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ASB 76TH ANNUAL MEETING

APRIL 1-4, 2015

University of Tennessee at Chattanooga and the Tennessee Aquarium

Meeting Site: Convention Center at the Marriott, Chattanooga, Tennessee

Abstracts of Papers and Posters
Presented at the Annual Meeting

Heritage Plaza on the campus of the University of Tennessee at Chattanooga

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PURPOSE

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

TIME AND PLACE OF FUTURE MEETINGS

2016 March 31-April 3: Hosted by the University of North Carolina at Charlotte, and Davidson College, Davidson, NC. Meeting site is the Embassy Suites Hotel, Charlotte-Concord, NC.

To Better Serve You

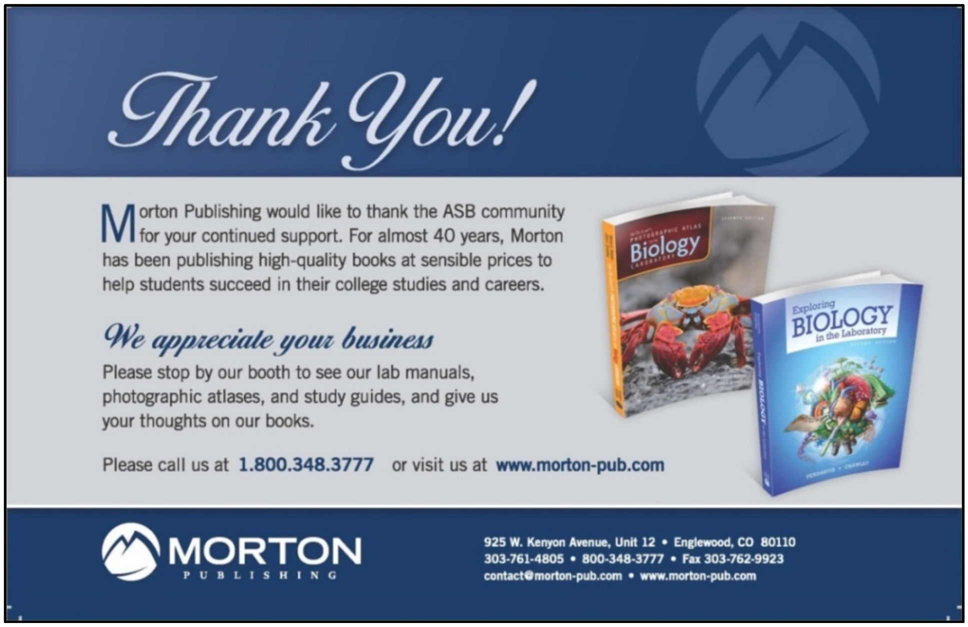
An Experiment on the Annual Meeting Time

Next year (2016), ASB will shift its traditional meeting time of Wednesday – Saturday to Thursday – Sunday. The traditional meeting time originated to provide schools with a convenient time to meet without interfering too much with classes. However, today, spring breaks occur earlier and a shift to later in the week will hopefully reduce the impact on classes for many people.

ASB will try out this new arrangement for one year, and then assess the suitability of this change with the ASB membership. If a majority favor this new schedule, ASB will make it routine each year. If not, ASB will go back to the original schedule in 2017.

Establishing a HARD Deadline for Abstracts

Beginning in the spring of 2016, there will be a hard deadline for the submission of abstracts. Late submissions put pressure on the program committee members and make it difficult to finalize the program before it has to be sent to the printers. Therefore, we will strictly enforce a firm deadline next year and there will not be any deadline extensions. Late abstracts can still be submitted, but will not appear in the formal, printed program. Instead, they will be added to a late submission file that will be available online for download.



CALL FOR NON-COMMERCIAL WORKSHOP AND SYMPOSIUM PROPOSALS FOR THE 2016 ANNUAL MEETING OF THE ASSOCIATION OF SOUTHEASTERN BIOLOGISTS

Deadline for Receipt of Proposals: September 1, 2015

Proposals for non-commercial Workshops (hereafter referred to as Workshops) and Symposia to be offered at annual meetings of the Association of Southeastern Biologists must be prepared and submitted for review as described in this Call for Proposals; the same criteria for proposal preparation, submission, and review apply to proposals originating from internal leadership bodies within ASB (such as standing committees) and from individuals or groups outside of ASB. **Commercial workshops are arranged through the President, and they are subject to separate guidelines that can be obtained from the President.** Written proposals for Workshops and Symposia must be submitted to the Chair of the Program Committee, the ASB Meetings Coordinator, and the ASB President no later than two weeks prior to the fall interim meeting of the ASB Executive Committee. Proposals for Workshops must clearly describe their structure (including maximum number of participants) and concept, as well as prerequisites, space and other facilities requirements, and request for funding from ASB (if any). Proposals for Symposia must clearly address all five of the criteria listed below and be accompanied by letters of endorsement (if any). All proposals will be peer-reviewed and ranked by the Program Chair of the LAC and the ASB Executive Committee. Decisions to accept or reject proposals will be made at the fall interim meeting of the ASB Executive Committee, and proposers will be contacted shortly thereafter.

Workshops

Structure & Concept: Workshops are flexible in their structure. They can be a half-day, full day, or two days in length. Lunchtime Workshops are also offered. Workshop structure is determined by the organizers. Workshops typically have maximum enrollments, and they may specify prerequisites for participation (Workshops should be open to all meeting attendees, first-come first-served, who meet these prerequisites). Workshops often have a registration fee to cover A/V equipment and preparation. Workshops are intended to convey specific knowledge or skills; they are not intended for the presentation of research papers. Workshops are frequently more interactive and informal than sessions within the formal scientific program, and they are not scheduled concurrently with Symposia, contributed oral sessions, or poster sessions. Workshops may involve one or several teachers/presenters, and they may include computer-based or other 'hands-on' training. Weekend Workshops may be linked with a scientific field trip. A Workshop proposal should make clear what participants might expect to gain, and how the Workshop furthers the overall goals of the Association of Southeastern Biologists (these two aspects are the major criteria for Workshop acceptance). Limits of space and time may make it impossible to accommodate all worthy submissions.

Symposia

Structure & Concept: Symposia are a half-day or a full day in length. The number of speakers and the length of each talk are determined by the session organizers; talks should be between 15 and 30 minutes long, and presentation times can vary between speakers. Each session should include at least one 30 minute break that will be synchronized with the coffee break of all concurrent sessions. Generally, Symposia should be focused, integrated presentations assessing current understanding regarding a particular research problem, concept, application, or educational theme. Symposia should have broad appeal to members of ASB or involve integration across sub-disciplines.

Symposium proposals will be assessed under the following criteria. Weighting of particular criteria may vary depending on the nature of proposals, but proposals should explicitly address these criteria, as appropriate. There is typically room for only three Symposia at the annual ASB meeting.

Criteria for Evaluation of Symposium Proposals

1. **Scientific strength:** Symposia are the scientific centerpieces of the meeting, and should:
   - offer significant contributions to biological understanding,
   - present innovative or interdisciplinary approaches, including novel collaborations or syntheses across subdisciplines, and
   - have broad enough appeal to generate large audiences (>100 people) at the meeting.
2. **Structure and organization:** Symposia should be more explicitly integrated than other sessions, and should be structured to:
   - provide overall synthesis or overview; they should not be simply a set of related case studies,
   - avoid taking a narrow perspective on the Symposium topic; organizers should carefully avoid appearance of biases toward their own perspectives, and
   - build a well-integrated whole; each talk should have clear relevance to overall synthesis.
3. **Speakers:** Invited speakers should bring new contributions to the session, not simply reviews of previous work. Inclusion of experienced or particularly engaging speakers can strengthen a proposal, but new voices are also important. Proposals with a larger proportion of confirmed speakers will be favored.
4. **Funding:** Workshop and Symposium proposers must certify that they have sufficient funding available to cover all costs of the program as proposed, including expenses (travel, meals, lodging, honoraria) for all invited speakers. If additional funds are needed beyond those available to the proposers, such funds must be identified and may be requested from the ASB Executive Committee (EC), which has some funding available for Symposium proposals, usually reserved for proposals that come from ASB standing committees. If requesting funds from the EC, the Symposium proposers must specify an amount and justify that amount. If the EC provides funds requested by the Symposium proposers, it is assumed that the Symposium is fully funded as described. If partial funding is offered by the EC, the Symposium proposers must subsequently secure the additional funds required to cover all costs.
5. **Integration:** Proposals may receive higher priority if they are clearly linked to the meeting's overall theme, or if they offer particular value or insight in the

context of other sessions proposed for the meeting or of Symposia at recent ASB meetings.

Endorsements

Workshops and Symposia are often endorsed by various groups, agencies, and organizations including international societies, private non-governmental organizations, governmental agencies, or internal leadership bodies within ASB, such as standing committees. These endorsements will be considered in review of proposals, particularly if they emphasize why the group finds merit (in terms of evaluation criteria above) in the proposal. **Each of these groups, organizations, or agencies is allowed to endorse only one Symposium proposal**. If a group submits a proposal, that group is considered to be endorsing its own proposal, and it cannot endorse another. Symposium proposers, in requesting endorsements, should make this policy clear. There is NO guarantee that a proposal endorsed by any group or organization will be accepted. Individuals preparing letters of endorsement should send them directly to those preparing the proposal for inclusion as part of the proposal package.

If Your Proposal Is Accepted

After proposals are accepted and the scheduling for the meeting is underway, cancellations and schedule changes are very disruptive to meeting planning. Hence, organizers of Workshops should obtain firm commitments from their teachers/presenters and organizers of Symposia should obtain firm commitments from as many of their invited speakers as possible before submitting their proposals. **Requests for additional funding will not be considered by the ASB Executive Committee.**

If a proposal is accepted, the organizers must submit a final summary description of the Workshop or Symposium to the Program Committee Chair at the same time abstracts are due. This summary will appear on the meeting website and should be written so as to stimulate interest and promote attendance. This description must include a complete and current listing of organizers' names and their affiliations, addresses, telephone and fax numbers, and email addresses; a 400-word narrative description of the session; a 50-word sentence description of the session; and a final, confirmed speaker list.

It is the responsibility of Symposium organizer(s) to see that each speaker submits an individual abstract of his/her talk using ASB's abstract submission criteria by the abstract submission deadline. It is not permissible to submit abstracts by any other means. Contact the Program Committee Chair if your situation precludes use of the abstract submission website.

It is suggested and encouraged that a written summary of the Workshop or Symposium be submitted to *Southeastern Biology* for publication.ଓ

Non-Commercial Workshop/Symposium Proposal Submission Form

Title:

Submitters' Contact Information (address, phone, and e-mail address):

Session Description: In 400 words or less and in sentence form, describe the theme and purpose of this session.

Session Justification: In 250 words or less and in sentence form, provide the justification for this session.

One-sentence Summary: Summarize your proposal in 50 words or less.

Speakers and Titles: List all teachers/presenters (Workshops) or speakers and their titles (Symposia). Next to each participant, indicate if they are confirmed or only contacted and have not yet decided (unconfirmed). Do not list individuals who have not yet been contacted.

Funding: Explain how the Workshop or Symposium as proposed is to be funded. Symposium proposers may request needed funds from the ASB Executive Committee.

This form must be submitted to the following individuals no later than two weeks prior to the fall interim meeting of the ASB Executive Committee (deadline is September 1, 2015).

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ASB

Paper and Poster Abstracts

From the 76th Annual Meeting

Hosted by

The University of Tennessee at Chattanooga
and
The Tennessee Aquarium
In Chattanooga, Tennessee

Meeting Site:

Chattanooga Marriott
Convention Center

April 1-4, 2015

76th Annual Meeting Association of Southeastern Biologists

Chattanooga, TN • April 1-4, 2015

Presentation Abstracts

1 Katherine G. Mathews
Biology, Western Carolina University, Cullowhee, NC

Introduction to Botany of Extreme Habitats Symposium

Regionally, the Southeastern U.S. is often viewed as temperate and mesic. However, on a finer scale there are many examples of climatically or edaphically extreme habitats, such as those characterized by fire, drought, salinity, and toxicity. As will be argued by Weakley, the Southeastern U.S. has a rich and diverse native vascular flora because of these many small patch, 'extreme' communities, and that these communities give the Southeast greater ecological resilience over time. The other speakers in this symposium will give examples of different extreme microcosms and the ecophysiological characteristics of the plants and their habitats. Sorrie and Bracey Gray will discuss how canebrakes are fire disclimax communities, currently dependent upon human-induced fires, that succeed to tree-shrub communities with lower fire frequencies. Morris will explain how salt marshes are both highly productive and also extremely toxic monocultures of *Spartina*, which represent a self-maintained ecophysiological feedback system. Horton and Culatta discuss high-elevation, shallow-soil, rock outcrop communities' dependence on cloud immersion to ameliorate water stress. They experiment with the potential effects of climate change on rock-outcrop plants, returning to Weakley's topic of ecological resilience. Pollard describes how metal toxicity can be dealt with by different species, including exclusion and sequestration, in relation to the evolution of metal-tolerant races in several species. Finally, Baker and Witsell discuss the conservation of hydro-xeric, saline subsoil outcrops for the survival of rare plants. As Weakley argues, we might conclude that extreme habitats act as 'nurseries' and refugia for the maintenance of plant diversity in the Southeast.

2 Alan S. Weakley
UNC Herbarium/North Carolina Botanical Garden, University of North Carolina at Chapel Hill

Life on the Edge: Vascular Plant Speciation in Small Patch Communities in the Southeastern United States

The Southeastern United States (SEUS) has a rich and diverse native vascular flora (high gamma diversity) with many 'new' species still being described; many of the plant species of the region are narrowly endemic and also associated with specialized and often 'small patch' communities: glades, fens, hillside seepage bogs, rock outcrops, barrens, river scours, high elevation peaks, sandy scrub, dunes. 'Azonal' communities of these kinds can be characterized as having edaphic or microclimatic conditions atypical for (or even extreme in relationship to) the general conditions of the region. Does this mean that these plants are doomed forever to be oddball, restricted rarities? No. Analysis of their relationships to congeners suggests that unusual small patch communities serve as 1) incubators of speciation and 2) refugia that maintain an ecologically diverse set of species regionally that can expand and contract over periods of millions of years in response to environmental change. The inclusion in the regional species pool of many species restricted to azonal communities (and therefore rare and narrowly endemic at a particular time) provides ecological resilience to the region. By examining the worldwide distributions of genera and families and the divergence times of finer lineages, we can demonstrate that the SEUS has had one of the most resilient temperate biotas in the world over the past 20 million years. An explicit appreciation of time as an additional dimension in the consideration of gamma diversity enriches our understanding of the past, present, and possible future of the SEUS biota.

3 Bruce A. Sorrie[1], Janet B. Gray[2]
[1]Research Associate, University of North Carolina, Chapel Hill; [2] DPW/Endangered Species Branch, Fort Bragg, NC

Canebrakes of the Carolina Sandhills

Canebrakes - dense colonies of river cane (*Arundinaria gigantea*) or switchcane (*A. tecta*) - were part of the presettlement landscape in the southeastern United States. Since that time, however, clearing for agriculture, livestock, and forestry, coupled with fire-suppression, has greatly reduced the area covered by canebrakes. Over much of the Southeast, canebrakes are now merely a memory. In the Sandhills region, switchcane (*A. tecta*) occurs as a narrow to broad ecotone along streamhead tree-shrub communities within a landscape of rolling pine-oak-grass uplands. Where fire frequency is very high (annual or biennial), switchcane may occupy the entire width of the streamhead and may extend downstream for 300 meters or more; here the name canebrake truly applies. At annual or greater fire frequencies, as occurs within military impact areas, canebrakes may be devoid of any tree canopy and extend a kilometer or more. Since the 1980s, controlled burns, natural lightning fires, and military activities have returned fire to local areas of the Sandhills. Intensity of fire appears to play a critical role in re-establishing canebrakes, by removing dense ericaceous shrubs and thinning the tree canopy. Particularly hot fires seem to act as a trigger event that induces the growth of switchcane throughout the streamhead. Thereafter, fire return intervals of 1-2 years are sufficient to maintain canebrake communities. As currently understood, canebrakes are fire disclimax communities that succeed to tree-shrub communities (with switchcane ecotones) with lower fire frequencies. In the Sandhills region of NC-SC, well-developed canebrakes occur currently at approximately 20 discrete locations.

4 James T. Morris
Belle W. Baruch Institute, University of South Carolina, Columbia

Life and Death of the Salt Marsh Redux

Many advances have been made in understanding salt marsh ecosystems since the classic publication, 'Life and Death of the Salt Marsh' (1969), by John and Mildred Teal. Salt marshes are highly productive yet also very toxic. Salt marshes on the East Coast and worldwide are dominated by a single plant species, smooth cordgrass (*Spartina alterniflora*) or its congeners. The physicochemical conditions in salt marshes may explain why plant species diversity is so low. Soil salinity there can be highly variable in space and time, commonly ranging up to 60 ppt or more, double the salinity of seawater, because of the concentration of salt by evapotranspiration. Many halophytes like *S. alterniflora* use nitrogen-based organic solutes to osmoregulate, but this does not solve the salinity problem as nitrogen availability regulates the production of these compounds, which limits marsh primary production. Nitrogen is growth-limiting in an environment with abundant NH4 because root respiration limits the oxygen necessary for uptake efficiency. The absence of oxygen also results in the production of large concentrations of H2S by sulfate reducing bacteria. H2S is highly toxic, yet *S. alterniflora* thrives. Moreover, the concentration of H2S increases as productivity increases, because sulfate reducers degrade the organic matter produced by the plants. Why this plant would indirectly produce a toxin and how it tolerates sulfide is a mystery, but is a likely explanation for salt marshes being essentially monocultures. These feedbacks among major nutrient cycles, sulfides, and plant growth appear fundamental to the survival and productivity of salt marshes.

5 Jonathan L. Horton, Katherine E. Culatta
Biology, University of North Carolina at Asheville, Asheville, NC

Influence of Cloud Immersion on High Elevation Rock Outcrop Plants

In the southern Appalachian Mountains, high elevation rock outcrops provide a unique habitat for plants adapted to cool temperatures and frequent cloud immersion. Cloud immersion may ameliorate water stress in these shallow-soil habitats by reducing leaf-to-air vapor pressure deficit (VPD). Climate change predictions propose that frequency of immersion will decrease, which may adversely affect rock outcrop plant populations. We observed environmental and physiological characteristics of several outcrop species at two outcrops in the Great Craggy Mountains near Asheville, NC. At one outcrop, cloud immersion occurred during almost 30% of daylight hours and at least one hour immersion occurred on 67% of days over an 81 day period. Stomatal conductance decreased with increasing VPD in all species, but transpiration responses varied among species, suggesting potential differences in water stress susceptibility. We used information from this field experiment to design a greenhouse microcosm experiment to test the effect of reduced immersion duration on plant growth and physiology of two outcrop specialists, *Hydatica petiolaris* and *Solidago simulans*. Plants were grown in microcosms simulating observed (6 h/d), reduced (3 h/d) and absent rates of immersion. Maximum photosynthetic rates, light saturation point and water use efficiency increased while transpiration decreased with decreasing immersion duration. Root mass, root:shoot ratio and specific leaf mass were greatest in the reduced immersion treatment. Results from this microcosm experiment indicate acclimation in response to immersion duration for some physiological parameters, suggesting some ability to adapt to changing climatic conditions. More research is needed to determine fitness effects of reduced immersion.

6 A. Joseph Pollard
Biology, Furman University, Greenville, SC

Heavy Metal Tolerance and Accumulation in Southeastern Plants

Heavy metals may be essential micronutrients in trace concentrations, but they are usually toxic at high concentrations. Physiologically stressful concentrations of heavy metals occur in natural geological outcrops or result from human activities such as mining and pollution. Although metal toxicity restricts the growth of sensitive species, some plants are more tolerant. The evolution of metal-tolerant races has been demonstrated in several species growing on anthropogenically contaminated soils in the southeastern U.S. Plants may tolerate edaphic metals by exclusion or sequestration. Plants known as hyperaccumulators take up and store metals at exceptionally high concentrations in their leaves. Hyperaccumu- lation is rare, with only about 500 species in the world. Only two examples of heavy-metal hyperaccumulation are known from the Southeast: cobalt in *Nyssa sylvatica* and manganese in *Phytolacca americana*; however, both of these are unusual cases in that the plants only occasionally occur on metal-contaminated soils where they can hyperaccumulate. Globally, the most common natural metalliferous outcrops are derived from ultramafic rocks such as serpentine and olivine, which contain elevated nickel, cobalt, and chromium. The southeast has few ultramafic exposures, but at the Buck Creek deposit in Clay County, NC, an endemic plant, *Packera serpenticola*, is a strong accumulator of nickel. Although there are no hyperaccumulators among the woody species at Buck Creek, the forest canopy as a whole accumulates significant amounts of nickel in the leaves, and our research has shown that decomposition of leaf litter releases a measurable pulse of soluble nickel into soils and streams.

7 C. Theo Witsell, Brent T. Baker, Thomas L. Foti
Arkansas Natural Heritage Commission, Little Rock, AK

Rare Plants with a Pinch of Salt: Extreme Botanizing in the Saline Barrens of the Arklatex

Saline barrens, sometimes called saline glades, are edaphic grasslands occurring on hydroxeric, naturally saline soils in several ecoregions of Arkansas, Louisiana, and Texas. These patch habitats support a mosaic of herbaceous and shrubby communities in a matrix of hydroxeric flatwoods or tallgrass prairie and savanna. Associated habitats range from 'slicks' (glade-like outcrops of saline subsoil with cryptogamic crust and little vascular plant cover) to annual and perennial grasslands, herbaceous marshes, savannas, and woodlands. The rarity of these habitats, along with a number of rare species they support, make them a high conservation and research priority. Many disjunct and state-rare species occur in these sites and global rarities include *Anthaenantia texana* (G3G4), *Bigelowia nuttallii* (G3G4), *Chloris texensis* (G2), *Geocarpon minimum* (G2, Federally Threatened), *Gratiola flava* (G3), *Hymenoxys perpygmaea* (G1), *Hymenoxys texana* (G2, Federally Endangered), *Rudbeckia texana* (G3), *Schoenolirion wrightii* (G3), *Thelesperma flavodiscum* (G3), *Thurovia triflora* (G2G3), *Valerianella florifera* (G3), and *Willkommia texana* (G3G4). Nebkhas, or 'pimple mounds,' (eolian features formed during past xeric climatic intervals) are a common feature in these habitats and recent data indicate these were formed as recently as 700 ybp at Warren Prairie Natural Area in Arkansas. An overview of the flora, ecology, geomorphology, and ecological history of these habitats will be provided. Disturbance processes appear to play a vital role in maintaining slicks, with a notable decline in this critical microhabitat following protection of sites in Arkansas from the 1980s to present. Two years of results from experimental disturbance plots at this site will be presented.

8 Kristin A. Bakkegard
Biological and Environmental Sciences, Samford University, Birmingham, AL

The Yawning Behavior of the Red Hills Salamander (*Phaeognathus hubrichti*)

Yawning has been observed in all vertebrate taxa. Hypotheses to explain yawning include the physiological (e.g. increase blood oxygen levels, maintain vigilance or increase arousal, to cool the brain) to the social (e.g. intraspecific communications, indicate boredom, or as dominance displays). The Red Hills Salamander (*Phaeognathus hubrichti*) is a large fossorial plethodontid endemic to six counties of south-central Alabama. They are mainly nocturnal and when active, keep their head and front feet outside, and the remainder of their body inside of a burrow. Using infrared (IR) capable video cameras to continuously document behaviors of salamanders at their burrow entrances, I observed 77 yawns from 40 salamanders, with (22.1%) and without (77.9%) tongue protractions (TP). Mean duration of all yawns was 5.6 +/- 3.4 sec (range = 1.0-15.0 sec); without TP = 6.2 +/- 3.5 sec (N = 60; range = 1.0–15.0 sec), and with TP = 3.5 +/- 1.5 sec (N = 17; range = 1.0–7.0 sec). Most yawns occurred with salamanders in their normal position at the burrow entrance and had no apparent stimuli. Yawns were also associated with salamander's heads emerging from the burrow, usually at the start of the evening activity. Salamander yawning is unlikely to have a respiratory or communication function. The most likely explanation is that Red Hills Salamanders yawn to increase vigilance, heighten arousal levels, or to prepare for feeding. This is the first detailed account of yawning behavior in any salamander.

9 James R. Kerfoot, Jr.[1], Micah P. Fern[2], Ruth M. Elsey[3]
[1] Biological Sciences, Union University, Jackson, TN; [2] United State Agriculture, Auburn University, AL; [3] Louisiana Wildlife and Fisheries, Rockefeller Wildlife Refuge, 5476 Grand Chenier Hwy, Grand Chenier, LA

Scaling the Feeding Mechanism of Captive *Alligator mississippiensis* from Hatchling to Juvenile

Small changes in size can lead to potential performance consequences and may influence an organism's ability to utilize resources in its environment. As the American alligator (*Alligator mississippiensis*) transitions between neonate, juvenile and adult habitats (ontogenetic niche shifts), there are inevitably dynamic changes in their feeding performance. This study sought to investigate the scaling of the feeding mechanism and its performance from hatchling to juvenile size classes in *A. mississippiensis*. Feeding events were recorded during March 2011 at Rockefeller Wildlife Refuge (Grand Chenier, Louisiana). Thirty-six captive individuals were randomly sampled, ranging from 30.5 cm to 91.5 cm total length, and feeding events were recorded using a high speed camera at a rate of 300 fps. Results indicated that many linear, angular and timing kinematic variables scale allometrically with cranium length; whereas maximum gape velocity and duration of feeding bout do not scale with cranium length and remain constant between these size classes. Although it has been shown that there is an isometric relationship between cranial elements and body size in *A. mississippiensis*, this relationship is not transferred to linear and timing variables of prey-capture events. These allometric relationships echo other investigations of scaling relationships such as bite-force production and terrestrial locomotion.

10 Annalee M. Tutterow, Shannon E. Pittman, Michael E. Dorcas
Biology, Davidson College, NC

Factors Affecting Survivorship in NC Bog Turtle (*Glyptemys muhlenbergii*) Populations

Turtles are among the most vulnerable to declines, extirpations, and extinctions, especially those species with specialized niches. Additionally, turtle life history traits, such as delayed maturity and high egg and juvenile mortality necessitate high adult survivorship to maintain stable populations. The bog turtle (*Glyptemys muhlenbergii*) is a small and cryptic species listed as federally threatened in the United States. Because survival estimates are critical to understanding population dynamics, I used a long-term dataset and applied a CJS model in program MARK to calculate annual adult and sex-specific survival for twelve intensively-sampled North Carolina bog turtle populations. I evaluated eight basic models for each site and found that adult survivorship remained constant over time for all populations and a sex-specific model was supported for all populations. However, adult survivorship varied between 0.872 and 0.934, all below the 0.95 marker of a stable population. My findings emphasize that bog turtle populations in North Carolina are in a critical state and warrant close monitoring of bog turtle sites. Future studies should focus on relating site- specific factors affecting adult survivorship to site management.

11 Scott P. Jones, David R. Chalcraft
Center for Biodiversity and Biology, East Carolina University

To What Extent Do Larval Predators Affect the Morphology and Performance of Juvenile Toads?

Many organisms have the ability to alter their morphology, behavior or life history in response to environmental cues. For example, many tadpoles alter their morphology to better escape from predators. It is unclear, however, whether morphological changes made by tadpoles in response to predators in their aquatic environment have important consequences after the tadpoles leave a pond. To examine these potential consequences, we conducted an experiment where we 1) raised tadpoles of the southern toad in artificial ponds with no predators, caged predatory dragonfly larvae, or caged predatory fish, 2) transferred metamorphosed individuals to outdoor enclosures, and 3) assessed whether the morphology, survival, and performance of larvae and metamorphosed individuals varied among these treatments. Rearing environment affected both the morphology and survival of toads during their aquatic stage. For example, tadpoles reared with caged predators developed wider tail muscles and shorter and wider bodies than tadpoles reared without predators, with dragonflies inducing larger changes than fish. The presence of caged dragonflies enhanced the survival of larval toads relative to environments with no predators but caged fish had no effect on survival. Rearing environment had no effect on toad morphology either at metamorphosis or several weeks after metamorphosis. Though toads reared with predators could generally jump further at metamorphosis than toads reared without predators this difference was not observed in older metamorphosed toads. Thus the larval rearing environment has little effect on many traits after metamorphosis but has important effects prior to metamorphosis

12 Matthew R. E. Erickson, David C. R. Rostal
Biology, Georgia Southern University, Statesboro

Influence of Diet on Growth and Health of Captive Hatchling Gopher Tortoises (*Gopherus polyphemus*)

Accelerated growth in tortoises has traditionally been associated with potential health risks, however empirical evidence in the literature is lacking. In captivity, growth rates of tortoises are generally expected to exceed those of natural populations and the main cause is probably due to differences in diet. In the context of captive management programs for the purpose of reintroduction, diets that increase growth rates are deemed important because larger animals are less subject to predation and rapid growth permits earlier release, reducing overall cost and effort. To assess the influence of diet on growth and health of captive hatchling tortoises, we compared growth rates, sprint speeds, and blood chemistry parameters of gopher tortoise hatchlings reared on four different diets over a period of 168 days. Tortoises fed Mazuri brand tortoise diet or a mixture of horse feed and vegetables had significantly higher growth rates and faster sprint speeds on average than those fed a mixture of supermarket greens. Calcium supplementation of supermarket greens had no effect on growth rate or sprint speed. Significant differences were also measured in blood chemistry results. We hope to use this information to make recommendations that improve the success and feasibility of captive management programs.

13 Anastacia Marcus
Biology, Jacksonville State University, AL

Frog Call Survey from Clay County, Alabama

Clay County is located in east-central Alabama. The county is rural with small communities and private residences scattered throughout. The landscape consists mostly of wooded habitat with small farms interspersed. There has been little herpetological interest in the county due to lack of nearby colleges. This study was conducted to fill in herpetological distribution gaps. This survey consisted of five ponds, a flatland with a creek, and a private residence within a three mile radius. The survey was conducted from

January, 2013 through January, 2015. Twelve species were observed and recorded: *Anayrus americanus, Anaxyrus fowleri, Acris crepitans, Hyla chrysoscelis, Hyla cinerea, Hyla gratiosa, Psuedacris crucifer, Pseudacris feriarum, Gastroph ryne carolinensis, Lithobates catesbeiana, Lithobates clamitans, and Lithobates sphenocephala.* Frogwatch USA guidelines were used to record species, location, time, temperature, wind speed, and call intensity. This data was used to monitor large scale changes in frog populations. Four species were found that had not previously been recorded in the county: *H. cinerea, H. gratiosa, P. crucifer,* and *L. sphenocephala.* Breeding seasons varied among species. Fall and winter breeders included *A. americanus, P. crucifer, P. feriarum,* and *L. sphenocephela.* Spring and summer breeders included: *A. fowleri, A. crepitans, H. chrysoscelis, H. cinerea, H. gratiosa, G. carolinensis, L. catesbeiana,* and *L. clamitans.* Further exploration and expansion of sites should take place for continued understanding of frog inhabitants of Clay County.

14 Lauren M. Bonee
Biology, Maryville College, TN

Effects of Various Basking Substrates on the Body Temperature of the Bonaire Whiptail Lizard (*Cnemidophorus murinus*)

Reptiles are ectotherms that obtain their heat from their environment by using a wide variety of behaviors such as basking. It is the dorsoventral flattening of the reptile's body to increase surface area to maximize heat absorption from the sun or from the substrate. Little research has been done to determine if lizards have a ideal basking substrate and if that substrate affects the lizards body temperature. The purpose of this study was to determine if the Bonaire whiptail lizard (*Cnemidophorus murinus*), which is endemic to Bonaire, Municipality of the Netherlands, has a preferred basking substrate and if the whiptail's body temperature varies on different types of substrates. The body temperature of the Bonaire whiptail lizard was monitored with a compact IR thermometer while basking, and the temperature of the basking substrate was also recorded. Overall, sand was the only basking substrate group to have a positive temperature difference. Rock-like and other/plant material substrate groups had a negative temperature difference. This study shows that sand and plant material substrate groups are vital for the thermoregulation of the Bonaire whiptail lizard. As natural vegetation is being lost on the island due to urbanization and grazing, the whiptails are losing their primary substrate needed for lowering their body temperature. More research would be needed to determine if the imported vegetation used by resorts have the same thermoregulatory effects as the native vegetation.

15 Barry P. Stephenson[1], David C. Byrd[1], Nikolett Ihasz[2], Lindsey Swierk[3], John Swierk[4]

[1] Biology, Mercer University, Macon, GA; [2] Psychology, Mercer University, Macon, GA; [3] Biology, Intercollege Graduate Program in Ecology and Center for Brain, Behavior and Cognition,The Pennsylvania State University, University Park, PA; [4] Chemistry, The Pennsylvania State University

Assessing Temperature-Dependent Color Change in Eastern Fence Lizards (*Sceloporus undulatus*) with Spectrophotometry: Implications for Badge Function and Color Production

A recent report described temperature-dependent color change in two populations of the Eastern Fence Lizard (*Sceloporus undulatus*) in the southeastern U.S. We extended upon this work by using spectrophotometry to characterize abdominal and dorsal color expression across a range of temperatures (24, 28, 32 and 36C) in both males and females from a population in central Georgia. In general, warmer temperatures were

linked to a decrease in the wavelength of peak reflectance (hue) for both abdominal and dorsal body color in both sexes, whereas other measured color traits (UV chroma and brightness) were unaffected. Specifically, males exhibited bright blue abdominal color when warm and pale green color when cool, consistent with earlier findings. However, temperature treatment sequence predicted the magnitude of abdominal color change; males that were progressively heated changed markedly (i.e., green to blue), whereas males that were cooled from a starting warm body condition did not show significant color change over the same measurement time period. As with abdominal color, male dorsal color changed with temperature, with cooler males exhibiting a longer-wavelength hue than warmer males. In contrast, female abdominal hue did not change significantly with temperature. However, dorsal color hue did change with temperature, and paralleled the pattern seen in males, with the longest wavelength hue observed in females at cooler temperatures. We consider these results in terms of the proposed functional significance of male abdominal color in this species, as well as models for badge color production in *Sceloporus*.

16 Alyssa A. Hoekstra[1], Eric J. Nordberg[2], Sarah J. Kirkpatrick[1], Vincent A. Cobb[1]
[1] Biology, Middle Tennessee State University, Murfreesboro; [2] College of Marine and Environmental Sciences, James Cook University, Townsville, QLD, Australia

Timber Rattlesnake (*Crotalus horridus*) Movement Patterns in Middle Tennessee

The movement of 18 timber rattlesnakes (*Crotalus horridus*) was studied using radio-telemetry during their active season from 2012 through 2014. The snakes that were tracked for 2 seasons (n = 8) and 3 seasons (n = 2) had considerable overlap in their home ranges and exhibited similar ingress and egress movement patterns from year to year. Body size influenced movements; smaller snakes had smaller home ranges, less frequent movements, and traveled less distance from their hibernaculum than larger snakes. Male snakes had larger home ranges and moved greater distances than female snakes. Overall, snake movement was highly directional during egress away from and ingress to hibernation sites. Rates of movement were greater during the egress and ingress migration periods than in mid summer when foraging activity dominated their behavior. Even though the landscape at this study site is fragmented with a variety of habitat types, including agricultural and human development, snakes exhibited movement patterns similar to some prior studies in very different environments.

17 Eric L. Margenau[1], Yong Wang[1], Callie J. Schweitzer[2]
[1] Alabama A&M University; [2] United States Forest Service, Southern Research Station

Breeding Bird Community Response to a Gradient of Forest Canopy Reduction in an Upland Hardwood Forest

Post-logging sites were historically assumed to provide unfavorable habitat to songbirds. Timber harvests have always been important for species that require disturbances, but while most studies focus on clearcuts, few examine the harvesting methods ranging between clearcutting and undisturbed forests, such as those created with shelterwood prescriptions. I studied breeding bird community response to different basal area retention levels during the second stage of a two-stage timber harvest, 12 and 13 years post-initial harvest in an upland hardwood forest in northern Alabama on the southern end of the mid-Cumberland Plateau through territory mapping. This study looked at how different retention cuts affect bird species with varying habitat requirements. Bird diversity, richness, and percent similarity were compared among treatments using analysis of variance with a post-hoc LSD test. The relationship between habitat features and bird diversity were examined using correlation analysis. Breeding bird diversity was significantly lower in the control stands than 50% retention stands (2013 $p = 0.002$, 2014 $p = 0.007$) in both years. Breeding bird diversity was positively correlated with sapling density in 2013 ($r = 0.65$); showed a quadratic correlation with sapling density in 2014 ($r = 0.85$), and canopy cover in both years (2013 $r = 0.96$, 2014 $r = 0.96$). Breeding bird diversity was similar across all four shelterwood treatments in both years, although these treatments had structural differences among them. These finding suggest that breeding bird diversity is dynamic and temporally dependent upon timber harvest and subsequent succession.

18 Marae C. Lindquist, Ray S. Williams
Biology, Appalachian State University, Boone, NC

The Role of Terpenes in Aphid Colonization of Multiple Species and Genotypes of *Solidago*

This study investigated the role of genetic diversity between different species and genotypes of *Solidago* in determining the abundance of a specialist aphid herbivore. Previous research in the Williams laboratory at Appalachian State University suggested the importance of terpenes in aphid colonization of *Solidago altissima* genotypes. To expand the research approach, this study focused not only on *S. altissima* but also co-occurring species *S. juncea* and *S. rugosa*. Colonization of the goldenrod aphid *Uroleucon nigrotuberculatum* on the different species and genotypes tested if terpenes were affecting aphid choice of both species and genotypes. A common garden design was used and the aphids were allowed to naturally colonize potted plants. There were 4 genotypes of each species and each plant was randomly assigned into one of the 48 plots. Aphid abundance was recorded every three days. Leaf samples were collected to quantify terpenes, N and C:N ratios and total plant biomass was determined to standardize aphid abundance. It became clear that *S. rugosa* could not be considered because it was at a different developmental state and was not accessible to the aphid. *Solidago altissima* and *S. juncea* showed no significant species affect (Nested ANOVA), but there were significant differences in some terpenes. In *S. altissima* we found significant genotype effects on aphid abundance and several terpenes were affected by genotype. A Partial Least Squares Regression (PSLR) analysis found that terpenes and not foliar nutrients were the major contributing factor in aphid abundance on *Solidago* species. This study gives us preliminary insight to how *S. rugosa* and *S. altissima* phytochemistry affect aphid abundance, and will help in future research on the role of terpenes in aphid colonization of *Solidago*.

19 Brian K. Bonville, Ray S. Williams
Biology, Appalachian State University, Boone, NC

Effect of Genotype and Environment on the Abundance of a Specialist Aphid in *Solidago altissima*

Genetic diversity within dominant plant species is important in governing the population dynamics of arthropods. One phenotypic attribute that plants possess affecting the colonization of herbivorous insects is phytochemistry. Allelochemicals, such as terpenes, may play a role in deterring or attracting insects such as aphids and can vary by plant genotype. We analyzed the effects of genotype and environmental factors in the form of nitrogen and phosphorous addition on leaf terpenes in tall goldenrod (*Solidago altissima*) and related this to the abundance of a specialist aphid species (*Uroleucon nigrotuberculatum*). This allowed us to differentiate effects of genotype (G) from environment (E) and examine potential interaction (GXE). In our experiment we planted six genotypes of tall goldenrod in a common garden design and provided plants different nutrient regimes; nitrogen addition, phosphorous addition and control (no nutrients).

Aphids colonized the plants naturally. We quantified aphid abundance throughout the growing season, taking estimates of plant biomass and leaf samples for analysis of plant phytochemistry during two times of peak aphid abundance. Our data analysis to date demonstrated that both genotype and nutrient treatment and their interaction were statistically significant in relation to aphid colonization. Our results show that plant genotypes responded to nutrients in a way that impacted aphid abundance. This suggests that genotypic variation in *S. altissima* may be a major contributor to insect community structure in old field ecosystems. This highlights the importance of genetic diversity in forming ecosystem complexity within terrestrial systems

20 Julie A. Ragsdale, Ray S. Williams
Biology, Appalachian State University, Boone, NC

Effects of Spatial Scale and Genotype on the Associated Pollinator Community of *Solidago altissima*

The field of community genetics attempts to understand how genotype identity and genetic diversity of plant species affects associated communities. We investigated how insect pollinator communities were influenced in the old-field dominant species *Solidago altissima* varying by genotype and spatially separated fields and investigated the possible role of plant secondary metabolites. Previous research demonstrates effects of plant genotypic diversity on arthropod communities in *S. altissima* and that terpenes are a possible mechanism for insect choice of genotypes, though little focus has been directed to flowers and pollinators. Because the effect of plant genotype and environment on associated arthropod communities is scale-dependent, our experiment addressed possible spatial effects using 4 sites (large-scale, representative of potential environmental effects) with 4 patches within each site (small scale, representative of genotypic effects). Pollinator surveys were conducted three times at each patch throughout the blooming period, during which observed pollinators were identified to the lowest possible taxa. Inflorescences were collected for biomass and terpene analysis. Terpenes were analyzed using gas chromatography. We used a general linear model (Proc GLM) to partition effects of site from genotype (r2) and ran regression analysis. Our model found that for total pollinator abundance, site was not a significant factor and explained a small amount of the variation (r2 = 0.13). We conclude from this that pollinator abundance is more influenced by differences among genotypes, which accounted for the majority of the variation (87%). This being the case, we now hypothesize there is correlation between pollinator abundance and terpenes in flowers, such that (1) terpenes will vary by plant genotype, and (2) terpenes influence pollinator choice of host plant.

21 Christopher J. Payne
Curriculum for the Environment and Ecology, University of North Carolina, Chapel Hill

Long-Term Forest Growth in a North Carolina Piedmont Forest: Species-Specific Patterns Influencing Stand-Level Biomass Trends

Studies show evidence of recent biomass increases across various forest types, including temperate forests. Additional research has shown that temperate forest composition has not remained consistent with classical succession predictions due to a myriad of hypothesized factors such as changing climate and fire suppression. We are interested in observing multi-decadal, species-specific growth trends to gain a better understanding about which underlying species might be driving whole-stand biomass trends and if previously-unexpected species seem to be driving recent observations. Using an 80-year tree-growth and mortality data set of 34 permanent sample plots in the Duke Forest, we examine trends of biomass accumulation and individual tree growth in a temperate

Piedmont forest. We examine if above-expected growth of hardwood species in successional pine plots is extending or even increasing peak stand biomass and if previously non-dominant hardwoods such as *Acer rubrum*, *Liquidambar styraciflua* and *Fagus grandifolia* are driving mixed-age, mature hardwood stand biomass unexpectedly upwards. Individual measurements of tree growth and death throughout Duke Forest plots allow us to track broad, forest-wide successional change. Identification of each individual to the species level allows us to determine stand-level biomass accumulation for each species. Further, individual-tree mortality data allows us to determine the extent to which observed biomass trends are due to growth rate shifts versus changes in mortality rates. Finally, knowledge of the age and disturbance history of the plots allows us to determine expected growth levels attributable to normal recovery processes in order to determine if growth rates are exceeding expected values.

22 Peter A. Wilfahrt[1], Fletcher W. Halliday[2], Robert W. Heckman[2], Charles E. Mitchell[2]

[1] Curriculum for the Environment and Ecology, University of North Carolina, Chapel Hill; [2] Biology, University of North Carolina at Chapel Hill

Plant Community Assembly in an Experimental Old Field System: The Role of Soil Nutrients, Trophic Controls, and Priority Effects

Environmental conditions, biotic interactions, and species' physiology interact as strong determinants of plant community composition. Community assembly theory predicts that these factors act as performance filters at the species level, and that their relative strengths will vary through time. Using an experimental old field study, we examine the responses of plant assemblages to fertilization via soil nutrient addition, insect herbivore and pathogen exclusions, and priority effects of extant vegetation. Six native, perennial herbaceous species were transplanted into denuded 1m2 plots in an old field in Durham, NC in 2011 at two different diversity levels, and factorially manipulated with soil nutrient addition and the exclusion of insect herbivores and foliar fungal pathogens. Exclusion of plant enemies (herbivores and disease) and fertilization both reduce species richness ($p<0.001$), indicating both top-down and bottom-up controls within the system. A significant interaction was also observed ($p<0.01$) between the treatments, which appears to show that the fertilization effect overwhelms that of enemy exclusion when they act in tandem. An analysis of Bray- Curtis dissimilarity index across time revealed that fertilization led to increased species turnover ($p<0.001$), while enemy exclusion led to decreased species turnover ($p<0.001$), relative to their controls. This indicates that while both treatments lead to decreased richness, fertilization promoted growth of non-planted species, while enemy exclusion promoted retention of the planted species which perhaps reduced further colonization events. This talk explores these results and analyses of plant physiological traits to highlight the implications for assembly principles in plant communities

23 Dennis D. Tarasi

Curriculum for the Environment and Ecology, University of North Carolina, Chapel Hill

Invaded Communities Differ in Composition and Structure from Uninvaded Communities

Do invasive species substantially impact the communities they invade? This question has driven many ecological studies in the past several decades, with mixed results. I examined this question in the forests of the southern North Carolina Piedmont with two different focalinvasive shrubs, *Ligustrum sinense* (Chinese privet, family Oleaceae) or *Elaeagnus umbellata* (autumn olive, family Elaeagnaceae). I identified stands dominated

by one of these invaders and systematicallydocumented species composition, cover and structure measures, as well as multiple abiotic components, across multiple spatial scales. I then collected similar data from paired control plots, forested patches nearthe invaded communities of similar composition and structure, but without the dominant invader and with no history of management or removal. These control communities allowed a 1-to-1 comparison in a natural experimental setting, with the only detectable difference in these communities being the presence (or absence) of the focal invader. Invaded communities differ from their uninvaded counterparts in several significant ways, demonstrating that invasive species dominance does in fact correlate to substantial changes in the structure, composition and outlook of forests experiencing biotic invasions. Invaders, however, are not consistent in their impacts, as privet dominance yields a different, and generally more substantial, change in forest composition than does autumn olive.

