises, learn about the key elements for successful graduate school applications. After a short introduction, an interactive discussion will ensue with the help of five experienced ASB panelists. We will also divide the discussion into blocks so that we can engage attendees with short exercises that will help them experience successful strategies for career development. To ensure the progress of the discussion, there will be a moderator from the Human Diversity Committee. The workshop will end with a short review of the take-home messages to remember.

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THE 83RD ANNUAL MEETING OF THE ASSOCIATION OF SOUTHEASTERN BIOLOGISTS

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30 MARCH-2 APRIL 2022

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Ecological Society of America
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SE CHAPTER

TRIBETA DISTRICTS I & II

Association of Southeastern Biologists 2022
Meeting-At-A-Glance

Wednesday March 30 – April 1, 2022

Statehouse Convention Center and Little Rock Marriott Hotel

Wednesday, March 30

Time	Event	Location
11:00 AM - 6:00 PM	Registration Open	Governor's Hall IV
1:00 PM - 6:00 PM	ASB Executive Committee Pre Event Meeting	Exhibit Hall
2:00 PM - 5:00 PM	SABS Executive Council Meeting	Izard
6:30 PM - 8:00 PM	Welcome: ASB 2022 R.H. Plenary Speaker - Dr. Marla Spivak	Wally Allen Ballroom D
7:30 PM - 9:30 PM	Welcome Reception	Wally Allen Foyer

Thursday, March 31

Time	Event	Location
7:00 AM - 5:00 PM	Registration Open	Governor's Hall IV
7:00 AM - 8:00 AM	ASB Past President's Breakfast Meeting	Fulton
8:00 AM - 5:00 PM	Exhibits Open	Governor's Hall IV
8:00 AM - 8:30 AM	Poster Placement	Governor's Hall IV
8:30 AM - 9:45 AM	Morning Poster Session (ASB Odd #'s) - with Coffee Break	Governor's Hall IV
9:45 AM - 10:15 AM	Lightning Talks	Governor's Hall IV
10:15 AM - 12:00 PM	Cell Block Symposium	Drew
10:15 AM - 12:00 PM	Plant Systematics	Wally Allen Ballroom A
10:15 AM - 12:00 PM	Aquatic Ecology	Wally Allen Ballroom C
10:15 AM - 12:00 PM	Ecology: Communities	Wally Allen Ballroom B
10:15 AM - 12:00 PM	Animals: Entomology	Wally Allen Ballroom E
12:00 PM - 1:30 PM	Lunch on own for majority of attendees	
12:00 PM - 1:30 PM	ASB Diversity Committee Lunch	Fulton
12:00 PM - 1:30 PM	ASB Education Committee Lunch	Pope
1:30 PM - 4:00 PM	Workshop: SERP (by invitation only)	Drew
1:30 PM - 2:30 PM	Microbiology	Wally Allen Ballroom A
1:30 PM - 2:30 PM	Aquatic Ecology	Wally Allen Ballroom C
1:30 PM - 2:30 PM	Ecology: Conservation	Wally Allen Ballroom B

1:30 PM - 2:30 PM	Symposium: Plant Conservation Genetics	Wally Allen Ballroom E
2:30 PM - 2:45 PM	Break	Wally Allen Ballroom Foyer
2:45 PM - 3:45 PM	Cell & Molecular	Wally Allen Ballroom A
2:45 PM - 3:45 PM	Ecology: Physiology	Wally Allen Ballroom C
2:45 PM - 3:45 PM	Ecology: Conservation	Wally Allen Ballroom B
2:45 PM - 3:45 PM	Symposium: Plant Conservation Genetics (continued)	Wally Allen Ballroom E
3:30 AM - 4:30 PM	BBB Mixer	Fulton
3:45 PM - 5:00 PM	Afternoon Poster Session (Even #'s, all SERP posters) with Coffee Break	
4:45 PM - 5:45 PM	SABS/BSA Student Reception	Great Room - Marriott
5:00 PM - 6:00 PM	ASB Business Meeting	Wally Allen Ballroom E
6:00 PM - 10:00 PM	Thursday Night ASB Social Live Music, Food, Drinks, Games	Margaret Clark Adventure Park and Vogel Schwartz Sculpture Garden