24 Mercedes M. M. Bartkovich,
Yong Wang Biological and Environmental Sciences, Alabama A&M University

Determining Breeding Origins and Stopover Patterns of Four Migrant Songbird Species in Northern Alabama Using Stable Isotope and Molecular Methods

Determining the breeding, or natal, origin of a population of migratory birds is essential for understanding factors that could be responsible for population changes. Migratory bird species have different migratory and energy reserve strategies that vary based on sex, age class, and breeding origin. This research examines the breeding origins and stopover patterns of four Neotropical migratory songbird species: Wood Thrush (*Hylocichla mustelina*; n=85), Eastern Wood-pewee (*Contopus viren*; n=79), Gray Catbird (*Dumetella carolinensis*; n=123), and Ovenbird (*Seiurus aurocapilla*; n=120). During the fall of 2007 and 2008 in the Walls of Jericho, Jackson Co., AL, 407 individuals were captured, banded, measured, and had two tail rectrices removed. Molt origin of these individuals was estimated using stable hydrogen isotope (deuterium) analysis of the collected feathers. In conjunction with isotope analysis, DNA extraction and polymerase chain reaction will be performed to determine the gender of each individual since these species are sexually monomorphic. Preliminary analyses indicate that the Ovenbird had the broadest and most northerly breeding grounds, while the Wood Thrush, Eastern Wood-pewee and Gray Catbird had more southerly breeding origins. There was a negative relationship between the deuterium values and timing of migration, meaning that individuals that bred the furthest north migrated through our stopover site later in the season. Examining breeding sites and stopover patterns, such as timing of migration and energetic conditions, will improve our understanding of the connectivity of migratory songbirds and enable the development of more effective conservation strategies for these bird populations.

25 Jacquelyn Fitzgerald[1], Thomas Wentworth[2], Clint Penick[1], Katherine Stuble[3], Robert Dunn1
[1] Biological Sciences, North Carolina State University, Raleigh; [2] Plant and Microbial Biology, North Carolina State University, Raleigh; [3] Plant Sciences, University of California, Davis, Davis, CA

Seasonal Effects of Climate Warming on Forest-Floor Arthropod Communities

Climate warming is predicted to reshape ecological communities on a global scale. The impacts of warming on community composition and diversity have been shown to vary with latitude, primarily as a result of differences in species' thermal tolerances. However, it is unclear how warming will differ in effects on co-occurring species that are active at different periods of the year. We used the results of a large-scale experimental temperature manipulation in Duke Forest, NC, to examine the effects of simulated forest-floor warming on arthropod community structure. Using monthly community samplings over a two-year period, we measured species' abundances and taxonomic diversity to assess the consequences of temperature increases. We show that experimental warming has significant effects on arthropod community structure, and that these effects vary strongly with season and taxonomic group. Our results suggest that sensitivities of species to climate warming depend on their seasonal activity patterns.

26 Christine A. Ricci[1], Albert Meier[1], Ouida Meier[2], T. Keith Philips[1]
[1] Biology, Western Kentucky University, Bowling Green; [2] Geography and Geology, Western Kentucky University, Bowling Green

The Effects of Fire and Other Habitat Characteristics on Habitat Selection of *Exyra ridingsii*, the Riding Pitcher Plant Looper Moth

Exyra ridingsii is a host specific moth that spends its entire immature life cycle in the *Sarracenia flava* pitcher plant. *Sarracenia flava* requires acidic, moist soil that undergoes frequent burns. Habitat selection and the effects of fire as well as other habitat characteristics were examined for *E. ridingsii* during this study. From summer 2012 to Fall 2013, five sites in the Croatan National Forest, North Carolina were surveyed four times each year. One site had no burn disturbances; the remaining four sites were evenly split with two having had burns occur in them and two having burns occur nearby in 2012. At each site seven to twenty quadrats were selected randomly for sampling. In each quadrat, trumpets were counted and measured for height. Also recorded was whether the trumpets were healthy or affected by herbivory, and the fraction affected was calculated (herbivory per clump). Highest median herbivory per clump values were found at the burned sites. Millis 2 had 100% herbivory for the late summer 2013 sampling date, and Millis 1 had an herbivory per clump value of 0.86; 86% of clumps at this site exhibited herbivory. All other values were above 50% with the exception of Catfish Lake Road which was 32%. Herbivory per clump was not found to be statistically correlated to site and therefore burn status. Burn status, soil saturation, and woody understory growth all seem to play a role in the habitat selection of *E. ridingsii* but there is much research still to be done.

27 Renee Fortner, Claudia L. Jolls
Biology, East Carolina University, Greenville, NC

Insights into the Habitat and Reproductive Biology of the Federally Endangered, Cooleys Meadowrue (*Thalictrum cooleyi*)

Thalictrum cooleyi Ahles, is a dioecious species, endemic to fire-dependent, wet pine savannas of the southeastern US, listed as federally endangered in 1989. Knowledge of habitat and breeding biology are crucial to conservation. My study, conducted in NC populations of *T. cooleyi,* examined 1) woody species associates, 2) sex ratios, 3) potential pollen limitation, and 4) seed germination requirements. Logistic regression showed that *T. cooleyi* presence decreased as canopy closure increased. In contrast, as percent cover of woody shrubs increased, so did the likelihood of *T. cooleyi* presence. *Morella cerifera* L., wax myrtle, was the only significant shrub predictor of Cooley's meadowrue (Wald = 13.823, df = 1, $p < 0.0001$). Twice as many males as female plants occur in these populations. Despite male-biased sex ratios, supplementation experiments showed that seed set is limited by pollen availability. Average seed set for plants with hand pollinated flowers was higher than for open pollinated controls (77.5 % vs. 34.5 %, respectively). Cooley's meadowrue seeds are dormant at maturity, requiring cold stratification at 1oC to break dormancy. Germination rates are low (11.3 %, n = 779 seeds), likely due to low seed viability and underdeveloped embryos. Germination rates might improve with a period of warm stratification followed by cold stratification to break morphophysiological dormancy. My work supports concerns that habitat loss (i.e., transition of open pine savanna to dense forest), pollen limitation to seed set, and poor seed viability threaten the recovery of Cooley's meadowrue.

28 Caryn D. Ross, Sujan M. Henkanaththegedara
Biological & Environmental Sciences, Longwood University, Farmville, VA

The Effects of Urbanization on Birds of the Southeastern United States

The human population is rapidly growing around the world, increasing urbanization while consequently affecting many wildlife species. Birds have become a model species for observing the effects of urbanization on wildlife; however, the majority of previous studies have been narrowly focused and confined to local sites. The purpose of this study is to determine the effects of urbanization on bird communities on a wide geographic scale covering five states of the southeastern United States (Virginia, North Carolina, South Carolina, Georgia, Florida). We used eBird citizen science database to collect bird occurrence and composition data from 30 state parks and 30 cities in each state.Additionally we conducted field surveys in five state parks and five cities in Virginia to ground-truth eBird data. Our results showed higher species richness in natural areas compared to urban areas and significant differences of feeding guild composition between urban and natural areas. This is most likely due to species-specific traits associated with urbanization sensitivity. Determining broad scale changes in bird communities due to urbanization will help conservation practitioners to implement better conservation management strategies within urban and non-urban areas.

29 Canceled.

30 John A. Jones[1], Anna C. Tisdale[1], Marja H. Bakermans[2], Jeffery L. Larkin[3], Curtis G. Smalling[4], Lynn Siefferman[1]
[1] Biology, Appalachian State University, Boone, NC; [2] Biology and Biotechnology, Worcester Polytechnic Institute, MA; [3] Biology, Indiana University of Pennsylvania, Indiana, PA; [4] Audubon North Carolina, Boone, NC

Ecological and Behavioral Consequences of Sympatry Between Golden-Winged and Chestnut-Sided Warblers in the Southern Appalachians

To mitigate the rapid decline of worldwide biodiversity, conservation biologists need integrative approaches that focus on spatial habitat requirements as well as the behavioral ecology of at-risk species. Although golden-winged warblers (*Vermivora chrysoptera*) are a conservation priority and despite the significance of interspecific competition on community structure, little research has focused on competition with (non- *Vermivora*) heterospecifics. In northwestern NC, agonism frequently occurs between golden-winged and chestnut-sided warblers (*Setophaga pensylvanica*), thus, we explored the potential consequences of sympatry.Using a correlative approach, we investigated the degree to which these species overlap and how chestnut-sided warbler density is related to individual quality, behavior, and fitness of golden-winged warblers. Additionally, we used remotely-sensed imagery to characterize habitat and to potentially tease apart the influences of habitat quality versus heterospecific density on measures of golden-winged warbler fitness. When golden-winged warblers settled in territories with high densities of chestnut-sided warblers, they displayed poorer individual quality, higher aggression, and occupied lower-quality territories. Further, golden- winged warblers that settled among high densities of chestnut-sided warblers commenced breeding later in the season, which resulted in smaller clutch sizes. These data suggest extensive habitat overlap and indirect negative consequences of sympatry for golden-winged warblers. Moreover, our results suggest that competition likely restricts golden-winged warblers to inhabiting poorer quality habitat, thus exacerbating the negative effects of coexistence between species in the

southern Appalachians. Thus, a better knowledge of competition and preferred habitat types for golden-winged warblers (or other species) can aid management efforts of at-risk study systems. 76th Annual Meeting ASB

31 Adam K. Morgan, Matt C. Estep, Zack E. Murrell
Biology, Appalachian State University, Boone, NC

Evaluation of Genetic Structure of *Spiraea virginiana* Using Microsatellite Markers

In the plant species *Spiraea virginiana*, this study investigated the relationship of geographic features to genetic structure. We focused on the relationship between subdrainages and genetic structure, and explaining patterns of low between-population variability and high within-population variability described by Brzyski and Culley (2011).We assessed the utility of a set of primers targeting microsatellite regions in quantifying genetic variation across multiple populations, and evaluated the efficacy of the RAPDs previously used on the species. Evidence was found to support the idea of southern ancestral refugia, our analysis points to the Tennessee subdrainage as more genetically diverse than the Cumberland drainage. Mantel tests report significant relationships between genetic distance and geographic distances (Rxy = .281, p = .001), as well as genetic distance and river network distances (Rxy = .201, p = .001) of *S. virginiana* sites. An AMOVA supports the hypothesis of genetic structure between subdrainages (p= .001). Microsatellite chromatograms also revealed tetraploid peak patterns that may indicate allopolyploidy or limited disomic inheritance.

32 Paige F. Phillips, Sharon E. Mason, John G. Barlett
Biology, Campbell University, Buies Creek, NC

A Frightening Future Without Honey Bees; What Will We Do?

Without nature's honey bee, the human and animal food population could be in grave danger. The recent bee decline over the past several decades has been the cornerstone of the environmental quality. If the honey bees continue to die, vitality of life will disappear forever. Honey bees are the most important pollinator are responsible for pollinating over one third of our food produced such as fruits, vegetables, nuts, seeds and cotton and are worth over 15 billion dollars in this nation. Multiple suspects are possible including toxic pesticides, parasites, malnutrition and viruses. CCD, Colony Collapse Disorder, is a mysterious syndrome that has caused up to 80% of the bee colonies to disappear in our nation. When bees become sick, they leave the hive to avoid fellow bees from becoming sick. This phenomenon is causing an entire colony to leave all at once, disappearing from the hives without a trace. As the honey bees are exposed to the pesticides sprayed on our crops, this affects the honey bee's memory and weakens their immune function and causes them to be more prone to infection. Also, these pollinators are asked to perform a natural task on an unnatural scale by mass producing crops and removing them from their natural habit. Expanding many bee habitats by using universities and educational settings, by also informing people on ways to improve the environment for humans, animals and honey bees, can assist with the challenges that lie ahead in the future of our food source.

33 Jaclyn N. Inkster, Claudia L. Jolls
Biology, East Carolina University, Greenville, NC

An Organic Insect Deterrent Does Not Affect Visitation by Native Insects to a Threatened Great Lakes Dune Endemic Plant

Larinus planus (Coleoptera: Curculionidae) is a non-native adventive biological control used to limit seed production by non-native weedy thistles in North America. These weevils oviposit in flowering heads and the developing larvae consume plant ovules and seeds. *L. planus*, however, also has non-target impacts and can reduce seed set of the federally threatened *Cirsium pitcheri* (Asteraceae) by 50-99%. *C. pitcheri*, a Great Lakes shoreline endemic, has no means of vegetative reproduction and relies solely on seed set for population persistence. *C. pitcheri* is primarily pollinated by native bees which are sensitive to conventional chemical pesticides. Surround WP (95% kaolin clay) is an insect deterrent used in organic agriculture. As a potential effective control for weevil seed predation, however, kaolin clay must not deter potential pollinators. Surround WP was applied to *C. pitcheri* seed heads as aqueous solutions of 9% and 18% to assess the effect of Surround WP on insect visitors to *C. pitcheri*. Our study site was located at Wilderness State Park in sand dunes along northern Lake Michigan. We recorded pollinator species, visits, and duration during 10 minute observations for 88 paired plants (control and 9% or 18% treatment). There were no significant differences in mean species richness, number of visits, or duration of visit between control and treatment groups. This pilot study suggests no negative effect on insect visitors. Surround WP may be a suitable deterrent to prevent non-target seed predation by a biocontrol insect on this rare dune perennial.

34 Kevin Trostel, Ashley B. Morris
Biology, Middle Tennessee State University, Murfreesboro

Reproductive Ecology of the Rare Cedar Glade Endemic *Astragalus bibullatus*

The federally endangered legume Pyne's ground plum (*Astragalus bibullatus*) occurs in a narrow range within Middle Tennessee. The eight known occurrences are all located within Rutherford County. A noticeable decline in population sizes has been observed over a ten-year time span. The short term decline is attributed to human expansion and encroachment of invasive species. Genetic studies have been conducted with this species in the past, but here we use novel microsatellite markers to determine genetic relationships within and among all of the remaining natural popula- tions. Loci were polymorphic within and among populations of *A. bibullatus*, suggesting that these markers may be a useful tool for conservation genetics in this species. Patterns of genetic structure will be analyzed in the context of a 10-year demographic data set tracking individual growth and fecundity. These results will lead to recommendations for conservation management strategies for the species. In particular, work is underway to better understand successes and failures of reintroduction attempts to improve the long-term genetic potential of these populations.

35 Carlen Hussey, Ashley Jessup, Dane M. Kuppinger
Biology, Salem College, Winston-Salem, NC

Determining the Fire History for Pilot Mountain State Park, North Carolina

In some ecosystems, fire has a large influence on the types of vegetation present. Determining the historical fire regime can help explain current vegetation patterns and aid future planning and management. This study utilized fire scars on three pine species (*Pinus pungens, P. rigida,* and *P. virginiana*) to assess the fire history of Pilot Mountain State Park. It was hypothesized that the fire history of Pilot Mountain would closely resemble that of previously studied xeric forests of the southern Appalachians. Fifty-four cross-sections were analyzed and a composite fire history was constructed from these samples. Thirty-five of the collected samples exhibited fire scars and between them they recorded 59 fire events between 1859 and 2014. The mean fire interval (MFI) of these samples was 2.87 years and the median fire interval was 2.00 years. Fire frequency was greatest between 1909 and 1934 with 15 distinct fires recorded within this period. The MFI for Pilot Mountain was shorter than what has been found in previous studies in the

Appalachians potentially indicating a greater degree of human influence (through anthropogenic fire initiation) than has been seen in previously studied ecosystems.

36 Margaret Bliss, Kristen K. Cecala
Biology, University of the South, Sewanee, TN

Implications of Behavioral Plasticity on Habitat Use by Appalachian Stream Salamanders Following Riparian Disturbance

Human activities frequently impact ecosystems resulting in wildlife declines, yet animals often continue to persist at low densities in impaired environments. Because habitat selection behaviors have evolved to maximize an individual's fitness, evaluating the behavior of animals that choose to inhabit degraded habitats provides insight into wildlife declines and effective targets for management. The objectives of our study were to evaluate whether fine-scale habitat selection behaviors differed between individuals inhabiting disturbed environments relative to undisturbed habitats. Specifically, we evaluated the potential selection and movement biases by blackbellied salamanders (*Desmognathus quadramaculatus*) to different contexts depending on the status of the surrounding riparian forest. Salamander individuals from deforested riparian zones were (1) less responsive to light and (2) exhibited greater reactivity than did salamanders from undisturbed riparian zones. Individuals originating from deforested habitats had poor body conditions, indicating that deforested streams are suboptimal relative to forested habitats. Although evidence suggests that salamanders decline following riparian disturbance, our results indicated that salamander individuals that exhibit high behavioral plasticity are capable inhabiting altered habitats.

37 Bianca Garner, Baraka Williams, Elrica Brown, Dominique Clark, Angel Garcia
Biology, Tougaloo College, MS

Iron and Temperature Regulation of *Bacillus cereus* Group Microbes Physiology

Both iron and temperature are important regulators of the growth of *Bacillus cereus* Group Microbes. Optimal temperatures are associated with the virulence of the various microbes, with the animal associated microbes optimal at upper temperatures. *B. cereus* group microbes associated with insects have optimal growth temperatures that are much lower. Iron availability has been directly linked to the regulation of iron acquisition mechanisms, including siderophore and heme uptake. We questioned how these two important environmental signals altered the response of *B. cereus* group microbes. We observed that low levels of iron at low temperatures had an increase in growth for *B. thuringiensis*. The level of catechol produced was much higher at these temperatures than at the higher temperature. The elevation of catechol coincides with an increase in the expression of the genes associated with iron chelators, compounds produced under iron limitation to aid in sequestering iron. We observed that the ferric uptake regulator, fur, was also upregulated. These studies suggest that temperature might be the more important regulator of iron uptake genes in *B. thuringiensis*, as opposed to the actual iron concentration.

38 Adrianna E. Eder[1], Manuel F. Santiago[2], David K. Giles[1]
[1] Biological and Environmental Sciences, University of Tennessee at Chattanooga; [2] Chemistry, University of Tennessee at Chattanooga

Exogenous Fatty Acids from Lotion Affect Phospholipid Structure and Alter Permeability Characteristics in *Acinetobacter baumannii*

Recent studies have highlighted the ability of some bacteria to utilize fatty acids as a membrane remodeling strategy. Considering this, we hypothesized that fatty acid-containing cosmetic products, such as lotions, may have an effect on skin-dwelling bacteria. The current study surveyed *Acinetobacter baumannii* for its growth under skin conditions (minimal media, pH 5.5, 150 mM NaCl, 30 C) and membrane lipid response to fatty acids found in daily-moisturizing lotions. Since phospholipid profiles from *A. baumannii* suggested structural changes, a crystal violet (CV) uptake experiment was performed to assess bacterial uptake of hydrophobic compounds, a key indicator of membrane permeability. Differences of up to 20% CV uptake were observed, demonstrating decreased membrane permeability to hydrophobic compounds following lotion fatty acid exposure. *A. baumannii* phospholipids were then extracted following growth in the presence and absence of lotion fatty acids and analyzed by high-performance liquid chromatography/mass spectrometry (HPLC/GC) to confirm bacterial synthesis of phospholipids possessing acyl chains corresponding to the supplied fatty acids. The ramifications of fatty acid utilization were explored by performing acid and salt stress assays on *A. baumannii* following growth with lotion fatty acids. Although minimum inhibitory concentrations were unaffected, the fatty acid treated bacteria exhibited variable growth effects upon exposure to increasing concentrations of sodium chloride and lactic acid. Increased biofilm formation was noted with *A. baumannii* after exposure 12:0, 14:0, 18:2, 18:3G, 18:3 a, 20:3, and 20:4. Ongoing experiments are investigating the ramifications of fatty acid assimilation following antimicrobial peptide and antibiotic treatment.

39 Saba A. Munir[1], Daniel J. Shults[2], Steven J. Symes[2], David K. Giles[1]
[1] Biological and Environmental Sciences, University of Tennessee at Chattanooga; [2] Chemistry, University of Tennessee at Chattanooga

Exposure to Exogenous Fatty Acids Impacts Phospholipid Composition, Membrane Permeability, and Virulence Phenotypes in *Acinetobacter baumannii*

Acinetobacter baumannii, a ubiquitous gram-negative bacillus found on a variety of surfaces, is a major human health concern because of its emergence as a nosocomial infection and its antibiotic resistant nature. Some gram-negative bacteria have the ability to acquire and incorporate fatty acids into their phospholipid membranes. This study was designed to determine whether structural alterations occur in *A. baumannii* upon exposure to a wide range of polyunsaturated fatty acids (PUFAs) as well as the significance of this phenomenon in terms of survival and resistance to stress. Thin layer chromatography of isolated phospholipids indicated phospholipid profile variation depending on the exogenous PUFA supplied. The fatty acids affected membrane permeability, as determined by a hydrophobic compound uptake test. At least a 20% range of uptake was observed between the PUFAs examined. Isolated lipids were analyzed by ultra-performance liquid chromatography/mass spectrometry. Numerous unique phospholipid species were identified and bioinformatically predicted to contain the exogenously supplied PUFA as one of their acyl chains. A biofilm assay indicated that bacterial growth in the presence of each PUFA caused an increase in biofilm production. Environmental stresses such as hydrogen peroxide, antimicrobial peptide, and antibiotic pressures were assayed as well. Sensitivity of *A. baumannii* to two different antimicrobial peptides, colistin and polymyxin B, increased following growth in several of the PUFAs. Since cationic antimicrobial peptides are believed to interact with bacterial lipid membranes for eventual pore formation, these results implicate exogenous fatty acids as modification moieties that may impact resistance to environmental stresses.

40 Mai H. Tran, Joong-Wook Park
Biological and Environmental Sciences, Troy University, AL

Effect of Freshwater Exposure on Tarballs Bacterial Community

Tarballs are remnants of petroleum found on the shoreline after oil spills or oil seeps. Many characteristics of tarballs resemble those of a biofilm- forming environment, making them a possibly favorable microcosm for bacteria. Much research has focus on oil-biodegrading microbial communities in marine tarballs. A study by Tao *et al.* in 2011 revealed that tarball samples collected on the Gulf coast contain an unusual accumulation of non-hydrocarbonoclastic bacteria *Vibrio vulnificus,* a human pathogen. This result further suggests the potential of tarballs as a reservoir for a variety of microbes. It has been observed that some of coastal tarballs float around and reach freshwater estuaries and lakes connected to the ocean. As no study has analyzed the microbial community in the freshwater tarballs, this study proposes to investigate the shift of bacterial community in marine tarballs collected on the Gulf coast after being exposed to freshwater. Total DNAs extracted from marine and freshwater tarballs will be analyzed using PCR-DGGE and DNA sequencing to identify dominant bacteria in the freshwater tarballs in comparison with those in the marine tarballs.

41 Benedict C. Okeke, Christiane Ingram, Andrew Paulk, Sharla Rafferty
Biology, Auburn University at Montgomery

Biomass Conversion by a High Beta-Glucosidase Producing Trichoderma Species SG2

Large quantities of lignocelluloses are produced annually and can be converted to fuels and chemicals. Moreover, fossil oil is non-renewable and a major cause of atmospheric pollution. Complete mixtures of enzymes are required for efficient conversion of biomass to fuels and chemicals. *Trichoderma* isolated from decaying biomass and surface soil mixture is a strong producer of mixtures of cellulolytic and xylanolytic enzymes. *Trichoderma* produces more β-glucosidase than *Trichoderma*RUT-C30 employed for cellulase production and coproduces amylase in lignocellulose medium. This study presents simultaneous production of cellulolytic-xylanolytic-amylolytic enzymes and optimization of lignocellulose biomass saccharification by *Trichoderma*SG2. Results indicate potential application of *Trichoderma*SG2 in biomass conversion to fuels and chemicals.

42 Kristin A. Keith, Amanda D. Williams
Biology, Lipscomb University, Nashville, TN

The Involvement of the JAK/STAT Pathway in the Regulation and Induction of Immunoproteasomes Following IFN-Stimulation

Immunoproteasomes differ from proteasomes in 3 key subunits: LMP2, LMP7 and MECL1 and vary in cleaving preference - optimizing the efficacy of cleavage of the antigen for MHC-class 1 antigen presenting cells. The immunoproteasome specific antigen peptides are presented on the outer surface of the infected cell via immunoproteasome and MHC-1 processing allowing the T-cells to phagocytize the infected cell lines. Previous studies have suggested that IFN-G, a major cytokine involved in the induction of immunoproteasomes during viral infections, induces the JAK/STAT pathway - specifically activating JAK2. We hypothesized that immunoproteasome subunits are activated through JAK2-mediated signaling pathway upon induction via IFN-G. To test our hypothesis, we treated a murine dendritic cell line and a murine macrophage cell line with AG-490, a JAK2/STAT3 chemical inhibitor, followed by IFN-G in order to study the regulation of the immunoproteasome subunits through the JAK/STAT pathway with the use of western blot protocol. The results suggest that immunoproteasomes are mediated through a JAK2-dependent manner. Our data suggests that in both the dendritic cell line and the macrophage cell line, 30uM AG-490 effectively inhibits JAK2 thereby mediating the return of immunoproteasome subunit expression levels to normal levels. In conclusion, our data indicates that immunoproteasomes are mediated through a JAK2-dependent manner.

43 Matthew J. Heard, Victoria J. Frost, Jordan Lewis
Biology, Winthrop University, Rock Hill, SC

Assessing the Abundance and Distribution of *Escherichia coli* on Oceanic Beaches in SC

Oceanic beaches are home to pathogens that can severely affect human health. However, we often have a limited understanding of how these microbial species vary in abundance and spatial distribution within oceanic beach communities. Understanding how these taxa are distributed across these habitats is critical because exposure to or increases in their abundance may lead to increases in human illnesses or public beach closures. In this study, we examined how the abundance and distribution of *Escherichia coli* (*E. coli*), an important fecal indicator bacteria species, varied across a set of oceanic beaches in Folly Beach, South Carolina. To assess this, we collected sand samples from three distinct habitats (sand dune areas, inter-tidal areas, and sub-tidal areas) at 30 beach locations. In addition, we also examined how both beach re-nourishment and bacterial levels in adjacent marine water sources may have influenced our findings. Our results show that *E. coli* is found in all three habitat areas we examined along the beach, but in varying levels of abundance. We also found that beach re-nourishment significantly altered *E. coli* abundance and distributions and that inter-tidal habitat areas on re-nourished beaches showed increased abundances of *E. coli* (which may make some sense as this is generally where re-nourished sand is added). Finally we found that *E. coli* was not present in nearby marine waters, which may suggest that the terrestrial pollutants and animals may be the likely source of bacteria when it is found on the beach or causes beach closures. Collectively, our findings suggest that *E. coli* is likely to be present in all zones of a beach and is an important source of bacterial pollution in coastal habitats. Furthermore, our findings suggest that fecal indicator surveys to assess bacterial pollution levels (conducted by organizations such as the EPA) may be better served by sampling sand instead of marine waters.

44 Blake W. Nelson, Leighanne R. Main, Horton H. Hobbs III, Andre L. Lorenz, Jay A. Yoder
Biology, Wittenberg University, Springfield, OH

Cricket Mummies in Caves and Identification of the Causative Entomopathogenic Fungus

A white pillowy fungus fastens dead cave crickets to walls of caves. The finding of these mummies is not correlated with any special habitat requirements or conditions. Our goals were to determine the identity of the fungus; find out if it is pathogenic to crickets; and determine if this fungus is part of the regular flora of healthy crickets. We analyzed crickets throughout the Cumberland Plateau (*Hadenoecus cumberlandicus* KY, *H. opilionoides* TN, *H. jonesi* AL) and mummies by water rinse and fungus culture. The primary fungal isolate was *Beauveria caledonica* (99% Blast match 18S rRNA ITS similarity to *B. caledonica* in beetles). In contrast, healthy crickets carry *Aspergillus* and *Penicillium* in addition to a rich fungal diversity, with *B. caledonica* being absent or isolated in low frequency. Applying Koch's postulates, healthy crickets treated with a *B. caledonica* inoculum died. *Beauveria caledonica* was subsequently re-isolated from the cadavers, and colony characteristics matched the original *B. caledonica* isolate. Thus, *B. caledonica* has potential in biocontrol and is a natural regulator of cricket populations. Because cave crickets are a keystone species, *B. caledonica* could have an indirect negative impact on other organisms in the cave community.

45 Anna R. Moravec[1], Andrew W. Siv[2], Daniel J. Shults[1], Steven J. Symes[1], David K. Giles[2]
[1] Chemistry, University of Tennessee at Chattanooga; [2] Biological and Environmental Sciences, University of Tennessee at Chattanooga

Polyunsaturated Fatty Acids (Pufas) Affect Phospholipid Composition, Membrane Permeability, Stress Resistance and Biofilm Formation in Pathogenic *Vibrio* Species

The pathogenic *Vibrio* species (*cholerae*, *parahaemolyticus* and *vulnificus*) represent a constant threat to human health, causing food-borne and skin wound infections as a result of ingestion or exposure to contaminated water and seafood. Recent studies have highlighted *Vibrio*'s ability to acquire and assimilate fatty acids from environmental sources, and the possession and conservation of such machinery provokes consideration of fatty acids as important factors in the dual lifestyle of *Vibrio* species. In this study, exogenous fatty acid exposure to *Vibrio* species is linked to changes in bacterial membrane phospholipid structure, permeability, biofilm formation and susceptibility to stress. Polyunsaturated fatty acids (PUFAs) supplied in growth medium were assimilated into bacterial phospholipids, as determined by lipid extraction and subsequent thin-layer chromatography and ultra-performance liquid chromatography/mass spectrometry. The incorporation of fatty acids affected (up to 40%) membrane permeability as assessed by uptake of the hydrophobic compound crystal violet. For each species, certain PUFAs were identified as affecting minimum inhibitory concentrations to peroxide stress and antimicrobial peptide treatment. Some fatty acids, such as eicosapentaenoic (20:5) and docosahexaenoic (22:6), conferred protection against hydrogen peroxide, whereas others, such as linolenic (18:3) and arachidonic (20:4), heightened susceptibility to polymyxin B in a species-specific manner. Significant fluctuations in biofilm formation were observed depending on the PUFA supplemented. Our results illuminate the important and complex roles of exogenous fatty acids in the membrane physiology and virulence of a bacterial genus that inhabits aquatic and host environments containing an abundance of diverse fatty acids.

46 Jennell Talley, Rebekah Ward, Christopher Brandon, Christopher Brown
School of Science & Technology, Georgia Gwinnett College

A Three-Tiered Approach to Improve Program Assessment for the Undergraduate Curriculum

Developing a comprehensive assessment of student understanding and progression through a degree program is challenging. Three common problems are (1) gaining a clear view of depth of content/concept knowledge, (2) obtaining informative, longitudinal information about ones program, and (3) burdening busy faculty with additional requirements. Assessment questions, for ease of grading, are often multiple choice questions which do not assess deeper levels of understanding, such as synthesis, and limit a students own expression of their knowledge. Assessments might be embedded in tests or at the end of the students academic career, thus conflating retention with cramming for the test and preventing the recognition of key moments when important concepts were reinforced or persistent misunderstandings took root. Finally, good assessment takes time and is too often given low priority by faculty and staff that are already pulled in many directions professionally and personally. In this talk, we will present a three-tiered, holistic approach to assessment that addresses these issues while trying to balance time input and quality data output. We will also present evidence that this method can be used to enhance faculty professional development.

47 Christopher Brown, Jennell Talley, Christopher Brandon, Rebekah Ward
School of Science & Technology, Georgia Gwinnett College

What We Can Know About Our Students Without Really Trying: A Longitudinal Study of Student Progress Reveals Some Surprising Information

One quality of a successful educator is to be attuned with how well students incorporate the content and skills they are taught in one's course and throughout the students' academic career. We must assess students to highlight and enhance our own teaching strengths and to discover and address their unsatisfactory progress. To better understand our students' progression through the biology program, the Biology Program Goals committee at Georgia Gwinnett College has designed and begun implementing a new method for assessing student progress on the biology program goals. Here, we present some of the more interesting preliminary results from the Fall 2014 and Spring 2015 semesters. We will highlight the added depth and breadth of knowledge about our students' progress and demography this new method provides. We will discuss why we feel this approach is a more meaningful way to understand student progression and achievement and how it can be utilized to enhance course and program design.

48 Christopher E. Barton
Biology, Belmont University, Nashville, TN.

Using *DNA Barcoding* to Supplement Classical Taxonomic Methods in Undergraduate Science Courses

The use of classical taxonomic methods to identify plant and animal species has long been a part of the core undergraduate biology curriculum. These methods have been fruitful over the years and have allowed the identification of numerous new species. However, it is also well known that there are times in which classical identification methods might prove difficult, especially in species with a high degree of phenotypic plasticity. In response to these challenges, we are proposing to incorporate *DNA Barcoding*, a molecular means of species identification, into our undergraduate course and research programs. As students learn these molecular techniques, they will accumulate multiple laboratory and bioinformatic skillsets typically not gained in some undergraduate courses. We believe that the incorporation of *DNA Barcoding* will allow students to keep up with the pace of molecular taxonomy, while instilling a greater appreciation for classical taxonomic methods.

49 Victoria L. Turgeon
Biology, Furman University, Greenville, SC

Inquiry-Based Teaching of Human Anatomy Moves Learning Beyond Memorization

Too often courses in human anatomy are seen by instructors and students as courses in memorization. Students are presented with the various systems and are instructed to recognize the structures, identify origins and insertions, and assign functions. While many students are capable of memorizing this large amount of information, they do not retain it beyond the exams. The failure to include evolution, case-studies, and hypothesis- based teaching has reduced the college-level human anatomy course to that of a non-majors science course. Human anatomy should build upon a student's knowledge of biology, chemistry, and physics. Therefore, to help students retain information and place human anatomy within the context of evolution, it is important to question the structural-functional relationships of the human body. Such methods including model-building and a flipped-classroom approach were used in an upper-level human anatomy course at Furman University. Students taught in this manner surpassed expectations when presented with novel material during class activities and on exams. Being fully engaged with the material and requiring the students to think about anatomy in terms of questions of evolution and function moved them beyond mere memorization. The final exam in each of two sections taught using this methodology contained novel questions that could only be answered if the students knew how to apply the concepts. Answers to similar questions asked of students taking a traditional human anatomy course, reveal that inquiry-based instruction of anatomy is associated with a deeper understanding of the material and interpretations of the relationships between structures.

50 James R. Rayburn
Biology, Jacksonville State University, Jacksonville AL

A Comparison of Student Response System Quizzes to Conventional Paper Tests (Multiple Choice) for General Biology Courses at Jacksonville State University

New technologies, such as the Student Response Systems (SRS), help motivate students to be more prepared, maintain concentration in lectures, stay interested during class, and maintain response anonymity. SRS can increase understanding of complex bioscience concepts and are becoming more common place in education. The SRSs allows an entire class to respond to multiple choice questions displayed on a projection screen or TV. Students input their responses using remote devices, the results are instantly collected, summarized and presented to the class in visual format. These systems are used in lectures and as standalone quizzes. How well the results from the in class clicker quizzes correspond to student performance on regular exams was determined. Over several years (~5) data were collected using SRS and compared to conventional test results. Regression analysis was made comparing correlations of SRS to conventional tests. Quizzes given during lectures and quizzes given as a standalone exam were compared to paper exams covering the same material. Correlations between the responses were performed. R2 values were often between 0.3 and 0.5 indicating there was a positive relationship between these values. The more questions given on quizzes led to better R2 values compared to the paper exams. Overall the comparisons suggest that the SRSs do well for assessing student learning.

51 Amy M. Wiles
Biology, Mercer University, Macon, GA

Figure Analysis: An Active Learning Technique Promoting Visual Literacy in Biology

Student learning is improved when active learning methods are utilized rather than when traditional lectures are given. A challenge, however, has been how to incorporate active learning into content-heavy courses, such as an upper-level cellular biology course. Many active learning techniques require students to apply knowledge, and therefore these techniques work best when students have already grasped concepts. An additional challenge is that visual literacy has often been overlooked in undergraduate biology education, including the interpretation of textbook diagrams or visual data presented in journal articles. A technique called Figure Analysis was developed and implemented in upper-level, biology lecture courses as a way to deliver content via active learning while increasing the visual literacy of the students. Students learn content while mastering figure interpretation, and they apply information from those figures by explaining them to their peers. Students also make connections between the figure material and previously acquired ideas. Importantly, the instructor does not lecture on the material but only gives an introduction to the concept before students analyze a figure. Students therefore grapple with the material with peers before formal instruction.Student visual literacy was improved after using Figure Analysis, as determined by self-reporting and by assessment.

Figure Analysis requires no technology and therefore may be used in any classroom or nontraditional space. This active learning technique requires no additional preparation over that of a traditional lecture. Best practices for implementation of Figure Analysis for a range of classes, including introductory and high school courses, will be discussed.

52 Kevin M. Drace
Biology, Mercer University, Macon, GA

Implementing Authentic Research as the Introductory Biology Laboratory

Introductory biology professors face a variety of challenges and opportunities in teaching today's students. Recently, the AAAS Vision and Change report and the President's Council of Advisors on Science and Technology encouraged science educators to evaluate more effective teaching strategies in the classroom and laboratory. To that end, two sections of Mercer University's Introductory Biology II course were completely redesigned. Historically, the laboratories emphasized the conceptual material covered in traditional lectures, while giving the students hands-on experience with biological techniques. In an effort to provide students with a more authentic research experience, the laboratory was designed around a single authentic research project. Students were provided soil samples collected from artisanal gold mining camps in Ecuador. Groups worked together to isolate bacteria and characterize strains for resistance to a variety of antibiotics. Each student worked with his or her own individual strains to isolate DNA and use PCR to amplify 16S rDNA. Then, these sequences were used to determine bacterial identity. Most students finished the entire project and submitted their results to the National Center for Biotechnology Information (NCBI) database. The students reported an overwhelmingly positive response to the experience, in comparison to previous student perceptions of the 'traditional' laboratory. This presentation will cover the challenges and rewards of designing and implementing this type of project in the introductory laboratory. Survey results strongly indicate that students placed a high value on this experience as an effective teaching strategy.

53 Kunsiri Chaw Grubbs
Biology, Winthrop University, Rock Hill, SC

Thinking Outside of the Book: Taking Biology Students Outside of Class

Teachers are challenged to go over comprehensive textbook material within a limited timeframe in many biology courses. In order to fulfill course objectives, teachers stress lectures and assignments. Students are not provided a lot of in-class time to experience the flora and fauna in their sur- roundings. I intend to share a few of the out-of-class activities that I do to encourage student thinking and promote a contextual understanding of biology. These activities include learning plant names through geocaching, chalk drawing of cell structures on the sidewalk, going on trips to local nature areas and grocery stores, visiting the campus greenhouse and herbarium/museum, and teaching classes outside. It is important to encourage active student learning by using the resources that are available for us. I believe that this is a key factor in encouraging more students to study biology.

54 C. Theo Witsell
Arkansas Natural Heritage Commission, Little Rock, AR

The Breath of the South Blows Through This Valley: Southeastern and Coastal Plain Influence in the Interior Highlands Flora

A number of plant taxa found primarily in the Gulf and Atlantic Coastal Plains are known to occur in the Interior Highlands Physiographic Region (Ouachita Mountains, Arkansas Valley, Boston Mountains, and Ozark Plateaus Ecoregions), many associated with rare or specialized patch habitats. However, no systematic biogeographic study has been made of the Interior Highlands flora and no systematic analysis of the habitats of disjunct taxa found there has been attempted. To meet this end, county level range maps were examined for the native flora of the Interior Highlands and a list was compiled of those species that exhibit disjunct or edge-of-range distributions in the region. Core distributions of each of these taxa were assigned to one or more of several categories (Northern, Appalachian, Coastal Plain, Great Plains, Southwestern, Rocky Mountains, etc.). For those taxa with a primarily Coastal Plain distribution (the first group considered in an ongoing, broader study), habitats were attributed to each taxon. Habitats found to exhibit notable Southeastern and Coastal Plain floristic influence include fens, acid seeps, river scour, natural depression wetlands (abandoned stream terrace channel scar ponds, karst sinkhole ponds, and 'Mastodon Wallows' or upland non-karst depression wetlands), bluffs, dry acidic woodlands, glades, prairies, saline barrens, and mesic hardwood forests. Each of these habitats will be discussed and representative Coastal Plain taxa given for each.

55 Kelly A. Anderson[1], Dwayne Estes[2]
[1] Center of Excellence for Field Biology, Austin Peay State University, Clarksville, TN; [2] Botanical Research Institute of Texas, Fort Worth

Floristics and Biogeography of Riverscour Communities on the Locust Fork of the Black Warrior River, Blount County, Alabama

Riverscour communities of the Southeast are shrub/herb/graminoid-dominated zones found along rocky high-gradient river systems in dissected regions. Exposed bedrock and deposits of sand, cobble and boulders are defining features of riverscour. Open conditions of these riverside bars are maintained by periodic flooding. The Locust Fork of the Black Warrior River in Blount County, Alabama lies within the Southern Table Plateau Ecoregion of the Southwestern Appalachian Province and is notable for its riverscour communities and outstanding biological richness. Despite the biological significance of alluvial bars these communities remain understudied and rarely surveyed due to their relative inaccessibility. Encroaching development, reservoir construction, invasive species, and toxic runoff from mining threaten the integrity of these unique communities. As such, swift baseline documentation of existing floristic composition is critical. The primary objective of this study was to conduct an inventory of the vascular flora of the Locust Fork riverscour communities. Fieldwork was conducted from March 2013 - October 2014. During this study 267 species were discovered representing 195 genera and 86 families. Noteworthy collections included *Baptisia australis*, *Calamovilfa arcuata*, *Fothergilla major*, *Hymenocallis coronaria*, *Marshallia mohrii*, *Phyllanthopsis phyllanthoides*, *Polygonella americana*, *Solidago arenicola*, and putatively undescribed species of *Amorpha*, *Amsonia*, *Helianthus*, and *Symphyotrichum*. The results of this study are discussed and compared to floristic and vegetation studies of other Southeastern riverscour systems to better understand the biogeography and ecology of these underexplored communities.

56 Zach Irick, Joey Shaw
Biological and Environmental Sciences, University of Tennessee at Chattanooga

Preliminary Vascular Plant Flora of the Big Soddy Creek Gorge

The premise of this study is to document the vascular flora of the Big Soddy Creek Gorge (BSCG). BSCG is located in Hamilton and Sequatchie Counties, Tennessee on the eastern edge of the Cumberland Plateau and it drains into the Ridge and Valley. From May until September 2014 I made approximately 12 collecting trips to upland plateau, gorge slope, and lowland Ridge and Valley habitats. Voucher specimens were collected and are being prepared for entry to UCHT. Preliminary results of the survey include 73 families, 114 genera and 206 species. Six species of conservation concern have been collected, including *Castanea dentata, Diervilla lonicera, Gelsemium sempervirens, Phemeranthus teretifolius, Ribes curvatum, and Scutellaria montana.* Future directions include collecting through the 2015 growing season, delineating the plant communities of the gorge, and a phytogeographic analysis to determine the nature of the BSCG vascular flora.

57 Austin Prater, Joey Shaw
Biology and Environmental Science, University of Tennessee at Chattanooga

The Vascular Flora of the Lula Lake Land Trust on Lookout Mountain in Walker County, GA and a Biogeographical Analysis of the Coastal Plain Element on the Cumberland Plateau

The vascular flora of the Lula Lake Land Trust was surveyed during the growing seasons of 2012 through 2014. The LLLT consists of 1780 h atop Lookout Mountain in Walker County, Georgia. A total of 60 collecting trips were made with 672 species and lesser taxa of vascular plants documented. These represent 119 families and 369 genera. Twenty-eight species of conservation concern were documented including the federally endangered *Spiraea virginiana*, *Lysimachia fraseri* (state listed as rare), and four species not previously known from the state (*Calamovilfa arcuata*, *Chelone lyonii, Populus grandidentata,* and *Solidago arenicola*). Ninety-one non-native species (13.5% of the flora) were documented. A legacy database handed down through the lab of Joey Shaw (UTC) was expanded to include 26 floras of Tennessee, Kentucky, Alabama, and Georgia and was used to measure the proportion of Coastal Plain endemics present in the Eastern and Western Highland Rim, Cumberland Plateau, Ridge and Valley, and Blue Ridge physiographic provinces of Tennessee, Alabama, and Georgia. ANCOVA results indicate the Cumberland Plateau floras contain a significantly higher proportion of Coastal Plain species than the surrounding provinces (F1, 19 = 16.2, p = 0.001).

58 O. Rayne Leonard, Ashley B. Morris
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The Search for the Holy Grail: Comparative Plastomics of Noncoding Chloroplast Regions in Basal Angiosperms, With a Focus on *Illicium*

Basal angiosperms are of interest to researchers because they provide insight into the diversity within angiosperms, polarize analyses of flowering plant evolution, and make functional inferences about the common ancestor of early angiosperms. However, information about extant basal angiosperms is limited. *Illicium* is a monogeneric, monophyletic group of basal angiosperms comprised of 30-40 species, most of which are located in southeast Asia. Disjunctions between the New World and Old World species raise interesting biogeographic questions. Comparative plastomics provides an opportunity to identify potentially informative noncoding chloroplast regions for ecological and evolutionary questions in this group. A Tortoise and Hare approach was used, assessing the number of potentially informative characters (substitutions, indels, and inversions) across all noncoding regions of the plastome within and among four species *of Illicium*. In addition, results of the comparison were assessed within the broader context of basal angiosperms. A total of nine basal angiosperm plastomes were included in the analysis. Preliminary results show that the most informative regions differ within the major orders in the basal angiosperms, as well as across all angiosperms. Contributions to the conversation surrounding the use of next-generation whole plastome sequencing versus

Sanger sequencing for targeted phylogenetic studies within this understudied region of the angiosperm tree of life are discussed.

59 Rebecca A. Dellinger-Johnston, Bruce K. Kirchoff
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Creating a Visually Based Plant Identification Key

Taxonomic keys are essential tools for species identification, used by students and professional biologists. In recent years, advancements in photography have allowed these keys to host high-quality photographs for aid in identification. However, most modern keys still rely heavily on text rather than images. Using text alone limits the user to a discrete number of characters, often described in esoteric terms. In order to create more effective keys, we are developing methods for constructing image-based taxonomic keys. These keys rely on visual pattern recognition to identify species. To ensure the strength of this method, our key focuses on the morphologically diverse genus, *Quercus*. A set of standardized photographs was taken of 43 species of oak native or naturalized in the Southeast. These photographs were used to create a survey that measured how botanists and botanical novices rate the pair-wise similarity of different plant structures, such as leaves or acorns. The mean of each rating was summarized across individuals into a similarity matrix, which was used to a construct dendrogram. This dendrogram will become the basis for the visual key, which will be constructed using standard photographs with limited text. This key will then be tested against an existing dichotomous key to determine if user can make more accurate identifications using the visual key. A t-Test will be used to compare the accuracy of both keys. Using this method of key creation, innovative keys could be constructed for students and professionals in other fields of biology.

60 Joshua Hamrick, Emily Gillespie
Marshall University

Using Herbarium Specimen Data: An Herbarium Informatics Study of the Order Ranunculales within West Virginia with Emphasis on Plants of Key Ethnobotanical Importance

The diverse ecology and anthropological history of West Virginia provides an area of particular ethnobotanical interest considering continued use of many native wild plants for food, material, and medicinal purposes. This study uses the occurrence of ethnologically interesting Ranuculales within a small herbarium collection, Marshall University Herbarium (MUHW), to highlight the complexities and benefits of biological collection digitization. Particular Ranunculales species are harvested regularly within the Mountain State for supplemental income. This study will compare herbaria records with annual harvest data to note the occurrence and distributions of these species and to understand how humans are using forests across the state. Biases and problems associated with using small collections for ecological studies will be discuessed in order to ullustrate why it is valuable to support continued specimen collection and collection digitization efforts that result in data that is fit-for-research use. The importance of herbaria digitization for the synthesis of collections into one accessible resource benefiting education and increased botanical awareness of the general public will also be dicussed.

61 Daniel M. McNair[1], Mac H. Alford[1], Brian J. Axsmith[2]
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Plant Fossils from the Miocene of Mississippi: Reconstructing a Deltaic Wetland

Edward W. Berry made fossil collections from the Hattiesburg Formation in the early 20th century and identified two species from very fragmented material. He concluded that the formation was poor in fossils. Berry was the last paleobotanist to give the formation any serious consideration, and very little knowledge has been added since then, with a total of four plant families identified. However, results of the current study provide a much fuller picture of the flora based on data from a fossil locality discovered in 2014. A total of 15 families and 18 genera have been identified from this locality, and we now suspect that the Hattiesburg Formation contains one of the largest Miocene floras in southeastern U.S. Several of the collections represent the oldest records of their kind for the eastern United States. Most of plant forms described will be familiar to botanists working in the southeastern U.S., but there are a few surprises.

62 Charlie Williams[1], Eliane Norman[2], Walter K. Taylor[3]
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Andre Michaux in Tennessee 1789–1796

The first European-trained botanist to visit Tennessee was the Frenchman Andre Michaux who traveled and collected here in 1789, 1793, 1794, 1795, and 1796. Parts of Tennessee were then the wild western frontier of the U.S. and George Washington was President. Our detailed study of all of Michaux's North American journeys using the primary sources is nearing completion. We will report on how the study was conducted and on some of our findings about Michaux's travels and discoveries in Tennessee.

63 Charles N. Horn
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Geographical Variation in *Heteranthera multiflora* (Pontederiaceae)

Heteranthera multiflora has a known distribution in three distinct regions of the New World, Atlantic coast of North America, the Great Plains and southern South America. It can be easily separated from its closest relative, *H. reniformis*, by the presence of a rounded leaf shape, shortened lower internode of the inflorescence stem (less than 1 cm), and purple filament hairs on the stamens. For *Heteranthera multiflora*, specimens from each of the geographic regions can be separated, based on a combination of floral features: the number of flowers (fewest in Atlantic coast form), proportion of flowers within spathe (highest in Atlantic coast form), and perianth tube and lobe lengths (shortest in Great Plains form). Perianth color is unique in each region, white in South America, purple, especially at the base, in the Great Plains, and lavender in the Atlantic coast. At this point the taxonomic differences will not be taxonomically recognized due to observed statistical overlap of measurable features. A recent find in North Carolina near Raleigh suggests that the population was introduced from the Great Plains into a man-made reservoir.

64 Alexis B. King[1], Jon M. Davenport[1], Blake R. Hossack[2]
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Re-Interpreting Geographic Variation in the Wood Frog, *Rana sylvatica*

Beginning in the 1800's, biologists noticed that many species become larger in colder climates (i.e., higher altitudes and latitudes). Support for this pattern has generally been found for many vertebrate groups. As a result of body size changes, it is hypothesized that life-history characteristics will also differ across latitudinal gradients. For example, large females may lay fewer, but larger eggs than small females at higher latitudes. Recent reviews have suggested that these general patterns of body size and life history characteristics are to be expected for amphibians. However, limited data is available on many species of amphibians to validate these generalizations. Therefore, we investigated variation in body size and life history characteristics of the wood frog, *Rana sylvatica.* Wood frogs are a great study species for this type of research because they are common and widespread across North America, spanning the southern Appalachians to the Arctic Circle. We combined field and literature data covering the entire range of the wood frog (over 30 degrees of latitude). We found that body size of adult wood frogs and egg size decreased as latitude increased. Surprisingly, clutch size was not associated with change in latitude. Wood frogs do not appear to follow the patterns predicted by previous researchers. Our study illustrates the need for additional data, even on common species, before generalizations can be applied. This type of data may also aid in understanding wood frog population dynamics at higher latitudes and vulnerability to future climate change.

65 Ethan J. Royal[1], Sarah A. Smiley[2], Terence M. Farrell[1]
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The Effect of Prey Species on Caudal Luring in Pigmy Rattlesnakes (*Sistrurus miliarius*)

Pigmy rattlesnakes are dietary generalists that eat amphibians, reptiles, mammals and centipedes. We investigated foraging in pigmy rattlesnakes in both field and laboratory behavior trials. In the lab, we videotaped field-collected snakes (n=29) in trials with Ground Skinks (*Scincella lateralis*) (n=29) and trials with the Florida Blue Centipedes (*Hemiscolopendra marginata*) (n=29) and quantified a variety of behaviors to determine if prey type influenced foraging. Caudal luring was observed in 17% of skink trials but never in the presence of centipedes. Cratering (partial burrowing in sand) occurred significantly more frequently in skink trials than centipede trials. Snakes were significantly more likely to actively pursue centipedes than skinks. In the field, we filmed 51 rattlesnakes that were found in typical foraging postures. We randomly exposed each snake to one of three treatments: frog, anole, or control. In the frog and anole treatments snakes were presented with either a green treefrog (*Hyla cinerea*) or a green anole (*Anolis carolinensis*) tethered approximately one meter from the snake using string, while control snakes were exposed to string with no prey. We observed three instances of caudal luring; twice in anole trials and once in a frog trial. There was no statistically significant difference in the frequency of caudal luring between the treatments. All snakes that used caudal luring in field trials were mature adults, contradicting previous studies that hypothesized caudal luring in pigmy rattlesnakes was limited to juveniles. The plasticity in foraging tactics exhibited by pigmy rattlesnakes may enhance their success as generalist predators.

66 Carlos D. Camp[1], Wally Smith[2], Jessica A. Wooten[3], Dirk J. Stevenson[4], John B. Jensen[5]
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Genetic Divergence in Populations of Slimy Salamanders (*Plethodon glutinosus* Species Complex) Across the Lower Piedmont and Coastal Plain of Georgia

The advent of modern molecular techniques has enabled the discovery of unimagined genetic diversity within what were believed to represent widespread, largely homogeneous species. While early work depended on genetic distances determined by the analysis of allozymes, researchers now rely heavily on gene sequences because of their ability to detect differences among silent-site mutations and non-coding genes. They can also determine relationships directly from ancestor-descendent lineages. A quarter of a century ago the widespread taxon *Plethodon glutinosus* (Slimy Salamander) was split into 14 parapatric species based on allozyme analysis. Many workers have investigated the relationships among the named forms using DNA-sequence data. However, virtually none has conducted a fine-scale analysis of the phylogeography of single purported species. We sequenced four genes (three mitochondrial and one nuclear) for populations across the range of *P. ocmulgee*, which is distributed across the lower Piedmont and Coastal Plain of Georgia. We also examined populations of neighboring taxa within these regions. We found that genetic divergence is significantly related to geographic distance and climatic similarity with major rivers possibly also contributing as a barrier to gene flow. Sequence data did not conform to currently recognized taxa. This could be due to (1) introgression, (2) incomplete lineage assortment, or (3) the failure of allozyme-based distance measures to accurately define species and their boundaries.

67 Caitlin T. Rumrill[2], David E. Scott, Stacey L. Lance[2]
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Chronic Effects of Larval Exposure to Multiple Stressors in Southern Toads, *Anaxyrus terrestris*

The complex life histories of amphibians allow for stressor exposure in aquatic and terrestrial life stages, and studies have also shown that exposure of the parental generation impacts offspring tolerance to novel stressors. Additionally, exposure to one stressor is almost always coupled with exposure to another, and the interactive effects of exposure to multiple stressors are generally unknown. To examine these issues we employed a 2x2x2 factorial design in outdoor 1000 L mesocosms (n = 24), where we bred southern toads (*Anaxyrus terrestris*) from uncontaminated and heavy metal contaminated sites, then exposed free-swimming larvae to an anthropogenic (copper - 0, 30 g/L) and natural (predator cues - present/absent) stressor. We then transferred metamorphs to terrestrial mesocosms and examined the chronic effects of early life stage exposure. We measured larval and terrestrial survivorship, time to/size at metamorphosis, post-metamorphic growth, and conducted a physiological assay targeting hopping ability 1wk. and 1mo. post-metamorphosis. We found a significant negative effect of contaminated parental source on size at metamorphosis and 1 wk. post-metamorphosis hopping measurements, as well as a significant source*Cu*predator interaction on 1 wk. hopping measurements. We found parental source to significantly affect juvenile size with contaminated source larger 3 mo. post-metamorphosis but by 5 mo. neither source was significantly different. Additionally, survivorship analysis indicated decreased survivorship due to source and larval Cu exposure, with fewer surviving to 5 mo. from contaminated source and 30 g/L Cu treatments. The presence of transgenerational effects and a 3-way interaction highlight the importance of conducting multistressor studies across generations.

68 Stacey L. Lance[1], Cara N. Love[1], Megan E. Winzeler[1], Rochelle Beasley[1], Schyler O. Nunziata[2], David E. Scott[1]
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Prevalence of Two Amphibian Diseases, Ranavirus and Chytridiocmycosis, in Contaminated and Uncontaminated Wetlands on the Savannah River Site

A variety of natural and anthropogenic stressors have been hypothesized to increase the emergence of wildlife diseases in amphibians via increased host susceptibility. In South Carolina, a high incidence of *Batrachochytrium dendrobatidis* (Bd) in bullfrog larvae was observed in constructed wetlands on the Savannah River Site (SRS), where there are also elevated levels of copper, zinc, and mercury. However, no studies to date have explicitly examined the linkages between metal contaminants and the disease ecology of ranavirus or chytridiomycosis in amphibians, and this knowledge gap impedes our understanding of disease transmission. We sampled adult and larval amphibians from four contaminated and eight reference wetlands on the SRS. We examined 1004 individual amphibians representing 14 frog and 7 salamander species. Overall, for Bd, *Pseudacris ornata* had the highest prevalence (48.1%), followed by *Lithobates catesbeianna* (27.4%) and *L. sphenocephalus* (24.5%). Three species of salamanders tested positive including *Ambystoma tigrinum*, *A. opacum*, and *A. talpoideum*, though all at low levels. For ranavirus, *P. ornata* again had the highest prevalence (100%), followed by *A. tigrinum* (85.7), *A. talpoideum* (53.1%), and *A. opacum* (45.9%). Significantly higher proportions of animals with *B. dendrobatidis* were observed in contaminated sites (19%) versus uncontaminated sites (6.4%). Slightly lower proportions of individuals at contaminated sites were ranavirus positive than at reference sites (32.1% vs. 39.1%, respectively). Opposite trends were observed for pathogen loads with higher fungal zoospore loads in reference wetlands and higher viral loads in individuals from contaminated wetlands. We discuss these results and ongoing follow-up studies.

69 Timothy E. Baldwin[1], Yong Wang[2], Callie J. Schweitzer[3]

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The Influence of Environmental Conditions and Land Cover on Pool Breeding Amphibian Diversity within Northern Alabama

Within this study, we assessed the connection between vernal pool environmental conditions, land cover, and pool breeding amphibian diversity. It was hypothesized that vernal pools overshadowed with more canopy cover and surrounded with more heterogeneous land cover would have a negative relationship with amphibian diversity. Twenty four vernal pools were sampled during this study, from James D. Martin Skyline Wildlife Management Area and William B. Bankhead National Forest in northern Alabama. Larval amphibians and metamorphs were inventoried biweekly, during three breeding seasons (2008-2011) using minnow traps. Vernal pool environmental conditions and morphology data were collected simultaneously with amphibian sampling. ArcGis 10.1 and ERDAS Imagine 2013 were used to assess the surrounding land cover. Canonical correspondence analysis was applied to document the relationship between amphibian species, local environmental conditions, and landscape variables. Finally, forward multiple linear regression was used to assess the influence that environmental conditions and land cover had on amphibian diversity. During this study, a total of 35,963 larval amphibians and 837 metamorphs were sampled. Across all three breeding seasons, there was a gradient between forest cover percentage when compared to soil and water temperature. Multiple regression results indicated that water pH, pool area, soil and water temperature, and leaf litter depth predicted larval amphibian abundance, R2 = 0.347, $p < 0.001$. Diversity indices were related to vernal pool environmental conditions, rather than land cover.

70 Joshua R. Ennen[1], Wilfredo Matamoros[2], Sarah C. Hazzard[1], Mickey Agha[3], Jeffrey E. Lovich[4]

[1] Tennessee Aquarium Conservation Institute, Chattanooga; [2] Facultad de Ciencias Biologicas, Universidad de Cencias y Artes de Chiapas, Museo de Zoologia, Tuxtla Gutiérrez, Chiapas, Mexico; [3] Forestry, University of Kentucky, Lexington; [4] U.S. Geological Survey, Southwest Biological Science Center, Flagstaff, AZ

The Where and Why of North American Turtles: An Explanation of Species Richness Patterns

Species richness is not uniformly distributed across the landscape, and these patterns are often associated with environmental gradients. In this study, we examine species richness patterns within North America turtles and use 14 abiotic variables (8 climatic, 2 topographical, 2 stream variables, as well as latitude and longitude) to construct regression models fitted to spatial data that predict species richness for all turtles (n = 85), freshwater aquatic and semiaquatic turtles (n = 75), turtles in the family Emydidae (n = 43), and those in the Kinosternidae (n = 21). Overall, species richness was positively related to maximum temperature of the warmest month (K), precipitation of the wettest month (mm), total stream length (km), and temperature seasonality. Species richness of aquatic and semiaquatic turtles was positively related with precipitation of the wettest month, total stream length, and temperature seasonality. Emydid species richness was only related (positively) to precipitation of the wettest month. Interestingly, only kinosternid richness was related (negatively) with latitude. Also, species richness within kinosternid was positively related to precipitation of the wettest month and total stream length. Given current and projected climate trends, especially alterations of temperature and precipitation patterns, species richness of North American turtles could be impacted.

71 Canceled.

72 Lori Tolley-Jordan[1], David Rickless[2], Joe Morgan[2]
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The Distribution of Trematode Parasites of Freshwater Periwinkles (Pleuroceridae: *Elimia*) in Alabama Streams

Alabama is a global hot-spot for freshwater periwinkle (Gastropoda: Pleuroceridae) snail diversity, including those in the genus *Elimia*. Interestingly, most freshwater snails have co-evolved with one or more species of trematode parasite. However, the diversity of these worms, that more than likely far surpasses its native snail hosts, is undescribed in Alabama. To examine parasite diversity, 50 individuals of each snail species per stream were collected. From each snail, gonads and digestive glands were removed, smeared onto a slide, and observed for parasite presence using a compound microscope. As there are no taxonomic keys for the parasite life stages found in snails, a catalogue that grouped cercaria morphotypes based on distinctive physical features and anatomical measurements was made. To date, 20 parasite morphotypes of nine snail species have been recorded. Of the 26 streams sampled, snails collected from four streams had no parasites while snails in the remaining streams were infected with up to four trematode morphotypes. In general trematode communities were unique to the location where the snails were collected. However, overlap in a parasite morphotype among snail species collected from multiple locations was found for three morphotypes while eight parasite morhotypes were found within a snail species collected from multiple localities. Overall, these results show that trematode richness is twice that of their snail host species. Thus, Alabama may also be a global hotspot for trematode diversity. Further research, including molecular analyses of these worms, is needed to gain a better understanding of this unique diversity.

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Differences between Barn Owl (*Tyto alba* L.) Pellet Remains Collected in 1988 and 1996 from a Silo Roost in Claiborne County, Tennessee

One hundred two barn owl (*Tyto alba* L.) pellets were collected in 1996 from the campus of Lincoln Memorial University, Harrogate, Tennessee, in extreme northern Claiborne County. Average weight, length, and width of intact pellets were 6.15 g, 46 mm, and 30 mm, respectively. Prey remains identified, from most to least abundant, included short-tailed shrews (*Blarina brevicauda*; 35.3%), southern bog lemmings (*Synaptomys cooperi*; 17.8%), *Sorex* spp. (12%), hispid cotton rats(*Sigmodon hispidus;* 7.7%), avian spp. (7.3%), prairie voles (*Mictrotus ochrogaster*; 4.7%), deer mice(*Peromyscus* spp.; 4.3%), eastern harvest mice (*Reithrodontomys humulis*; 3.1%), least shrews (*Cryptotis parva*; 3.1%), pine voles (*Microtus pinetorum*; 1.9%), house mice(*Mus musculus*; 1.2%), eastern cottontails (*Sylvilagus floridanus*; 0.8%), one black rat (*Rattus rattus*; 0.4%), and one Norway rat (*Rattus norvegicus*; 0.4%). Chi-square 2 x 2 contingency analysis comparing 1988 (Copeland and Caldwell) to our 1996 data, revealed significantly higher proportions of short-tailed shrews to least shrews ($\chi 2 = 19.5$; d.f. = 1; $P = 0.05$, 3.84) and significantly higher proportions of voles (*Microtus* sp.) to southern bog lemmings (χ 2 = 13.7; d.f. = 1; $P = 0.05$, 3.84) identified from pellet remains. Prey selected by barn owls is influenced by individual preference, density of prey species, and seasonal differences in hunting strategies. Reciprocal fluctuations between southern bog lemming and vole populations have been previously reported however. Reflection of such interspecific competition in owl pellet remains should be investigated.

74 Chelsea R. Hinton, Renee Yetter
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Foraging Behaviors of the Bumble Bee (*Bombus* sp.) with the *Lobelia siphiliticus* Population: A Closer Look at Thieving Versus Legitimate Foraging Frequencies

Foraging behaviors of bumble bees have been studied in a variety of contexts that include thieving, legitimate foraging and pollen collecting. In this investigation we observed the foraging patterns of the bumble bees (*Bombus sp.*) in a population of *Lobelia siphilitica* in the Daniel Boone National Forest. In particular, we documented the frequency of thieving versus legitimate visits, the incidence and consistency of both types of visits by the individual bees when observed in a sequence of visits, the incidence of pollen collection when involving both types of foraging techniques, and the possibility of variation in types of visits at the different times of day. Over the course of the flowering season, 60 bees were observed. Each visit to a flower was recorded as a singular event. The preliminary data are indicative of bees showing consistency with their respective foraging behavior and providing evidence to their frequency as well. However, closer looks at the data and more results will be forthcoming.

75 Christopher P. Randle[1], Brandi C. Cannon[1], Angela K. Hawkins[2], Michelle L. Lewis[1]
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Explaining Local Host Preference in *Phoradendron leucarpum*: Response to Host Cues in Leafy Mistletoe

Phoradendron leucarpum (Raf.) Reveal & M.C. Johnst. is a common parasite of trees occurring from southern New Jersey to California and south to central Mexico. It has often been noted that *P. leucarpum* exhibits host preference on a local scale, primarily parasitizing one or a few hosts over a small geographic scale, even when other plants are available that *P. leucarpum* readily parasitizes elsewhere. To explain this apparent local host preference, we investigated radicle orientation and haustorial formation in response to variation in light, host substrate, and proximity to hosts. Successful radicle orientation depends on proximity to hosts, suggesting a role for gaseous host metabolites in infestation. Further, *P. leucocarum* exhibited similar growth responses to some monoterpenes as has been reported in *Cuscuta pentagona*. Additionally, haustorial establishment depended on light and host substrate. Physical substrate was primarily important in adherence to the host. Variation in chemical composition of cork between local hosts and hosts in other locations result in significant differences in haustorial establishment. The distribution of *P. leucarpum* on hosts can therefore be explained in part by differences in host cues. However, data are insufficient to eliminate the role of selection for host-races in *P. leucarpum*.

76 Christopher Adams, Caleb Krebs, Jacob McClain, Jonathon Terrell
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Dormancy-Breaking and Germination Requirements for Seeds of the Kentucky Endangered Yellow Gentian *Gentiana flavida* A. Gray (Gentianaceae)

Seeds of *Gentiana flavida* are dormant at maturity. Studies were conducted to determine adequate dormancy-breaking conditions to allow maximum seed germination and to determine the necessary growth medium for maximum seedling establishment. Mature seeds were placed in a 5°C incubator for varying time periods (0-12 weeks) simulating the cold stratification that seeds would receive in the field during winter. Each group of seeds was then moved to a 25°C incubator, and subsequent germination was monitored. Seeds also were subjected to gibberellic acid (GA3) treatments to confirm the specific type of dormancy present. To determine ideal growth medium conditions, *G. flavida* seedlings were placed in six different soil treatments, both sterilized and non-sterilized: site soil, forest soil, and regular potting soil and then monitored for survivorship over three months. Results indicated that the 12 week cold stratification treatment produced a significantly higher percent germination (76%) than stratification at 10 (68%), 8 (44%), 6 (22%), 4 (6%), or 0 (0%) weeks. These data indicate that seeds require exposure to low temperatures to overcome seed dormancy. Seeds exposed to GA3, with no cold stratification, germinated to 78% (1000 ppm) and 70% (500 ppm), which confirmed the presence of physiological dormancy. Seedling survivorship, overall, was low; however, survivorship was significantly higher in site soil, non- sterilized (36 %) than in any other treatment (0-17%). In conclusion, for maximum germination and juvenile survivorship, seeds should receive 12 weeks of cold stratification and have exposure to parent soil with intact microbial flora.

77 Kevin S. Burgess[1], John A. Barone[1], Scott B. Whitley[1], JoVonn G. Hill[2]
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Determination of Grasshopper Diets Using DNA Barcoding

DNA barcoding is a molecular technique that allows for the identification of taxa from small tissue samples. By barcoding the plant material in the feces, several studies have reported on the diets of species of herbivorous mammals as well as some tropical leaf beetles. Here we describe the use of DNA barcoding to determine the diet of grasshoppers from their feces (or frass). At three prairie sites in eastern Mississippi, grasshoppers were captured, identified, and held in test tubesuntil they produced a frass pellet. They were then released, unharmed. Plant DNA was extracted from the frass, and theDNA was amplified through PCR using primers for the rbcL gene region found in the chloroplast genome of plants. After the PCR product was sequenced, the sequences were aligned and manually edited. From 187 initial samples, 56 yielded high quality, bi-directional sequences (with three additional uni-directional sequences) from 17 species of grasshoppers. Of these, 35 were homozygous, consisting of plant DNA from a single species. These were blasted to a pre-existing DNA barcode library for prairie plants from Mississippi and Alabama. Twelve samples were identified to a single plant species with greater than 99.5% pairwise identity, while 16 were identified to genus. The remaining seven samples were likely derived from plant species not in the barcode library. Twenty-four frass samples appeared to contain plant DNA from more than one species. Thus, DNA barcoding can be used non-destructively to determine the diets of grasshoppers.

78 Zachary Masters, Kunsiri Grubbs
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A Study of the Pollinators of Schweinitzs Sunflower (*Helianthus schweinitzii*), Asteraceae

Schweinitz's sunflower (*Helianthus schweinitzii*) is listed as an endangered species by the US Fish and Wildlife Service. Sexual reproduction of the species relies on the pollinators for seed production. The objective of the study was to determine the types of pollinators for this endangered species. In the fall of 2013 and 2014, populations located in the Winthrop Recreation & Research Complex, and the Blackjacks Heritage Preserve were observed to identify pollinators of this sunflower. Insects from the orders of both Hymenoptera and Lepidoptera were found to be the most frequent visitors to this sunflower. The insects from order Diptera were less commonly found. For the unintentional pollinators, we found that the solider beetles (Chauliognaths spp.) were the most commonly found on every single capitula. Most pollinators were found mainly during the middle of the day, and when the wind was not strong.

79 Madelyn N. Woods, Daniel A. McCarthy
Marine Science Research Institute, Biology and Marine Science, Jacksonville University, FL

The Development of a Baseline for Spatiotemporal Variability in Planktonic Communities of the Lower St. Johns River Estuarine System

Estuarine waters worldwide are facing increased habitat destruction, over-exploitation, and rapid species decline. High temporal variability of estuarine systems renders health assessments difficult without baseline knowledge of the local interactions occurring at the primary producer and consumer levels. Shifts in these community compositions, such as cyanobacterial blooms, can alter food-web dynamics and the flow of carbon and energy, thus compromising the stability of the surrounding ecosystem. To better understand these interactions, spatiotemporal distributions of meso-, microzooplankton and phytoplankton taxa were quantified to develop a baseline for seasonal planktonic community structure and the relative influences of biotic and abiotic factors. Monthly neuston 200 and 20m net samples with continuous and discrete abiotic data (temperature, conductivity, D.O.) were collected at three distinct sites along the Lower St. Johns River (LSJR) salinity gradient, (Marine, Estuarine, and Freshwater) in northeast Florida from September 2013 to October 2014. Mesozooplankton between 200 and 1000 dominated the majority of samples at all sites, though taxonomic composition varied significantly between freshwater and marine sites throughout the sampling period (p*Bosmina* spp.) dominated freshwater samples, with maximum average abundances of 0.21 individuals/L. Abiotic factors did not appear to significantly affect zoo- or phytoplankton community structures. However, a large Microcystis bloom from October to December corresponded significantly to a decrease in mesozooplankton richness at the freshwater site ($p<0.05$). This relationship may correspond to competitive exclusion by larger zooplankton during times of increased phytoplankton richness.

80 Michael E. Held[1], Joe E. Winstead[2], William S. Bryant[3]
[1] Biology, Saint Peter's University, Jersey City, NJ; [2] College of Science and Engineering, Southern Arkansas University, Magnolia; [3] Biology, Thomas More College, Crestview Hills, KY

Long-Term Recovery Dynamics of a Tornado-Damaged Forest in Boone County, Kentucky

This 40-year study reports on the changes in the structure and composition of an old-growth forest after a windstorm in 1974. Tree density, basal area, and species composition were measured in Dinsmore Woods, an old-growth maple dominated forest in Boone County, Kentucky in 1974, both prior to and following a tornado, and then subsequently in 1985, 1994, 2004 and most recently in 2014 to assess the recovery patterns. Tree density declined from 1974 to 1985, increased in 1994 and 2004, but showed a decline in 2014. Basal area showed a decline immediately following the tornado [1985 survey] but has increased and stabilized at 30 m2/ha in 2004 and 2014. Species composition of the tree layer has changed over the 40 years. *Acer saccharum* was still the dominant species, but the subdominant layer was now composed of *Fraxinus americana*, *Celtis occidentalis*, and several *Quercus* species though the importance of *Quercus* showed decline by 2014. The dominance of *A. saccharum* was seen in all strata (tree, sapling, and seedling). The disturbance appears to have maintained the dominance of *A. saccharum* over the last 40 years. The close similarity of the basal areas documented in 1974 and 2014 of approximately 30 m2/ha indicates the development or degree of stability in a forest preserve in this mixed hardwood Ohio River basin habitat.

81 Bailey A. Hunter, Brian C. McCarthy
Environmental and Plant Biology, Ohio University, Athens

Challenges to American Chestnut Restoration: Allelopathic Effects of Three Invasive Plant Species (*Ailanthus altissima*, *Alliaria petiolata*, *Lonicera maackii*) on American Chestnut

Since the loss of *Castanea dentata* (American chestnut) due to chestnut blight, many changes have taken place in the forests *C. dentata* once inhabited, including the proliferation of invasive species. To date, no one has evaluated the possible impacts of invasive plants on the reintroduction of *C. dentata*. Aqueous extracts and biomass of three invasive plant species with known allelopathic influences (*Ailanthus altissima, Alliaria petiolata, Lonicera maackii)* were used to understand how invasive species might impact proposed *C. dentata* restoration efforts. Blight resistant hybrid chestnut seeds were planted in the Ohio University Greenhouse and treated weekly with aqueous extracts of biomass from the invasives. Extracts were diluted so that there were high (0.05 or 0.2 g ml-1) and low (0.025 or 0.1 g ml-1) treatments along with non-treated controls. Chestnut seedlings were also planted in a parallel field experiment at the West State Street Research Gardens in Athens, OH, where biomass was used instead of extracts. Chestnuts were treated with high (40 or 15 g) and low (20 or 7.5 g) levels of roots or shoots of the invasives, along with non-treated controls. Chestnut height was measured weekly. High levels of *A. altissima* extracts negatively impacted chestnut height. However, results differed between the two experiments. Biomass of the invasives did not negatively impact chestnuts growing in the garden. Differences between experiments were likely due to environmental difference. The results suggest that the allelopathic effects from *A. altissima* might negatively impact chestnuts if seeds are planted at invaded sites.

82 Andre L. Lorenz[1], Blake W. Nelson[1], Jay A. Yoder[1], Lynn Royce[2]
[1] Biology, Wittenberg University, Springfield, OH; [2] Mitebee Farm Inc., Corvallis, OR; Entomology, Oregon State University, Corvallis

Tree Hive Colonies as a New Approach to Beekeeping and Its Implications for Enhancing Beneficial Fungi

Lynn Royce from Oregon mounts beehive boxes in trees (http://treehivebees.com). Her methodology was developed in response to colony collapse disorder (CCD) as an attempt to minimize colony stress by returning bees (*Apis mellifera*) to their native habitat in the trees. Some of the noticeable benefits of this approach are treatment-free conditions, easy attraction of swarms into empty hives, fewer predators bothering the colonies, and more successful overwintering. To determine if tree colonies are exposed to different symbiotic fungi that keep the bees healthy, we analyzed the fungi in bee bread (fermented pollen fed to bee larvae) by pitting these fungi against *Ascosphaera apis* (chalkbrood larval disease). Bee bread from tree colonies contained twice as much *Aspergillus* (mainly *A*. *niger*), *Penicillium*, *Cladosporium*, and *Mucor*, and a total fungus inoculum exhibited enhanced chemical antagonism, overgrowth, and speed of response at inhibiting or slowing growth of *A*. *apis*, compared to ground colonies. Individual fungal components were not as effective as the overall quantity. We conclude that tree colonies seem to be healthier, because they can support a heavier fungus load and are better protected against disease by having a greater quantity of beneficial fungi.

83 Jessica L. Allen
Institute of Systematic Botany, The New York Botanical Garden, Bronx, NY; Graduate Center, The City University of New York, New York, NY

High Elevation Endemics and Climate Change: The Future of Rare Lichens in the Southern Appalachians

High elevation species worldwide are increasingly threatened by mountain top extinction. Data documenting climate change in the southern Appalachians suggest that this region is no exception. This situation warrants considerable attention as it poses a threat to the unique biological communities that inhabit the high elevations of the southern Appalachians. Lichens, symbioses between fungi and algae, are abundant and diverse in the southern Appalachians, including a number of species that are narrowly endemic to the high elevations. In this study, I documented the current distributions of nine endemic lichens throughout the high elevations in the southern Appalachians and used niche modeling to predict how much suitable habitat will exist within their current ranges by 2050 and 2070. Considerable data exist for lichen distributions in the Great Smoky Mountains National Park (GSMNP), so I performed a focused inventory of the target species on high elevation ridges outside of GSMNP. To conduct the modeling in Maxent I used the resulting localities from my field work and locality data from collections held at The New York Botanical Garden. During my field work I located at least one previously undocumented population of each target species on high elevation ridges outside of GSMNP. Regardless of the climate model and carbon dioxide concentration used, the Maxent models predict little to no suitable habitat for all species within their current ranges by 2070. The implications of these results and future research directions in light of them will be discussed.

84 Joshua F. Hashemi, Reuben Hilliard, Chelsea Harris, Paula C. Jackson
Ecology, Evolution and Organismal Biology, Kennesaw State University

The Impact of Mycorrhizal Colonization on the Growth of American Sycamore (*Platanus occidentalis*) and Black Willow (*Salix nigra*) Under Drought Conditions

This experiment is part of a larger investigation to examine the suitability of using American Sycamore (*Platanus occidentalis* L.) in addition to, or as an alternative to Black

Willow (*Salix nigra* Marshall) in riparian restoration. Climate change is significantly affecting environmental systems and is expected to cause a greater frequency in severe droughts and flooding. Black Willow has been used extensively in the southeastern United States in riparian restoration sites because of its putative tolerance to flood and drought conditions and ease of vegetative reproduction. Little information has been collected on American Sycamore and therefore little is known regarding its potential use in riparian restoration. This research compared species under field and greenhouse conditions. For the field component, roots were collected from ten trees of each species (*Salix nigra* and *Platanus occidentalis*) growing alongside a small (< 1 m width) perennial stream on the campus of Kennesaw State University. Roots were stained (acid fuchsin or trypan blue) and the presence of mycorrhizal structures was quantified using the root piece method. Greenhouse experiments were conducted subjecting 10 individuals of each species to well watered conditions or drought, with and without mycorrhizal colonization. (Detailed methods presented separately).Preliminary results for field data indicate that *Platanus* samples exhibited higher levels of mycorrhizal colonization, and therefore are expected to be more strongly influenced by mycorrhizal presence in the greenhouse experiments. Results and implications will be discussed.

85 Ismael Gomez, Clayton Lynch, David A Beamer
Natural Science, Nash Community College, Rocky Mount, NC

Diversification of Seepage Salamanders (*Desmognathus aeneus*) Across a Complex Geological Landscape

The seepage salamander, *Desmognathus aeneus*, occupies many distinct physiographic regions and several independent river drainage basins. Within this range, seepage salamander populations tend to be localized and most are apparently disjunct. The disjunct nature of these populations coupled with a complex geological and ecological history of the region occupied by these salamanders provides conditions which are conducive to lineage diversification. During the course of a range wide survey of seepage salamander, we visited nearly every historical site from which this species has been reported; in addition we discovered many previously unknown populations. Here we report the first phylogeographic survey of these minute salamanders. A Bayesian phylogenetic reconstruction of the mitochondrial DNA gene, ND2, reveals the presence of several well supported, distinct evolutionary lineages. The presence of multiple lineages within seepage salamanders has important conservation implications. The results of this survey provide a strong case for the importance of molecular systematic techniques in revealing the biodiversity of the southeastern United States.

86 Eric Byrd[1], Carolyn Cray[2], Scott Citino[3], Marcie Oliva[3], Rose Borkowski[1]
[1] Jacksonville University; [2] Comparative Pathology, University of Miami; [3] White Oak Conservation Holdings, LLC

Determination of Serum Amyloid a Ranges in Clinically Healthy Anesthetized Grevy Zebra (*Equus grevyi*) and Somali Wild Ass (*Equus africanus somaliensis*)

Acute phase proteins (APP) are a class of plasma proteins that play a variety of immunologic roles during the acute phase response (APR), when a host is first battling an infectious, traumatic, or other stressor which triggers inflammation. The baseline level of serum amyloid A (SAA) in anesthetized Grevy's Zebra (*Equus grevyi*) and Somali Wild Ass (*Equus africanus somaliensis*) was documented for the first time in this project. Blood serum was obtained from clinically normal animals residing at White Oak Conservation Holdings, LLC, as well as from animals that were known to be affected with illness. Samples were analyzed by an immunoturbudiometric assay for SAA. Resulting levels were then compared to SAA values documented for non-anesthetized clinically normal

horses (*Equus caballus*). Serum amyloid A levels from the exotic equids were also analyzed relative to other indicators of inflammation such as white blood-cell counts and fibrinogen levels as enabled through archived data. Results from this project may facilitate diagnosis and monitoring of inflammatory illnesses in endangered species of equid.

87 Angela K. Burrow, Melissa Caspary
School of Science and Technology, Georgia Gwinnett College, Lawrenceville

Plant Pollinator Networks of the Coosa Valley Prairies

The Coosa Prairie system is a unique and diverse community of flora and fauna, including many rare species, located in northwest Georgia. This project focuses on the wet prairie community, specifically whorled sunflower (*Helianthus verticillatus*), federally listed as endangered, and its associated Apoidea (bee) pollinators. Sustaining whorled sunflower populations requires knowledge of their distribution, population structure, and associated pollinators. We hypothesized that the occurrence of whorled sunflower would be correlated with the occurrence of rare pollinators and that some of these interactions will be characterized as monolectic. Vegetation was sampled for species identification, cover class, and number of flowering stems. Apoidea were sampled, pinned, and identified through morphological analysis. Whorled sunflower, big-leaf black-eyed Susan (*Rudbeckia fulgida)*, bushy aster (*Symphyotrichum dumosum*) and New England aster (*Symphyotrichum novae-angliae)* were among the dominant flowering plants, with over 70 floral species documented in the fall survey season. While *Apis mellifera* individuals were the most abundant bee species collected, native genera, such as *Megachile* and *Svastra*, were also well represented, with a total of ten native bee genera documented. While preliminary results suggest that bee richness and diversity in the wet prairie is similar to an apple orchard, a notable difference is the presence of the sunflower specialist genus *Svastra* in the prairie. The majority of bees collected appear to be generalists, however we are still analyzing species interactions in the prairie network. Given the abundance of rare flora and pollinator diversity, further research into this system is important to ensure its continued persistence.

88 Nathan M. Hoover, Eric Holzmueller
Southern Illinois University

Succession Over 34 Years in an Oak-Dominated Forest in Southern Illinois

Under reduced disturbances of the last century maturing oak-dominated forests have begun to be replaced by more mesophytic shade tolerant species. In this study we analyzed the compositional and structural changes occuring at Trail of Tears State Forest (TTSF) in the Ozark Hills of southern Illinois over 34 years. Data from forest inventories in 1980 and 2000 were compared against recent overstory sampling in 2014. Regeneration data was also compared between 2000 and 2014. Sample plots within the forest were further categorized by azimuth and slope postion into Ecological Land Types to classify site specific successional patterns. While more xeric sites show some resiliency to mesophytic invasion, preliminary results show loss of oak dominance on all topographical positions. Our results serve as an additional example of the well known phenomena of decreasing oak abundance in communities lacking adequate management to regenerate shade intolerant species.

89 Richard W. Nesslar, Margaret Anderson, James Zaczek
Southern Illinois University Carbondale

Mowing as a Management Tool in Rehabilitating Giant Cane (*Arundinaria gigantea*)

Giant cane (*Arundinaria gigantea*) is one of three bamboo species native to North America. Canebrakes or large continuous cane stands were one of the dominant ecosystems in the Southeastern United States and were maintained by periodic disturbances such as wildfire and windstorms. Canebrakes provide habitat for rare species such as the Swanson's warbler, creole pearly eye butterfly, and swamp rabbit. Canebrakes are also effective riparian buffer filters. However, former canebrakes have been largely converted to agriculture and only 2% of canebrake habitat remains. Thus, there is interest in restoration and rehabilitation of canebrake ecosystems. Previous studies have shown that fire and fertilization may increase cane density and spread but these treatments can be expensive, labor intensive, and can require a cumbersome permitting process for managers. Mowing may provide an alternative effective disturbance in place of fire where it is not practical. The objective of this study is to compare the effects mowing and fire on the growth and expansion of giant cane in eight remnant stands in the Cache River watershed. Measurements were taken in 2012 prior to a single mowing and a single fire in late winter, and after each growing season thru 2014. Data collected in burned, mowed, and control plots included culm density, culm height/diameter, and percent cover of giant cane. We will report on the change in density, height, and diameter of the cane located interior and exterior to the canebrake. Data collected from this study will improve the understanding how mowing and fire effects canebrakes. This information will benefit resource managers interested in rehabilitating and restoring giant cane.

90 Brent T. Baker, C. Theo Witsell
Arkansas Natural Heritage Commission, Little Rock, AR

Arkansas Status Assessment and Monitoring Summary for the Federally Threatened *Geocarpon minimum* Mack. (Caryophyllaceae)

We report on the current status of the federally threatened *Geocarpon minimum* Mack. (Caryophyllaceae) in Arkansas following extensive monitoring and survey work conducted from 2012 to 2014. All four previously known populations (Branch Saline Barrens, Hall Creek Barrens, Kingsland Prairie, and Warren Prairie) were found to be extant in 2012, although few individuals were observed at the Branch and Hall Creek sites. In 2014 no *G. minimum* was observed at the Branch site following recent alterations to the habitat. This was the only population then known from Arkansas Valley Ecoregion and the only one in the state not at least partially under protection by conservation ownership. However, a previously undocumented Arkansas Valley population was discovered the same year in saline barrens on federal land, the first new population discovered in the state in 30 years. Previously undocumented patches were also discovered at Kingsland Prairie and Warren Prairie in the West Gulf Coastal Plain Ecoregion. To test the hypothesis that some level of periodic habitat disturbance is necessary to maintain suitable microhabitat conditions for *G. minimum*, a small-scale habitat manipulation experiment was initiated in 2012 in areas that supported *G. minimum* in the mid-1980s but are currently unoccupied. Two seasons of observations are reported from these experimental plots. The ecology and habitat needs of *G. minimum* are summarized and major threats to populations are highlighted, including a noted increase in disturbance by feral hogs.

91 Robert H. Floyd[1], Jason R. Applegate[2], Stefanie Ferrazzano[3]
[1] Colorado State University, Center for Environmental Management of Military Lands (CEMML) at Fort A.P. Hill, VA; [2] Fort A.P. Hill Directorate of Public Works, Environmental & Natural Resources Division; [3] Oak Ridge Institute for Science and Education at Fort A.P. Hill, VA

Using GIS to Predict Habitat for Two Endangered Wetland Species at Fort A.P. Hill, VA: *Helonias bullata* and *Juncus caesariensis*

Fort A.P. Hill manages threatened and endangered species to ensure no net loss in military readiness and to provide a conservation benefit to listed species. In partial fulfillment of its requirements under the *Endangered Species Act* and the *Sikes Act*, Fort A.P. Hill's Directorate of Public Works, Environmental & Natural Resources Division (ENRD) reviews all installation projects for potential impacts to protected species, and field reconnaissance (i.e. a search for listed species) is conducted prior to ground disturbing activities. To assist in this process, ENRD developed two Global Information System (GIS) models to improve the efficacy of their search for two listed wetland species: the Federally-Threatened, State- Endangered, *Helonias bullata* and State-Threatened *Juncus caesariensis*. To predict *Helonias bullata* habitat, wetlands were assigned a habitat probably score based on the presence and spatial extents of three criteria: (1) proximityto known *Helonias bullata* locations, (2) palustrine forested wetlands, and (3) acidic seepage swamps. The United States National Vegetation Classification (USNVC) was used to identify acidic seepage swamps while spatial data for the first two criteria were provided by installation subject matter experts. To validate this methodology, ENRD reconnoitered 212 ha of predicted *Helonias bullata* habitat; 173 ha (82%) were found to be either ideal *Helonias bullata* habitat (i.e. acidic wetland seepages) or at least a mosaic of *Helonias bullata* habitat mixed with other wetland types, and two new *Helonias bullata* sites were discovered. ENRD's preliminary attempt to generate a similar model to predict *Juncus caesariensis* was not initially effective. However, using known spatial data for this species, ENRD observed that known occurrences of *Juncus caesariensis* were frequently located adjacent to a non-standard USNVC map unit identified as 'semi-permanent impoundments' (e.g. beaver ponds). To validate this observation, ENRD identified and reconnoitered 134 ha of wetlands adjacent to other 'semi-permanent impoundments,' and the result was the discovery of three new locations with *Juncus caesariensis*. ENRD has since incorporated both models into their field reconnaissance process, which has resulted in the discovery of more previously unknown sites with *Helonias bullata* and *Juncus caesariensis*.