Friday, April 1

Time	Event	Location
7:00 AM - 5:00 PM	Registration Open	Governor's Hall IV
7:00 AM - 8:00 AM	SABS/BSA Breakfast Meeting	Fulton
8:00 AM - 8:30 AM	Poster Placement	Governor's Hall IV
8:00 AM - 5:00 PM	Exhibits Open	Governor's Hall IV
8:30 AM - 9:45 AM	Morning poster sessions: ASB Odd #'s, all CURE posters, all BBB posters	Governor's Hall IV
8:00 AM - 6:00 PM	BBB Officers & Judges Room	Caraway 1
8:00 AM - 8:30 AM	BBB Joint Business Meeting (all delegates MUST attend)	Caraway 2/3
8:30 AM - 9:45 AM	Morning Poster Sessions (ASB Odd #'s, all CURE posters, all BBB posters)	Governor's Hall IV
10:15 AM - 12:00 PM	Plant Floristics	Wally Allen Ballroom A
10:15 AM - 12:00 PM	Animals: Herpetology	Wally Allen Ballroom C
10:15 AM - 12:00 PM	Ecology: Climate	Wally Allen Ballroom B
10:15 AM - 12:30 PM	Symposium: SERP (OPEN)	Wally Allen Ballroom E
10:15 AM - 12:00 PM	BBB Presentations	Caraway 2/3
11:30 AM - 12:00 PM	eBio Info	Drew - Panel
12:00 PM - 1:30 PM	Lunch on own for majority of attendees	
12:00 PM - 1:30 PM	SHC SE Chapter Lunch and Business Meeting	Fulton
12:00 PM - 1:30 PM	ESA Lunch and Business Meeting	Pope

1:30 PM - 2:15 PM	Symposium: SE Grasslands	Drew
1:30 PM - 2:15 PM	Microbiology	Wally Allen Ballroom A
1:30 PM - 2:15 PM	Workshop: Graduate School	Wally Allen Ballroom C
1:30 PM - 2:30 PM	Ecology: Conservation	Wally Allen Ballroom B
1:30 PM - 2:30 PM	Scholarship of Teaching and Learning	Wally Allen Ballroom E
1:30 PM - 3:30 PM	BBB Presentations	Caraway 2/3
2:45 PM - 4:00 PM	Symposium: SE Grasslands	Drew
2:30 PM - 2:45 PM	Break	Wally Allen Ballroom Foyer
2:45 PM - 3:45 PM	Cell & Molecular	Wally Allen Ballroom A
2:45 PM - 3:45 PM	Workshop: Graduate School (continued)	Wally Allen Ballroom C
2:45 PM - 3:45 PM	ASB DEI Talks	Wally Allen Ballroom B
2:45 PM - 3:45 PM	Scholarship of Teaching and Learning	Wally Allen Ballroom E
3:30 PM - 4:00 PM	BBB District Meeting	Caraway 2/3
3:45 PM - 5:00 PM	Afternoon Poster Session (ASB Even #'s Posters) with Coffee Break	Governor's Hall IV
4:00 PM - 5:00 PM	BBB Joint Session and Award	Caraway 2/3
6:30 PM - 9:00 PM	ASB Awards Banquet	Wally Allen Ballroom D

Field trips take place on Wednesday and Saturday.

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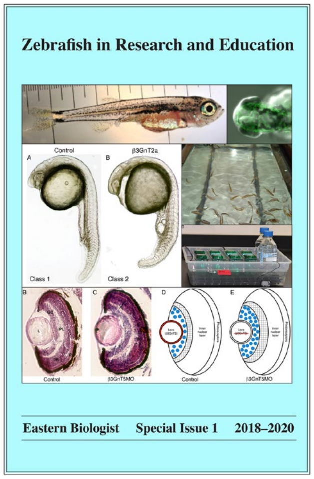

eBio (ISSN 2165-6657), is a peer-reviewed official journal of ASB that publishes original articles and notes focused on the biology of organisms as it relates to the structure, function, and development of their internal systems, and as it pertains to their use in medical and other applications not directly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

The Southeastern Naturalist (Print ISSN #1528-7092 and Online ISSN # 1938-5412) is a peer-reviewed official journal of ASB 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.