92 Victoria A. Roy, Kimberly A Hays
Natural Sciences, Dalton State College, GA

Antimicrobial Effects of Yarrow (*Achillea millefolium*) Essential Oil

Achillea millefolium (Yarrow)has been used as a medicinal herb for thousands of years. There is historical evidence that many cultures including the Greeks, Native Americans, and Dutch have used yarrow medicinally. In the United States, there has been a recent resurgence in the use of essential oils and other homeopathic treatments. Many companies claim that some essential oils, including yarrow, have antimicrobial properties. Our study tested the antimicrobial capabilities of four commercially produced yarrow extracts against four bacterial strains. We used the Kirby Bauer Disk Susceptibility Test on two Gram negative bacteria species, *Pseudomonas aeruginosa* and *Escherichia coli*, and two Gram positive species, *Bacillus cereus* and *Staphylococcus aureus*. Distilled water was used as a control. Each species was treated with all four oils and the control with three replicates of each treatment. After 24 hour incubation, we measured the zones of inhibition and used paired t-tests to determine if the effects differed significantly among the treatments and the species. All four purchased oils showed significant growth inhibition on *B. cereus*. Two of the oils showed significant zones of inhibition on *S. aureus* and *E. coli* when compared with controls. *P. aeruginosa*, which is known for having very high antibiotic resistance, showed no measurable zones of inhibition for any of the four oils. In the future, we plan to use steam distillation to prepare yarrow extracts from local plant material and test this known oil in the manner described above.

93 Kimika Tsukide, Kasi Quinn, Austin Leavell, Henry Spratt
Biological & Environmental Sciences, University of Tennessee at Chattanooga

Evaluating Bioremediation Methods Efficacy for Degradation Rate of Hydrocarbons Using Bioaugmentation among Various Soil Textures

With continuing increases in population growth, industrial development, and urbanization, the demand for petroleum increases. Hydrocarbons from petroleum and its waste products have immensely contributed to global contamination, negatively affecting ecosystems and human health. In previous experiments, microcosms were prepared by adding waste motor oil to various soil samples and incubated for different durations. Passive degradation by indigenous soil microbes was measured by hexane-extractions involving a gravimetric technique. Approximately 53% (1 week) and 87% (4 weeks) of oil degradation were observed in these experiments. Data obtained were subject to a high degree of technical and human errors. The objective of current experimentation is to evaluate the efficiency of microbial oil degradation using bioaugmentation, as well as to correct/minimize errors made in previous experimental methods. Bioaugmentation is an approach in which inoculation of indigenous/exogenous microbes enhances degradation rates. Data collected will serve as a comparison to validate previously obtained degradation rates and determine whether there is a statistical difference between passive and active bioremediation techniques employed. Oil degrading microbes will be isolated from soil sampled in close proximity to a University of Tennessee Chattanooga parking lot. Isolated microbes will be inoculated with 3 soil mediums (forest soil, clay, and sandy soil). Further hexane extractions performed using a separatory funnel. Finally, the data collected will be statistically analyzed to test for differences in degradation rate among the soil mediums. Efforts of this experiment will contribute to improving the methods employed to degrade harmful hydrocarbons.

94 Kaitlin Pearce, Rebekah Ward, Lee Kurtz
School of Science and Technology, Georgia Gwinnett College, Lawrenceville.

Effects of Phytoremediation on Contaminated Soils from Urban Gardens

Heavy metal contamination continues to cause serious environmental impacts including damage to human health. Sources of heavy metal contamination are widespread, especially in urban environments. Therefore, it is important to develop strategies to reduce the negative impacts of heavy metal contamination in the emerging urban gardening movement. Preliminary studies have indicated that both chemical and biological additives to soils can help plants sequester heavy metals in their root systems, a process known as rhizofiltration. This project aimed to evaluate the impact of additional of bioavailable phosphate and heavy-metal tolerant bacteria on soil concentrations of lead in the rhizosphere of sunflowers. The rhizosphere-associated bacterium *Bacillus megaterium* has been shown to uptake and store lead intracellularly, making it an ideal candidate for amendment to soils to enhance rhizofiltration. Preliminary results suggest that lead sequestration was increased by almost 100 ppm in amended soils relative to controls. The microbial community composition in non-amended soils was also investigated through phylogenetic analysis and compared to soil communities without plants. These data suggest a relative enrichment of lead tolerant bacteria in soils with sunflower rhizospheres. These studies may indicate simple methods for enhanced bioremediation in the growing sector of urban agriculture.

95 Kimika Tsukide, Kasi Quinn, Austin Leavell, Henry G. Spratt, Jr.
University of Tennessee at Chattanooga, Biological and Environmental Sciences

Evaluating of the Efficacy of Different Bioremediation Methods for the Degradation of Waste Motor Oil Added to Soil

With continuing increases in population, industrial development, and urbanization, the demand for petroleum increases. Hydrocarbons from petroleum and its waste products have contributed to global contamination, negatively affecting ecosystems and human health. In previous experiments conducted in this lab, microcosms were prepared by adding waste motor oil to soil samples and incubated for up to 4 weeks. Passive degradation by indigenous soil microbes was measured by hexane-extractions, and quantified using a gravimetric technique. Approximately 53% (1 week) and 87% (4 weeks) of added oil was degraded in these experiments. The objective of current experimentation is to evaluate the efficiency of microbial oil degradation using bioaugmentation. Bioaugmentation is an approach in which bacteria, specifically selected to use the target toxic organic material (in this case waste motor oil), are added to contaminated soils. For this study oil degrading microbes have been isolated from soil in close proximity to a University of Tennessee Chattanooga parking lot. Enrichment cultures of the isolated microbes will be inoculated into 3 different soil types (forest soil, clay, and sandy soil) contaminated with waste motor oil. Oil remaining in the soils over time will be determined using hexane extractions performed using separatory funnels. Data collected will be statistically analyzed to test for differences in degradation rates among the different soil types. Data collected will then be compared with previously obtained degradation rates to determine whether there is a statistical difference between passive and active bioremediation techniques employed.

96 Henry G. Spratt, Jr.[1], David Levine[2], Randy Walker[2]
[1] University of Tennessee at Chattanooga, Biological and Environmental Sciences; [2] Physical Therapy, University of Tennessee at Chattanooga

Potential for Deep Tissue Bacterial Contamination as a Result of Dry Needling

Dry needling (DN) is a therapy used to treat problems associated with skeletal muscles or connective tissue. Concern exists for potential contamination of deep tissue due to DN. This study was designed to determine the potential for the transfer of bacteria via DN. The study involved 27 volunteer subjects, sampled at five typical DN locations: latissimus dorsi, sternocleidomastoid, semispinalis capitis, infraspinatus, and dorsal interossei. Sampling from each subject was as follows: a site was swabbed using a sterile swab, followed by adjacent needling two times. After DN, needles were aseptically transferred into tryptic soy broth (TSB) and mannitol salt broth (MSB). At the lab swabs were streaked onto tryptic soy agar (TSA) and mannitol salt agar (MSA) plates. All media was incubated at 37 oC for 48 hours. Bacterial growth occurred on TSA or MSA from at least one sample site swabbed for every subject (27/27, 100%). For the needles, no growth was observed in any MSB. For needles incubated in TSB, 15 out of 27 (55%) subjects had growth. Both *S. aureus* and *S. epidermidis* were detected on swab samples. A follow up experiment to monitor potential transmission of Staphylococci into simulated skin was also preformed. Overall, bacteria found on needles appear to be normal skin associated, and represent the potential for deep tissue infection at the DN sample sites studied here. The use of antiseptics to clean skin prior to DN is not routinely done, and will be the subject of a follow up study.

97 David A. Beamer
Natural Sciences, Nash Community College, Rocky Mount, NC

Undergraduate Research in a Community College Setting

Undergraduate research opportunities are one of the transformative events in many beginning scientists' careers. However, conducting scientific research in a community college setting presents several challenges. The student bodies at many community colleges are often comprised of students that are underrepresented in science; women, minorities and first generation college students. As a result, these students are often not aware of scientific research or ways that they might engage in its pursuit. Here I present some of the ways I have introduced scientific research to my classes and students at Nash Community College and highlight some of the scientific accomplishments of these students.

98 Valarie A. Burnett
Science and Mathematics - Biology, Newberry College, SC

Enhancing Student Engagement and Active Learning in Face-to-Face and Online Classroom Settings

Recent trends in innovative teaching strategies advocate a shift from traditional instructor-led teaching methods to more 'student-centered' active learning models. By engaging students in their own educational process, they are better equipped to identify their strengths and weaknesses and take responsibility for learning and retention. Furthermore, active learning is a practice that should persist beyond the classroom experience into lifelong learning. Therefore, I have incorporated a number of activities into the face-to-face and online classroom environment to ensure active student participation in the learning process. These individual and group activities have been added stepwise to the course curriculum and have been modified over time based on student feedback and performance. Details and data on the long-term use of literature reviews and presentation assignments were reported previously. Study questions and case studies have also been utilized long-term and continue to evolve. More recent additions have focused on incorporating use of smart phones, quiz games, online discussion forums, and course-embedded research. Students were involved in the development of some activities. At the end of the course, they were required to assess various aspects of course activities, including their effectiveness in engagement, learning, retention, interest, and fun. Most students scored the quiz games and scientific investigations highly effective in these areas but did not find the discussion forum assignments useful. There is also a correlation between improved test scores with the incorporation of these activities. Future goals include development of more interactive and hand-on activities and increased use of technology and course-imbedded research.

99 Marlee B. Marsh
Division of Business, Mathematics and Sciences, Columbia College, SC

Who Killed Yew? Development, Implementation and Assessment of a New Case Study to Teach Mitosis

Case studies are often used to break up the monotony of lecture and to most importantly, promote active learning in the classroom. The purpose of this case, Who Killed Yew? , is to teach introductory college biology students the basic process of mitosis, focusing on the fundamental cellular processes that occur during each of the stages- prophase, prometaphase, metaphase, anaphase, telophase and cytokinesis. This case is framed around solving a murder. The murder plot involves a naturally-occurring poison derived from Yew trees of the genus *Taxus*, known as paclitaxel. Paclitaxel is a mitotic inhibitor that works by inhibiting the depolymerization of microtubules so that the cell is arrested in metaphase. The discovery of paclitaxel lead to the development of the chemotherapeutic drug, Taxol, and the case concludes by having students think about the correlations between poisons and chemotherapies. In this presentation, the author will discuss the strategies for developing this new case for the National Center of Case Study Teaching in Science, as well as how it was implemented in her courses this fall, and preliminary formative and summative assessment of the case.

100 Erica R. Krimmel[1], Debra L. Linton[2], Travis D. Marisco[3], Anna K. Monfils[2], Ashley B. Morris[4], Brad R. Ruhfel[5]
[1] Sagehen Creek Field Station, Truckee, CA; [2] Central Michigan University, Mt Pleasant, MI; [3] Arkansas State University, Jonesboro, AR; [4] Middle Tennessee State University, Murfreesboro; 5 Eastern Kentucky University, Richmond

Connecting Students to Citizen Science and Curated Collections

College-level plant diversity courses (e.g., plant systematics) often involve a collection project. These projects are designed to help students learn to correctly identify, document, and preserve specimens useful for scientific study. While these projects are invaluable learning tools, the specimens and associated data are often not incorporated into herbaria or online databases. Furthermore, students are not exposed to the emerging online citizen science initiatives and herbarium databases of our information-rich digital age. Here we present a new project and associated website (http://collectionseducation.org/ http://collectionseducation.org) designed to enhance traditional collection projects that can easily be incorporated into any plant diversity course. Our project integrates traditional taxonomic practices, ongoing citizen science initiatives, and digita-- age curatorial skills. The final goal is to produce archival-quality, research-ready plant observations and collections that will become part of our national biodiversity archive. Students will keep a detailed field notebook, collect and document specimens for archival purposes, and use traditional and emerging tools to reliably identify plant species. Additionally, students will interact with iNaturalist, an observation-based online tool designed to bring together professionals and citizen scientists documenting biodiversity. Data can then be directly exported from iNaturalist into the Symbiota digitization platform creating an opportunity to work with the virtual herbarium community and incorporate student collections into a database without creating legacy data. Due to the importance of collections in hand and online, this project emphasizes the skills and best practices required to facilitate downstream applications of student collections and documentation of plant biodiversity.

101 Pratima C. Darr, Wendy A. Dustman
School of Science and Technology, Georgia Gwinnett College, Lawrenceville

Engagement of High School and College Students in Authentic Research through Investigation of a Deadly Pathogen of Hibernating Bats

Increasing enrollment and specific training in STEM disciplines has been at the forefront of the higher education agenda in recent years. In this connection Georgia Gwinnett College (GGC) has undertaken to implement the 4-year Undergraduate Research Experience with offerings in both independent research and course-embedded research. Work described here showcases the implementation of an independent research experience that has engaged multiple undergraduates and a high school student over the last two years. It has provided a low cost yet broad focus research plan ideally suited to a small college with limited research infrastructure. This independent research experience has yielded significant gains in motivation, attitudes and research skills by involving students in the investigation of a very current problem in ways that are relatively simple and inexpensive to realize. The focus is on White Nose Syndrome (WNS), a fungal infection that has killed millions of hibernating bats, mainly of the genus *Myotis* in the last 8 years. A two-pronged approach to studying WNS involved use of an insect model to delineate details of pathogenesis and, sampling for the environmental presence of *Pseudogymnoascus destructans*, the agent of WNS, within a bat hibernaculum. Work described here will focus primarily on environmental sampling for *P. destructans* and how that provided students with a highly engrossing field experience followed up by engagement in widely employed microbiological and molecular research methods.

102 Rebekah J. Ward, Wendy Dustman, Lee Kurtz, Julia Shearer, Pratima Chakrabarti Darr
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Implementation and Impacts of the Small World Initiative: Hypothesis-Driven Undergraduate Research to Crowdsource New Antibiotics

An innovative approach to hypothesis-driven laboratory work was implemented in Microbiology courses during the 2014-2015 academic year. Our purpose was to improve student attitudes toward science and research ownership. The project, The Small World Initiative (SWI) sponsored by Yale's Center for Scientific Teaching, involves the discovery and cultivation of novel antibiotic-producing bacteria. The effect of this initiative can be evaluated through both attitudinal assessments and student learning outcomes. We hope to inspire participants to pursue careers in science and develop an appreciation for the scientific process. It is well established that undergraduate research experiences enrich STEM student learning outcomes. And in our increasing global society, student exposure to issues that affect diverse communities is imperative for career success. Incorporating SWI into biology courses will significantly contribute to 1) undergraduate research experiences 2) improving student's perspective of global scientific collaboration 3) enhancing student's marketable skills and critical-thinking abilities and finally, 4) addressing an urgent global health-crisis (proliferation of antibiotic resistance). In this presentation we will describe our implementation of the Small World Initiative and also disseminate our findings thus far with regard to student attitude and performance in experimental and control sections of the course.

103 Jeffery W. Bonner
Biology, Middle Tennessee State University, Murfreesboro

Thinking Critically About Yellow Fever in West Tennessee: A Historical Case for Teaching Principles of Microbiology

Critical thinking is an important skill for students to practice within any scientific discipline. The ability to think critically about scientific problems among peers is a skill that leads to a deeper understanding of content. The practice of this skill is beneficial to students and is efficiently adaptable to undergraduate biology courses; therefore, faculty should consider implementing a student-centered component such as this to the traditional lecture-only teaching. Higher-order cognitive process involved with critical analysis are often under-utilized in a lecture setting due to constraints of time and specific curriculum resources available to faculty. For this presentation I will give an overview of a set of time efficient, inquiry-based exercises developed for promoting critical thinking among peers in an introductory microbiology course. I will demonstrate one of these exercises that utilize the Yellow Fever epidemic that ravaged West Tennessee in the 1870s. This collaborative, inquiry-based exercise is grounded in principles of microbiology as it guides students on an exploration of public health crises that led to sanitation reform and scientific inquiry, which paved the way for current knowledge about host-pathogen interactions. By implementing discipline-based exercises that foster critical thinking, faculty can provide students an opportunity to prepare for peer collaboration in graduate school and professional careers, which rely on higher- order cognitive skills and less on rote memorization of facts.

103B Kristin M. Bliss, Shana M. Nelson
Biology, Randolph College, Lynchburg, VA

Inquiry-based lab approach encourages intellectual risk taking and development of higher level thinking skill in students

To motivate and inspire students, a classroom with enthusiasm, high expectations and flexibility is desirable. Inquiry based labs are uniquely suited to, and exemplify these attributes. Additionally, student-designed labs encourage discovery, risk taking, and can enhance student development as a scientist. This presentation will offer novel lab exercises that encourage active learning, discovery and intellectual risk-taking by the student. Exposure to such labs encourages a positive, inquisitive attitude and facilitates development of higher-level thinking skills.

104 J. Richard Carter
Biology, Valdosta State University, Valdosta, GA

Contributions to the Southeastern Flora

Field work by the author in the southeastern United States, particularly southern Georgia, over the past three decades has resulted in discovery of plants in the coastal plain that seem to represent undescribed taxa. Morphometric, distributional, and ecological data comparing these plants with related species will be presented. There are two *Cyperus* (Cyperaceae): One, an inhabitant of xeric white sandy uplands with myrtle oak and Chapman's oak,is presumably related to *C. nashii* and *C. retrorsus*, and the other, found in exsiccated karst ponds, has affinity with *C. strigosus* (Cyperaceae). An *Eleocharis* (Cyperaceae) related to *E. albida* inhabits sandy banks of tidal creeks, and an *Oxalis* (Oxalidaceae) and a diminutive *Juncus* (Juncaceae) are associated with sandstone outcrops.

105 Ralph L. Thompson[1], Katrina Rivers Thompson[2], G. Neil Douglas[1], Douglas R. Bruce[3], Paul F. Threadgill[4]
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Orange-Eye Butterfly Bush (*Buddleja davidii*, Scrophulariaceae) Naturalized in Tennessee

Buddleja davidii Franch. (orange-eye butterfly bush), an introduced Chinese shrub in the Scrophulariaceae, has been widely grown as an ornamental throughout the temperate eastern US. Through field studies in 2012-2014, we documented *B. davidii* as locally naturalized from seven populations in culturally disturbed sites from four Tennessee counties: Knox (3), Anderson (2), DeKalb (1), and Davidson (1). Butterfly bush has broad ecological amplitude for establishment, colonization, and naturalization in a diversity of open, insolated ruderal habitats. It has been recorded in 25 states; but, it is often not well-defined whether its status is cultivated, waif, persisting, naturalized, or invasive. A similar study in Kentucky recently determined *B. davidi*i to be naturalized in six counties; and, it should not be classified as a state-listed invasive species. While the SE-EPPC does not treat butterfly bush as invasive in TN, the TN-EPPC classifies it as an 'Alert' rank. We propose the local naturalization of *B. davidii* in TN clearly does not indicate invasive status. The restrictions of *B. davidii* to escape and migrate in TN is partly due to it being a shade-intolerant, pioneer species with a short-life span, a poor competitor to encroachment by native and non-native vegetation, a low adaptability to unseasonably cold temperatures, and a high sensitivity to herbicides. *Buddleja davidii* appears to be limited to disturbed areas with little ecological impact or potential to colonize Tennessee natural areas. Tennessee and other southeastern state EPPC personnel could benefit from evaluating *B. davidii* with a rational assessment system as developed by Trueblood for North Carolina.

106 Jesse C. Harris, Joey Shaw
Biological and Environmental Sciences, University of Tennessee at Chattanooga

Phylogeographic Study of *Castanea ozarkensis* Ashe to Determine the Geographic Distribution of Genetic Variability across the Ozarks

Castanea Mill. (Fagaceae) consists of three species within eastern North America: *Castanea dentata*, *Castanea pumila*, and *Castanea ozarkensis.* Previous molecular studies have shown intraspecific variability within the three eastern species, (Shaw et al, 2012, *Castanea*), (Li & Dane, 2013, *Tree Genetics & Genomes*). Shaw et al. showed three distinct haplotypes among allegheny chinquapin and ozark chinquapin, O3, O11, O12. While all of the ozark chinquapin samples represented the O3 haplotype, the O3 haplotype was also shared with two samples of allegheny chinquapin as well as O11 and O12 being represented by one specimen each of allegheny chinquapin. This determination was based on an approximately 300bp non-coding cpDNA region *trnV-ndhC*. These haplotypes are located throughout a wide geographic range from southwest Arkansas to northern Georgia, but sampling for the ozark chinquapin was done in a narrow geographic range between Missouri and Arkansas. We are therefore currently uncertain whether this entity lacks the genetic variability of the other two taxa or is merely the result of a deficient sample size due to prior focus mainly being on the southern Appalachian species of *Castanea*. Through the addition of hypervariable plastid markers and increased phylogeographic sampling to our preexisting database, we hope to gain increased resolution in the geographic distribution of genetic variability within the ozark chinquapin.

107 Travis D. Marsico[1], Jeremy J. Caron[2], Anna K. Monfils[2]
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The Role of Small Natural History Collections in Contributing to Understanding Species Distributions: Case Studies from Arkansas and Michigan Herbaria

How do small natural history collections contribute to our understanding of biodiversity patterns through space and time? To begin addressing this question, collaborators in eight states (AR, CA, CO, FL, GA, MI, TN, and WV) gathered vouchered vascular plant collection information from large and small institutions in their respective states. In each state, 40 species were randomly selected, 10 from each of four categories: rare S1, rare S2, common native, and invasive. Collection data were partitioned into large (>100,000 specimens) and small (<100,000 specimens) collections. From the resulting data sets, occurrence data were analyzed by collection size, county, specific locality, and date of collection. The distributions of the four species categories were compared to determine the relative contribution of small collections to the distribution from large collections in the states. We will present data from two states, Arkansas and Michigan. We found that small collections contribute to county-level and even more so to site- level spatial distribution knowledge, and that the proportion of these contributions differ by state, species category, and interests of personnel from individual collections. Our study quantifies and summarizes the patterns. Yet we found that there is no universal or predictable pattern of what or how much small collections contribute to species distribution knowledge. Therefore, we conclude that small collections are important, often uniquely so, and that the only guaranteed approach to making sure spatial and temporal contributions of small collections are utilized in research is to include collections of all sizes in digitization and data sharing efforts.

108 Emily Gillespie, Joshua Hamrick, Kristen Hammond
Biological Sciences, Marshall University

Management of the Modern Herbarium: Building a Student-Centered Approach to Conducting Digitization Projects

Herbarium digitization efforts in the southeastern United States have recently been given a significant boost from recent NSF ADBC Thematic Collections Networks funding for the SERNEC 'Key to the cabinets: Building and Sustaining a Research Database for a Global Biodiversity Hotspot.' As a result, 100+ herbaria in the Southeast are building workflows involving undergraduate and graduate students, in addition to faculty researchers and volunteers. Here we present a framework focused on inclusion of young undergraduates in the workflows of this project. At the Marshall University herbarium (MUHW), twelve students currently work in the collection. Many of these students are supported by the Federal Work Study program. We have developed a successful protocol for training geared especially for botany-naive students. We also present a framework for employing more advanced students as managers as part of providing meaningful job training opportunities. Data will be presented relating to student workflow efficiency, student management efficiencies and lessons learned. While the ideas and data presented here are anecdotal to the Marshall herbarium, our framework is completely scalable for varying institutional needs. We contend that students at all levels can and should be included as equal partners in our emerging and ongoing digitization efforts in herbaria and other natural history collections.

109 Eunjee Lee, Benjamin J. Thornton
Biology and Allied Health, Southern Adventist University, Collegedale, TN

The Effect of Caffeine on the Dry Mass of Mung Bean (*Phaseolus aureus*) 17 Days Post Germination

Garden enthusiasts hold a popular belief that adding coffee grounds to the soil will enhance plant growth. Some question if this affect is due to the presence of caffeine. Studies have shown that caffeine can influence the growth of the hypocotyl of mung beans *(Phaseolus aureus)*. In this study, mung beans were treated with various concentration of caffeine: 0.0772 mM, 0.772 mM, 7.72 mM, and 77.2 mM for 17 days. Mean dry mass (n = 10) of plants exposed to each concentration was compared to the control - mung beans grown without caffeine. Mung beans treated with 77.2 mM of caffeine did not sprout. Results did not meet parametric assumptions thus a Kruskal Wallis test was performed (a = 0.05; p < 0.001). By comparing the overlap of 95% confidence intervals of each group, the data appear to indicate that at concentrations higher than 0.772 mM mung bean growth is inhibited. These data support studies that demonstrate the negative impact of caffeine on plant growth.

110 Jay F. Bolin[1], Salim Al Rahbi[2], Abdulrahman Al-Hinai[2], Darach Lupton[2], Lytton J. Musselman[3]

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A Review of the Taxonomy and Phylogenetics of the Holoparasitic Hydnoraceae and Notes on a Potentially New Arabian *Hydnora* Species from the Sultanate of Oman

The Hydnoraceae is a small family of holoparasites within the Piperales that comprises two genera, *Hydnora*and *Prosopanche.* The under-collection of the hypogeous root holoparasites and the poor preservation of fertile material have contributed to taxonomic confusion within the family. Currently we recognize six old world *Hydnora* taxa and synonymize 11 additional names. Within *Prosopanche* we accept four new world taxa and synonymize 5 other names. Our taxonomy is based in part on a three loci *(accD*, *nad6*, ITS) phylogeny of Hydnoraceae. *Hydnora*and *Prosopanche*, were resolved as sister clades in rooted (with*Piper nigrum*) maximum parsimony and Bayesian analyses. *Hydnora* are parasites on three rosid plant lineages. The ancestral *Hydnora* host association seems to be on members of the Fabaceae and *Commiphora* (Burseraceae) followed by a single host- shift to*Euphorbia*spp. Significant work may be needed to revise the taxonomy of the Fabaceae-*Commiphora* parasitizing (FCP) clade of *Hydnora*, where only three species are currently recognized, but at least six descriptions of species from east and northern Africa remain unevaluated. Among the FCP clade is a *Hydnora* species from the southern region of the Arabian Peninsula that is represented by only a handful of herbarium specimens and was initially misidentified in the literature as *Hydnora africana*. We will review the available information regarding the poorly known Arabian *Hydnora* and present new taxonomic data from 2014 field work in the Dhofar region of Oman.

111 Scott D. Silvis[1], Michele Elmore[2], Julie Ballenger[1], Kevin S. Burgess[1]

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Documenting the Biodiversity of a Local Sandhill Flora Using DNA Barcodes: An Investigation into the Patterns of Resolution in Polytypic Taxa

DNA barcode libraries are fast becoming incorporated into the restoration and conservation management plans of local floras, especially where taxonomic complexity can confound plant identification based on morphology alone.This study outlines a preliminary evaluation of a barcode library based on the*rbcL*gene region of the chloroplast genome and thenuclear ribosomal gene region,*ITS.*Specifically, we establish a barc odelibrary for the Sandhill Flora of Georgia, a fragile and threatened habitat of moderate phylogenetic dispersion that holds a large number of rare and endangered plant species. To assess DNA sequence variation for this barcode region, DNA and Herbarium vouchers were collected for 62 species (37 genera, 28 families) across a series of 11 habitats near Fort Benning, Georgia. To conduct an initial evaluation of percent sequence recovery and percent species resolution for this flora, forward and reverse sequencing was conducted on a subset of taxa for the*rbcL*gene region. Sequence recovery (91% of specimens sequenced, 72% of total specimens screened) was relatively high and comparable with studies of similar taxonomic complexity. Species resolution (61%) was relatively low, but expected, for this flora of moderate composition (27% polytypic genera). This study underscores the potential utility of establishing a barcode library for the Sandhill region of Southwest Georgia for future ecological, conservation and restoration applications.

112 Andrew P. Hart[1], Kristian Theqvist[2], Kathleen Kron[3], Emily Gillespie[1]
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Inferred Phylogenetic Relationships within *Rhododendron* Subsection *Ledum*

Ledum, officially *Rhododendron* Subg. *Rhododendron* Section *Rhododendron* Subsect. *Ledum*, comprises a small group of lepidote rhododendrons collectively recognized by abaxial leaf scales. *Ledum* most likely forms a monophyletic group with another subsection of lepidotes (*Edgeworthia)* based on the presence of long-crisped multicellular trichomes on stems and abaxial leaf surfaces. Formerly a separate genus, several species are recognized within the group; three in North America and three additional species in Eurasia. Previous accounts have included up to eight species, some of which have been reclassified and subsumed within other species following morphological and broad scale molecular analyses. The current study attempts to investigate previous classifications with respect to newly generated molecular data and generate a novel cladogram for the group. Sampling for the current study included all known species of *Ledum*, experimentally generated hybrids, as well as lepidote and non-lepidote *Rhododendron* taxa. Molecular markers included two nuclear coding regions and three chloroplast intergenic spacers. Aligned DNA sequence data were subjected to Maximum Parsimony, Maximum Likelihood, and Bayesian inference. Existence of *Ledum* as a clade and placement of *Ledum* within *Rhododendron* based on highly supportive preliminary evidence will be discussed. A final subject of investigation comparatively explores the results of incorporating known hybrids into these data sets.

113 Ashley B. Morris[1], O. Rayne Leonard[1], Charlotte Germain-Aubrey[2], Joey Shaw[3]
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The State of Plant Phylogeography: A Review of Methodological Approaches

The term 'phylogeography' was coined more than 25 years ago to define the comparison of intraspecific gene trees with a species' spatial distribution on the landscape. Since then, the field has exploded, with nearly 11,500 articles published. Interestingly, plant phylogeographic studies represent roughly 10% of the total. To understand the current state of the field, we reviewed the literature between 2007-2014. We are specifically interested in what molecular markers were used and why, and whether time and space were explicitly considered in analyses. Using Web of Science, we used the topic search terms 'phylogeography or phylogeographic' and '*aceae' limited to the years 2007-2014. We narrowed our focus to the top five journals. Our goal was to quantify marker choice and the use of temporally and spatially explicit analyses. The majority of papers used cpDNA sequence data, but rarely were these regions the same as those identified by the Tortoise and Hare series as being 'top performers'. A small number of papers implemented divergence time estimation, with the majority descriptively linking observed patterns to the Pleistocene. An even smaller percentage of papers included spatial analyses of the genetic data or species distribution models. Given the importance of both space and time in the definition of phylogeography, these omissions are a considerable stumbling block for our field. Our results suggest that plant phylogeography could easily progress by integrating more rapidly evolving markers that are already identified as such, and including explicit analyses of time and space in relation to genetic data.

114 Lacey M. Genard[1], Charley F. Saylor[2], Mark S. Schorr[3]
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Ecoregion-Specific Patterns in the Distribution and Abundance of Introduced Redbreast Sunfish (*Lepomis auritus*) and Native Longear Sunfish (*L. megalotis*) (Centrarchidae) in Mainstem

The Redbreast Sunfish (*Lepomis auritus*) was introduced in the Tennessee River drainage (TRD) in the 1940s by intentional stocking. Our study objective was to characterize temporal patterns in population abundances of *Lepomis auritus* and *L. megalotis* in mainstem reservoirs on the Tennessee River based on multiyear analyses of historical (cove rotenone) and contemporary (shoreline electrofishing) datasets. Data were analyzed using longitudinal regression to assess sunfish population trends (species vs. time) within ecoregion-reservoir-specific river sections (overall alpha = 0.05, with sequential Bonferroni adjustment). Historical rotenone data (1947-1997) suggest two major points of *L. auritus* entry into the TRD in the 1950s: (1) Fort Loudon (1953)-Watts Bar (1957) in the upper reaches and (2) Wilson-Wheeler-Guntersville (1950 in each) in the middle reaches. Populations of *L. auritus* exhibited increasing trends in the Chickamauga-Nickajack and Guntersville sections (Ridge and Valley- Southwestern Appalachians), but such patterns were not observed in the other mainstem river sections. Populations of *L. megalotis* have remained robust in the Wilson-Wheeler and Pickwick-Kentucky sections (Interior Plateau-Southeastern Plains), but have declined in Chickamauga-Nickajack and Guntersville sections where *L. auritus* was found in high or increasing numbers. Contemporary electrofishing data (1993-2012) suggest that *L. auritus* has surpassed *L. megalotis* in mean abundance in the Nickajack-Chickamauga section. Patterns of change observed in *L. auritus* were not observed in other native *Lepomis* species.

115 Kaitlyn D. Peters, Kenneth Fortino
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Terrestrial Leaf Litter Alters Nutrient and Oxygen Flux in the Sediments from a Small Man-Made Pond in Central Virginia

Small man-made ponds are the dominant lentic habitat in the southeastern United States. Terrestrial leaf litter is known to significantly affect the nutrient cycling and ecology of lotic systems but much less is known about the impact of terrestrial leaf litter on lentic systems, particularly small man-made ponds. We hypothesized that leaf litter would increase sediment oxygen demand (SOD) and reduce the flux of inorganic N and P into the water column from the sediments. We evaluated the impact of terrestrial leaf litter on nutrient cycling and SOD with a lab experiment using sediments from a 0.06 ha pond in central Virginia. Litter-free pond sediment plus overlying pond water were incubated in 300 ml BOD bottles unamended, with added leaf litter (20, 10 mm diam. leaf discs), with added inorganic N and P, or with both added leaf litter and inorganic N and P. The samples were incubated in the dark at a constant temperature for 22 days. Sediment oxygen demand and nutrient flux was determined on 5 dates during the incubation. Our results show that sediments with leaf litter had greater SOD during the first week of the experiment but returned to control levels by day 22. Nutrient additions also significantly increased SOD but there was no interaction between the effects of leaf litter and nutrient additions. The presence of leaf litter in the sediments altered the timing and magnitude of nitrate and nitrite flux but had a smaller effect on ammonia and ortho-phosphate.

116 Jessica L Littlefield, Nicholas R. Ravagli, Krystal T. Ream, Dina M. Leech
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Implications of Freshwater Browning on Zooplankton: Using Superhume as an Artificial Source of Dissolved Organic Carbon for Experimentation

In recent decades, freshwater ecosystems in the Northern Hemisphere have increased in dissolved organic carbon (DOC) concentration, and consequently, in brown color. Environmental factors driving the 'browning' of fresh waters are currently under intense investigation. However, less is known about the direct and indirect effects browning will have on aquatic food web dynamics. One of the challenges to studying 'browning' is identifying a feasible source of organic carbon in which to experimentally manipulate DOC concentration. Superhume, a liquid humic acid concentrate produced by UAS of America, has been suggested as a potential artificial source of DOC. We used Superhume to test the effects of increasing DOC concentration on zooplankton, which serve as important prey for planktivorous fish and grazers of phytoplankton. Zooplankton from a local reservoir were placed in replicate 19 L tanks of Superhume ranging from 2-15 mg/L DOC. Equivalent amounts of algae and nutrients were also added to each tank. Over a 6-week period, zooplankton decreased in number in all tanks, particularly in the highest DOC (i.e., Superhume) treatment. Zooplankton community composition also shifted from predominantly copepod-dominated to cladoceran-dominated at all DOC concentrations. Interestingly, the guts of cladocera species, but not copepods, were often dark brown in color, suggesting their consumption of flocculent organic matter. Our results suggest that increasing DOC concentration, as manipulated with Superhume, reduces zooplankton abundance and shifts zooplankton community composition. Future work will compare these laboratory results with zooplankton abundance and species composition in ponds and lakes across a DOC gradient.

117 Raquel A. Fagundo[1], Michael Perkins[1], David Campbell[2], Andrew Mahon[3], Lynn Siefferman[1], Ken Halanych[4], Michael Gangloff[1]
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The Tree of Broken Dreams: A Molecular Analysis of *Elliptio*

The freshwater mussel genus *Elliptio* is currently believed to be the most diverse and widespread in North America. However, *Elliptio* is also known for its remarkable phenotypic plasticity. Numerous recent attempts at resolving species boundaries in this group using conventional molecular markers have revealed that species boundaries in this group are unclear and that genetic introgression among seemingly morphologically distinct taxa is widespread. We conducted an extensive meta-analysis of the 910 published cytochrome oxidase subunit I (COI) and NADH dehydrogenase subunit 1 (ND1) gene fragments as well as new sequences from our own recent collections. We obtained data from 20 of the 36 currently- recognized *Elliptio* taxa occurring in Gulf and Southeast Atlantic Slope drainages. We calculated genetic distance estimations, generated haplotype networks, and reconstructed phylogenetic relationships using maximum likelihood and Bayesian algorithms. Phylogenetic analyses suggest that *Elliptio* is paraphyletic and taxa currently included in *Elliptio* comprise at least 5 evolutionarily distinct lineages. Additionally, extensive haplotype introgression was observed among putative species with extensive introgression observed among Coastal Plain populations. These data strongly suggest a molecular based re-evaluation of this group is urgently needed in order to quantify genetic species boundaries and understand the role of physiographic variability and gene expression in shaping shell morphology.

118 Cook F. English, Gregory P. Lewis, Daniel T. Talley
Biology, Furman University, Greenville, SC

Relationships Between Total Heterotrophic Bacteria, Stream Water Chemistry, and Land Cover in the Piedmont Region of South Carolina

Streams in both urban and agricultural watersheds often receive increased nutrient inputs relative to streams in forested watersheds. Elevated nutrient inputs in turn might lead to greater abundance of bacteria in streams influenced by urban and agricultural land covers. However, few studies have examined the relationship between watershed land cover and stream bacterial abundance. During summer 2014 under baseflow conditions, we collected water samples from streams in 36 watersheds (1-24 km2 in area) in the South Carolina piedmont. Watersheds were placed into four land cover categories: mostly (>90%) forested, urban (including commercial and residential land covers), mixed forest/pasture, and mixed forest/pasture/row crops. Samples were analyzed for turbidity and concentrations of total heterotrophic bacteria (THB), major ions, ammonium, total dissolved nitrogen, and dissolved organic carbon. Nitrate concentrations were highest in the urban and forest/pasture/crop watershed groups and lowest in the mostly forested group. Streams in the mostly forested watersheds also had significantly lower turbidity and lower concentrations of THB and dissolved iron than streams in the other groups. Concentrations of THB were most variable in streams draining watersheds with crop cover and were significantly positively correlated with water temperature, turbidity, specific conductivity, and concentrations of dissolved iron, potassium, and chloride. Our results support the hypothesis that both urban and agricultural land covers affect not only stream nutrient concentrations but also bacterial abundance. Future research should examine potential links between elevated nutrient concentrations and bacterial abundance, as well as whether bacterial diversity differs among streams draining different land covers.

119 Sarah Fishburne, John Hains
Biological Sciences, Clemson University, SC

Metabolism of *Bellamya japonica*: Hypothesis, Experimental Design and Results

In spite of its expanding range and ecological importance as an invasive species in North America, little is known about the Japanese Mystery Snail, *Bellamya japonica*, as an invasive species. While our research includes ecological investigations of distribution, behavior, and fecundity, we also are beginning basic biological studies related to growth and metabolism. At this time we have begun studies using oxygen consumption to estimate respiration rates. Once cleaned, the specimen is placed in a sealed container with an optical dissolved oxygen probe and filled with pond water. A separate chamber without a snail is employed as a control for any oxygen consumption by organisms in the water. Our study employs water at room temperature (21oC). The water is allowed to equilibrate to room temperature to prevent it from being supersaturated with oxygen as it warms. Oxygen consumption rates are then measured over a period of 24 hours. Results are calculated on a volumetric basis and related to organismal mass.We hypothesized that there is a linear relationship of organismal mass to the respiration rate. We also hypothesized that respiration would predictably increase with temperature and that there would be both upper and lower limits to this trend. Our results thus far indicate that the mass relationship is linear but we have not yet completed enough observations to identify the thermal relationship or the metabolic-thermal limits. Our plans are to extend this research to identification of these and other metabolic niche characteristics for this invasive species.

120 James L. Wood
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Podostemum ceratophyllum: What Is a Torrenticolous Macrophyte and What Might We Learn from It?

Podostemum ceratophyllum, commonly called Hornleaf Riverweed, is an angiosperm known to play an important role in structuring riverine ecosystems in eastern North America. The plant grows attached to rocks and stable substrates in swift, aerated water in rivers with sufficient light reaching the benthos, but is reported to be in decline in much of its range. *Podostemum* provides nutrient resources and habitat for many invertebrates and vertebrates alike, plays in role in elemental cycling, and may accumulate heavy metals present in river water. My research questions have focused on how urbanization may influence the elemental composition of the plant, specifically looking at isotopic signatures of nitrogen and the accumulation of metals in plant tissues. During the summer/fall of 2014 I collected plant samples from rivers in North Carolina, Georgia, Tennessee, and South Carolina for analysis of ΔN-15, Al, Cr, Cu, Fe, Pb, Zn and other metals. Additional plant samples were collected above and below the Duke Energy coal ash spill site on the Dan River at Eden, North Carolina to investigate the possibility of metal accumulation in plant tissues as a result of the coal ash spill in 2014. The widespread distribution of the plant in eastern North American may make this plant a prime candidate to focus research on urbanization and river ecosystem health.

121 Amelia K. Atwell[1], Dan Huser[2], Joshua B. Smith[3], Mark S. Schorr[4]
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Environmental Correlates of Lotic Macroinvertebrate Diversity in the Lookout Creek Watershed (Tennessee River Drainage)

We examined relationships of catchment land-use features with lotic habitat (instream, riparian) and benthic macroinvertebrate assemblages (family richness) at eight tributary sites in the Lookout Creek system (Tennessee River drainage). The Lookout Creek watershed (485 km2; Tennessee River drainage) encompasses parts of northern Alabama (DeKalb County) and Georgia (Dade and Walker County), and southeastern Tennessee (Hamilton and Marion County). Study reaches (all in northwestern Georgia) were approximately 35 times the mean stream width and represented different tributaries in the Ridge and Valley ecoregion; however, portions of the upper catchments of certain sites fell within the Southwestern Appalachians. Study catchments yielded land-use results ranging from: 60.3% to 86.2% forested; 0.7% to 20.5% agricultural; and 2% to 32.3% urbanized. Benthic macroinvertebrate assemblages at the sites exhibited family richness values ranging from: 6 to11 EPT (Ephemeroptera, Plecoptera, and Trichoptera) families, 1 to 7 intolerant families, and 19 to 30 total families. Landscape-stream relationships were analyzed using Spearman's rank correlation procedure ($P < 0.05$). Family richness indices (EPT, intolerant, total) were directly correlated with pebble size in the streambed and inversely correlated with catchment housing density and inadequate riparian habitat. Total family richness was directly related to pool abundance. Agricultural land use in the catchment was inversely correlated with stream width and large woody debris. These relationships reflect the sensitivity of macroinvertebrates assemblages to catchment and habitat changes.

122 Megan E. Gibbons
Birmingham-Southern College

Six Years of Intensive Trapping and Removal of an Invasive Species of Crayfish from Roebuck Springs, Alabama: Impacts on Invasive and Native Crayfish Populations

Invasive species can have devastating impacts on local communities, including the elimination of native species throughcompetition, predation, or hybridization.*Orconectes virilis* is species ofcrayfish that isinvasive across the southeastern United States. When a dam removal at Roebuck Spring, Alabama destroyed the habitat of the largest known population of endangered watercress darter (*Etheostoma nuchale*) in the world, numerous measures were taken to preserve the remaining individuals. One such measure was to commence intensive trapping and removal of *O. virilis*, which was incredibly abundant atthe site and considered a potential threat to the darter. We trapped and removed almost 20,000 *O. virilis* usingminnow traps baited with cat food from 2008-2014. We recorded body size, sex, and catch rates of trapped crayfish and found that reductions in population size (based on catch rates) were cyclical and short lived, possibly because of inconsistent trapping effort. Over time, body size of trapped crayfish decreased, suggesting we were removing the largest crayfish from the population. After 1 yr of the study, we began findingtwo species of native crayfish, *Cambarus striatus* and *Procambarus acutus,* in our traps; the number of native individuals increased throughout the rest of the trapping period. It is not known how *O. virilis* impacts *E. nuchale* or the native crayfish speciesat Roebuck Spring, but our study opens the door for investigating these and other questions.

123 Alexander U. Edwards[1], Clifton Ruehl[1], Carlos Echevarria[2], Bill Bouthillier[2]
[1] Columbus State University; [2] Warm Springs National Fish Hatchery

Effects of Feeding Frequency on Alligator Gar Mortality

Atractosteus spatula (alligator gar) populations have declined due to overfishing and habitat loss during the past decades. Attempts to restock alligator gar using hatchery-reared fish have met with limited success because they are cannibalistic, especially at the relatively high densities occurring in hatcheries. We hypothesize that increasing feeding frequency might deter cannibalism. We measured alligator gar mortality and estimated cannibalism in a culture (n=5512) at Warm Springs National Fish Hatchery (WFSH) and compared results to data on mortality and cannibalism from similar studies. Cannibalism was 11% at WFSH compared to 44% and 19% in two other studies. The Warm Springs cultures were fed most frequently, suggesting that cannibalism decreased with increased feeding frequency.

124 Scott T. Cory, Howard S. Neufeld, Lauren K. Wood
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Ecophysiological Responses of Fraser Fir (*Abies fraseri*) Christmas Trees along an Elevational Gradient

Fraser fir (*Abies fraseri* (Pursh) Poir.) is endemic to high-elevation peaks of the southern Appalachians (>1500 m), but this species is grown commercially as Christmas trees from 650 m to 1400 m. Therefore, Christmas trees experience stressors they would not encounter in their native range (*e.g.* increased temperature, decreased frequency of cloud immersion) and may be particularly vulnerable to further stress from climate change. To better understand Fraser fir's response to climate change, we studied growth rates and carbon budgets on genetically similar Fraser fir Christmas trees along an elevational gradient from 660 to 1320 m in western NC and eastern TN. We found that bud break began ~14 days sooner at low elevations than high elevations. Trunk diameter increased the least at low elevations, although new stems grew faster and longer. Throughout the growing season, net photosynthesis (*Anet*) generally reached daily maximum before noon at low elevation, but peaked after noon at higher elevations. Mid-summer (June 2014) dark respiration, *Anet*, and daily carbon assimilation were greatest at high elevation, but later in the season (October), elevational differences were less significant. These results suggest that Fraser fir Christmas trees at low elevation are limited by mid-summer high temperatures; however, they compensate by extending their growing season relative to high elevation trees. Even though Fraser fir demonstrates some capacity to adapt to warming, trees growing at the lowest elevations may be especially susceptible to further climate change if mid-summer heat stress outweighs the benefit of a longer growing season.

125 Taylor E. Spillman[1], Finn B. Furstenwerth[1], Duncan D. Cameron[2], Jay F. Bolin[1]
[1] Biology, Catawba College, Salisbury, NC; [2] Animal and Plant Sciences, Sheffield, UK

An Isotopic and Molecular Study of Mycoheterotrophy in the Southern Blue Thread (*Burmannia capitata*)

The Burmanniaceae contain several lineages of achlorophyllous mycoheterotrophic plants that may associate with arbuscular mycorrhizal fungi (AMF). Here we investigate the isotopic profile of a green and potentially mycoheterotrophic wetland plant in situ, *Burmannia capitata*, the Southern Blue Thread, and associated vegetation. We generated Δ13C and Δ15N stable isotope profiles of a population of *B. capitata* from the Sandhills Game Lands in Scotland County, North Carolina. The highest Δ15N values were observed in the *B. capitata* shoot, congruent with similar reports in other mycoheterotrophic plants. Reference vegetation shoot and root fractions (C3 and C4) were statistically indistinguishable, whereas *B. capitata* shoot and root fractions were statistically different from each other. Interestingly *B. capitata* is a C3 plant and the *B. capitata* root fraction resembled C4 reference vegetation. This indicates that *B. capitata* has access to a carbon source with an isotopic signature different from C3 photosynthesis, an indication of mycoheterotrophy. We are applying 18S fungal specific primers (AML1-AML2 and GEOA2-GEO11) to identify AMF associates.

126 Kimberly C. Smith[1], Pieter A.P. deHart[1], Geoffrey W. Cox[2]
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Redefining How Biologists Analyze Data: Augmenting the Two-Dimensional Proportional Contribution Model with a Three-Dimensional Approach to Enhance Analysis of Stable Isotope Data

Currently biologists use two-dimensional models to visualize data obtained from studies utilizing stable isotope analysis (SIA). Two-dimensional models are accurate and allow for useful interpretation of ecological and physiological patterns, but are limited in the depth of interpretation they can provide about relationships between multiple disparate data points. Given recent advancements in computer programming and multidimensional presentation, we sought a more intuitive approach to modeling and analyzing isotopic data. To create this new opportunity, we used a recently produced and open-sourced Graphical User Interface program MixSIAR as our template, and modified the code to allow for simultaneous statistical comparison, computation, and graphing of three isotopic models. To test the accuracy of and interpretations yielded by our model, we inputted Δ13C, Δ15N, Δ18O, and ΔD data from samples analyzed in concurrent SIA studies focused on arthropod communities, and attempted to model multiple isotopes on three or more spatial planes on the same graph. Next, we inserted random noise that followed a standard normal distribution to this inputted data, and ran it through our multidimensional model to test the degree if accuracy of our model compared to the unedited data. Our initial analysis yielded accurate, true-to-life, three-dimensional graphs of isotopes, so we then enhanced the visual model to allow for intuitive data interpretation and analysis. Our new proportional-contribution model allows for a more robust examination of existing and future SIA data, and may provide a statistically significant increase in the accuracy of modeling isotopic data.

127 Leighanne R. Main, Blake W. Nelson, Jay A. Yoder
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Bioindicator of High Quality Water Based on Water Balance for Survival of the Parasitic Hairworm in Fresh Water Streams

When infected with hairworms, crickets, caddisflies, and beetles jump into streams and burst open releasing the worms into the water. The worms travel in the drift, tangle around each other, and form knots around twigs and grasses at the water's edge for laying eggs. Eggs are eaten which allows worms to develop internally within the arthropod. To explore how worms maintain body water to function outside the host, we determined water balance characteristics by applying kinetic model equations to mass changes made with a microbalance. Features of male worms (*Paragordius varius*, ID *cox1* barcode) were: ability to survive down to one-half their body water, enabling high water loss rates, and impermeability of the cuticle to water that restricts the amount of water influx to prevent overhydration. As knot size increased, water loss rate decreased due to reduced respiratory water loss from being immobile as an anti-predator behavior against fish. We conclude that worms rely on water gain from fresh water to counter high water loss. Thus, hairworms are signs of streams with high quality water and likely healthy fish populations that originate from a steady input into the stream of arthropod hosts that these worms parasitize.

128 Jennifer L. Newbrey, Renata C. Paiva, Michael G. Newbrey, Jaleesa E. Clarke
Biology, Columbus State University, GA

Seasonal Variation in Yolk Carotenoid Concentrations and Egg Metrics in Eastern Bluebirds Breeding in West-Central Georgia

Carotenoids are biologically-active, yellow, orange, and red pigments that are synthesized by plants and photosynthetic microorganisms. Birds are unable to synthesize carotenoids, and therefore they obtain all of their carotenoid resources from their diets. Female birds allocate high concentrations of carotenoids to their egg yolks, and eggs with higher concentrations of carotenoids are more likely to hatch and produce healthy chicks than eggs with lower concentrations. Despite this critical role that yolk carotenoids play in avian reproduction, surprisingly little research has focused on the yolk carotenoids of North American songbirds. Therefore, we studied seasonal variation in yolk carotenoid concentrations and egg metrics in Eastern Bluebirds (*Sialia sialis*) breeding in nest boxes at two locations in west-central Georgia; Columbus State University (CSU) in Columbus, GA (21 nests), and Callaway Gardens in Pine Mountain, GA (27 nests). The third-laid-egg was collected from each study nest and carotenoids were extracted and quantified in the laboratory using high performance liquid chromatography. At CSU, we found a positive correlation between Julian Day and concentrations of yolk carotenoids, which suggests that carotenoid-rich foods likely became more abundant later in the breeding season. We also found that later breeding female bluebirds at both locations produced eggs with larger yolks than females that bred earlier in the season. To better understand the trends that we found, future research will focus on the link between seasonal changes in diet, and the allocation of carotenoids and other resources to the eggs of bluebirds.

129 Glenn A. Marvin, Kayla Davis
Biology, University of North Alabama, Florence

Lower Temperature Limit for Feeding Behavior in the Semi-Aquatic Plethodontid Salamander *Desmognathus conanti*

Variation in food intake at different seasons or temperatures has been examined for some ectothermic animals; however, the lower temperature limit for salamander feeding behavior is unknown. We examined the lower temperature limit for feeding behavior in a semi-aquatic plethodontid salamander species (*Desmognathus conanti*). We quantified variation in the feeding responses of individuals to an iPhone video-recording of a walking cricket at 1oC, 3oC, 5oC, and 7oC. At each test temperature, we conducted three feeding trials for each individual in an experimental group (N=14). Three feeding trials for each individual in a control group (N=15) were conducted at the same times that experimental animals were tested. All feeding trials for individuals in the control group were conducted at 15oC. Experimental-group salamanders exhibited vigorous feeding responses at 5oC and 7oC, large variation in feeding responses among and within individuals at 3oC, and little to no feeding response at 1C. Feeding responses at both 1oC and 3oC were significantly less than at each higher temperature (repeated-measures ANOVA, P<0.001; Holm-Sidak multiple comparisons, P<0.001). Feeding responses of control-group individuals did not vary among the times when experimental-group individuals were tested. We conclude that the lower temperature limit for individual feeding behavior is quite variable, but the lower temperature range for feeding behavior is between 1oC and 5oC for this species. Our study is unique because we determined the effect of temperature on feeding behavior of a predator, independent of any temperature effect on movement or availability of prey.

130 Pieter A.P. deHart, Julie A. Lozier Biology,
Virginia Military Institute, Lexington

Size May, in Fact, Matter: Breed-Specific and Ontogenetic Dietary Differences in Free- Ranging Dairy Goats

The past decade has witnessed nationwide increases in abundance of free-ranging dairy goat (*Capra hircus*) farms. Concomitant with this growth have been new research efforts aimed at assisting producers in refining herds and their diets to increase production. One approach has been to increase breed diversification. Little evidence exists, however, on innate differences between breeds in digestive physiology, which may dictate both herd health and milk quality. Given inherent differences in size, behavior, and diet selectivity between breeds, there are likely breed-specific physiological differences dictating overall herd characteristics. To determine what dietary differences may exist, and bridge a critical knowledge gap, we examined the carbon and nitrogen isotopic signatures from hairs of 109 dairy goats from four breeds, across five farms with similar vegetation profiles, within Appalachian Virginia. Our results indicate that while the mean (+/-SD) values obtained for all breeds varied widely, with (Δ15N=6.3+/-1.4, Δ13C=-23.2+/-1.5), the differences between breeds (=2.3 ?15N, =1.7 ?13C) are much greater than those between farms (=0.3 for both Δ15N and Δ13C). Expected ontogenetic differences yielded more exaggerated distinctions between breeds, with variations between kids of different breeds =3.8 and =2.2 for Δ15N and Δ13C, respectively. Variation in Δ15N and Δ13C of kids is likely due to differential protein investment in milk by does, which could have implications for milk production rate and quality, and ultimately breed selection for specific environments. This work suggests that future research on free-ranging ruminants, their diet, and health effects of dietary supplementation should be performed at breed-specific levels.

131 Eric C. Niederhauser, Glenn R. Matlack
Environmental and Plant Biology, Ohio University, Athensio

Secondary Dispersal of Forest Herb Seeds from Raccoon Dung

Many deciduous forest herb species are dispersed by frugivores, resulting in deposition of seeds in dung. Seeds may be secondarily moved by abiotic and biotic processes which potentially affect microsite quality. We followed secondary movement of mayapple (*Podophyllum peltatum*) seeds deposited in raccoon (*Procyon lotor*) dung to understand the role of secondary dispersal in determining reproductive fitness. To observe seed movement and test the influence of environmental factors, marked seeds were incorporated into raccoon dung, placed in the forest, and relocated at regular intervals. Experimental watering was applied to test the potential for abiotic movement of seeds by rain. Motion/heat triggered cameras were trained on dung with and without incorporated mayapple seeds to determine the character of animal interaction with raccoon dung. The dung began to disintegrate and shed seeds within one week of deposition. Seeds can move < 30 cm by rainwash in a single rain event. Mayapple seeds appear to be actively removed from raccoon dung by white-footed mice and chipmunks beginning within 24 hours of deposition. Other animals interact with dung in various ways. Seeds appear to have been moved away from the dung location by water or animals up to 1.7 meters with distance influenced by both slope and litter cover. Seed germination was increased by the presence of litter and by landscape position. Thus, secondary movement by both biotic and abiotic processes can affect seedling fitness by changing seed location at the scale of microsite patchiness.

132 Kesley J. Gibson[1], Jonathan M. Miller[1], Paul D. Johnson[2], Paul M. Stewart[1]
[1] Biological and Environmental Sciences, Troy University, AL; [2] Alabama Aquatic Biodiversity Center, Conservation and Natural Resources, Marion, AL

Acute Toxicity Testing on Freshwater Mussels (Bivalvia: Unionidae) and Freshwater Snails (Gastropoda: Caenogastropoda)

Mollusca has the highest documented number of extinctions of any phyla, with 72% of freshwater mussels and 74% of freshwater snails classified as imperiled. Mollusk populations are declining due to anthropogenically caused physical and chemical habitat degradation. Toxicity tests are important tools that provide information for risk assessment of chemicals and are used in developing USEPA Water Quality Criteria (WQC).The objectives of this study were to determine the sensitivity (LC50) of three freshwater juvenile mussel species (*Villosa nebulosa, Villosa umbrans,* and *Hamiota perovalis*) and two freshwater non-pulmonate snail species (*Leptoxis ampla* and *Somatogyrus* sp.) to five toxicants (SDS, Cl, K, Ni, Zn) in need of new or updatedWQC. *Hamiota perovalis* and *L. ampla* are federally threatened species while *V. nebulosa* and *V. umbrans* are petitioned for federal protection. Results showed that *H. perovalis*, *L. ampla,*and*Somatogyrus* sp. had LC50 values lower than current WQC for Ni and Cl, and *L. ampla* had a lower LC50 value for Zn. *Leptoxis ampla* was also found to be extremely sensitive to SDS (LC50 = 26 g/L). With this study, data is now available to aid in establishing and updating WQC based on values inclusive of more sensitive species. *Leptoxis ampla* was found to have LC50 values lower than any mollusk species previously tested, indicating that this is a very sensitive species that may need stringent regional criteria and protection. Until USEPA WQC are updated, current regulations may not be protecting many of our nation's imperiled aquatic mollusk species.

133 John Enz, Taylor Montgomery, Laine Peterson
Biology & Marine Science, Jacksonville University, FL

A Comparison of the Population Dynamics of the Gopher Tortoises at 2 Distinct Sites within the Timucuan Ecological Historic Preserve in Northeast Florida American Beach, Nassau County, FL and the Theod

The land-dwelling gopher tortoise is listed as a Threatened species in much of the southeastern United States. Gopher tortoises are considered a keystone species, mainly because the burrows they dig provide shelter for numerous other species as well the tortoises themselves. In order to effectively manage gopher tortoise populations, an accurate population count must be known. Population estimates using burrow counts have been made at the TimucuanNational Park. However, burrow counts alone are not a direct reflection of the number of individuals within a population. The purpose of this study is to use 'burrow' cameras and remote game cameras to measure the population size, activity patterns, and other animals' burrow use at 2 known tortoise populations in the Timucuan National Preserve that encompass both isolated and human impacted populations. Comparisons between these populations will be made with particular interest in the human impacts on the population dynamics and activity patterns of the 2 populations.

134 Howard S. Neufeld
Biology, Appalachian State University, Boone, NC

Not Quite Like Making Sausage: How the EPA Sets National Ambient Air Quality Standards for Ozone and Other Criteria Pollutants

Every five years, the Clean Air Act Amendments of 1977 mandate the U.S. EPA to review the national ambient air quality standards (NAAQS) for the six criteria pollutants (NOx, SO2, O3, CO, Pb, and PM2.5 and PM10) regulated by this law. I was privileged to be a consultant member of the Clean Air Scientific Advisory Committee (CASAC) during the current five year cycle. We were charged with approving (1) a review of the scientific data accumulated in the past five years (Integrated Science Assessment, ISA), (2) a risk assessment (RA) derived from these data, and (3) EPA's policy assessment (PA), wherein the EPA makes its recommendation on whether to change the current standard. In this talk, I discuss how CASAC assists EPA in making recommendations about the NAAQS to the Administrator and how science is transformed into law. The process begins by summarizing new science developments in the ISA. Once this document is approved, EPA prepares the RA to determine whether the current standard protects human health and welfare with an adequate margin of safety, as required by law. Then the EPA makes recommendations about the NAAQS in the PA, and sends this document to the EPA Administrator, who makes the final decision. CASAC has recommended that the primary NAAQS for ozone be set < 70 ppb but above 60 ppb, which is lower than the current 75 ppb standard. I will discuss this standard setting process and whether recent criticisms of its membership and functioning are warranted.

135 Martin L. Cipollini, N. Royce Dingley, Patrick N. Felch
Biology, Berry College, Mount Berry, GA

Changes in Vegetative Structure After 10 Years of Restoration Management in an Old Growth Mountain Longleaf Pine Forest

The Berry College Longleaf Pine Management Area (BCLPMA; Floyd County, GA) harbors one of few remaining old-growth Mountain Longleaf Pine (*Pinus palustris* L.) forests. Like most remnant longleaf pine forests, stands at Berry College have been fire-suppressed for decades. Since 2003, an area of about 160 ha has been managed using low-intensity burns and herbicide treatment of hardwoods, with the goal of restoring an open, pine- dominated canopy, with low duff and litter levels, high grass and herbaceous plant cover, low fuel loads, and a stable longleaf pine population. Tree community structure was assessed using the point-quarter method at +/-25 random points in each of eight managed and five unmanaged stands in 2004 and 2014. Other vegetative variables (litter, duff, grasses, pine seedlings) were measured in 2 m2 plots at each point in a subset of stands in 2004/05 and 2013/14. Fuel loads were estimated during the same time frames using a modified plane-intersect method. Tree surveys in old- growth Mountain Longleaf Pine stands in Alabama (Talladega National Forest and Mountain Longleaf Pine National Wildlife Refuge) were included as external reference datasets. Results showed that density of longleaf pines has decreased in managed areas (mostly as a result of tree death associated with duff smoldering after prescribed burning). Nevertheless, managed stands were vegetatively similar to frequently burned external reference stands. In contrast, unmanaged stands were similar to fire-suppressed external reference stands and to managed stands when first surveyed in 2004. Results show progress is being made in restoring the overall vegetative structure to desired conditions.

136 John E. Quinn[1], Jenny Warnken[1], Melanie Cozad[2]
[1] Biology, Furman University, Greenville, SC; [2] Economics, Furman University, Greenville, SC

Determinants of Forest Biodiversity Value in a Rapidly Urbanizing Area of Upstate SC

Land use and land cover change is driving loss of biodiversity and associated ecosystem services. This change is particularly evident in the Piedmont ecoregion of the United States. The loss ecosystem services has given rise diversifies the stakeholders interested in restoring lost ecosystems to retain the benefits received. However, data on the value of these benefits are not easily available to researchers and practitioners. Using contingent valuation survey methodology, we assessed residents' willingness to pay (WTP) for forest preservation. WTP was assessed using a multiple- bounded discrete choice elicitation question that allows respondents to value forest preservation across a wide-range of monetary thresholds in addition to incorporating varying levels of uncertainty within responses. Tax and donation collection mechanisms were considered. For a 5% increase in forest cover over 10 years, we find WTP values of approximately 20 dollars per year across donation and tax bid vehicles. The WTP values increase as respondents' uncertainty across responses is allowed to vary demonstrating that the estimated value represents a lower bound. Perceptions regarding the reduction of society's current use of the environment for the benefit of future generations played a large role in determining WTP across both bid vehicles, while respondents' level of familiarization with biodiversity was significant in the donation vehicle where larger amounts of respondents' uncertainty was accounted for. Results suggest that it would possible to reach a conservation target of reversing forest cover loss from the last 40 years but that conservation efforts may need to focus on biodiversity education efforts.

137 Betsy Cuenca, Michael Erwin
Biology, Georgia Gwinnett College, Lawrenceville

Haplotype Frequency of Cytochrome Oxidase 1 (CO1) Among Black Crappie Inhabiting Southeastern Lakes

Black crappie, *Pomoxis nigromaculatus,* is one of the most fished-for species among freshwater anglers making the conservation of the species important to recreational fisheries. Despite the increasing interest of black crappie, there is little information available on the genetic aspects of the species. Molecular markers such as the mitochondrial DNA marker, cytochrome c oxidase subunit, CO1, are used in DNA barcoding and analysis of genetic diversity of pelagic fish populations. The aim of this study was to sequence the CO1 gene from pectoral fin tissue and examine the haplotype frequency of black crappie in four southeastern United States lakes. Samples were retrieved from East Lake Tohopekaliga and West Lake Tohopekaliga in Florida, Lake Marion in central Florida, and Lake Seminole that is found on the western border of Georgia and Florida. Results from this study may be used to produce a genetic baseline to counsel future management of this recreational fishery in the southeast.

138 James B. McGraw[1], Michael Elza[1], Sara Souther[2], Amy Hruska[1]
[1] Biology, West Virginia University, Morgantown; [2] Biology, West Virginia Wesleyan, Buckhannon

The Importance of Conserving Mutualists for Plant Conservation in a Changing Climate: A Case Study with Two Appalachian Icons

An expanding literature suggests that local adaptation in plants could become maladaptive in the face of climate change. Long-distance dispersal of pollen or seed by animals therefore could be critical for persistence in a warming climate. Yet for most plants, little is known about the identity of dispersers, let alone dispersal distance. In this study, we deployed wildlife cameras collecting both still images and video to examine seed dispersal of the widespread, economically-important understory plant, *Panax quinquefolius* L. (American ginseng). Small mammals and songbirds were the most frequent visitors to ginseng plants, and songbirds, specifically those in the thrush family, interacted directly with infructescences. Still images captured birds with red berries in their beaks. Videos captured the birds swallowing the berries. Experiments with caged thrushes at the Tennessee Aquarium in Chattanooga demonstrated that birds regurgitated the seeds without pulp and intact after 5 - 37 minutes. Viability tests demonstrated that the seeds were alive. Dispersal of ginseng seeds by thrushes could play a key role in moving genes northward or upward to track 'home climate' conditions of locally adapted plants such as ginseng. This places increasing importance on wood thrush conservation as an important component of American ginseng conservation. Both species, valued as icons of Appalachia, have shown marked declines in recent decades.

139 Hana M. Henry
Division of Natural Sciences, Maryville College, TN

Reef Fish Populations and Coral Reef Health as Affected by Anthropogenic Impacts on Bonaire, Municipality of the Netherlands

Coral reefs are experiencing degradation worldwide from climate change, sedimentation, nutrient enrichment, ocean acidification, disease, and overfishing. Bonaire, Municipality of the Netherlands, is an island located in the Caribbean Sea 80km north of the coast of Venezuela. Bonaire is surrounded by fringing coral reefs that are regarded as some of the most pristine reefs in the entire Caribbean due in part to the extensive conservation efforts of the Bonaire Marine Park and Washington Slagbaai National Park. The aim of this study was investigate the health of Bonaire's coral reefs by surveying fish diversity and abundance and the level of coral bleaching in a pristine control area and an anthropogenic influenced, high impact area. Overall no significant difference was found between the control and impact study areas in terms of reef fish species richness, species evenness, and coral bleaching ($P > 0.1$ for all). However, there was low abundance of two bioindicators species, butterflyfish (family Chaetodontidae) and parrotfish (family Scaridae), while a high abundance of damselfish (family Pomacentridae) was recorded in both study areas. This suggests that the coral reefs in both study areas are equally deteriorated and declining due to different anthropogenic impacts. Further research that compares the coral reefs in the Washington Slagbaai National Park, an area of both low direct and indirect anthropogenic impact, to the sites studied here is strongly suggested. This study provides a baseline assessment for further research on the fish diversity and health of the coral reefs in Bonaire, Municipality of the Netherlands.

140 Gil Nelson[1], Kevin Robertson[2]
[1] iDigBio/Florida State University; Tall Timbers Research Station; [2] Tall Timbers Research Station

Mobilizing Dark Data: Bringing Biological Field Station Biodiversity Collections into the Light

There are about 265 biological field stations in the United States, no fewer than 30 of which are located in the Southeast. These stations play critical roles as repositories of biodiversity specimens, progenitors of ecological and biological research, and partners in undergraduate and secondary education. A recent nationwide survey of field stations conducted by iDigBio, the National Science Foundation's national coordinating center for the digitization and mobilization of biodiversity specimen data, with additional data provided by the California Natural Reserve System, revealed that as many as 90% of field stations contain biodiversity specimen collections spanning all sorts of preparation types and organisms ranging from vascular plants, fungi, and algae to birds, fish, herps, invertebrates, marine organisms, and fossils. Many of these station-specific collections likely represent the best available documentation for narrowly defined biodiversity hotspots. This session will highlight strategies for facilitating the digitization of field station data for greater use by scientists, enthusiasts, the general public, and undergraduate and secondary students and educators. Overviews of recently completed digitization activities at Tall Timbers Research Station and Archbold Biological Station will provide examples.

141 Ketaki Deshpande, DeEtta Mills
International Forensic Research Institute, Biological Science, Florida International University, Miami

Major Histocompatibility Complex Genes as Additional Markers for Wildlife Conservation, as Modeled in *Equus caballus*

Major histocompatibility complex (MHC) class I and II gene products are responsible for an individual's body odor, and can also be a reflection of their fitness, health or diseased state. The inherent polymorphic nature of the MHC genes has the potential to generate unique combinations of genotypes and odor phenotypes within related and unrelated individuals. Many social interactions within mammals are thought to be driven by MHC-odor phenotypes. For example, given free choice, a mare will select a stallion based on dissimilar odor thus avoiding inbreeding to close relatives. Eight MHC microsatellites were genotyped using various domestic horse breeds and samples obtained from Oregons' wild horse herds using non-invasive hair sampling. MHC profiles could determine relatedness. The next phase of this project will be obtain the odor profiles from the domestic horses tested and assess if a correlation between MHC genotypes and the volatile organic compound (VOC) odor profiles exists. By understanding the relationship between MHC and odor using domestic horses with known relatedness or outbreeding, will provide evidence that these same correlations may be applicable to wild equids and help understand their behavior, harem hierarchal social structure and mate selection.

143 Beshoy Fahmy, Spencer Richardson, Samantha Stewart, Rebecca E. Conway
Biology, Lipscomb University, Nashville, TN

Investigating Endothelial Cell Activation and Angiogenesis by Glutamate Carboxypeptidase II- Derived Peptides

Angiogenesis is an important step in tumor progression and growth. Glutamate Carboxypeptidase II (GCPII), a transmembrane protease that cleaves carboxy-terminal glutamates from small peptides, is highly expressed in tumor-associated vasculature and positively regulates angiogenesis in a laminin-dependent manner. We previously demonstrated that GCPII cleaves small peptides from laminin to activate angiogenesis. Recently, we hypothesized that the tripeptide LQE, which is found throughout multiple isoforms of human laminin, may be cleaved by GCPII to produce the dipeptide LQ and free glutamate (E).Our lab subsequently demonstrated that both LQ and E activate primary endothelial cells, suggesting they may be important in angiogenesis. The focus of this study was to test these fragments for angiogenic stimulation *in vivo* using Matrigel implant assays, followed by analysis of hemoglobin content by Drabkin's assays and quantitation of microvessel density by analysis of hematoxylin and eosin staining of Matrigel implant sections. Additionally, we performed *in vitro* adhesion assays in the presence of GCPII inhibitors to investigate the ability of the peptides to rescue endothelial cell adhesion.Here, we report that LQ significantly activates angiogenesis *in vivo*, and preliminary results indicate it rescues endothelial adhesion *in vitro* in the presence of GCPII inhibitors. Free glutamate (E) failed to significantly induce angiogenesis or rescue adhesion in the presence of an inhibitor. In summary, we found LQ to be a GCPII-specific activator of endothelial cell activation and angiogenesis.

144 John M. Herr, Jr.[1], Erika Balogh[2], Soumitra Ghoshroy[1]
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A Method for Air-Drying Fresh Stem Sections of *Plectranthus amboinicus* (Lour.) Spreng and *Coleus blumei* Benth for Scanning Electron Microscopy (SEM)

Fresh stem sections 22 μm to 160 μm thick of *Plectranthus amboinicus* (Lour.) Spreng and Coleus blumei Benth were made with a hydro-microtome, mounted between strips of Teflon in water on standard slides, and covered with 0 thickness cover glasses. Each slide was placed in a covered petri dish and air-dried slowly at room temperature or rapidly dried at 32oC or 60oC in an open dish. During the drying process, the stem section was subjected only to the weight of the specimen cover glass or to the additional weight of ten 1 thickness cover glasses, cemented together with piccolyte or elvicite resin, or one or two standard slides placed atop the specimen cover glass. The applied weight ranged from 1.87 to 7.56 g. To determine a method for air-drying stem sections that would closely match the results achieved with the use of the standard critical point drying procedure was the objective of this study. Section quality and level of distortion was accessed by examining the surface in contact with the slide during the drying process in reflected light with a Wild M-5 microscope. Rapid drying of heavily weighted thick sections above room temperature markedly distorted anatomical features rendering the sections unsuitable for study. Thin stem sections (c. 22 μm thick), dried slowly at room temperature (c. 21oC) or in absolute ethanol dried rapidly at 60oC, and minimally weighted during the drying process (1.87 g) were anatomically comparable to those subjected to the critical point drying procedure.

145 Victor Hong, Benjamin J. Thornton
Biology and Allied Health, Southern Adventist University, Collegedale, TN

Differential Protein Expression During Tail Regeneration of *Anolis carolinensis*

Some invertebrates can regrow almost any part of their bodies, such as sea stars, planarians, and hydras. Vertebrates such as newts and lizards also possess regenerative abilities. Studies in lizard tail regeneration have been performed focusing on morphological and physiological changes. Advances in knowledge of cell signaling pathways have broadened the scope identified on various mechanisms of control for regeneration of limbs, and their implications in regenerative medicine. For this study, total proteins from regenerating tails of green anoles (*Anolis carolinensis)* were separated by pH using isoelectric focusing and then by size using a 14% (w/v) acrylamide gel. The protein gels were stained with Coomassie blue. Normalized protein differences were analyzed using SameSpots software from Nonlinear Dynamics Ltd. Spots of interest were sent to the University of Nebraska Mass Spectrometry Core Facility (Lincoln, NE) for protein identification using tandem mass spectrometry (MS/MS). We eleven proteins that were differentially regulated during tail regeneration in male green anoles.

146 Alexandra T. Barbour[1], Jason Braco[2], Matthew Whitmill[2], Erik Johnson[2]
[1] Biology, Guilford College, Greensboro, NC; [2] Biology, Wake Forest University, Winston-Salem, NC

Exploring Corazonin Receptor Expression in the Fruit Fly and Its Relevance to Human Fertility

For many organisms across the Metazoa, hormone signaling is essential for the facilitation or inhibition of numerous physiological and behavioral functions.The neuropeptide hormone called corazonin that is found in *Drosophila melanogaster*, among other arthropods, is known to be a signal for stress response and metabolism. Similarities to mammalian gonadotropin-releasing hormone (GnRH) suggest that corazonin may also play a role in reproduction.The purpose of this study was to identify corazonin receptor expression in the *Drosophila* brain to identify the neurons to which it binds. Adult *Drosophila* brains were dissected and corazonin producing neurons were tagged with green florescent protein (GFP) using the GAL4- UAS system. The tissue was treated with cy3 red florescent antibodies that are designed to bind to the corazonin receptor. The treated brains were analyzed with confocal microscopy. The staining results revealed that corazonin neurons and receptors are colocalized, which is consistent with autocrine signaling. This result may correlate to corazonin affecting its own production. Further investigation will help in determining the entire signaling pathway and full function of this neuropeptide in *Drosophila*. Due to the similarities between corazonin and GnRH, there is potential to use corazonin in fruit flies as a model to study causes and treatments of infertility in humans that are related to GnRH abnormalities.

147 Roger A Sauterer, Linda A Major
Biology, Jacksonville State University, AL

Histone-Induced Cytochrome C Release from Mitochondria: A Broadly Conserved Process?

Apoptosis is a process conserved across eukaryotes, including unicellular eukaryotes, even though the mechanisms differ between phyla. In animals a critical step of the apoptotic pathway is the release of Cytochrome c from mitochondria that causes the assembly of an apoptosome, which activates a cascade of caspases. Cascone (2012) demonstrated in mammalian cells that the core and linker histones bind to mitochondria to induce the mitochondrial Cytochrome c release, linking nuclear orDNA damage to the initiation of apoptosis. In our lab, Major (Thesis 2014) demonstrated that H3 from salt-extracted nuclear histones bind to isolated mitochondria in cauliflower (an angiosperm) and induces Cytochrome c release, even though published studies indicate that the release of Cytochrome c has no role in plant apoptosis. Even though the role of Cytochrome c in the divergent apoptotic pathways is not thoroughly known, we hypothesize that histone-induced Cytochrome c release is broadly conserved across eukaryotes. We propose to perform preliminary investigations of histone-mitochondrial binding and histone-induced Cytochrome c release in yeast (unicellular fungus), *Chlamydomona*s (chlorophyte), *Tetrahymena* (ciliate) and *Monosiga* (choanoflagellate) in order to determine whether this process is limited to specific eukaryotic kingdoms or is more broadly conserved. Additionally, we propose to investigate in more depth the histone- mitochondria interactions in cauliflower using HPLC-purified individual histones and the appropriate antibodies to determine which angiosperm histones bind to mitochondria and induce Cytochrome c release. These projects will provide a deeper understanding of the evolution of mechanisms incorporated into the different apoptotic pathways.

148 Nicole L. Vanderbush, Brian St. Clair, Marilyn Davis, Dan Davis
Chemistry and Biochemistry, University of Arkansas, Fayetteville, AR

Expression and Characterization of Cytochrome C6 from *Chlamydomonas reinhardtii* using a Designer Gene

Cytochrome c6 is a lumenal redox carrier in oxygenic photosynthesis. Its midpoint potential ranges from +340mV to +390mV. A synthetic gene, constructed by the removal of introns and the substitution to *E. coli* biased codons, was incorporated into a pUCF2 plasmid downstream of the lac operon and a pelA leader sequence. The protein is expressed by co-transformation in *E. coli* of the pUCF2 plasmid and the PEC86 plasmid, which contains genes for the covalent attachment of the heme. The spectral characteristics were determined by UV-Vis spectrophotometry and include a reduced alpha peak at 553 nm, beta peak at 523 nm, Soret band at 417 nm, the oxidized peak at 423 nm, and a peak at 693 nm indicative of the His- Met ligation of the heme. Mutants K29I and K57I, constructed using site-directed mutagenesis, show a shift in the alpha peak to 552 nm. The midpoint potentials at pH 7 as determined by redox titrations are 365 +/- 5 mV for the wild type and +322+/- 5 mV and +335 +/- 5 mV respectively for the K29I and K57I mutants. Differential scanning calorimetry reveals the folding of the wild-type protein and mutants to be irreversible. The Tm for the wild type is 78oC and 70oC and 71oC for the K29I and K57I mutants respectively. Cytochrome c6 from *C. reinhardtii* shows a typical spectrum, but the midpoint potential is not pH dependent as far as pH 10 differing from any previously described c6. Also, the conserved K29 and K57 residues contribute significantly to the midpoint potential and stability of the protein.

149 Tsu-Yi Su, Wanda T. Schroeder
Wesleyan College, Macon, Georgia

Effect of Exogenously Administered Estradiol and Progesterone on the Expression of Tgase1 Protein in Immature Mouse Vaginal Epithelia

Transglutaminase 1 (TGase1) is a calcium-dependent enzyme essential for the normal differentiation process of vaginal epithelial and epidermal cells. Both estrogen and progesterone play central roles in the normal physiological changes in vaginal epithelium that occur during the estrous cycle in mice. Recent studies have shown that in sexually mature mice, expression of TGase1 occurred in stratified vaginal epithelia during all stages of the estrous cycle, while the unstratified vaginal epithelium of immature mice lacked TGase1. Furthermore, exogenous administration of estradiol to immature mice induced expression of TGase1 and stratification in vaginal epithelia in 6-12 hours post-injection. In the current study, the effect of exogenously administrated progesterone in conjunction with estrogen has been examined to determine if progesterone alters the effect of TGase1 expression by estradiol. Twenty-day old immature mice were injected with estradiol, progesterone, estradiol and progesterone, or vehicle control and sacrificed at 6, 12, 18, 24, and 48 hours post-injection. Vaginal tissues were excised, sectioned, and examined using immunohistochemistry to determine whether or not TGase1 protein was expressed. Preliminary results have shown that when administered in conjunction with estradiol, progesterone delays the estradiol-induced expression of TGase1 in mouse vaginal epithelium. The results of this study will further the understanding of how estradiol and progesterone affect expression of key proteins in the differentiation process of vaginal epithelium.

150 Joseph A. Tierno, Matthew L. Oliver, Kayleigh T. Bradley, Marbuelis O. Carter, Michael L. Gleason
Biological & Environmental Sciences, Georgia College & State University, Milledgeville

Dynamics of Sup35 Amyloid Aggregations under the Effects of Cinnamon Extract

The protein Sup35 is the eRF3 of *Saccharomyces cerevisiae*, is responsible for the non-Mendelian phenotype [*PSI*+] and is widely used as a model prion. Using this protein to study the formation of amyloid *in vitro*, we have monitored its aggregation rates using a thioflavin T, a small fluorogenic compound that emits at 482 nm when bound to an amyloid motif. Using this assay we monitor kinetics of amyloid formation and are studying the dynamics by which a cinnamon extract (CEppt) interferes with its formation. Notably, this same extract disassembles amyloid-beta *in vitro* and *in vivo* in mice (Frydman-Marom et al., Tel Aviv University). To facilitate our studies we express a truncated of the prion, Sup35NM-6His, which includes domains necessary for stable prion formation and a His tag for affinity purification using Ni-NTA resin. To directly determine the fraction of Sup35NM that aggregrates, and to some extent the size of those aggregates in the presence of CEppt we use two electrophoretic techniques: boiled- gel/SDS-PAGE and SDD-AGE. Our findings indicate the CEppt may lead to the disassembly of amyloid fibrils composed of Sup35 which will hopefully lead to a better understanding of the mechanisms behind amyloid assembly and disassembly. It has been hypothesized that therapeutic compounds that could disassemble amyloids made of Sup35 would have a similar effect on other amyloids that are common in diseases such as Alzheimer's disease or even variant Creutzfeldt-Jakob disease (vCJD).

151 Natalie J. Hargrave, Mijitaba Hamissou
Jacksonville State University

Investigating Insulin-Like and Glucosidase Activities in Bitter Gourd (*Momordica charantia*) and Cucumber (*Cucumis sativus*) Extracts

Diabetes mellitus affects millions of people globally with a new person being diagnosed every 30 seconds. The prevalence of this disease encourages us to find new, less invasive ways to manage the disease. Bitter gourd (*Momordica charantia*) has been shown to possess several medicinal properties including hypoglycemic activity. Cucumbers also possess medicinal properties but has not been shown to own any hypoglycemic activity to date.We propose to test the extracts of these fruits for their β-glucosidase activity and the presence or lack of insulin. We hope to narrow down the cause of bitter gourd's hypoglycemic activity so that in the near future we can isolate it. If the cause and the strength of bitter gourd's hypoglycemic activity is found it may be possible to manufacture a supplement that can be used in replacement of insulin injections. That supplement would allow managing diabetes to become a much simpler and cost-effective task.

152 Ashley Morris
Biology, Middle Tennessee State University, Murfreesboro

Brief Introduction to Symposium Including Comments on Dr. Quarterman

153 Dwayne Estes[1,2]
[1] Botanical Research Institute of Texas, Fort Worth, TX; [2] Center of Excellence for Field Biology, Austin Peay State University, Clarksville, TN

A Review of the Ecology, Flora, and Phytogeography of Southeastern US Glade Communities

Glades are related to but distinct from other naturally open communities such as outcrops, barrens, prairies, and cliffs. These edaphically- maintained, small-patch, insular communities are associated with exposures of bedrock (limestone, dolomite, sandstone, granite, and shale). Most are level to gently sloping and may be partially covered with a thin mantle of soil. Most are characterized by saturated soils and pools of water in winter and spring, supporting small ephemeral wetlands. All become dry by summer and fall and desert-like. The combination of fluctuating moisture levels, high solar insolation, shallow soil, bedrock chemistry, and limited resources makes glades especially difficult places for plants to survive. As such, most glade types are dominated by annual grasses and various annual/perennial herbs; stunted shrubs and trees develop in pockets of deeper soil but are frequently killed by drought. Each of the major glade systems supports a distinctive flora and unique vegetation associations. Glades are relatively stable communities through time as evidenced by their high number of endemic species. Numerous new species have been described in recent years and undescribed species continue to be discovered from glade systems with regularity. The various glade types tend to share species with each other and with other naturally open communities such as prairies, cliffs, fens, and bogs. Many glade species have unusual phytogeographic patterns characterized by widely disjunct populations. In this talk I present an ecological overview of Southeastern glades, highlight their unique flora and biogeographic connections, and discuss hypotheses concerning the origin and evolution of glade flora.

154 Kimberly R. Taylor, Robert J. O'Kennon
Botanical Research Institute of Texas, Fort Worth, TX

Characteristic Flora of Walnut Limestone Glades: A Little Known Glade System in North Central Texas

Glade systems are prevalent across the Eastern United States. While each system is unique and possesses its own characteristic flora, there are many similarities between systems that unite them. The Walnut Limestone Glades of North Central Texas are a system that has previously received little attention. These glades form on limestone substrate within the Fort Worth Prairie and Lampasas Cut Plain ecoregions of North Central Texas. The glades within this prairie-barren-glade matrix have a characteristic flora that share many similarities with other limestone glade systems. The geology, edaphic conditions, vegetation patterns, characteristic flora, endemic species, and similarities to other glade systems will be discussed.

155 Matthew A. Albrecht, Quinn G. Long
Conservation and Sustainable Development, Missouri Botanical Garden

Effects of Habitat Structure and Herbivory on the Reintroduction of an Endangered Glade Plant: *Astragalus Bibullatus* (Pynes Ground‑Plum)

Conservation reintroductions are an increasingly important strategy to reduce species extinction in the wild, but they have a high-risk of failure when species habitat requirements are poorly understood. In this study, we used experimental reintroductions combined with habitat manipulations in natural populations to examine how variation in woody vegetation influences the demographic success of *Astragalus bibullatus* (Pyne's ground-plum), a federally endangered perennial endemic to limestone cedar glades (LCGs). Because populations previously reintroduced to undisturbed glade-forest ecotones went extinct, we tested the hypothesis that altered disturbance regimes have increased woody vegetation encroachment and reduced habitat quality in LCGs. In natural populations, we observed a significant negative relationship between tree canopy cover and plant size, flowering, legume production. Following the reduction of woody vegetation cover (primarily eastern red cedar) in natural populations, demographic vital rates improved and populations that were once senescent became reproductive. In the experimental reintroduction, transplant survival and growth declined significantly along a canopy cover gradient. Transplants in a glade-barren mosaic maintained by fire exhibited significantly greater survival, growth, and reproduction than transplants in previously unburned and more heavily encroached glade-forest ecotones. Caged transplants exhibited significantly greater survival, growth, and flowering than uncaged transplants across all sites, indicating that herbivores influence the establishment of restored plant populations in LCGs. Although edaphic factors (thin, infertile soil) are considered the primary driver of the origin and maintenance of limestone cedar glades, our data indicate that woody vegetation encroachment due to altered disturbance regimes threatens the population viability of glade endemics.

156 Jesse E. D. Miller, Ellen I. Damschen
Zoology, University of Wisconsin, Madison

Long‑Term Landscape Change in Ozark Dolomite Glades, 1939‑2012

Woody encroachment, or the invasion of shrubs and trees into grasslands, is one of the greatest threats to biodiversity in Ozark dolomite glades— rocky grasslands with diverse plant communities. Little is known, however, about what factors drive encroachment at a local scale, the extent to which glades have already become wooded at a regional scale, or how effective management practices have been for maintaining open glade landscapes. In this study, we used historic aerial photos to analyze rates and potential drivers of woody encroachment in dolomite glades in southwest Missouri. We hypothesized that local environmental variables, landscape context, and prior woody cover would all affect encroachment rates. We compared long-term change in glades managed with prescribed fire and mechanical thinning with unmanaged glades. We found that woody vegetation has increased significantly across the landscape since 1939, with only minor sensitivity to local environmental factors and landscape context. Previous cover of woody vegetation was, however, a predictor of encroachment rates, suggesting that propagule arrival has a stronger influence on encroachment than environmental filters. Contemporary woody vegetation cover was higher in unmanaged glades than managed glades, but managed glades still had significantly higher woody vegetation cover in 2012 than they did in 1939. Our findings suggest that woody encroachment in glades exhibits hysteresis, meaning that restoring encroached glades will likely require more intensive management efforts that maintaining existing open glades.

157 Matthew L. Niemiller
Illinois Natural History Survey, Prairie Research Institute, University of Illinois, Champaign

The Amphibian and Reptiles of the Cedar Glades and Barrens of the Central Basin of Middle Tennessee

The cedar glades and barrens of the Central Basin of middle Tennessee support a unique community of flora and fauna, representing some of Tennessee's most valued natural areas. Herpetofaunal inventories and associated studies, particularly those conducted over the last 15 years, have documented an impressive assemblage of amphibians and reptiles at several state- or federally-owned lands in Rutherford and Wilson counties, such as Stones River National Battlefield, Flat Rock State Natural Area, and Cedars of Lebanon State Forest and Natural Area. Sixty-three species (28 amphibians and 35 reptiles) have been documented to date, including four species considered rare, threatened, or endangered in Tennessee: *Ambystoma barbouri*, *Aneides aeneus*, *Cryptobranchus alleganiensis*, and *Gyrinophilus palleucus*. I will discuss the results of past inventory studies as well as the composition, relative abundance, threats, and conservation of the herpetofauna of the cedar glades of middle Tennessee.

158 Christopher R. Herlihy[1], Jeremiah W. Busch[2]
[1] Middle Tennessee State University, Murfreesboro; [2] Washington State University

What Maintains the Flower Color Polymorphism in the Cedar Glade Endemic *Leavenworthia stylosa*?

Leavenworthia stylosa is a winter annual endemic to the cedar glades of Tennessee. Plants produce either yellow or white petals, and most populations contain only a single flower color morph. Here we present the results of several experiments aiming to explain the evolutionary maintenance of this flower color polymorphism and its geographic distribution. We examined differences between yellow and white flowered individuals, performed reciprocal transplants between yellow and white-flowered populations, documented geographic variation in pollinator abundance and color preference, and observed how pollinators foraged amongst *L. stylosa* and other co-flowering *Leavenworthia species.* We found only weak evidence for local adaptation of the color morphs. Although there was variation in the abundance of pollinators and their preference for yellow or white flowers, this did not occur in a way that would maintain the flower color polymorphism. White flowers are larger than yellow flowers, and produce more seeds. However, fruits produced by white flowers suffer greater damage from seed predators. This tradeoff between fecundity and protection may help explain the maintenance of the polymorphism, but does not explain its geographic pattern. In sympatry with other white-flowered *Leavenworthia* species, *L. stylosa* often has yellow flowers. Pollinators tend to move among flowers of the same color, including moving between different species. The shift to yellow flowers in populations of *L. stylosa* where co-occurs with congeners may represent a case of reproductive character displacement to reduce costly hybridization, and may help explain both the maintenance of the flower color polymorphism and its geographic pattern.

159 Kim Cleary Sadler
Biology, Center for Cedar Glade Studies, Middle Tennessee State University, Murfreesboro

Cedar Glades as Outdoor Classroom Experiences for Grade K-12 Students

Creating public understanding about protecting and preserving biodiversity should begin during the formative years.Although most Middle Tennessee K-12 students can identify a feature and organism in the rainforest, few are able to say anything about a cedar glade, which is a unique ecological system that occurs in their backyard. With this in mind the Center for Cedar Glade Studies at Middle Tennessee State University has developed resources that promote student engagement with cedar glades. Teacher teams designed and developed grade-level appropriate and standards-basedresources for K-12 educators interested in teaching about limestone glades. Preservice educators at MTSU learn how to use glade resources and partner with K-12 students during glade field trips to learn how to teach in field settings. Bringing the cedar glade to school has been another successful approach in that two local schools have created glade gardens on their campus by rescuing glade plants from areas under development. Other aspects of the cedar glades as an outdoor classroom and student outcomes will be discussed.

160 Kunsiri Chaw Grubbs
Biology, Winthrop University, Rock Hill, SC

***Eupatorium rotundifolium* Complex: Investigating Its Origin**

Eupatorium rotundifolium s.s. is a member of the sunflower family (Asteraceae) that includes both sexual diploids and apomictic polyploids. The unique characteristic of the diploids is its ability to produce viable pollen, whereas the polyploids are almost pollen sterile. In this study, plant samples of *Eupatorium rotundifolium* diploids, polyploids, and its hybrids were collected from various sites around the Southeast. Nuclear DNA (ITS) and cpDNA (trnH, psbM, ycf6) sequences were used to investigate the intraspecific and interspecific variations among the collected samples. Additionally, morphological data were used as a supplemented tool to support the confirmation of the diploid pure type and the hybrid origins of some samples. Among the *E. rotundifolium* diploids that were collected from a narrow range around the Gulf Coast and the Atlantic Coast, both molecular and morphological data show that there is differentiation within the diploids. This might have led to some previous misidentification of the species and its related hybrids.

161 Randall L. Small, Jennifer L. Schilling
Ecology and Evolutionary Biology, University of Tennessee, Knoxville

Genetic Diversity and DNA Barcoding in Invasive Chinese Privet (*Ligustrum sinense*)

Chinese Privet (*Ligustrum sinense*, Oleaceae) is an invasive tree/shrub from eastern Asia. Privet often forms dense thickets in places where it establishes and crowds out native species. Despite its importance as an invasive, relatively little is known about its population structure, the origin of individual populations, or gene flow among populations. To begin to address patterns of genetic diversity within and among populations, and to test previously described DNA barcoding loci for Privet we sequenced gene regions of the nuclear ribosomal ITS and chloroplast psbA-trnH intergenic spacer from 10 individuals each from 6 populations in Knox County, TN. Little genetic variation was detected, but the variation that does exist is shared among populations suggesting multiple introductions and/or gene flow among populations. Finally, when comparing species identifications suggested by DNA barcodes, discrepancies were found in species assignment suggesting either mislabeling of samples, or confusion about the taxonomic identity of invasive vs. native Chinese populations.

162 Alexander Krings[1], Bruce K. Kirchoff[2], Piyush Agarwal[3]
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Image Sort Visual Learning for Field Botany Courses: Facilitating Higher-Level Active Learning in the Field through First Exposure Pattern Recognition Exercises in the Classroom or at Home

Field trips have long been an integral and important component of teaching plant identification at the university level. Field trips can be an important learning tool to teach identification because they help expose students to the variation in character states needed to train their minds to recognize features and patterns like domain experts. Observational repetition plays an important role in developing domain expertise. However, the effectiveness of field time may be limited depending on the extent to which (1) field time constitutes first exposure to new material and (2) lessons are delivered essentially as show-and-tell, thus limiting active learning. We here discuss the application of an open-access, customizable, html/javascript-based visual learning tool to create a series of active learning exercises in morphological terminology, keying, and species recognition through image sorting. We discuss experience employing the exercises in an undergraduate field botany course to transition first exposure from the field to the classroom or at home, and the possibilities for higher-level field exercises such a transition may facilitate.

163 Nathan D. Howell[1], Alexander Krings[1], William A. Hoffmann[1], Richard R. Braham[2]
[1] Plant and Microbial Biology, North Carolina State University, Raleigh; [2] Forestry and Environmental Resources, North Carolina State University, Raleigh

The Littoral Zone Flora of Carolina Bay Lakes in Southeastern North Carolina

Carolina bays are elliptic, directionally aligned basins of unknown origin that occur on the Atlantic Coastal Plain from southern New Jersey to northeast Florida. In southeastern North Carolina, several large, natural, lacustrine systems (i.e., Carolina bay lakes) exist within the geomorphological features known as Carolina bays. Within the current distribution of Carolina bays, Bladen and Columbus counties contain the only known examples of Carolina bay lakes. The Carolina bay lakes can be split into two major divisions, the 'Bladen Lakes Group' which is characterized as being relatively unproductive (dystrophic - oligotrophic), and Lake Waccamaw, which stands alone in Columbus County and is known for its high productivity and species richness. Although there have been several studies conducted on these unique lentic systems, none have documented the flora comprehensively. In the present study, we opportunistically sampled the littoral zone flora of eight Carolina bay lakes during the 2013-2015 growing seasons; literature reviews and herbarium voucher specimens complemented this field work to produce an inventory of the vascular plant species present. To date, this survey detected 193 species/subspecies in 134 genera and 79 families of vascular plants. Of the 193 total taxa, seventeen species were of conservation concern. Lake Waccamaw exhibited the highest species richness with 141 catalogued taxa and 14 species of conservation concern. Across all sites, the Cyperaceae (23 spp.), Poaceae (22 spp.), Asteraceae (11 spp.), Ericaceae (8 spp.), Juncaceae (7 spp.), and Lentibulariaceae (6 spp.) were the most species-rich vascular plant families encountered.

164 Kipp P. Callahan, Alexander Krings, David L. Lindbo, William A. Hoffmann
Plant and Microbial Biology, North Carolina State University, Raleigh

The Vascular Flora of Pondberry Bay Preserve (Sampson County, North Carolina)

Pondberry Bay Preserve is a 2,067 acre property that is managed by the North Carolina Plant Conservation Program (PCP) located in Sampson County, North Carolina. The property was acquired by the PCP in 2002 in an effort to preserve habitat for Pondberry (*Lindera melissifolia*), a federally endangered species. Under previous ownership much of the property was utilized for the cultivation of Loblolly Pine (*Pinus taeda*) but the site is currently being managed to maintain habit for the Pondberry and restore the site to its historical Longleaf Pine (*Pinus palustris*) dominated system. The aim of this study is to produce a taxonomic manual of the vascular flora of the preserve utilizing field collections and herbarium records. To date, approximately 450 specimens have been collected. Herbarium research, continued site visits, and specimen identification are ongoing. This manual will be available for public use and will provide a baseline to assess restoration efforts and future management of the property.

165 Gerald L. Smith, Whitney K. Schlick, J. Derek Huffstetler
High Point University, NC

An Intriguing Population of *Hymenocallis* in the Pittman Creek System in the Central Florida Panhandle

Populations of *Hymenocallis* in the Florida Panhandle continue to intrigue and present taxonomic challenges. *Hymenocallis gholsonii* deep in the Apalachicola National Forest was published in *Novon* (2009). An interesting population of *Hymenocallis* located on floating muck islands in the Pittman Creek system, Florida were brought to the attention of G. L. Smith in 1999. We have been undertaking studies on its morphology, cytology, genetics (ISSR) and its unique ecology. We will present the results of our studies and offer our ideas about its taxonomic status.

166 Karen P. Fawley[1], C. Theo Witsell[2], Marvin W. Fawley[1]
[1] School of Mathematical and Natural Sciences, University of Arkansas at Monticello; [2] Arkansas Natural Heritage Commission, Little Rock, AR

The Taxonomic Status of *Cardamine dissecta* (Brassicaceae) in Arkansas

Cardamine dissecta (Leavenworth) Al-Shehbaz, a wildflower in the mustard family (Brassicaceae), is widely distributed in the southeastern U.S. (Alabama, Georgia, Kentucky, Mississippi, North Carolina, South Carolina, Tennessee, and Virginia) and northward into Indiana and Ohio. A disjunct group of populations occurs in Polk County, Arkansas, several hundred miles to the west of the main range. All of the known Arkansas sites occur in the watersheds of Blaylock Creek, Sugar Creek, and the Saline River in a rugged area of the Ouachita Mountains. We were curious about the taxonomic status of *Cardamine dissecta* in Arkansas, specifically we wondered if Arkansas populations of *C. dissecta* are morphologically and genetically distinct enough to be considered a new taxon. We evaluated the status of the Arkansas populations of *C. dissecta* using DNA sequence analysis of the ribosomal internal transcribed spacer region. Analyses of these data produced an unexpected result. Arkansas specimens of *C. dissecta* were actually more closely related to *C. concatenata* than to southeastern populations of *C. dissecta*. However, the Arkansas specimens of *C. dissecta* are morphologically distinct from *C. concatenata*. These results suggest that the Arkansas populations of *C. dissecta* are actually a new species found only in a narrow part of the Ouachita Mountains.

167 Wendy B. Zomlefer[1], Steven Hughes[1], J. Richard Carter[2], David E. Giannasi[1], Alan Harvey[3], David Morgan[4]
[1] University of Georgia; [2] Valdosta State University; [3] Georgia Southern University; [4] University of West Georgia

Patterns of Biodiversity Documented by Four Herbaria in Georgia: Do Small Collections Data Make a Difference?

Current specimen digitization efforts target smaller herbaria: these collections likely comprise unique records (such as rare taxa), documenting species from the area surrounding the institution. To test this hypothesis, preliminary data from four Georgia herbaria of various sizes were assessed, with focus on specimens collected from the state at the county level. In Georgia, the county represents a particularly refined geographical unit for documenting biodiversity: although the twenty-fourth largest state, Georgia comprises 159 counties, the second highest after Texas (254). Color-coded maps generated by ArcMap served as a visual aid to compare per county number of specimens and species for herbaria at the University of West Georgia (ca. 4,000 specimens collected in Georgia), Georgia Southern University (11,000), Valdosta State University (40,000), and University of Georgia (86,000). The vouchers from the two largest herbaria show relatively good state-wide coverage, reflecting exchange programs from current floristic projects and from those going back many decades. Valdosta State University Herbarium has strong representation in the coastal plain, while University of Georgia Herbarium has better coverage for northern Georgia. County gaps for both herbaria include the west-central border of the state. The two smaller herbaria have the greatest concentration of specimens/species from their home county, with much fewer in adjacent counties. However, the results indicate that records from these two herbaria complement the holdings of larger ones, filling in several county record gaps. This supports the supposition that smaller collections are crucial for complete sampling coverage and confirms the scientific value of these herbaria.

168 Megan Scholer, Brad Ruhfel
Eastern Kentucky University

Phylogenetic Placement of the Newly Described Clover *Trifolium kentuckiense* (Fabaceae)

In this study we attempt to resolve the phylogenetic placement of the recently described clover, *Trifolium kentuckiense* (Fabaceae). To do so, we analyzed data from non-coding plastid (*trnL* and *ndhA* introns) and nuclear (ITS) nucleotide sequence data using maximum likelihood inference. We also examined the ability of the little utilized *ndhA* intron to resolve relationships in *Trifolium,* in comparison to the more widely used *trnL* region. We present evidence indicating that *T. kentuckiense* is strongly placed within a clade of annual clovers including *T. reflexum,* a morphologically similar species. Additionally, we find that the *ndhA* intron is more variable than *trnL* and thus more successful at resolving relationships within *Trifolium*. Furthermore, analysis of the *ndhA* intron revealed strongly supported conflict between the plastid and nuclear genomes that was not evident in analyses of *trnL*.

169 Justin Hendy[1], Melody Sain[2], Randy Small[1], John Placyk[2], Josh Banta[2]
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Using Genetic Data to Distinguish *Hibiscus dasycalyx* from Its Closest Relatives, *H. laevis* and *H. moscheutos*, and to Assess Patterns of Interspecific Hybridization

Hibiscus dasycalyx (Malvaceae) is currently found in only three counties in east Texas and has recently been listed as 'threatened' under the U.S.F.W.S. Endangered Species Act. Evidence exists of hybridization between *Hibiscus dasycalyx* and two related sympatric species *Hibiscus laevis* and *Hibiscus moscheutos*. A possible hybrid origin of *Hibiscus dasycalyx* has also been suggested. To facilitate ongoing conservation efforts a clear understanding of the taxonomy and phylogeny are required for these species. Sequences of low copy nuclear genes are being used as they display a considerable higher level of variation than cpDNA sequences. These data will be able to determine each species genetic boundaries while also determining the amount of hybridization occurring between the three species, and the direction of that hybridization. It will then be determined if *Hibiscus dasycalyx* is in fact its own distinct genetic species or not. If it is in fact distinct it will be considered worthy of conservation priority. The impact hybridization has had on the genetic integrity on *Hibiscus dasycalyx* and on the individual populations will be assessed to determine how much of a threat hybridization is having on species integrity. If hybridization is found to be a threat conservation efforts will need to take this into account. If any of the three populations are found to be distinct then conservation efforts should focus on those populations.

170 Neil Billington
Biological and Environmental Sciences, Troy University, AL

A Review of the Frequency of Hybridization between Walleye and Sauger in North America

Walleye (*Sander vitreus*) and sauger (*S. canadensis*) are large predatory fishes that are valued in fisheries in North America. They also have been stocked outside of their natural ranges to provide additional angling opportunities. Hybridization between these two species is rare in natural populations, but may occur at higher frequencies in impoundments or as a result of stocking if they have not evolved together in the same system. Moreover, their F1 hybrid the saugeye (a cross between a female walleye and a male sauger) is propagated and stocked by fisheries managers as it performs well in impoundments. Walleye and sauger hybrids can backcross with both parental species resulting in introgression. Based upon original protein genetic data collected by cellulose acetate gel electrophoresis at four diagnostic loci, and data from the literature, hybridization rates between these species ranging from 1-39% are reported. Protein electrophoresis was more reliable than morphological examination, in many of these studies, for identifying hybrid and introgressed fish. To date, DNA markers have only been used in a few studies, but have provided additional useful information.

171 Todd A. Egerton[1], Matthew R. Semcheski[1], Kimberly S. Reece[2], Wolfgang K. Vogelbein[2], Katherine C. Filippino[3], Margaret R. Mulholland[3]
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Expansion and Toxicity of *Cochlodinium polykrikoides* and *Alexandrium monilatum* Harmful Algal Blooms in Chesapeake Bay

Chesapeake Bay has been subject to long-term eutrophication and experiences a succession of seasonal algal blooms throughout the year. Of particular concern, the harmful dinoflagellate *Cochlodinium polykrikoides* forms immense months-long blooms throughout the lower Bay and its tidal tributaries. *C. polykrikoides* has been associated with increasing algal blooms worldwide along with mass mortalities of finfish and shellfish. While this species has been observed in the region for over 50 years, it has greatly expanded its range and abundance since the mid 1990's. In addition, for the last eight years, the region has experienced a dramatic increase in blooms of the toxic *Alexandrium monilatum*. Dense blooms of *A. monilatum* and associated fish mortalities have long been observed in the Gulf of Mexico, but were first observed in Chesapeake Bay in 2007. Both species form blooms with densities in excess of 104 cells/ml, during which, the individual dinoflagellate taxa can account for greater than 99% of the total phytoplankton biomass. Laboratory bioassays have illustrated the devastating effects these blooms can have on living resources, including significant mortality (up to 100%) in zooplankton, and larval fish and oysters. Both dinoflagellate species are known to produce resting cysts, which may act as a transport mechanism for expansion in the estuary allowing for the establishment of new initiation sites of blooms in subsequent years. Monitoring efforts have identified bloom initiation sites within the James and York River estuaries as well as potential triggering mechanisms including precipitation and wind events, tidal cycling and water temperature.

172 Gabriel I. Herrick
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Response of Floating Aquatic Plant Communities to Nutrient Loading in Florida Waters

With the implementation of the Numeric Nutrient Water Quality Criteria for Florida, waters will be considered impaired through a combination of nutrient concentrations and imbalances in floristic composition. Due to limited experimental data, floristic responses to increased nutrient loads have been inferred from presence/absence in reference healthy waters. Meanwhile, direct experimental evidence showing stressor-response relationships between increased nutrient concentrations and switches in competitive interactions among aquatic plants would provide more sound support for plant community measures of aquatic ecosystem health. I am currently running a series of experiments aimed at showing direct experimental responses of native and exotic plant species to nutrient levels both within and exceeding the new nutrient criteria. Current data show that three co-occuring species of floating aquatic plants, *Azolla caroliniana*, *Lemna valdiviana*, and *Salvinia minima*, all increase in biomass and population sizes as nutrient concentrations increase to levels that exceed nutrient criteria. Future work will be directed at determining interactions between nutrients and competitive outcomes resulting in shifts in community structure.

173 Stefania M. Ward, Lori Tolley-Jordan
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Comparing Parasite Communities of the Freshwater Snail, *Elimia comma*, Among Tributaries of the Upper Black Warrior River, AL

Alabama is a global hot-spot for freshwater periwinkle (Gastropoda: Pleuroceridae) snail diversity, including those in the genus *Elimia*. Interestingly, most freshwater snails have co-evolved with one or more species of trematode parasite. However, the diversity of these worms, that more than likely far surpasses its native snail hosts, is undescribed in Alabama. We examined parasite diversity in *Elimia comma*, a Black Warrior River Basin endemic that occurs mostly within the Bankhead National Forest, AL. As there are no taxonomic keys for the parasite life stages (redia and cercaria) found in these snails, a catalogue that grouped cercaria morphotypes based on distinctive physical features and anatomical measurements was made. Cercaria collected from 26 infected *E. comma* in six streams were categorized based on unique morphological characters along with measurements of parasite size. Parasites were photographed and measured in µm under a compound microscope using MoticX imaging software. Results showed four morphotypes of trematodes occurred among the six streams. One morphological character, presence/absence of eyespots was used to differentiate trematodes into two morphs while further differentiation into another 2 morphs in each group was based on differences in size. One morph occurred in all streams while another occurred in two streams. All other parasites occurred only in one stream each. These results suggest that diversity of trematode parasites can be far greater than the diversity of their native snail hosts. Further molecular work is needed to assess if morphological characters and measurements estimate true differences among the worm morphotypes. Four different types of parasites in one species of snail from six small streams of the Black Warrior Basin found suggest that parasites are diverse in this region. As this is just one small portion of one Basin, much more work is needed to understand trematode diversity in Alabama. The data collected and analyzed indicates that the single tail, no eye spots parasite types are the most abundant at this time in the part of the Black Warrior River Basin that was examined; verses single tail, with eye spots. For farther identification of the parasites micro- research would need to be done.

174 Ellen Winant, William Ensign
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Conchological and Life History Differences in Three Species of *Elimia* from the Lower Etowah River Basin

Pleurocerid snail diversity in the Southeastern United States is thought to be high, but estimates of overall diversity are compromised by uncertain taxonomy. This is particularly true for the genus *Elimia*, where reliance on conchological characters by early naturalists for species designation failed to recognize significant variability in shell morphology. In this study we examine three putative species of *Elimia* to determine if quantifiable conchological characters are associated with differences in life history characteristics. Individuals of *E. modesta, E. carinocostata,* and *E. carinifera* were collected monthly from tributary sites in the lower Etowah River Basin and returned to the lab. Females were separated by species and placed in mono-specific tanks where egg deposition could be monitored. Conchological characters, including shell angle and sculptural characteristics, were also assessed on specimens not used in tank observations. Differences in egg deposition were observed in the lab and in substrate samples obtained from the field. Although there is overlap, shell angle measurements differ among the three forms and there are definable sculptural differences. Shell differences appear early in juvenile forms and the three species are distinguishable by the establishment of the fourth whorl. Our results suggest that there are at least three distinct species of *Elimia* occurring in lower Etowah River Basin tributaries.

175 Troy R. Mutchler[1], Daniel Hoffman[1], Mark M. McCarthy[2], Silvia Newell[3], Wayne Gardner[2]
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Nitrogen Cycling in Coastal Ecosystems: A Case of Too Much Recycling?

Bacterial nitrogen (N) transformations are likely to be key determinants of the fate of N in seagrass meadows, but transformation rates within vegetated sediments are not fully understood. To measure these rates, sediment cores from vegetated and un-vegetated sites in St. Joseph Bay, FL were incubated in a continuous flow system with tracer additions of 15NO3- and 15NH4+ in 2012 and 2014. Samples from the inflow and outflow of the cores were analyzed for net O2 and N2 fluxes. Initial estimates in 2012 showed no evidence of anammox or simultaneous heterotrophic N fixation. Net 28N2 fluxes in unamended cores may then represent ambient denitrification rates, which were higher in

un-vegetated versus vegetated sediments. Denitrification rates were not enhanced during the incubations suggesting that denitrifiers were either incapable of accelerating their metabolism in response to the N additions and/or a tight coupling with nitrification. Dissimilatory nitrate reduction to ammonium produced more NH4+ in vegetated sediments than in un-vegetated sediments in both 2012 and 2014. Together, these results suggest that N inputs accumulate and recycle as NH4+ within seagrass systems, potentially contributing to eutrophication that threatens coastal systems.

176 Natalia L. Traver, Dave Unger
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Impact of a Small Woodlot on Biotic and Chemical Stream Quality

The effects of forest fragmentation and disturbance on stream health have been widely studied as native riparian habitat is increasingly subjected to anthropogenic land-use change. To date, no research has been performed on the impact that the Maryville College woods, Maryville, Tennessee exerts on Brown Creek as it flows from areas of high rural and agricultural land-use into a deciduous forest fragment. The goal of this study was to investigate the effects of the Maryville College woods, a 57 hectare mixed mesophytic deciduous forest fragment, on both the chemical composition and the aquatic macroinvertebrate community structure. Macroinvertebrates were sampled at two sites, where the stream entered the college woods and where it exited, using two sampling methods (artificial leaf-packs (n=20) and standard kick-nets (n=16)). Dissolved oxygen, temperature, and flow rate were measured in-stream, and water samples were collected for analysis in the lab. Stream depth and width were measured. Downstream sites showed significant differences in macroinvertebrate measurements including: evenness, richness, abundance, number of sensitvie families, number of sensitive individuals, number of *Ephemeroptera, Plecoptera,*and*Trichoptera* (EPT) taxa, and Family-level Biotic Index. Dissolved oxygen was improved and stream depth increased at downstream sites. The Maryville College woods appears to induce certain habitat changes, which promote a shift in macroinvertebrate communities from more disturbance and low water quality tolerant assemblages at upstream sites to greater biodiversity overall as well as more sensitive assmblages at downstream sites. This study strongly supports previous research indicating that forested riparian habitat is imperative for greater stream quality, higher biodiversity, and overall improved watershed health.

177 Dalisa R. Kendricks, Barry K. Rhoades
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Effects of Lithium Chloride on Synaptic Efficacy in *Procambarus clarkii*

Despite the use of lithium to treat Bipolar disorder, its functionality in the nervous system is still not completely understood. Previous research has shown that lithium may have an effect on calcium-induced processes, including its role in the elicitation of post synaptic potentials. *Procambarus clarkii,* a species of crayfish, were used to perform electrophysiological recordings from nerve and muscle cells. Microinjections of LiCl were secreted into the vicinity of the neuromuscular junction and recordings across the IIIrd nerve root and superficial flexor muscles were correlated to determine alteration in latency and intensity of elicited post-synaptic potentials. By inputting current into the IIIrd nerve root of the crayfish abdomen via suction electrode and measuring the elicited potentials of the innervated muscle cells via microelectrodes we have been able to gain an understanding of the general effect of Li+ at the neuromuscular junction. We measured the amplitude of the post-synaptic potentials and the time base between the injected current and the elicited post synaptic potential. This data has shown that Li+ has an inhibitory effect on post- synaptic potentials by way of decreasing the intensity of the post-

synaptic response to the input stimuli while increasing the latency between the action potential and post-synaptic potential.

178 Caitlin E. Elam
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Tennessee Wetlands: Rapid Assessment and Future Directions

The Tennessee of Environment and Conservation (TDEC) is responsible for managing, protecting and enhancing the quality of the state's water resources and was granted authority to regulate impacts water resources through the 1977 Tennessee Water Quality Control Act (TCA 69-3-108) 401 Certification and Aquatic Resource Alteration Permitting requirements. Detailed chemical and biological indices of stream impairment and guidelines for stream mitigation have been developed as a result of these rules. These indices are used as assessment tools for regulatory functions such as determinations of impairment and availability for proposed impacts. Wetlands are currently moving to the forefront of regulatory questions and new tools are being developed and evaluated to assist in the assessment and regulation of these unique 'waters of the state'. A Tennessee Rapid Assessment Methodology (TRAM) based on the Hydrogeomorphic Approach to assessing wetland condition is currently being tested for regulatory use. Models have been developed for five wetland HGM types in Tennessee: Slope, Depression, Riverine, Flat and Fringe. Wetlands that do not fit these HGM types can be assessed using the Non-HGM TRAM. These tools allow for the rapid assessment of a potentially impacted wetland's availability and natural resource value to assist in determining mitigation that will result in an overall 'no net loss' of resource value. TDEC is also focusing efforts on wetland reference site identification, wetland plant community classification and ecological sampling methods to further inform the wetland regulatory framework in Tennessee.

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Relationships Between Benthic Macroinvertebrate Assemblages, Stream Habitat, and Catchment Landscape Features in the Lookout Creek System (Tennessee River Drainage)

We examined relationships of catchment land-use features with lotic habitat (instream, riparian) and benthic macroinvertebrate assemblages (family richness) at eight tributary sites in the Lookout Creek system (Tennessee River drainage). The Lookout Creek watershed (485 km2 Tennessee River drainage) encompasses parts of northern Alabama (DeKalb County) and Georgia (Dade and Walker counties), and southeastern Tennessee (Hamilton and Marion counties). Study reaches (all in northwestern Georgia) were approximately 35 times the mean stream width and represented different tributaries in the Ridge and Valley ecoregion; however, portions of the upper catchments of certain sites fell within the Southwestern Appalachians ecoregion. Study catchments yielded land-use results ranging from: 60.3% to 86.2% forested; 0.7% to 20.5% agricultural; and 2% to 32.3% urbanized. Benthic macroinvertebrate assemblages at the sites exhibited family richness values ranging from: 6 to 11 EPT (Ephemeroptera, Plecoptera, and Trichoptera) families, 1 to 7 intolerant families, and 19 to 30 total families. Landscape-stream relationships were analyzed using Spearman's rank correlation procedure ($P < 0.05$). Family richness indices (EPT, intolerant, total) were directly correlated with pebble size in the streambed and inversely correlated with catchment housing density and inadequate riparian habitat. Total family richness was directly related to pool abundance. Agricultural land use in the catchment was inversely correlated with stream width and large woody debris. These relationships reflect the sensitivity of macroinvertebrates assemblages to catchment and habitat changes.

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Toxicity of Cigarette Butts and Electronic Cigarette Cartridges, and Their Chemical Components, to *Xenopus laevis* Embryos

Potential developmental toxicities of three different cigarette butt leachates were evaluated using the frog embryo teratogenesis assay-Xenopus (FETAX). Xenopus laevis embryos were exposed to regular cigarette butt (RCB), menthol (MCB) and electronic (ECB) in concentrations ranging from 0 - 4 butts/l for RCB and MCB and 0 - 10 butts/l for ECB. The embryos were from stage 8 to 11 and were exposed for a 96-h period in static renewal test conditions. Median lethal concentration (LC50), malformation (EC50), non-observed adverse effect concentration (NOAEC), and lowest observed adverse effect concentration (LOAEC) were calculated. Results from these studies suggest that each tested leachate is teratogenic for X. laevis embryos. The highest LC50 was determined for ECB exposure at 17.9 cigarette butts/L. The LC50 value was the lowest with RCB and MCB having LC50s of approximately 1 cigarette butt/L. There were notable EC50 differences with RCB having the lowest and ECB the highest. The NOAEC and LOAEC levels for RCB and MCB were below 1 cigarette butt/L for both mortality and malformations; over 8 butts/L for ECB mortality and over 4 butts/L for malformations. From these results, we conclude that RCB leachate is the most toxic compound, while MCB leachate has the higher teratogenicity. ECB leachate has the lowest toxic and teratogenic effects on embryos but there were still noticeable effects. The results confirmed that the FETAX assay can be useful in an integrated biological hazard assessment for the preliminary screening for ecological risks of cigarette butts, and electronic cigarettes, in aquatic environment.

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Assessing Avian Use of Forested Stopover Habitat along the Mid-Atlantic Flyway During Fall Migration

Migration is demanding and the most vulnerable of life history stages for many avian species. This journey generally requires individuals land at stopover sites between breeding and wintering grounds where they must compete for limited resources to meet high energetic demands. Thus, the identification and protection of high quality stopover habitat is essential for preserving migratory species. While the importance of stopover sites for migratory populations is well-known, information is lacking. To assess migratory landbirds use stopover habitat during fall migration, we surveyed at 48 forested sites along the Delmarva Peninsula in fall 2013 and 2014. Avian detections were recorded along 500 m transects using distance sampling methods. Additionally, food abundance measurements were recorded each visit to assess seasonal availability, and habitat structure and composition data was collected once mid-season. Understanding use of stopover habitat is paramount to prioritizing conservation efforts. Recognizing and protecting important stopover sites means migrants can meet basic metabolic requirements faster, thus storing energy more efficiently and increasing their likelihood of surviving the journey. This information can be used to inform the scientific community and interested general public, influence public policy, and help promote the conservation of lands critical for migratory species.

182 Margaret J. Pryatel[1], Verl Emrick[2], J. E. Barrett[1]
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Ecosystem Services Associated with Switchgrass Plantings in Agricultural Landscapes

Agricultural activities have a major impact on global biogeochemical cycles, particularly nitrogen, phosphorus and carbon. Cultivation accelerates the decomposition of soil organic matter, which contributes to atmospheric carbon and further decreases the ability of soils to retain nutrients. Planting perennial warm season grasses are a useful management alternative to row crop agriculture because they are effective at increasing soil carbon storage and may facilitate higher rates of nitrogen and phosphorus retention in agricultural watersheds. In this project, we are interested in examining the advantages of converting row crops to a native perennial warm season grass (*Panicum virgatum*, common name switchgrass) as a potential nutrient management and carbon sequestration strategy in agricultural systems within the Shenandoah Valley of Virginia. Soil samples were sieved into three particle size classes and analyzed for carbon and nitrogen to evaluate where carbon is stored and nitrogen is retained in conventional row crops (maize and soy beans) and in soils below switchgrass. Contrary to what we expected, the results suggest a change in soil physical properties and an initial decline in soil organic matter from row crop soils converted to switchgrass. In addition, soil samples will be analyzed for mineral carbon and nitrogen pools through short term incubations, and carbon within microbial biomass using a chloroform fumigation extraction. The results from this study will be used to understand the environmental and economic benefits of implementing warm season grass plantings within agricultural watersheds as a means to mitigate agriculturally-induced effects on carbon sequestration and nitrogen retention in soils.

183 Chloe Connolly, David Vandermast
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The Impacts of Ice Storm Damage to the Structure and Composition of Elon University Forest

Extreme and infrequent natural disturbances, such as an ice storm can have profound effects on the structure and composition of a forest. The ice storm of March 6th, 2014 was an unusual precipitation event (over 0.5 inches of ice) for the central Piedmont of North Carolina. The objective of this study was to understand the effect of this ice storm on Elon University Forest (EUF). As a relatively young forest dominated by-early successional pines, we hypothesized that this storm accelerated the successional trajectory of EUF. For this study, we used data collected in 2011 and we resampled eight 1000 m2 (20 x 50 m) permanent vegetation plots established in EUF. In each plot, all trees 10 cm and greater in DBH (diameter breast height) were identified to species and measured for their diameter, in accordance with Carolina Vegetation Survey protocol. We found that 4.2% of trees and 5.3% of basal area were lost to storm-caused tree mortality. Of 27 tree species, Virginia pine (*Pinus virginiana*) was most frequently affected this storm (of 19 fallen trees 18 (94.7%) were Virginia pine). Plots dominated by early-successional species suffered greater mortality and loss of basal area than did late-successional plots. Furthermore, blocked-MRPP (Multi-response Permutation Procedure) and ordination using NMS (non-metric multidimensional scaling) in PC-ORD indicated that, by selectively removing pines, this event altered early- successional plots more than it did late-successional ones. Our data support our hypothesis that the ice storm hastened the loss of early- successional species and accelerated the pace of secondary succession on EUF.

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The Effect of Controlled Burns on Abundance of Woody Species at Buck Mountain, WV

Each year the U.S. Forest Service prescribes burns within the George Washington and Jefferson National Forest (GWJNF). Burns are prescribed both in the growing (May-October), and dormant season (November-April). The goal of the burns is to reinstate the natural fire regime, and consequently, return the forests to their original species composition, dominated by oak species in the canopy. Currently in GWJNF, Appalachian pine-oak forests are experiencing an increase in fire-intolerant species while *Quercus* spp. and herbaceous groundcover are declining. In the summer of 2014, a vegetation survey was conducted on Buck Mountain, West Virginia to determine if there was a significant difference between dormant and growing season burns compared to a no-burn control with regard to woody vegetation abundance. We were specifically interested in regeneration of *Quercus* spp. and the endangered *Gaylussacia brachycera* (box huckleberry). A total of sixty plots, 40 m in diameter, were established within a site burned once, a site burned twice (one growing, one dormant season), a site burned twice (both dormant), and a site protected from fire (control). We hypothesized that burns would have an effect on abundance of woody vegetation. We predicted that *Quercus spp.* and *G. brachycera* would increase after burns due to the decrease in competition from fire-intolerant species. We found that *Quercus prinus*, the most dominant canopy oak species, and *G. brachycera* were significantly more abundant after dormant season burns. The results of this study suggest that seasonality is an important component when determining when to prescribe burns.

185 Ryan Dorkoski, Jared L. DeForest
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Does Phosphorus Luxury Uptake Occur in Soil Microbial Communities?

Microbial communities process matter to maintain homeostasis, which affects ecosystem function. Microbial homeostasis can be described through a stoichiometric approach that predicts microbial C:N:P based on limiting elements. Since modern ecosystems may be shifting from strict nitrogen- limitation to phosphorus having a stronger influence, more focus is needed on how phosphorus limitation affects microbial stoichiometry. Luxury uptake, or the ability to 'hoard' scarce resources, is documented in aquatic systems and terrestrial plants, but little is known about soil microbial communities. We hypothesized that soil microbial phosphorus luxury uptake should be lower in microbial communities that have chronic access to more labile phosphorus than communities deficient in phosphorus. Luxury uptake was measured in native soils, and soils annually amended with phosphorus for 5 years. Treatments were incubated for 5 months to cause carbon-limitation, followed by a phosphorus pulse to saturate phosphorus and induce luxury uptake. There was no significant change in the microbial community composition, biomass, or soil pH caused by the pulse between treatments. Microbial C:P doubled ($P<0.05$) in the elevated phosphorus treatment following the pulse, which occurred above an available phosphorus level of ~13 mg P kg soil-1. This suggests that an overabundance of labile phosphorus caused a decrease in microbial phosphorus, requiring us to reject our hypothesis and propose that the pulse may have inhibited luxury uptake instead of stimulating it. Regardless, it is clear that labile phosphorus concentration altered microbial C:P, which should be considered when using microbial stoichiometry as a predictor of ecosystem status.

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Bird Diversity and Abundance on Reclaimed Surface Coal Mines in Alabama: Temporal and Habitat Related Variations

Few publications investigate landscape-level effects of mining or mine-reclamation on wildlife populations, assess cumulative impacts of mining from multiple sites at the landscape scale, or consolidate existing information for management decisions. We contribute to these knowledge gaps by investigating temporal and habitat relationships of avian communities on reclaimed mines by using unlimited-detection radii point-counts for bird community data, and fixed radii vegetation plots across 27 small-scale surface coal-mines throughout north-western Alabama. Mines were grouped into three habitat categories (grassland, conifer, mixed [$P = 0.047$); no other treatments showed significant differences. Mines greater than 14 years since closure showed non-significantly higher diversity than younger mines ($P = 0.086$). With the exception of 9 -14 year old grasslands, 9-14 year old mines had the lowest diversities, and older mines had the highest diversities. Even in productive eco-regions with small-scale mines, reclamation can take more than a decade to maximize effects in songbird communities. Short-term reclamation goals can be better met by targeting grassland species with grassland reclamation or targeting more species by diversifying vegetation composition.

187 Victoria A. Peters[1], Albert Miere[2], Michael May[3], Thomas Brackman[4]
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Influences of a Filled Valley and Deep Soil Water Saturation on Tree Growth in the Green River Floodplain

In January 2006, 10,000 bare-root seedling bottomland hardwood trees were planted in a hay meadow in the alluvial floodplain of the Green River. Tree growth of planted and volunteer seedlings is heterogeneous. The apparent patchiness appears to be unrelated to the NRCS soil types and lighting. We hypothesize that characteristics of the substrate well below the depth of the roots of the saplings is responsible for variation in tree growth. In order to characterize subsurface conditions, we utilized Electrical ResistivityTomography (ERT) to map resistivity of earth materials to a depth of 20 m. We found that a valley had been buried beneath portions of the relatively flat field, and that patches of tall trees were located over the sediment filled valley. Stunted tree growth was detected away from the valley. Tree height was most closely correlated with soil saturation as determined by resistivity at 1.1 m below the surface. We measured root depth for some of the largest planted and unplanted saplings in areas of rapid growth and slow growth. In both cases, few roots extend below 30 cm. We suspect that the trees are obtaining water from below the depth of root penetration via capillary action from the saturated soils in the buried valley. Should such buried valleys be common phenomena in karst regions of Kentucky, they may have substantial influences not only on the growth of trees but also on the growth of crops.

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Historical Land Use Drives Community Composition of Stream-Associated Salamanders

Human activities leading to land-cover change can result in persistent influences on ecosystems. Biodiversity-rich Piedmont of the Southeastern US was subject to extensive historical (1840-1920) cotton farming resulting in changes in the biota and the landscape. Widespread urbanization took place upon the abandonment of cotton farming in the Piedmont leading to multiple, transitional land uses whereas Blue Ridge quickly recovered the forest cover with little subsequent change in the land cover. We surveyed 100 m-transects at 70 low-order streams for Plethodontid salamanders and collected habitat data. Using USGS land-cover dataset (2006) and aerial photographs (1940) as current and historical data sources, we assessed the percent land-cover in 1 Km-radii-buffers at the riparian zone and watersheds for each sampling site. Using percent land-cover as predictors and species richness and Shannon Index as response variables, we developed a model via a stepwise multiple regression. Optimal model parameters that predict species richness and Shannon Index indicated the importance of historical land-uses (human settlements, raw-crop agriculture, forest cover) on stream-dwelling salamanders, despite vegetation recovery. Specifically, protected areas with agriculture or timber-based legacy were species-deprived, compared to those that were not farmed or lumbered. Conversion of forests into farmlands lead to soil erosion, sedimentation, higher discharge, and destabilization of uplands rendering those streams unsuitable for many salamanders. Our findings provide insights to assist stream restoration and landscape-scale conservation of regions with long-term historical land-uses.

189 Robert E. Evans, David Welch, Lesley Starke
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Differential Species Response to Severe Fire in a Carolina Bay Wetland in the Coastal Plain of North Carolina

Although fire suppression has been implicated in the degradation of longleaf pine vegetation, the impact of suppression on inclusional wetlands has received far less attention. Carolina Bays are isolated wetlands of the Atlantic Coastal Plain that have been heavily impacted by incompatible land- uses. Relatively few high quality examples remain; especially with intact landscape context. We will briefly discuss the considerations affecting our decision to reintroduce fire to a Carolina Bay wetland supporting a federally endangered shrub species (*Lindera mellisifolia*). We will also present data from randomly located, post-burn sample plots which document the species-specific effects of fire on tree survival. Loblolly Pine (*Pinus taeda*) the pre-fire dominant, was heavily reduced across all size classes, while Pond Cypress (*Taxodium ascendens*) mortality was concentrated in the smaller size classes. Changes in species composition following fire appear to have met preliminary ecological restoration goals for the site and suggest fire may be important for maintaining the structure and composition of these imperiled habitats.

190 Edward Schwartzman
NC Natural Heritage Program

Montane Red Cedar Glades of Western North Carolina

Western North Carolina is home to a number of unique outcrop communities, referred to as 'cedar glades' or Montane Red Cedar-Hardwood Woodlands by the NC Natural Heritage Program. Given the lack of limestone in the area, red cedar (*Juniperus virginiana*) is an uncommon species in the mountains of NC. Its role as a community dominant on these glade-like outcrops makes this community distinctive in the region. These cedar glades occur on a variety of geologic substrates but in a restricted geographic range in several mountain counties. Montane Red Cedar Glades are also repositories for a number of rare and unusual plants, including endemic and disjunct species, and are a significant component of the natural diversity of the Southern Appalachians.

191 Patrick A. Smallwood, Melissa Caspary, James E. Russell
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Investigation of Genetic Structure of Louisiana Bluestar (*Amsonia ludoviciana*) Populations in Georgia

The Louisiana bluestar (*Amsonia ludoviciana*) is a rare, herbaceous plant known to historically occur in Louisiana, Mississippi, and Georgia, although populations in Mississippi are believed to be extirpated. Within its disjunct range, the Louisiana bluestar can be found in granite outcrops of Georgia and in pine flatwoods, small-stream riparian forests, and bottomland forests of Louisiana (Lemke 1987). In Georgia, the Louisiana bluestar grows in small clusters along the margins of outcrop habitats within the Piedmont Physiographic Province. The goal of this research was to better understand genetic structure and diversity of *A. ludoviciana* populations in Georgia. Until recently it was thought that there were only six populations present in Georgia, although now there are 33 separate populations reported in the state (Allison 2013). Analysis of genetic diversity of six populations of *A. ludoviciana* was used to determine the level of inbreeding, degree of isolation, and heterozygosity within and among each population. Our intention for conducting this research was to prioritize conservation efforts and guide future research for Georgia and Louisiana populations of this species. Allison, J. R. (2013) Status of Rare Plant Species on Outcrops of Lithonia Gneiss and on Granite Outcrops in Heard County. Georgia of Natural Resources, Social Circle, GA. Lemke, D. E. 1987. Recent collections and a redescription of Amsonia ludoviciana Vail (Apocynaceae). Sida: contributions to botany 12:343-346.

192 Michael A. Erwin
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Haplotype Diversity Analysis of Black Crappie, *Pomoxis nigromaculatus* (Family Centrarchidae), Inhabiting Lake Sydney Lanier, Georgia

Molecular markers have been used to analyze the genetic structure of many pelagic fish populations. In this study haplotype diversity will be examined for the nuclear rhodopsin gene (RHO) and the mitochondrial cytochrome c oxidase I gene (COI) of *Pomoxis nigromaculatus,* Black Crappie, in Lake Sydney Lanier, Georgia. This species is a popular freshwater sport fish in the southeastern United States, and data released by the U.S. of the Interior shows that *P. nigromaculatus* is the third most targeted freshwater fish in Georgia. This fishery has been sustainable due to the species' fecundity, monitoring by wildlife management, and enforced bag limits by the state. Data on the genetic structure of this population may provide a useful tool for wildlife managers to more effectively manage this species. Mitochondrial DNA (mtDNA) and nuclear DNA (nuDNA) sequence data were collected for the purpose of developing an initial genetic baseline for black crappie inhabiting Lake Sydney Lanier, Georgia.

193 Sunny A. Fleming, Andrea S. Bishop, David Lincicome, Allan Trently
Tennessee Division of Natural Areas

An Update on the Status of the Federally Endangered *Xyris tennesseensis* in the State of Tennessee

Xyris tennesseensis Kral, Tennessee yellow-eyed grass, is a federally endangered vascular plant species in the Xyridaceae. Globally, it is known from six counties across Alabama, Georgia and Tennessee. Within Tennessee it is known only from the Western Highland Rim physiographic province in Lewis County. It is an endemic of calcareous seepage fens. These seepage fens are fed by aquifers recharged by precipitation, and are typically dominated by *Parnassia grandifolia*. Several species observed adjacent to these populations include *Scleria verticillata, Fuirena squarrosa* and *Desmodium ochroleucum*, which are typically associated with more open land cover. Many areas where calcareous seepage fens are found also support barren-like characteristics, limestone glades and prairie-like remnants. It appears likely that historically, a disturbance regime was necessary to maintain a more open canopy and sustain populations of *Xyris tennesseensis.* Management of this species in Tennessee, Alabama and Georgia has included hand-thinning of woody vegetation from margins of seeps where *X. tennesseensis* occurs, however a recent publication by Georgia Division of Natural Resources shows that this is not a viable long term management strategy. These observations and reports have provided a new context for interpreting long-term monitoring data collected at the Tennessee sites, and provide direction for future management and monitoring at these sites.

194 John B. Taggart
UNC Wilmington

Distribution and Management of Invasive Plant Populations in State Park Properties of the North Carolina Coastal

The North Carolina Division of Parks and Recreation manages 32,063 ha of coastal plain lands divided among 26 properties comprised of state parks, state natural areas, and a state recreation area. Of 35 invasive plant species found at 25 reporting sites, Japanese honeysuckle (*Lonicera japonica* Thunberg) and privets (*Ligustrum* spp. L.) occurred most frequently followed by: sericea (*Lespedeza cuneata* [Dumont-Cours.] G. Don), Japanese stiltgrass (*Microstegium vimineum* [Trinius] A. Camus), alligatorweed (*Alternanthera philoxeroides* [Martius] Grisebach), Bermuda grass (*Cynodon dactylon* [L.] Persoon), common reed (*Phragmites australis* [Cavanilles] Trinius ex Steudel ssp. *australis*), silverberries (*Elaeagnus* spp. L.), mimosa (*Albizia julibrissin* Durazzini), and wisterias (*Wisteria* spp. Nuttall). Current management measures for these species and others include herbicide applications, hand pulling to intensively-focused labor with equipment, or use of biological controls. These activities challenge missions, budgets, and staff time of each park unit such that early detection and rapid response are difficult. A dedicated staff position, invasive plant management team, and development of simple control guidelines for vines and herbs are recommended to enhance on-site efforts and provide consistency, whereas contractual assistance and collaborative efforts will be needed to control difficult or wide-spread populations. Regular monitoring and proactive management at sites with few to no invasive species should be given priority to avoid future problems. In addition to current challenges posed by invasive plant populations found at most sites, species introductions and spread as a function of climate change, sea level rise, and tropical storms are likely.

195 Jason R. O'Bryhim[1], Tayler M. Clarke[2], E.C.M. Parsons[1], Stacey L. Lance[3]
[1] George Mason University, Fairfax, VA; [2] University of Costa Rica, San Jose; [3] Savannah River Ecology Laboratory, Aiken, SC,USA

Forensic Identification of Sharks and Rays Being Caught and Sold in Costa Rica

In the past two decades shark populations have declined as a direct result of global increases in shark fisheries, resulting in one quarter of shark species being listed as vulnerable, endangered, or critically endangered. However, few nations have developed catch limits and no international or bilateral catch limits exist. One barrier to establishing catch limits is a lack of accurate species-specific extraction rates because many species look similar, distinguishing characteristics of sharks are commonly removed, or sharks are simply grouped together in fisheries data. To better under- stand the species specific impacts different fisheries are having on sharks along Costa Rica's Pacific coast we used forensic genetic techniques (DNA barcoding of a 652 base pair region of the cytochrome c oxidase I gene) to identify the types and quantities of shark species being landed in artisanal fisheries and being sold at markets around San Jose. Our results show that at least six species of shark and one ray are being sold in these markets, with *Carcharhinus falciformis* representing the vast majority of samples. The endangered scalloped hammerhead, *Sphyrna lewini,* and the smooth hammerhead, *S. zygaena*, were also identified in market samples. Within the artisanal fisheries, six species of shark were identified, with *S. lewini* accounting for the majority of all sharks landed. Estimated total lengths for *S. lewini* in artisanal fisheries, suggests that sharks sampled were either juveniles or neonates. It appears sharks being caught in artisanal fisheries are not the same as those being sold in markets around San Jose.

196 Claudia L. Jolls[1,2]
[1] Biology, East Carolina University, Greenville, NC; [2] University of Michigan Biological Station, Pellston

Panacea, Pandoras Box, Anna Karenina, and a Double-Edged Sword: Perceived Rewards and Risks of Biological Control

More than 1100 releases of more than 500 taxa have been released globally for biological control, largely of invasive plants. Testing for efficacy and negative non-target impacts of biocontrol agents has become increasingly rigorous; yet, different reviewers come to different conclusions. Fewer than 10% of the insect taxa released as biocontrols and perhaps no more than 15% of the cases documented have sufficient study for evaluation of rewards and risks. Of concern is the relative lack of 1) long-term study, 2) ecological and evolutionary perspectives on potential impacts, and 3) objective, quantifiable assessment of risk and effect sizes. Our work on the demography, ecology, and genetics of a Great Lakes endemic, Pitcher's thistle (*Cirsium pitcheri*), illustrates the challenge of detecting non-target impacts, the so-called 'Achilles heel' of biological control. As cautioned by others, documenting ecological or evolutionary change at the population-, community-, or ecosystem-level requires long-term, specific investigation. Phenological differences among target invasive and non-target native plants, population differences in agent feeding preferences, and variation in palatability of plants are not always included in pre-release testing. Non-target impacts require time to appear; lag-phases complicate detection. Range extensions by biocontrols are difficult to predict, even if investigated. Lack of records, particularly unauthorized introductions, also prevents critical evaluation of non-target impacts. The problem of invasive plants and the need for easy, effective control methods are very real. Given the relative rewards and risks, however, use of biological control should be less frequent, more carefully tested, and more extensively regulated.

198 Ruthie Barbas, Matthew R. Gilg
Biology, University of North Florida, Jacksonville, FL

Tests of Reproductive Isolation Between *Fundulus heteroclitus* and *F. grandis*

The goal of this study is to elucidate the speciation of salt marsh fishes by investigating barriers to reproduction between similar species. Barriers to reproduction between *F. heteroclitus* and *F. grandis* are being investigated by analyzing the prevalence or lack of hybridization in a variety of laboratory experiments. This study focuses on two questions:

1) How strong is pre-zygotic isolation (barriers to the formation of hybrid zygotes) between *F. heteroclitus* and *F. grandis* and their hybrids under conditions when individuals do and do not have the opportunity to choose between conspecific and non-conspecific mates? 2) How strong is post-zygotic isolation (barriers to survival and reproduction of hybrid offspring) among *F. heteroclitus* and *F. grandis* and their hybrids? Preliminary results of no-choice breeding trials have revealed the presence of both pre-zygotic and post-zygotic barriers between these species. Specifically, the results indicated a decrease in heterospecific mating and fertilization success relative to the mating and fertilization success of conspecifics. Hatching success of heterospecific embryos was also lower than that of conspecifics. Post- zygotic barriers appeared to be stronger in one of the two heterospecific crosses, revealing a possible asymmetry in post-zygotic barriers between *F. heteroclitus* and *F. grandis*.

199 Whitaker M. Hoskins, Randall L. Small
Ecology and Evolutionary Biology, University of Tennessee, Knoxville

The Role of Polyploidization in the Spread of *Hibiscus* Section *Furcaria*

Neopolyploids constitute at least 35% of the known species of angiosperms, and polyploidization is an important process in plant diversification. *Hibiscus* section *Furcaria* includes several groups of polyploids in addition to ten known diploid species. Genome groups for *Hibiscus* section *Furcaria* determined through artificial hybridization experiments have been used to elucidate the biogeography and evolutionary relationships of these species groups. For instance, the Australian hexaploids contain 3 genomes (designated G, J, and V) and are thought to have developed from a polyploidization event between an African diploid relative (G) and two unknown donors (J and V). This study seeks to use phylogenetic analysis of a suite of chloroplast regions to determine the maternal genetic relationships between the diploids and the Australian hexaploid lineage to reconstruct the origin of this group and determine if any surviving diploid donors exist related to the unknown J and V genomes. Four nuclear regions are also being explored to determine if markers can be useful for reconstructing genome relationships. Preliminary results suggest differences are limited in chloroplast regions but more prevalent in nuclear regions.

200 Macy Key, Fengjie Sun
School of Science and Technology, Georgia Gwinnett College, Lawrenceville

A Phylogenetic Study of Molecular Structures in Tmrna

Transfer-messenger RNA (tmRNA) is a bacterial RNA molecule containing combined features of transfer RNA and messenger RNA. The tmRNA is known to form ribonucleoprotein complex (tmRNP) together with Small Protein B (SmpB), Elongation Factor Tu (EF-Tu), and ribosomal protein S1. Despite its important roles in diverse biochemical functions, e.g., recycling the stalled ribosome, adding a proteolysis-inducing tag to the unfinished polypeptide, and facilitating the degradation of the aberrant messenger RNA, the evolutionary history of tmRNA remains elusive. In this study, we apply an award-winning phylogenetic approach using RNA structural information to reconstruct evolutionary history of tmRNA components. Using both geometrical and statistical data, we generate trees of molecules to reveal the phylogenetic history of three domains of life (Eukarya, Bacteria, and Archaea) and trees of RNA substructures to show the evolutionary history of the major molecular domains in tmRNA. This study demonstrates the application of the phylogenetic analysis of RNA structural evidence in support of the existing tree of life.

201 Rebecca E. Hale[1], Natrieifia T. Miller[1], Robert A. Francis[2], Caroline Kennedy[1]
[1] Biology, University of North Carolina Asheville; [2] Wildlife, Fisheries, and Aquaculture, Mississippi State University

Does Parental Care Alter Selection on Developmental and Life History Traits? A Case Study in Two Ambystomatid Salamanders

Obligate parental care and the inability of offspring to develop properly without parents occurs in many animals, including birds, reptiles, fish, and amphibians. However, loss of the ability to develop properly without parental care is difficult to explain. The variable egg-laying strategies and parental care of the salamander genus, *Ambystoma*, provide an excellent system in which to examine the evolutionary process. Phylogenies of the *Ambystoma* strongly support aquatic egg-laying and absence of parental care as ancestral in this group. Parental care has evolved just once in this genus, in *A. opacum*, and is associated with terrestrial egg-laying. We propose that development in a terrestrial environment followed by a prolonged stasis during which females guard eggs may alter selection on *A. opacum* embryos, favoring individuals that are larger and at a later stage at hatching, even though a prolonged embryonic stage could reduce survivorship if the female were to abandon her nest. We compared embryonic development of *A. opacum* with the co-occuring, non-caring *A. maculatum* under a range of laboratory conditions over two breeding seasons for each species. We found species differences in age and stage at hatching, consistent with the hypothesis of reduced selection for fast development in *A. opacum*.

202 Curtis J. Hansen, Leslie R. Goertzen
Biological Sciences and Auburn University Museum of Natural History, Auburn University, AL

Wildflower Genomics Within the Genus *Marshallia* (Asteraceae)

High-throughput DNA sequencing allows for the development of a variety of genomic data resources for non-model systems. We follow a genome- skimming approach with the wildflower genus *Marshallia* (Asteraceae) to explore various basic questions of genome structure, ecological adaptation and diversification. We present a simple example of the utility of these data with a pipeline to examine the validity of nrDNA ITS as a barcode marker in *Marshallia*, sequencing multiple individuals of all species. With the exception of the putative hybrid *M. mohrii*, all species of *Marshallia* had a unique ITS sequence and intraspecific variation was very low. The ITS sequences bolstered specific status for the recently described *M. legrandii* and suggest a relationship between *M. trinervia* and the federally listed *M. mohrii*. Additionally we have characterized the chloroplast genomes for all species of *Marshallia* and compared them to existing chloroplast genomes within Asteraceae. Transcriptome sequences for several species in varying environmental conditions have additional utility in developing phylogenetic markers and better understanding *Marshallia* genetics.

203 Eleanor Diamant, Elliot Carter, Lauren Carter, Joe Cullen, Patrick Devlin, Drew Gill, Spencer Gill, David Reagan, Mark Stanback
Biology, Davidson College, NC

Factors in the Ejection of Parasitic Eggs by Eastern Bluebirds (*Sialia sialis*)

Understanding the rules with which birds discriminate between their own eggs and those of brood parasitic brown-headed cowbirds (*Molothrus ater*) is complicated by the fact that most species can be categorized as either acceptors or rejecters: few species exhibit intraspecific variation in egg ejection behavior. We investigated the mechanisms underlying discrimination and ejection of parasitic eggs by Eastern bluebirds (*Sialia sialis*). In 2013 and 2014, we monitored approximately 250 nest boxes once per week, adding a model egg when we first found Eastern bluebird eggs in the nest. By artificially parasitizing nests with large and small blue, white, and tan-speckled wooden eggs during or after laying, we attempted to elucidate Eastern bluebird host ejection behavior and costs of egg ejection. We added an orange earplug to the nest one week following the model egg addition to test for an association between fastidiousness/sanitation and egg ejection. Eastern bluebirds ejected speckled eggs at a significantly higher rate (68.9%) than white (16.3%) and blue (13.3%) eggs, suggesting that Eastern bluebirds recognize and eject cowbird eggs as a threat to their fitness. Speckled egg size did not significantly affect ejection rates, suggesting that Eastern bluebirds are not gape-limited. Speckled eggs added after laying were ejected at a significantly higher rate than those added during laying, contrary to expectations. Speckled egg ejectors tossed orange earplugs at a significantly higher rate than acceptors. Thus, ejection is associated with fastidiousness/sanitation, suggesting experience or age could be linked to ejection.

204 John B. Reese
Ecology & Evolutionary Biology, University of Tennessee, Knoxville

Effect of Genome Duplication on Male Gametophyte (Pollen Tube) Development

Genome duplication (polyploidy) has been a major force in eukaryote evolution, especially in flowering plants (angiosperms). Despite the essential role of the male gametophyte in mediating fertilization, very little work has focused on what effect polyploidy may have on its development. Potential effects include nucleotypic effects on cell size and structure and higher metabolic rates due to gene dosage effects. In addition, diploid pollen tubes (from tetraploid donors) can have heterozygosity, which may also have differential effects on development depending on the genetic variation of the parent plants. The limited existing literature that compares pollen tube growth in plants with ploidy level variation (whether within a species or between closely related species) does not show a clear trend in either direction. However no study has intensively examined the complete male gametophyte development between different ploidy levels. This talk will introduce a plan for ongoing research comparing the development of the male gametophyte between closely related individuals with ploidy variation.

205 Alex T. Edwards
Ecology and Evolutionary Biology, University of Tennessee, Knoxville

A Comparison of the External Microbial Assemblages Between Native Southern and Wild Northern Strain Brook Trout, *Salvelinus fontinalis*, of Hatchery Ancestry

Hatchery reared, northern strain brook trout have been stocked in streams within the home range of southern strain brook trout in an effort to restore or enhance native trout populations since the late 1800s. However, brook trout native to the southern Appalachians are genetically distinct, raising ecological and ethical concerns regarding the impact of the past stockings. In this study, external mucosal samples of native southern and wild northern strain brook trout of hatchery ancestry were plated and their microbial assemblages were compared by characterizing colony morphologies and estimating densities of colony-forming units (CFUs). The hatchery-ancestry fish had significantly higher CFU densities than those of the southern strain fish. These results suggest that the native southern strain brook trout may exhibit a greater ability to inhibit microbial growth in their epidermal mucus than do the northern strain fish of hatchery ancestry.

206 Li-Jun Yan[1], Kevin S. Burgess[2], Lian-Ming Gao[1], De-Zhu Li[1]
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Evaluating the Role of Asymmetric Introgression in Potential Hybrid Speciation Between Two *Rhododendron* Species in Yunnan, China

Natural hybridization is ubiquitous in plants and the creative force of species formation through this process has been documented. Although hybridization can also lead to the genetic assimilation of taxa through asymmetrical gene introgression, the evolutionary significance of this process in hybrid speciation has not been fully explored. In this study, we investigated natural hybridization between *Rhododendron spiciferum* and *R. spinuliferum* across nine allopatric populations and 15 putative hybrid zones in Yunnan Province, China (N=566). To investigate the magnitude and direction of hybridization for each hybrid zone, we determined the genetic structure of parental and hybrid taxa using 13 nuclear microsatellite loci and the trnL-F region of the chloroplast genome. Based on STRUCTURE analysis, parental taxa formed two genetically distinct clusters (*R. spiciferum* [N = 113, 23.2%]; *R. spinuliferum* [N = 132, 27.1%]) and the frequency of hybrids was high (N = 242, 49.7%) across all hybrid zones but varied from population to population. Furthermore, NEWHYBRID analysis revealed that hybrid zones are dominated by F2 or later generation hybrids, indicative of a relatively old hybrid lineage. Both nuclear and chloroplast analyses indicate that the majority of hybrids are the result of backcrossing to the *R. spiciferum* genome indicating that asymmetric gene introgression plays an important role in the genetic structure of this hybrid zone. Collectively, our study indicates that the process of asymmetrical introgression may facilitate hybrid niche formation and subsequent hybrid speciation via adaptive introgression in hybrid species '*R. duclouxii*'.

207 Victoria A. Burgess, James E. Russell
School of Science and Technology, Georgia Gwinnett College, Lawrenceville

The Cost of Sex and *Wolbachia* Infection in *Trichogramma* Wasps

Sex allocation is an important reproductive trait that involves optimizing the number of female and male offspring a female can produce. For many insects this trait has been coopted by a bacterial parasite called *Wolbachia*. Parasitic wasps in the genus *Trichogramma* are infected with a form of *Wolbachia* that feminizes male offspring and allows them to reproduce parthenogenetically. The ultimate consequence of this type or reproductive manipulation is female-biased sex ratio distortion of populations and, in some cases, entire species. The spread of this type of *Wolbachia* infection in populations and species is often associated with a loss of sexual reproduction. The proximate cause of the loss of sexual reproduction though is unknown. We address this question by testing two distinct hypotheses related to sexual reproduction in *Wolbachia*-infected populations: 1) Female sexual fuction is costly, and 2) *Wolbachia* infection is costly. Using antibiotically-cured *Trichogramma* wasps survival and reproduction was analyzed for asexual, sexual, and cured laboratory populations. The results will be discussed in terms of bacterial transmission in populations and the potential to change modes of reproduction.

208 Loren D. Hayes[1], Luis A. Ebensperger[2]
[1] Biological and Environmental Sciences, University of Tennessee at Chattanooga; [2] Departamento de Ecología, Pontificia Universidad Católica de Chile, Santiago

Mammalian Plural Breeding: Why Bother?

Evolutionary theory predicts the persistence of social strategies that maximize individual reproductive success. A challenge for behavioral ecologists is to explain the evolutionary significance of strategies that seemingly are in conflict with theory. One such strategy is plural breeding with communal care (multiple females in group breed and rear offspring together). In mammals, plural breeding occurs in ~10% of species with known social systems across 8 orders and can involve the transfer of energetically expensive milk to non-descendent offspring. Across mammals, plurally breeding females have lower direct fitness than singularly breeding (one individual dominates reproduction) females. This observation leads to the important question: 'Why do female mammals breed plurally?' This talk will summarize our decade-long effort to answer this question using the degu (*Octodon degus*), a short-lived, plurally breeding rodent endemic to Chile. Our initial work showed that the per capita direct fitness of females decreases with increasing female group size (potential for communal care). Genetic analyses revealed that groups lack strong kin structure, limiting the potential for indirect benefits that would offset direct fitness costs. Neuroendocrine analyses suggest that immediate direct fitness costs are not explained by trade-offs between current and future reproduction. Recent evidence supports the hypothesis that plural breeding with communal care improves reproductive success during the most ecologically challenging years, possibly by buffering offspring from developing poor stress responses. Current research aims to determine if sociality-direct fitness relationships are habitat-specific and how the experimental reduction of predation risk influences these relationships. Funding: NSF, CONICYT

209 Jennifer R. Mandel[1], David E. McCauley[2]
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Pervasive Mitochondrial Heteroplasmy in Natural Populations of Wild Carrot, *Daucus carota* spp. *carota* L.

Exceptions to the generally accepted rules that plant mitochondrial genomes are strictly maternally inherited and that within-individual variation in those genomes, i.e., heteroplasmy, should be minimal are becoming increasingly apparent. These findings raise questions about the potential significance of heteroplasmy for plant mitochondrial genome evolution. We previously found evidence for recombination amongst mitochondrial genes in wild carrot, *Daucus carota* ssp. *carota*, indirectly pointing to the existence of heteroplasmy in this species. In order to assay directly for heteroplasmy in wild carrot, we designed a novel quantitative PCR assay that can detect and quantify intra-individual SNP variation in two mitochondrial genes (*Cox1* and *Atp9*). We found heteroplasmy in > 60% of all wild carrot populations surveyed and in > 30% of the 140 individuals that were genotyped. Heteroplasmy ranged from a very small proportion of the total genotype (e.g., 0.995:0.005) to near even mixtures (e.g., 0.590:0.410) in some individuals. These results have important consequences for the role of intra-genomic recombination in the generation of plant mitochondrial genome genotypic novelty. The consequences of such recombination are evident in the results of this study through analysis of the degree of linkage disequilibrium (LD) between the SNP sites at the two genes studied.

210 Thomas M. Hart, Wade B. Worthen
Biology, Furman University, Greenville, SC

The Effect of Water Mite Parasitism on Fluctuating Asymmetry and Immune Response of Two Dragonfly Host Species, *Argia fumipennis* and *Pachydiplax longipennis*

Water mites (*Arrenurus* spp.) parasitize dragonflies when adult odonates emerge from their larval exuvia. Parasite load can reach 400 mites/dragonfly and can reduce dragonfly survivorship. Some dragonfly species respond immunologically by melanotic encapsulation. They clog the mite's stylet, and the starved deflated mite remains attached. We sampled dragonflies and found significant differences in the frequency of mite parasitism across dragonfly species. In addition, only one species (*Argia fumipennis*) had deflated mites, showing evidence of melanotic encapsulation. We measured right and left forewing lengths of *A. fumipennis* and *Pachydiplax longipennis*, and compared the fluctuating asymmetry of wing length between parasitized and unparasitized individuals. There was no significant difference in asymmetry between parasitized and unparasitized individuals for either species. However, wing asymmetry in *A. fumipennis* was positively correlated with the number of inflated mites (one-tailed Spearman rank correlation, N = 55, r = 0.238, p = 0.040). We also evaluated differences in melanotic encapsulation between species. We inserted a 2.0 mm piece of sterile monofilament fishing line into the thorax of *A. fumipennis* and *P. longipennis* individuals for 24 hours, and compared mean greyscale scores of inserted and emergent ends using image-J software. There was no difference between these species in response to this methodology, even though *A. fumipennis* encapsulates mites in nature while *P. longipennis* does not. High rates of parasitism may exert a subtle effect symmetry, but the effects are typically weak; probably because parasite loads are usually low (median = 2) and occur late in development.

211 Joseph M. Taylor[1], Lawrence E. Hurd[1], Pieter A. P. deHart[2], Meredith C. Campbell[1]
[1] Biology, Washington and Lee University, Lexington, VA; [2] Biology, Virginia Military Institute, Lexington

Stable-Isotope Analysis Reveals Trophic Differentiation of Lycosids Feeding in Fields and Forests

As generalist predators, spiders have been shown to have substantial impact on arthropod communities. As one of the most abundant and pervasive predators in temperate terrestrial ecosystems, they are found in many different habitats, with flora ranging from purely herbaceous (e.g., old field) to almost entirely woody (e.g., late succession forest). As ground-level foragers, cursorial spiders encounter wide arrays of herbaceous arthropods supported by this varying vegetation. Given this, the trophic impact these predators can have could be highly variable between individual spiders, even within identical taxonomic families. To identify the degree to which the trophic level of these generalist predators may vary between herbaceous and woody habitats, we examined the stable isotope ratios of carbon (Δ13C) and nitrogen (Δ15N) in cursorial wolf spiders (*Lycosidae*) captured in forested lots to those caught in field lots. Our results indicate wide variation between the two habitats: average Δ15N values of lycosids found in fields (Δ15N = 7.69) were significantly higher than those found in forests Δ15N = 4.72), and this difference equates isotopically to an entire trophic level. This large difference observed may be due to variation in ground-level flora between the two habitats, which is then trophically enriched into herbaceous arthropods. Alternatively, given the large levels of depletion in 15N observed in lycosids from forest habitats, we propose that instead of feeding on herbivores as expected, these spiders are more reliant on detritivorous arthropods. Future work on these habitats should therefore examine the isotopic signatures of detritivores between these two habitats.

212 Christopher J. Paradise
Biology and Environmental Studies, Davidson College, NC

Effect of Sticky Tree Bands on Accumulation of Non-Target Arthropods and Reduction of Defoliation from Cankerworms (*Alsophila pometaria*)

I monitored the accumulation of non-target insects and spiders on tree bands used for cankerworm control for a 4-week period in the autumn of 2013 prior to the beginning of cankerworm emergence. In addition, I estimated the effect tree banding has on reducing defoliation in comparison to non-banded trees over a 3-year period. Banding is known to capture high numbers of certain forest pests such as fall cankerworms (*Alsophila pometaria* (Harris)), although conclusive evidence that it results in a pronounced reduction in defoliation is lacking. I found that non-target arthro- pods and leaves accumulated at a steady rate over the course of the study prior to emergence of cankerworm adults. Many predatory arthropods, including spiders, assassin bugs, praying mantids, lacewing larvae, and ladybird beetles were observed entangled and walking free on bands outside the Tanglefoot-covered area. Both unbanded and banded trees can suffer high densities of cankerworm larvae and high rates of defoliation the following spring, although the effect of banding on reducing defoliation is small and non-significant in some years. Tree bands were often installed improperly. Early installation of tree bands prior to cankerworm adult emergence has negative consequences for the rest of the arthropod community, and proper installation, with no gaps and regular maintenance will be most effective in reducing larval populations and defoliation.

213 Andrew Bennett, Miranda Bowman, Matthew S Lehnert
Biological Sciences, Kent State University at Stark, North Canton, OH

Flies and Butterflies Use Capillarity for Fluid Uptake from Porous Surfaces: Evidence Supporting the Limiting-Pore Size Hypothesis

Butterflies and moths (Lepidoptera) and flies (Diptera) have independently evolved mouthparts modified for fluid uptake. Both groups face the common selective pressure of acquiring fluids from pores in porous substrates (e.g., rotting fruit, films of floral nectar) that cannot be acquired via suction alone due to the innate capillary pressure within the small pores; therefore, we hypothesized that capillarity is initially employed for fluid uptake when feeding from porous surfaces. Capillarity could bring liquids into the food canal to form stable liquid bridges for the sucking pump to act on for fluid uptake. To test the importance of capillarity, we employed the limiting-pore size hypothesis, which assumes that stable liquid bridges can form as long as the radius of pore sizes = the radius of the food canal. We fed four butterfly species and two fly species a mixture of a 20% sucrose solution with fluorescent, magnetic nanoparticles (MNP) from filter papers with specified pore sizes (11 to 60 m). Insects were dissected, and a magnet was subsequently waved by the dissected crop on a fluorescent microscope to visualize movement of the MNP. As predicted, our results indicated a trend where butterflies with food canals of smaller radii fed from pores of smaller sizes. Flies, however, successfully fed from all pore sizes, probably due to a multi-channel hierarchy system whereby fluids are first transported from pores into the small pseudotracheal channels.

214 Valerie R. Kramer[1], Catherine P. Mulvane[1], Aubrey Brothers[1], Patrick D. Gerard[2], Matthew S. Lehnert[1]
[1] Biological Sciences, Kent State University at Stark, North Canton, OH; [2] Mathematical Sciences, Clemson University, SC

Studies of Allometry among Structures of the Lepidopteran Proboscis in Relation to Fluid Uptake Abilities

Most butterflies and moths (Lepidoptera) feed on fluids using a proboscis, which is a conduit composed of two elongated maxillary galeae and cuticular structures of different shapes and wettability. Although the proboscis and its components act as a functional unit for fluid uptake, the structures that comprise the proboscis each play a particular role(s) in the fluid uptake process, such as capillary pull of liquids from films. The purpose of our study was to determine how the structural configurations of proboscises of Painted lady butterflies (*Vanessa cardui*) might be affected among individuals of different body weights, proboscis lengths, and fluid uptake rates. We hypothesized that differences in structural configurations might impact fluid uptake abilities. To test this hypothesis, we fed larvae different treatments of artificial diet of varying water concentrations to induce size differences in the adults. We measured six proboscis characters and used the allometric growth equation with log- transformed data and linear regression analysis to determine patterns of allometry. In general, there was positive allometry among measured characters when fluid uptake rate was used as the independent variable; however, negative allometry was observed when proboscis length and butterfly weight were the independent variables. Our study, therefore, indicates that fluid uptake rates are influenced by the proboscis architecture.

215 Ashley L. Lash, Matthew S. Lehnert
Biological Sciences, Kent State University at Stark, North Canton, OH

Feeding Abilities of Butterflies with Split Mouthparts

Butterflies and moths (Lepidoptera) represent the most diverse group of fluid-feeding insects with 160,000+ species. Most Lepidoptera use specialized mouthparts (proboscis) that consist of two C-shaped maxillary galeae that join to form a food canal, which acts as a conduit for channeling and transporting fluids from pools and wetted surfaces to the gut. The functionality of proboscises is commonly described with the drinking-straw model, relying on the sucking pump located in the butterfly's head to induce fluid rise. Recent studies, however, have provided evidence that the proboscis also incorporates capillarity and wettability dynamics for fluid rise. The purpose of this study was to determine if action of the sucking pump is necessary for fluid rise and subsequent feeding. We used four feeding treatments and the Painted lady butterfly (*Vanessa cardui*) to test the hypothesis that fluid rise is independent of the sucking pump. Butterflies in each treatment had the proboscis split for different lengths and the distal 20% of the proboscis was submerged in a pool of 20% sucrose solution with green food coloring. After feeding, the butterflies were dissected to confirm if fluid had traveled along the split proboscis to the gut. Our results indicated that butterflies with split proboscises retained the ability to feed; however, the amount of fluid that entered the gut decreased with increasing proboscis separation. Our results suggest that butterflies with split proboscises in the wild could retain feeding abilities

216 Danielle D'Amato, John Enz
Biology & Marine Science, Jacksonville University, FL

A Survey of Dragonflies and Damselflies (Order *Odonata*) in the Timucuan Ecological Historic Preserve of Northeast Florida with an Analysis of Mercury Levels in the Preserve Using Dragonfly Larvae as Indicators

Dragonflies and Damselflies (Order Odonata) are good indicators of water quality since they can live in the aquatic larval stage for up to 5 years. In addition, they are organisms that can be seen and appreciated by citizens with ease when visiting National Parks. The purpose of this study was to conduct a Park wide survey of Odonata within the Timucuan Ecological & Historic Preserve (a National Park) in Northeast Florida. Five areas across Timucuan were surveyed for both adult and larvae Odonata throughout the summer of 2014. Adults were captured using aerial nets while larvae were sampled using d-nets. In addition, larvae were collected for mercury analysis in order to generate a baseline mercury level for the Park. The results of the survey, including 11 new Park records, will be discussed along with the mercury analysis results. Finally, an educational pamphlet on the Odonata of the Timucuan Preserve that was produced during this study will be shared.

217 Peter A. Van Zandt, Caleb Bonds, Andrew NeSmith, Brandon Perry, William Pitts, H. Wayne Shew
Biology, Birmingham-Southern College, Birmingham, AL

Night Movers: An Investigation of Moth Species for the Presence of Pollen as a Measure of Their Potential Role in Pollination

The natural history of pollination has been studied for centuries, and the mutually beneficial relationship between diurnal insect pollinators and flowering plants is well documented. However, the role of nocturnal insect pollinators is not as well understood. There are notable cases of well- known moth pollination systems, such as yucca moths and many members of the sphinx moth family (Sphingidae), but given the enormous diversity of nocturnal Lepidoptera, the full extent of the involvement of moths in pollination is poorly known. In this study, we surveyed moths from six families to look for evidence of flower visitation as indicated by the presence of pollen grains on the head, mouthparts, or bodies of dried museum specimens. Each specimen had its mouth parts and proboscis swabbed with a cube of glycerin jelly containing basic fuchsin stain, and samples were examined at 400x magnification. All pollen grains were counted and identified to the lowest taxon possible. We looked for patterns in flower visitation based on moth taxonomy, body size, wingspan, and proboscis length. There was high variability among individuals within species, with many species ranging from 0 to 200 grains per specimen. The percentage of individuals per species with abundant pollen grains ranged from 0 - 80%, suggesting that some species are likely to be acting as pollinators, while many are not. Family and subfamily identity appeared to be the best predictors of pollen abundance, in accordance with patterns observed in the literature.

218 Matthew S. Lehnert[1], Charles E. Beard[2], Patrick D. Gerard[3], Konstantin G. Kornev[4], Peter H. Adler[2]
[1] Biological Sciences, Kent State University at Stark, North Canton, OH; [2] School of Agricultural, Forest, and Environmental Sciences, Clemson University, SC; [3] Mathematical Sciences, Clemson University, SC; [4] Materials Sciences and Engineering, Clemson University, SC

The Architecture of the Butterfly Proboscis in Relation to Feeding Habits

Butterflies use modified mouthparts (proboscis) to acquire a range of fluids from diverse substrates, including floral nectar, tree sap, rotting fruit juices, and carrion excrement. We studied 21 characters of the proboscis structural landscape among five butterfly species to test the hypothesis that proboscis structure relates to nectar and sap feeding habits. We used scanning electron microscopy to acquire proboscis dimensions and to study possible sexual dimorphisms, the shapes and sizes of proboscis linking structures (dorsal legulae), cuticular patterns, and sensilla. A hierarchical cluster analysis revealed that nectar feeders do not group well; however, proboscis architecture is relevant for phylogenetic classification. Although an overall sap- or nectar-feeding proboscis was not supported, individual characters that might relate to floral entry, such as the arrangement, distribution and sizes of chemosensilla, presence of a Zone 3 (i.e., a tip void of dorsal legulae), and extent of proboscis tapering are potentially good predictors for flower visiting butterflies.

Poster Abstracts

P1 Tasha J. Stryker, Jennifer S. Borgo, Kelley Godbout, Kristen Oliver
Coker College, Hartsville, SC

Coyote Diet at Carolina Sandhills National Wildlife Refuge: Implications for Deer Recruitment

Recent increases in coyote (*Canis latrans*) populations have caused concern regarding their potential to impact white-tailed deer (*Odocoileus virginianus)* recruitment. This study has evaluated coyote diet at Carolina Sandhills National Wildlife Refuge in McBee, South Carolina since May 2010. Coyote scat samples were collected from roadways and trails within the refuge. The scat was distinguished from the waste of other predators based on appearance and, if present, the tracks near the waste. The collected samples were labeled with the location and date of retrieval, and then brought back to Coker College and frozen until processing. Before dissection, the samples were dried at 65 C for approximately three days. We randomly selected one scat per month to ensure that each scat came from a different meal. Using dissecting microscopes and tools, food material was separated out based on characteristics into the following prey categories: mammal, reptile, insect, avian, plant, and other/unknown. Thus far, we have found evidence of heavy predation on mammals (highest average percent composition), followed by plant and arthropod remains. In addition, we will be conducting a finer scale of identification on mammalian remains, using jaw fragments and hair in the scat. The hair will be laundered and then identified under microscope using a diagnostic key of hair from southeastern mammals (including fawn and adult deer). The anticipated completion date for this research is March 2015. The results obtained during the study may lead to a greater understanding of coyote ecology in South Carolina.

P2 Robert Carter, Logan Miller, Chris Pellecchia
Biology, Jacksonville State University, AL

Breeding Bird Populations of a Highly Fragmented Urban Habitat in Oxford, AL

Point counts were conducted in a highly fragmented urban environment adjacent to Choccolocco Creek to determine breeding bird habitat use. The narrow riparian zone is dominated by a hardwood overstory and understory of Chinese privet and surrounded by urban development including an airport, interstate, and mall. The breeding birds were compared to an intact forested landscape adjacent to Shoal Creek on the Talladega National Forest (TNF). The urban environment avian species richness was 43 compared to 54 for the TNF. The total number of individuals was 339 on the TNF compared to 254 for the Choccolocco Creek area. Fragmented habitats had fewer species but included some species, such as killdeer, Eastern meadowlark, swallows, and Eastern phoebe, not found on the TNF. The open grassy and shrub habitats adjacent to the interstate and airport likely account for the presence of these species.

P3 Nicole Huie[1], R. Malia Fincher[1], Scot Duncan[2], Dreshun Buford[2], Kevin Willson[3], Hannah Gousse[4]
[1] Biological and Environmental Sciences, Samford University, Birmingham, AL; [2] Biology, Birmingham Southern College, AL; [3] University of Maryland, College Park; [4] University of Connecticut, Storrs

Temperature Facilitates Longleaf Pine Persistence in Fire-Suppressed Montane Habitats

Since the arrival of European settlers, and especially during the last century, the distribution of *Pinus palustris* longleaf pine) has been reduced by as much as 98% in the United States. Long term fire suppression has likely played a large role in the decline of this species, allowing fire-intolerant hardwood species to displace longleaf pines. In areas where longleaf pine has persisted, often in patchy stands, it has been suggested that other abiotic stressors may be suppressing competition from hardwoods. We examined the role of abiotic stressors, including soil depth, canopy cover, and temperature, on longleaf pine density in a remnant population of montane longleaf pine at Oak Mountain State Park, Alabama. We compared longleaf density and size in two habitats within the park, the southeast facing ridge of Double Oak Mountain, which we predicted would experience more stressful abiotic conditions, and the tops of foothills to the northwest of Double Oak Mountain, where we anticipated that conditions would be less stressful. Surveys were repeated in 2003 and 2014. Juvenile longleaf pine density was higher in the ridge than the in the foothills, and the abiotic variable that appears to be driving this pattern is average daily temperature in the summer. The plots which reached the highest temperatures had the highest juvenile longleaf pine densities. In fire-suppressed habitats, high temperatures may suppress competition by hardwood species, allowing longleaf pine to persist.

P4 Kaitlin A. Anstrom[1], Leigh Anne Harden[1], Malcolm A. Campbell[1], Gabrielle J. Graeter[2], Michael E. Dorcas[1]

[1] Biology, Davidson College, NC; [2] North Carolina Wildlife Resources Commission

Developing an Effective Edna Field Protocol for the Detection of Bog Turtles (*Glyptemys muhlenbergii*)

Environmental DNA (eDNA) is the DNA an organism leaves behind in the environment, in the form of mucus, feces, urine, shed skin, etc. The DNA can be collected in water or soil samples and analyzed through PCR and electrophoresis to determine the genus or species of origin. eDNA techniques have the potential to strengthen species distribution studies, particularly of secretive and cryptic species. Bog turtles (*Glyptemys muhlenbergii*) in North Carolina are state and federally listed as an Endangered Species. Current methods of locating bog turtles are time intensive, physically laborious, and yield low numbers because the turtles are extremely reclusive. Our main objective was to develop field and lab eDNA protocols to positively detect bog turtles from a tank containing bog turtles, which included testing sampling methods, filtration systems, two DNA extraction methods (commercial kit and a phenol-chloroform method (PCI)). We used nanodrop technology in addition to Polymerase Chain Reaction and electrophoresis to obtain results. We collected 11 water samples from a closed tank containing four bog turtles throughout July, 2014. Nanodropping indicated that both the commercial DNA extraction kit and the PCI method successfully extracted DNA from the water samples. However, all samples failed to amplify in PCR and no bands were seen from electrophoresis.

P5 Miranda L. Camp[1,2], Brandon O'Brien[1,3], Torey Bowser[1,4], Linda Amaral-Zettler[5,6], Erik Zettler[1], Amy Siuda[1]

[1] Sea Education Association, Woods Hole, MA; [2] Stetson University, DeLand, FL; [3] Cornell University, Ithaca, NY; [4] University of Maine, Orono; [5] Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, Woods Hole, MA; [6] Earth, Environmental, and Planetary Sciences, Brown University, Providence, RI

Caribbean Spiny Lobster (*Panulirus argus*) Dispersion Dynamics in the Sargasso Sea

Larval dispersion via ocean currents connects adult populations of Caribbean spiny lobster, *Panulirus argus*, throughout the Caribbean Sea. We assessed connectivity between populations in the Caribbean and Bermuda via the Sargasso Sea. Sequences of the hypervariable domain of the control region of the mitochondrial DNA (HV-CRd1) for 6 Bermudian adult samples were compared to two existing data sets of adult samples (Diniz et al., 2005; Naro-Maciel et al., 2011). There was no indication of an isolated Bermuda population, but rather a mixture of individuals from several different lineages and locations. Additionally, we carried out twice-daily net tows at both surface and subsurface depths to collect *P. argus* larvae along a transect of the western Sargasso Sea. A total of 132 phyllosoma were collected at 18 of 34 sampling stations, representing every developmental stage except stage III, though mature individuals were most prevalent. We compared HV-CRd1 of select larval individuals to existing genetic sequences from adult populations to pinpoint an origin, and calculated the amount of time an individual would need to reach their collection location based on ocean current speed and direction. In each case, our calculations suggested that larvae were experiencing longer travel times and distances than were possible according to existing larval development duration data. Though some individuals are likely lost, the combination of travel calculations, and the presence of individuals of multiple developmental stages in single tows support the delayed development theory (Phillips and McWilliams, 1986) for indirect transport through the Sargasso Sea.

P6 Emily C. Thyroff, Heather P. Griscom
Biology, James Madison University, Harrisonburg, VA

Experimental Field and Greenhouse Trials on American Ginseng, *Panax quinquefolius*: Implications for Restoration in Appalachia

Panax quinquefolius, American ginseng, is one of the most valuable non-timber forest products, NTFPs, by providing economic, cultural, and ecological ecosystem services in forests. Although ginseng has a broad distribution range, it is not abundant anywhere due to overharvesting and deer browse. This study included experimental field and greenhouse trials to determine optimal growing conditions given discrepancies regarding aspect and soil. Three soil series were tested and either aspect (in the field) or soil moisture (in the greenhouse), a component of aspect, were manipulated in a factorial design resulting in six treatments. We hypothesized that there would be significant differences in ginseng performance (germination, survival, height, and leaf area) due to soil, aspect (field), and soil moisture (greenhouse). We predicted that ginseng would grow best in loam soil that was limed and perform the poorest in sandy loam soils. We also predicted that ginseng would grow best on northern sites or high soil moisture and poorest on southern sites or low soil moisture. We found that soil type had a significant effect on height and leaf area in greenhouse and field trials (< 0.05). On average, field ginseng from the limed loam soil was 6 mm taller and 1250 mm2 larger in total leaf area than ginseng from sandy loam. Surprisingly, we found no effect of aspect or soil moisture on ginseng growth or survival. Having a better understanding of the ecology of ginseng, especially soil series, will help create a ginseng habitat model for national forests and private lands.

P7 Valentina Ochoa[1], Katie McDermott[1], Amanda Long[1]
[1] Biology, Florida Southern College, Lakeland; [2] Integrative Biology, University of South Florida

Why Do Non-Native Pipevine Host Plants Have Different Impacts on Two Native Butterfly Specialists?

Larvae of swallowtails in the genus *Battus* feed exclusively on plants of the genus *Aristolochia* (pipevines). The nephrotoxic and carcinogenic aristolochic acids of the

Aristolochia confer an effective chemical defense mechanism against predators. Although many species of *Aristolochia* are native to Florida, there are a considerable amount of non-native species in cultivation, some of which pose a threat to many plants and animals alike. Many people grow non-native Aristolochia species because of their showy flowers and quick growth as opposed to native species, which are also not widely available in the nursery trade. During the course of breeding two species of native Florida butterflies (*Battus philenor* and *Battus polydamas*), we observed that *B. polydamas* had a wide tolerance for different species of pipevine (native and non- native).Alternatively, *B. philenor* eggs deposited on non-native *Aristolochia* resulted in low larvae survivorship. These observations indicate a difference in plant tolerance between the two butterfly species. Our goal was to test the hypothesis that levels of aristolochic acid were higher in non-native *Aristolochia* species than native species. Preliminary studies gathered from various published papers support this hypothesis. Leaves of five species of *Aristolochia* (two Florida native species: *A serpenteria, A. tomentosa* and three non-native species: *A. littorallis, A. trilobata and A. fimbriata*) were subjected to a solid-phase extraction, followed by high-performance liquid chromatography to compare concentrations between species. Identifying the mechanisms underlying the differential tolerance of two *Aristolochia* specialist butterflies to non-native host plants will improve our understanding of their co-evolutionary dynamics and improve preservation strategies.

P8 Alexandria N. Albers[1], Joshua T. Ackerman[2], Frances Bonier[3], David W. Bradley[4], Russell D. Dawson[5], C. Alex Hartman[2], Robert W. Klaver[6], Michael P. Lombardo[7], Emma McIntyre[8], Jim W. Rivers[9], Dave Shutler[8], Mark T. Stanback[10], Carol M. Vleck[11], Lynn Siefferman[1]

[1] Biology, Appalachian State University, Boone, NC; [2] Western Ecological Research Center, U.S. Geological Survey, Dixon Field Station, Dixon, CA; [3] Biology, Queen's University, Kingston, ON; [4] Bird Studies Canada, Port Rowan, ON; [5] Ecosystem Science and Management, University of Northern British Columbia, Prince George; [6] Iowa Cooperative Fish and Wildlife Research Unit, U.S. Geological Survey, Iowa State University, Ames, IA; [7] Biology, Grand Valley State University, Allendale, MI; [8] Biology, Acadia University, Wolfville, NS; [9] Forest Ecosystems and Society, Oregon State University, Corvallis, OR; [10] Biology, Davidson College, NC; [11] Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, IA

Behavioral Response to a Novel Object Varies with Geographical Location in Tree Swallows

Tree swallows (*Tachycineta bicolor*) are currently undergoing a range expansion in southern North America. However, populations are declining in northeastern North America while remaining stable or increasing at other breeding sites. Thus, tree swallows provide a unique opportunity to study traits associated with range expansion. We quantified neophobic behavior in tree swallows across their breeding range: stable northern breeding sites (Michigan, British Columbia), western breeding sites (Oregon, California), declining northeastern breeding sites (Ontario, Nova Scotia), and newly colonized western and southern sites (Iowa, North Carolina). We measured neophobia by monitoring parental behavior before and after we placed a novel object (a rubber duck) on their nestbox. We measured latency time to 1) return to their territory and 2) enter the nestbox to feed nestlings both before and after placement of the novel object, as well as quantifying reproductive effort before object placement. Geographic location significantly predicted behavior and reproductive effort; birds at the front of the range expansion fed offspring more often, and had larger broods of heavier offspring at the same nestling age. Additionally, birds at the front of the range expansion were less neophobic (i.e. entered nest boxes more quickly) and were slower to return to their territories during neophobia trials. Our data suggest that birds at the front of the range expansion are less neophobic, but perhaps forage further from their nest box.

P9 Marietta D. Shattelroe, Jennifer Rhode Ward
Biology, University of North Carolina Asheville

Determining Genetic Variation among Western North Carolina Ginseng (*Panax quinquefolius* L.) Populations

American ginseng (*Panax quinquefolius*) is a medicinal herb that has been used for centuries in North America, and more recently in Asia. Ginsenosides, the biologically active compounds, are used to treat conditions such as diabetes and cancer. Market demand for wild-grown plants has reduced population sizes to dangerously low levels, resulting in *P. quinquefolius* being listed on Appendix II of CITES. Loss of individuals has been correlated with reduced genetic variation within and among populations in some regions, but this relationship has not been well characterized in western North Carolina. We used 7 microsatellite loci to analyze DNA from 7 western North Carolina populations under different harvesting pressures. Initial results showed that 1 of 4 of the populations had a high number of private alleles. Heterozygosity was also high among this population. AMOVA showed that 79% of detected variation was among individuals within populations, suggesting historic or recent gene flow. These data will be correlated with collection regime and ginsensoside quantity and quality to better inform management strategies of wild populations.

P10 E. Natasha Vanderhoff, Jennifer R. Brehm
Biology & Marine Science, Jacksonville University, FL

Avian Dispersal of Invasive Plants in the Southeastern United States

Invasive plants alter community dynamics including seed dispersal networks. The southeastern United States is home to numerous invasive trees and shrubs. Many of the invasive plants bear fruit that attracts avian dispersers, including *Lonicera maackii, Sapium sebiferum, Cinnamomum camphora, Schinus terebinthifolius,* and *Elaeagnus umbellate*. We examined the literature on seed dispersal of invasive species in the southeastern region to determine the scope of research that has been conducted and prioritize goals for future research.

P11 Jared A. Elmore, Clinton S. Major, Joel Borden
Biology, University of South Alabama, Mobile, AL

Avian Species Richness, Abundance, and Diversity of Langan Park, Botanical Gardens and Japanese Gardens in Mobile, Alabama

Birds are a large component of the terrestrial vertebrate ecosystem and are often used as bio-indicators of habitat quality. However, the factors that affect their community composition, such as vegetation type and cover, proximity to water, and level of urbanization, are very complex and often understudied. Understanding the interactions between these factors and birds are important for ornithology, ecology, and conservation. We performed a study in a city park in Mobile, Alabama focusing on determining the above stated relationships in a small area with diverse habitat types. We carried out a bird survey using the avian point count method to obtain avian occurrence data over a period of approximately two months in the fall of 2014. Birds occurring at points covering the different vegetation covers were recorded by both visual and auditory methods throughout the study. Site characteristics were recorded by both visual observations and GIS data. All data was compiled and mapped using ARCGIS to ease visual relationships. Avian abundance, richness, and diversity were calculated for order, family, and species for the site as a whole and for each point. Bird orders and families were compared with site characteristics such as vegetation type and proximity to water. The results suggest that both vegetation type and proximity to water play a major role in determining the avian community, which is well known but still somewhat misunderstood. This data can be used to improve conservation and management plans for the avifauna in this city park and other similar urban areas.

P12 Jennifer R. Brehm, E. Natasha Vanderhoff
Biology & Marine Science, Jacksonville University, FL

Do American Robins Have the Gut? The Role of Gut Passage on Seed Germination of Invasive Camphor

Birds play an important role in the dispersal of fruit. Seed passage through an avian frugivore's gut can play a vital role in the germination process; once ingested, seeds may undergo chemical and/or mechanical treatment within the gut that can influence germination. American Robins *Turdus migratorius* regularly consume camphor fruit *Cinnamomum camphora* during winter migration in Florida. We compared germination rates of camphor seeds that passed through an American Robin's gut to seeds in fruit that fell naturally to the ground.

P13 Kendall S. Cooper, Gaius Augustus, Joel R. McNeal
Ecology, Evolution, and Organismal Biology, Kennesaw State University, GA

Microsatellite Primer Design for Population Genetic Studies of *Cuscuta rostrata* (Beaked Dodder)

Cuscuta rostrata is a parasitic vine that occurs in the southern Appalachian Mountains from West Virginia south to extreme northeast Georgia. The populations in Georgia often contain few individuals, are widely scattered, and often have relatively low seed set compared to populations further north at higher elevations. Microsatellite markers are being mined from transcriptome data in order to assess genetic diversity within and among populations, and initial results of the primer design process will be presented. Patterns in genetic structure and diversity of *C. rostrata* may help explain why populations at the core of *C. rostrata's* range are thriving while populations in Georgia may be more susceptible to climate change.

P14 Aaron Schrey, Jennifer Zettler, Kyle Adams, Bridget Frederick, Amy Gutting, Nicholas Ingebretsen, Alexandria Ragsdale
Biology, Armstrong State University, Savannah, GA

Genetic Structure of Populations of Mealybugs on Epiphytic Orchids of South Florida

In 2012, the orchid mealybug *Pseudococcus microcirculus* was first collected from a single plant in North America's most diverse orchid region, the Big Cypress Basin (Collier County, FL). Though often associated with orchids grown in greenhouses, this insect had not been recorded from orchids *in situ*. Follow-up surveys showed that mealybugs were more widespread and were collected in both the Fakahatchee Strand State Preserve (sites B and F) and the Florida Panther National Wildlife Refuge (sites C and M). Mealybugs (n = 54) were collected from multiple orchid individuals and were screened by optimizing seven microsatellite loci. We estimated genetic diversity and differentiation among all sites. All loci were variable; expected heterozygosity ranged from 0.501 to 0.629. We detected genetic differentiation between C and M (FST = 0.019, P = 0.05) and M and B (FST = 0.026, P = 0.05). We detected significantly lower mean pairwise relatedness among individuals from B compared to all other locations, and site B had the lowest observed inbreeding coefficient. We found genetic diversity and mean pairwise relatedness were highly variable among plants with multiple individuals. However, plants form sites F and M tended to have higher mean pairwise relatedness compared to B and C. We plan to optimize 7 more microsatellite loci and screen variation from additional individuals and sites. We expect to detect additional genetic differentiation and to address individual-level genetic characteristics after screening the additional microsatellites.

P15 Haylee A. Trotter, Mycah Sewell, Lisa Kelly
Biology, University of North Carolina at Pembroke

Does Colony Social Form of Invasive Fire Ants (*Solenopsis invicta*) Affect Microhabitat Choice in Wetlands of North Carolina?

For fire ants (*Solenopsis invicta* Buren), colony social form is a major factor in terms of reproduction and possibly in the invasion ecology of this species. During summer 2014, fire ants were collected from one or two transects within five wetlands in southeastern North Carolina. We will examine the effects of colony social form on the choice of microhabitat and on the distribution of colonies relative to habitat edge. In an earlier study, we found both monogyne and polygyne fire ants in two other wetlands within the region. However, the monogyne social form (one egg- laying queen) appears to be more common than the polygyne form (multiple egg-laying queens) within the southeastern United States. Multiplex PCR will be performed on the ant samples to detect the Gp-9 gene, which is responsible for colony social form. Colony locations will be mapped using topographic software and GPS coordinates. We predict that monogyne colonies will be more common than polygyne colonies. We also predict that polygyne colonies will be more common near the edges of these habitats. Such outcomes may be related to differences in invasion strategies.

P16 Allison E. Griffin, Anthony D. Tata, II, Mary Sledge, John Lewis
Biology, Lipscomb University, Nashville, TN

Determining Genetic Structure of Feral Pig Populations in Tennessee Using Microsatellite Markers

Feral pigs (*Sus scrofa*) are an invasive species that cause agricultural damage, spread diseases, and decimate habitats, especially wetlands. Feral pigs are a problem in Tennessee given their broad distribution and rapid and prolific reproduction. They tend to aggregate around the Tennessee River, the Cumberland Plateau, and in the Appalachian region of east Tennessee. The distribution of feral pigs increased drastically in the past fifteen years due to natural range expansion and illegal translocations. The study's objective is to gain information about the genetic structure of Tennessee's current feral pig population through the use of microsatellite markers in order to determine the population structures created by the distribution increase. DNA extractions were performed on blood samples received from the Tennessee Wildlife Resources Agency (TWRA), and that DNA was amplified through Polymerase Chain Reactions (PCR) using fluorescently labeled markers from the U.S. Pig Genome Coordination Program. 96 samples were amplified using primers S0026 and S0005. Fragments were separated on the ABI 3730 capillary array sequencer, and analyzed with ABI's Genemapper software. Allele sizes were rounded to integers and bins determined using TANDEM. S0026 amplified 11 alleles from 73 to 97 bp, and S0005 amplified 10 alleles from 216 to 234 bp. Population clusters will be determined using STRUCTURE 2.3.4. Understanding population structure will help determine interbreeding patterns and illegal translocation, which will be useful to TWRA biologists, veterinary officials, and landowners determining the most appropriate population management methods to control the spread of disease, population growth, and agricultural and environmental damage.

P17 Sean G. Kellogg, Edward Lowry
Hampden-Sydney College, VA

Invasive Potential of the Invasive Plant Species *Centaurea stoebe* in Competition with the Native Species *Lespideza capitata*

Spotted knapweed, *Centaurea stoebe* ssp. *micranthos*, long recognized as a problem in western North America, is an invader of increasing concern in the east. Broadly different environmental conditions between the regions invite consideration of different invasive dynamics and potential contrasts with patterns in the west. Changing patterns of land-use in eastern regions make this a critical time in understanding how invasive plants opportunistically exploit habitat availability. One of the most common native species occurring at sites of invasion in the Mid-Atlantic is *Lespideza capitata*. Our goal was to examine the potential for knapweed to competitively displace the native through experiments in the greenhouse and census data from the field. Field observations were from the High Bridge Trail, a 50 kilometer greenway in Virginia developed from a recently decommissioned railway. Invaders and native plants were grown together to observe the effects of competition. Measurements were taken of root length, shoot length, longest leaf length and leaf count, in addition to dried mass of roots and shoots at the end of the experiment. *C. stoebe* was more than 2.5 times more likely to survive in competition with the native *Lespideza*. Competitively dominant knapweed plants were smaller in size and mass than those in pots where the bush clover survived. The greater size of *C. stoebe* with living bush clover may be attributable great nutrient availability, either incidental in the soil from the clover or from AMF. A better understanding of competitive interactions between invaders and natives is timely in this natural system.

P18 Erik W. Kellogg, Edward Lowry
Hampden-Sydney College, VA

How Well Does an Aggressive Invasive Plant Species, *Centaurea stoebe* (Asteraceae), Perform When Grown in Different Substrates

Centaurea stoebe ssp. *micranthos* is increasingly recognized as an aggressive invasive species in eastern North America as well as out west. The purpose of this experiment was to test and observe the growing patterns of Centaurea stoebe when placed in different substrates. C. stoebe is commonly found in dry sandy soils that have lower nutrient levels. Greenhouse experiments were set up to reflect the range growing conditions found in the field: three sold types of increasingly sandy composition were tested for early seedling establishment. Accessions were made from field sites of invasive plants which were transferred initially to growth chambers and to 3 treatments of increasingly sandy-soil pots in the greenhouse. Sandy soil plants had roots that were 63% larger than the medium sand treatment and 79% larger than the low sand. Conversely, above ground growth was lower in the sandy soil, possibly more constrained by nutrient availability. Sandy soil produced plants with 59% to 61% less above ground growth than the less sandy treatments. Statistical significance was high to very high for pairwise comparisons of the sandy soil to other treatments. Notably, mortality rates were lowest in the sandiest soil, below 3%. In the least sandy soil there was 18% mortality and in the medium treatment mortality was above 65. Great root growth is linked to more successful establishment, especially in dry soils, and is a likely characteristic associated with invasiveness.

P19 Lyle J. Hardee[1], William H. Dees[2], Lacie C. Petticrew[1], Caleb M. Ardizzone[2], Omar E. Christian[3], Ning Zhang4, Sandesh Thapa[4], Hannah G. Fogg[1], Janet R. Woolman[1]

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Establishing a Web Presence for the Louisiana Environmental Research Center at McNeese State University

The Louisiana Environmental Research Center (LERC) at McNeese State University, Lake Charles, Louisiana, was established to conduct research focused on environmental problems of importance to southwest Louisiana (SWLA) and the Gulf of Mexico region. The Center also provides information and data to agencies, researchers and industry on impacts of environmental events on the SWLA coastal region. The Center's mission is to conduct basic and applied research, accumulate and disseminate information, and create awareness through education on SWLA environmental issues and concepts with a primary emphasis on the Chenier Plain. To publicize information related to ongoing and completed research and environmental projects at LERC, a plan was formulated to develop, launch, and operate an Americans with Disabilities Act (ADA) accessible LERC website featuring LERC news, staff, media, projects and publications. Several projects and administrative and outreach activities are highlighted on the website, including: the Louisiana Native Plant Initiative, Phytoremediation Studies in Contaminated Soils using *Spartina alterniflora*, Effects of Native Plants and Plant Derivatives on Medically Important Arthropods, Biomedical Research in the Chenier Plain, Phytochemical Investigation of Native Louisiana *Hypericum* Species, Calcasieu River Dredging Project, and Investigations of Excessive Sedimentations in Calcasieu Ship Channel and Surrounding Watersheds (Hydrodynamics and Sediment Transport). These projects increase understanding about the natural resources of the Chenier Plain and contribute to the preservation and sustainability of Louisiana's coastal region.

P20 Gail M. Moruza, Gregory E. Mansour, Dean Cocking
Biology, James Madison University, Harrisonburg, VA

Background Mercury Presence in Air, Soil, Duff, and Macro-Invertebrate Compartments of "Uncontaminated" Forest Ecosystems Located in Rockingham County, VA

Forest ecosystems in the Shenandoah Valley of Virginia are not directly exposed to major sources of mercury (Hg) contamination. Therefore, Harrisonburg, located in Rockingham County in the Shenandoah Valley of Virginia, was assumed to be suitable as a low level control in comparison with sites in Waynesboro, VA (30 miles away) which were exposed to industrial mercury contamination in the 1900's. Subsequently, the presence of low level Hg from regional background sources has been demonstrated. This study examines various trophic levels and compartments within two late successional forests located in Rockingham County. A variety of invertebrates including, but not limited to, flies, beetles, hymenopterans, and spiders were digested in hot concentrated nitric and sulfuric acid and analyzed for total Hg concentrations using a Perkin Elmer Flow Injection Spectrophotometer dedicated to Hg analysis. Similar digestion procedures were used for soil, duff, and air-borne passive samplers to evaluate ambient Hg. The results demonstrated that Hg is present within the various compartments and patterns emerged. For example, samples of Japanese Beetles had relatively high concentrations of 31.4 mg/kg dry biomass of digested material, while soil samples contained only 0.03 mg/kg dry weight. It is thought that none of the concentrations attained at these sites are great enough to be considered a health hazard and no adverse effects on the biota were observed. Mercury is identified as merely associated with these organisms; this study does not confirm whether the association is superficial or internal.

P21 Jennifer Tyson[1], Alicia Reigel[1], Daniel Gleason[2], Scott Harrison[1]
[1] Biology, Georgia Southern University, Statesboro, Georgia; [2] Institute for Coastal Plain Science, Georgia Southern University, Statesboro

Relative Abundances of the Recently Introduced Barnacles, *Megabalanus coccopoma*, and an Unidentified Species of *Megabalanus*, in the Southeastern US

Megabalanus coccopoma is an abundant introduced species currently found along the southeastern U.S. coastline. Recently, among collected samples thought to be *M. coccopoma,* several individuals of an unidentified species of *Megabalanus* were found. To date we have been unable to identify the samples to species level due to unknown origin, morphological variation, and inconsistent taxonomic keys. Cytochrome Oxidase I (COI) sequences show >10% divergence between the unidentified species and *M. coccopoma*, providing an easy tool for distinguishing the two taxa. In this study we used a restriction enzyme digest of COI to estimate the relative abundance and distribution of the two *Megabalanus* species off the coast of Georgia and South Carolina. Specimens were sampled from 4 coastal and 4 offshore sites. To date, from the offshore sites 73% of the specimens collected were identified *M.coccopoma* and 27% were identified as the unidentified species. Therefore, the unidentified species is limited to offshore sites only where *M. coccopoma* occurs at both offshore and coastal sites.

P22 Caitlin M. Gallagher, Jennifer Newbrey
Biology, Columbus State University, GA

Determining the Level of Carotenoids in Herbivorous Grasshoppers as Food for Insectivorous Birds

Carotenoids are biologically active pigments that are synthesized by plants, fungi, bacteria and algae, and are important dietary requirements of animals. In birds, carotenoids help to reduce free radical damage to DNA and proteins, and are incorporated into sexual signals of many species. Herbivorous insects, like grasshoppers, are likely an important source of carotenoids for insectivorous birds; however, very little work has been done on the carotenoid content of insects. Therefore, we sampled herbivorous grasshoppers from different sites in Columbus, Georgia to identify and quantify their carotenoid pigments. We freeze-dried and crushed the grasshoppers, extracted the carotenoids using acetone, and identified the carotenoids using high-performance liquid chromatography. Four confirmed carotenoids, β-carotene, canthaxanthin, lutein, and zeaxanthin, and seven unidentified carotenoids, were found within the sampled grasshoppers. Total carotenoids and concentrations of β-carotene were significantly different across the four sampled grasshopper subfamilies, with grasshoppers of the subfamily Oedipodinae having the highest concentrations and grasshoppers of Tettigoniidae having the lowest. However, total carotenoid concentrations and the concentrations of β-carotene were not significantly different across genera within the subfamily Gomphocerinae. There was also no significant difference in grasshopper carotenoid concentrations between the sampling locations. This research was successful in providing new knowledge on grasshopper carotenoids, which had not previously been studied. Compared to studies of other invertebrates, the average total carotenoid concentrations found in grasshoppers were much higher, although grasshoppers had lower levels of lutein and zeaxanthin than other invertebrates.

P23 Calla L. Telzrow, Joshua W. Campbell
Biology, High Point University, NC

Arthropod Communities in Various Successional Forest Habitats

Logging schemes can result in numerous habitats that arthropods utilize. The type of logging (e.g. clear-cutting, select-harvesting, etc.) and state of succession can result in very different arthropod communities. Arthropods play an integral role in the ecological balance and utilize logged areas. This project examined the effects of various logging management schemes on insect abundance and diversity. Sweep net samples of arthropods were collected from loblolly pine forests in Mississippi. Five different forest treatments were studied: (1) 1-3 years since re-planting, (2) 3-5 years since re-planting, (3) 5-10 years since re-planting, (4) 1-5 years since thinning, and (5) >6 years since thinning. Collected arthropods were counted and classified to the lowest taxonomic level possible. Samples from the early successional forests had greater arthropod abundance and diversity than those collected from the late successional forests. Beneficial and pest species of arthropods can be affected by the type of logging and the age of the logged area, which can have a cascade of effects on vertebrate organisms that utilize them for food.

P24 Lauren E. Whitehurst[1], Holly R. Prendeville[2], Laura F. Galloway[2], Kevin Burgess[1]
[1] Biology, Columbus State University, GA; [2] Biology, University of Virginia, Charlottesville

Determining the Effects of Herbivory on an Herbaceous Plant, American Bellflower (*Campanulastrum americanum* L.)

Deer are overabundant and are dramatically affecting herbaceous plants through herbivory, possibly leading to selection for tolerance. Plants subjected to herbivory tend to suffer from reductions in fitness, such as delays in reproduction, which can negatively affect life history traits. We used the American Bellflower (*Campanulastrum americanum*) to investigate whether plants have evolved to tolerate deer herbivory through delays in reproduction and if this tolerance is greater in certain populations. In a common garden experiment, we evaluated whether the differences in phenology between populations result from a response to herbivory by using three clipping treatments 1) plants clipped at the same calendar date, 2) plants clipped at a similar phenological stage, and 3) controls (unclipped). Additional plants open to natural deer herbivory were also observed and the fitness components of these plants were compared to those kept from natural herbivory. The reproductive fitness of plants was compared among treatments using one-way ANOVA. Plants clipped at similar phenological stages showed a significant increase in biomass production indicating a strong response to herbivory compared to unclipped. Our data suggests that deer herbivory affects the performance of *C. americanum*.

P25 Annie Slayton, Lori Tolley-Jordan
Biology, Jacksonville State University, AL

The Impacts of a Small Dam Removal on the Distribution of Parasitized Snails (Pleuroceridae: Elimia) in Choccolocco Creek, Alabama

In general, parasitized snails are found in patchy distributions in freshwater systems due to, in part, the preferential use of particular habitat types by snails. Dams, even small ones, cause marked changes in water velocity, depth, substrate type which alters the distribution of available habitats to snails. In this study, we examined the effects of the removal of a small, rock dam (1 m high) on the distribution of parasitized snails in a 200m reach of Choccolocco Creek in the Talladega National Forest, Alabama. On 27 August

2014 (pre dam removal) and again on 15 November 2014 (2 months post dam removal), snails and habitat data were collected from a 100 m reach upstream and a 100 m reach downstream of the dam. Using a stratified random sampling design, snails were collected from 15 quadrats (0.09m2) in each 100 m reach for both sampling dates. In addition, velocity (m/s), depth (m), substrate type, and distance from edge were recorded for each quadrat. Results showed that although overall snail densities increased following dam removal, no differences in percent of snails infected were found. In addition, no significant differences in velocity or depth were found before and after dam removal but significantly smaller substrates were found before dam removal. No differences in the relationship of infected snails with substrate size, depth, velocity, or distance from edge were found due to dam removal. These results suggest that infected snails are not aggregated in the stream due to changing habitat conditions from dam removal.

P26 Luisa Santiesteban, Allison Armstrong, Jordan Hartman, Thomas Lee, Christy T. Carter
Biology, Wingate University, NC

Investigation of Soil Seed Banks from Two Habitat Types in a Freshwater Wetland

The soil seed bank representing two distinct areas of an inland wetland on the campus of Wingate University in Wingate, North Carolina, was investigated in order to determine whether differences in species composition occurred. Species presence was determined using a germination assay of the transient seed bank. Soil was collected in March 2014 before spring germination in a monotypic stand of *Typha latifolia* and in an open mudflat on the opposite side of the lake. Ten 0.25 m2 plots were randomly constructed along a 30-m transect in both sites, for a total of twenty plots. Four soil cores (28.3 cm2) were collected from the four corners of each plot. Soil was pooled within each plot and spread-out in plastic trays (21.8 cm × 21.8 cm). Trays were placed in the greenhouse, regularly watered, and randomized throughout the growing season. Overall, nine species and eight genera were found representing seven plant families. Seven species were found in both sites, but only five were shared. *Diodia virginiana* and *Cyperus polystachyos* were found only in the *Typha* site whereas *Hypericum mutilum* and *Reimarochloa oligostachya* were only found in the mudflat. Frequencies from the mudflat and *Typha* sites, respectively, included *Cyperus polystachyos* (0%, 10%), *Diodia virginiana* (0%, 50%), *Fimbristylis autumnalis* (40%, 10%), *Rotala ramosior* (20%, 60%), *Murdannia keisak* (20%, 10%), *Anagallis arvensis* (10%, 70%), *Hypericum mutilum* (10%, 0%), *Cyperus flavescens* (10%, 20%), and *Reimarochloa oligostachya* (10%, 10%). Follow-up soil sieving is being conducted to identify species that failed to germinate in the greenhouse.

P27 Mycah Sewell, Haylee A. Trotter, Lisa Kelly
Biology, University of North Carolina at Pembroke

Colony Social Forms of Invasive Fire Ants (*Solenopsis invicta*) in Wetlands of North Carolina

Solenopsis invicta Buren, the red imported fire ant, has two social forms that are key to the fire ant's reproductive biology and possibly to its invasive strategies. The social form of a colony is determined by one gene, Gp-9. A genotype of BB results in a monogyne colony that has only one egg-laying queen, while a Bb genotype results in a polygyne colony that has multiple egg-laying queens. To study the distribution of these social forms, living ants were collected in 2013 from two wetlands in southeastern North Carolina and then genotyped using multiplex PCR and agarose gel electrophoresis. Similarly, ants collected from five additional wetlands in 2014 will be genotyped. Monogyne and polygyne colonies were nearly equally represented in the wetlands sampled in 2013. We wish to compare the incidence of social forms across all wetlands sampled. These wetlands supported a wide range of vegetation types, from completely herbaceous to nearly closed canopy forest. This study could reveal different patterns of environmental selection for the two social forms. Factors that could be important include tree cover, flooding, and the availability of suitable microhabitats.

P28 Waydon T. Yates[1], Mickey Agha[1], Joshua R. Ennen[2], Jeffrey E. Lovich[3], Carl H. Ernst[4], Evelyn M. Ernst[4], Steven J. Price[1]

[1] Forestry, University of Kentucky, Lexington; [2] Tennessee Aquarium Conservation Institute, Chattanooga, TN; [3] Southwest Biological Science Center, US Geological Survey, Flagstaff, AZ; [4] Division of Amphibians and Reptiles, Smithsonian Institution, Washington, DC

Delayed Emergence Dynamics in Emydid Neonate Turtles of North America

Delayed timing of nest emergence has been reported in eight turtle families and occurs over a wide range of localities in North America. In this study, we examined the relationship between phylogeny, geographic location and climate to timing of emergence in hatchling turtles in the family Emydidae. We obtained data on nesting emergence from original summaries provided by Gibbons and Nelson (1978), Gibbons et al. (2013) and Lovich et al. (2014). Overall, we compiled exact nest emergence dates in 14 species, 22 localities and over four decades. Preliminary results indicate a positive relationship between environmental variables (precipitation and temperature) and geographic location to timing of nest emergence. After removing the effect of phylogeny, we found a significant negative correlation between body mass and average date of emergence in delayed emerging hatchling turtles, suggesting that the largest species exit the nest first. Because delayed emergence may be controlled by environmental cues, it is increasingly important to study these effects as they relate to current climate trends.

P29 Mickey Agha[1], Benjamin Augustine[2], Jeffrey E. Lovich[3], David Delaney[4], Barry Sinervo[5], Mason O. Murphy[6], Joshua R. Ennen[7], Jessica R. Briggs[8], Steven J. Price[1]

[1] Forestry, University of Kentucky, Lexington; [2] Fish and Wildlife Conservation, Virginia Tech, Blacksburg; [3] Southwest Biological Science Center, US Geological Survey, Flagstaff, AZ; [4] US Army Construction Engineering Laboratory, Champaign, IL; [5] Ecology and Evolutionary Biology, University of California Santa Cruz, Santa Cruz, CA; [6] Biology, University of Kentucky, Lexington; [7] Tennessee Aquarium Conservation Institute, Chattanooga, TN; [8] Warner College of Natural Resources, Colorado State University, Fort Collins, CO

Using Motion-Sensor Camera Technology to Infer Seasonal Activity and Thermal Niche of the Desert Tortoise (*Gopherus agassizii*)

Understanding the relationships between environmental variables and wildlife activity is an important part of effective management, especially for threatened species such as the desert tortoise (*Gopherus agassizii*). Because of current warming trends, ectotherms in desert environments may have increasingly restricted windows for activity. Therefore, we studied the effects of temperature, sex, and day of year on the activity of a population of threatened desert tortoises at a large-scale wind energy facility wind energy generation facility during one activity season. In summer 2013, we deployed 48 motion sensor cameras at the entrances of tortoise burrows to investigate activity (entry, exit) in desert tortoises. Using generalized estimating equations, we found that the relative probability of activity was associated with temperature (linear and quadratic), sex, and day of the year. In addition, we found significant support for interactions between sex and day of the year, and sex and temperature in predicting the probability of activity. Sex effects showed that male tortoises are generally more active than female tortoises. Lastly, temperature had a quadratic effect, indicating that tortoise activity was heightened at a range of temperatures. Using our models, we then made population- level estimates of air temperatures and times (days and hours) that were associated with maximum activity during the study. Because tortoise activity is constrained by environmental conditions, it is increasingly vital to continue to conduct studies on how tortoises vary their activity throughout the Sonoran Desert based on abiotic influences such as temperature.

P30 Mickey Agha[1], Jeffrey E. Lovich[2], Joshua R. Ennen[3], Benjamin Augustine[4], Terrence R. Arundel[5], Steven J. Price[1]

[1] Forestry, University of Kentucky, Lexington; [2] Southwest Biological Science Center, US Geological Survey, Flagstaff, AZ; [3] Tennessee Aquarium Conservation Institute, Chattanooga, TN; [4] Fish and Wildlife Conservation, Virginia Tech, Blacksburg; [5] Southwest Biological Science Center, US Geological Survey, Flagstaff, AZ

Exploring the Spatial Dynamics of Tortoise Burrow Placement in an Industrial Landscape

Technological advances, climate change and market regulatory changes are the catalyst for a promising future in utility-scale renewable energy. However, landscape modification caused by these industrial developments may cause adverse effects, especially for threatened wildlife; investigations designed to identify these human-wildlife interactions are important for strategic management. We examined patterns of burrow site selection by desert tortoises (*Gopherus agassizii*) as related to anthropogenic features in a large-scale wind energy facility in California, USA. Specifically, through extensive field surveys and radio-telemetry, we collected locations of active tortoise burrows between 1997-2001 and 2009- 2014 along with number and sex of turtles found in each burrow. Kernal density estimation of burrow locations across the landscape revealed a lower density of burrows in the area of both high road and turbine density. Using Ripley's K function, we demonstrated that burrows were more clustered than spatially random, which may reflect habitat selection by tortoises. Spatial patterns in mean number of tortoises found in each burrow per year (activity level index) indicated that the most active burrows were in areas of low road and turbine density. Thus, our research suggests that roads and turbines may influence burrow placement by threatened desert tortoises.

P31 Crispian F. Shelton, Christopher B. Manis, G. John Lugthart
Biology, Dalton State College, GA

Multi-Year Investigation of a Turtle Community in a Northwest Georgia Lake and Wetland Prior to Restoration

A three year study was conducted to determine the characteristics of the turtle community at Lakeshore Park in Dalton prior to a pending habitat restoration. Hoop traps were used to collect turtles from Threadmill Lake, a 2.5 acre subdivided lake, and an adjoining 1 acre wetland. Sampling occurred during three two-week sampling periods in June 2012, July 2013, and June 2014. A total of 471 turtles were captured representing four families and six species. *Trachemys scripta* was the most abundant Emydid observed (23%). Other Emydids, *Pseudemys concinna* (16%) and *Chrysemys picta* (6%), were less common. Kinosternidae, Chelydridae, and Trionychidae were represented by one species each: *Sternotherus odoratus* (42%), *Chelydra serpentina* (11%), and *Apalone spinifera* (2%), respectively. Sex ratios were calculated for *T. scripta* (1.0 : 1.8), *C. picta* (1.0 : 1.6), *P. concinna* (1.0 : 4.1), *S. odoratus* (1.5 : 1.0) and *C. serpentina* (1.0 : 2.1). Sexual size dimorphisms were noted in *S. odoratus* and *C. serpentina* with significantly larger male body measurements. Larger female body sizes were observed in all Emydid species.

P32 Scott M. Weir[1], David E. Scott[1], Christopher J. Salice[2], Stacey L. Lance[1]
[1] Savannah River Ecology Laboratory, University of Georgia, Aiken, SC; [2] Environmental Science and Studies, Towson University, MD

Understanding the Population-Level Consequences of Copper Toxicity and Climate Variability on Amphibians Inhabiting Contaminated Environments

A great deal of amphibian ecotoxicity data has been generated in the last 15 years, with excellent insights obtained from both laboratory and mesocosm studies. In wild populations, however, a single instance of exposure to lethal or sublethal levels will not necessarily translate into population-level declines. A powerful tool to investigate the population-level consequences of contaminant toxicity is to incorporate the toxicity data into population models. Here we present a stochastic matrix population model for frogs inhabiting a copper-contaminated environment. We parameterize the model with published demographic data available for the southern leopard frog (*Lithobates sphenocephalus*) and other anuran species when southern leopard frog data were not available. We used laboratory-generated toxicity data to inform adjustments to survival parameters for embryos and larvae in the model. We investigated a range of copper concentrations that correspond to laboratory data. We also incorporated catastrophic reproductive failure (CRF) which has previously been shown to be important for amphibian population persistence. Our results suggest that copper toxicity in the absence of CRF has little impact on population persistence. High probabilities of CRF resulted in extinction for all simulations, which has been reported previously and is quickly coming to consensus. However, an important interaction was found in which copper toxicity significantly raised the probability of quasi-extinction at low CRF probabilities. Future research efforts include modeling additional species (and associated copper toxicity) while also adopting a metapopulation approach to model a landscape of wetlands that vary in failure probabilities and copper contamination.

P33 Justin Seibert, P. Brent Nichols
Spokane Tribal Fisheries, Spokane, WA

Walleye Population Trends from 2002-2012 in Lake Roosevelt, WA

Walleye were introduced to Lake Roosevelt in the 1950's and have since become abundant. However, Walleye are an apex predator and have shown potentially negative effects on native fish. In order to evaluate population trends of Walleye, a random stratified sampling design was started in 2002. This is conducted yearly via gill nets (n = 150) during the first week of November. Length (g), weight (g), and sex was recorded and sagittal otoliths were removed from Walleye. From 2002-2012 Walleye showed increasing catch per unit effort. Length frequency histograms revealed that growth slowed down considerably once walleye reach ≈300 mm and very little Walleye grow past ≈400 mm. Age frequency histo- grams showed few fish greater than four years of age with a wide range of ages (0-19 years). Annually mortality ranged from 28% to 47% (mean = 39.3%). Walleye condition was poor during all years with an average relative weight of 82.5 (range = 79.4-85.5). Once Walleye grew past the aforementioned bottleneck they tended to exhibit a higher average Wr. During this period Walleye exploitation was considered to be low. There- fore, these population characteristics are indicative of an overabundant Walleye population and likely having negative effects on native fauna.

P34 Kristen Oliver[1], Jennifer S. Borgo[1], Jennifer McCarthey Tyrrell[2]
[1] Coker College, Hartsville, SC; [2] The Center for Birds of Prey, Awendaw, SC

Bacterial Growth Inhibition Ability of Uropygial Gland Secretions of Passerines Based on Foraging Behaviors

Birds must preen their feathers to ensure the precise placement and position of the barbules that make up each feather. While preening, the bird accesses the uropygial gland located at the base of the tail, which usually contains either wax (waterfowl) or oil components (passerines). There is evidence that constituents of the uropygial gland secretions prevent the growth of certain bacteria such as *Bacillus licheniformis*. We found that passerines in the inland areas of South Carolina might be better able to inhibit *B. licheniformis* than passerines found in coastal areas of South Carolina. In an effort to identify how and why birds in inland environments are able to inhibit this bacterium, this project looks at whether foraging techniques correspond to a bird's ability to inhibit *B. licheniformis*. Specifically we predict that ground foragers will have the highest ability to inhibit the bacterium, opportunistic foragers will have an intermediate ability to inhibit the bacterium, and arboreal foragers will have the lowest ability to inhibit the bacterium. Sampling has occurred since November 2014 in Darlington County, South Carolina. The target species will be captured via passive and target (using play black) mist netting. Lab techniques acquired through our previous study will be used to obtain bacterial inhibition rates for each sample. The project will be completed by March 2015. Samples collected so far range from an average growth inhibition of -219344% to >99%. In particular, 8 samples from North American Cardinals (*Cardinalis cardinalis*) showed high levels of inhibition of growth (80->99%).

P35 A. Lawrence Bryan[1], John R. Robinette[2]
[1] Savannah River Ecology Laboratory, Aiken, SC; [2] Savannah Coastal Refuges, USFWS, Savannah, GA

Activity Patterns of Nesting Male and Female Wood Storks During the Breeding Season

Behaviors of male and female Wood Stork (*Mycteria americana*) parents were documented at seven nests throughout a single breeding season in a colony on the Harris neck NWR (coastal GA) to examine potential gender-specific differences in parental activities. Specifically, for 1500+ nest- hours of observations, we comapred nest attendance, incubation rates, foraging and nest material trips/hour, and durations of foraging trips. We further examined these activities relative to stage of nesting: incubation, young nestling (0-28 days post-hatch), older nestling (28-50 days post- hatch) and flying young (>50 days post-hatch). Males attended the nest more frequently and made more nest material trips per hour than females during the incubation and young nestling stages. The higher attendance rate may result from the female needing time to recover energetically from egg-laying or reduced risk of conspecific aggression at the nest with the male in attendance. There were no gender-specific differences in incubation rate, feeding rates or foraging trip duration,

P36 Nathan R. Webb, Sydney Richards, Nicholas Spalsbury, Richard Phillips, James Welch, Jennifer L. Ison
Biology, Wittenberg University, Springfield, OH

Morphologic and Genetic Data from a Northern Mississippi Population of Cricket Frogs

Amphibian populations have been in decline in the United States for decades. Changes in population status of cryptic species may often go undetected, but their appropriate identification is essential for any rigor associated with documenting trends. Assessment of cricket frog populations has proven problematic due to taxonomic uncertainty and potential hybridization as well as the inability to reliably identify species morphologically. As a pilot study aimed at larger scale analyses, we scored 30 cricket frogs based on both morphologic and genetic markers from an area of sympatry in Northern Mississippi. Using five morphologic characters aimed at distinguishing *Acris crepitans* from *A. gryllus*, 30 individuals were assigned morphological scores. We then compared individual morphological scores with genetic scores calculated from four published neutral genetic markers with potential cross-species utility. To date, our data suggests a mismatch between assignment scores based on morphologic and genetic data. Individuals with all five morphological indicators of *A. gryllus* showed genetic marker patterns consistent with *A. crepitans*, while others shared genetic markers associated with both species. Our results may be explained by hybridization, greater than previously documented morphological variation in *A. crepitans*, or as an artifact of marker specificity. Currently, we are investigating call character displacement, habitat partitioning, and increased sampling areas to assess potential barriers or levels of hybridization.

P37 Amber M. Kincaid, James E. Russell
School of Science and Technology, Georgia Gwinnett College, Lawrenceville

Population Genetic Analysis of *Trichogramma kaykai* Using Molecular Markers

Population structure and genetic diversity are interrelated factors that play a significant role in the evolution and ecology of all species. We investigated the population genetics of *Trichogramma kaykai,* an endoparasitoid wasp that parasitizes eggs of the butterfly *Apodemia mormo* in the Mojave Desert. Trichogrammatid wasps are known to exhibit phoretic transportation. This poses the question of whether *T. kaykai* breeding is limited to local geographical areas or the larger host range. To answer this, *A. mormo* eggs were collected, *T. kaykai* were cultured and DNA extracted for population genetic analysis using the mitochondrial cytochrome oxidase subunit one (CO1) gene region. If *T. kaykai* breeding is limited to a local geographical area, then a subdivided population genetic structure is expected. Additionally, these endoparasitoid wasps may be host to the cytoplasmic bacterium *Wolbachia. Wolbachia*-infection within the *T. kaykai* population is known to be associated with feminization of males; asexual reproduction; and co-inheritance of mitochondria and infection. On a phylogenetic tree *Wolbachia*-infected individuals would be expected to occur within groups of related taxa, since mitotype and infection are vertically co-inherited. We hypothesized that the *T. kaykai* population structure is not subdivided. Additionally, we hypothesized that unique mitotypes will group by infection status. Phylogenetic analysis supported the first hypothesis, with a panmictic population characterized by mutations divided amongst diverse geographical locations. Unexpectedly, *Wolbachia*-infection did not strictly follow grouping by infection status. Multiple *Wolbachia*-associated mitochondria observed were descended from uninfected lineages. This is suggestive of *Wolbachia*-infection horizontal transfer, and the need for further study.

P38 Kathleen A. Carroll[1], Loren Hayes[1], Luis Ebensperger[2]
[1] Biological and Environmental Science, University of Tennessee at Chattanooga; [2] Departamento de Ecología, Pontificia Universidad Católica de Chile, Santiago

How Ecological Variables Influence Social Network Structure and Fitness in *Octodon degus*

Within a population, animal social structure can influence the types and extent of competitive and socio-sexual interactions with conspecifics. Thus, understanding social structure is critical to developing a comprehensive understanding of the evolution of sociality and cooperation. Ecological variation is an important driver of social interactions that influence social structure. Evidence suggests social interactions are beneficial to species that live in unpredictable environments where ecological conditions cause some years to be harsher than others. Across taxa, social network analyses are repeatable and comparable methods to examine how social structure relates to environmental variation. The objective our study was to determine if environmental conditions influence social network structure in the degu (*Octodon degus*), a semifossorial rodent endemic to Chile. To achieve this objective, we conducted social network analyses using live-capture data from multiple seasons and across 8 years. We are determining if sociality is increased in years with low food abundance, high animal density and high burrow density. We also examine if increased interactions among group members enhance the direct fitness of adults by examining the slopes of regressions of social network structure and direct fitness across years. Funding: NSF IRES, UTC PRSA

P39 Lauren K. Wood, Howard S. Neufeld, Scott T. Cory, Jessica N. Stevens
Biology, Appalachian State University, Boone, NC

Water Relations and Tracheid Anatomy of Fraser Fir (*Abies fraseri*) Christmas Trees Along an Elevation Gradient

Fraser firs (*Abies fraseri* (Pursh) Poir.) are an integral part of the southern Appalachian Mountains, both as an endemic species in high elevation (>1500 m) cloud forests and a staple in the regional agro-economy, where they are grown as Christmas trees. These Fraser firs are grown below their natural elevation range, where temperatures and subsequent evaporative demand are higher. We studied water potential (ψ), hydraulic conductance (Kh), and tracheid anatomy among genetically similar Fraser firs along an elevation gradient from 660 to 1320 m in western North Carolina and eastern Tennessee. Maximum stomatal conductance was lowest at the lower elevation site. Stomata also tend to close earlier in the day compared to those at the two higher elevation sites, where they remain largely open until late afternoon. Water potentials at all sites are highest in the morning but the lower elevation trees tend to have a significantly lower water potential midday early and late in the season. On one day in July, the highest elevation site had very low relative humidity and exhibited the most negative water potential. These results suggest that, at lower elevations, Fraser fir exhibit increased water stress and lower rates of gas exchange due to warmer temperatures. Studies of tracheid anatomy are being done to see if increased demand for water is accommodated by either increased tracheid diameters, or increased pit-pore densities. Our results suggest that further climate warming may make the growing of Christmas trees at the lowest elevations somewhat problematic, especially in drought years.

P40 Clay S. Crippen, Matt C. Estep, Gary L. Walker
Biology, Appalachian State University, Boone, NC

Comparison of Newly Developed Microsatellite Markers to Previous Allozyme Diversity Analysis in Select Southern Populations of *Thuja occidentalis*

Thuja occidentalis, more commonly known as northern white cedar, is a species native to the Great Lakes region of North America. It has a southern disjunct range, reaching down the Appalachians to parts of Eastern Tennessee that are believed to be remnants of a once continuous population at the last glacial maximum 20,000 YBP. This study seeks to compare a previous allozyme based study with newly developed microsatellite markers to assess the utility of these markers and to examine the genetic diversity from selected populations.

P41 Joshua Grier, John Counts, Heather M. Joesting
Biology, Armstrong State University, Savannah, GA

Investigating the Function of Leaf Inclination in the Sand Dune Herb *Hydrocotyle bonariensis*

Coastal sand dunes can be an inhospitable habitat for plants. In addition to unique abiotic factors (i.e., salt spray and periodic saltwater inundation), the sand dune environment is characterized by high incident sunlight, especially at midday, during the growing season. *Hydrocotyle bonariensis*, a large-leaf herb common to sand dunes, has been shown to increase leaf angle from horizontal during the growing season, thereby reducing midday leaf sunlight incidence. The aim of this study was to investigate the function of leaf inclination in *H. bonariensis* by comparing diurnal leaf sunlight exposure, leaf temperature, and photosynthetic efficiency between naturally inclined leaves (control) and experimental leaves restrained in a horizontal orientation monthly from June to August 2014. Results showed that experimental leaves received 5 - 7 times more incident sunlight on the top leaf surface than the bottom surface at midday, compared to 2 - 4 times more sunlight exposure on the top leaf surface in control leaves. This increased sunlight exposure on top surfaces in experimental leaves corresponded to significantly greater diurnal leaf temperatures compared to control leaves in each month measured. Furthermore, photosynthetic efficiency (measured as *Fv/Fm*) was significantly lower in experimental leaves during midday in August, suggesting that these leaves experienced higher light stress compared to control leaves. These results indicate that increased leaf inclination during the growing season in *H. bonariensis* functions to reduce negative effects associated with high sunlight absorption (i.e., increased leaf temperature and reduced photosynthesis), and therefore likely facilitates daily photosynthetic carbon gain in the sand dune habitat.

P42 Ridma Bandara[1], Jeffrey L. Walck[1], Siti N. Hidayati[1], Kayri Havens[2]
[1] Biology, Middle Tennessee State University, Murfreesboro; [2] Plant Biology and Conservation, Chicago Botanic Garden, Glencoe, IL

Temperature Ranges for Dormancy Loss and Germination Between Species Differing in Dispersal Strategies

Dormancy loss and germination have an optimum temperature and minimum and maximum thresholds (hereafter, tolerance range). This range may be influenced by dispersal strategy: species with gravity-dispersed seeds may be expected to be specialized to local climate conditions (narrower tolerance range) compared to species with wind-dispersed seeds. We selected two eastern North American genera contrasting in dispersal strategies: *Penstemon digitalis* (gravity) and *Asclepias syriaca* (wind). We hypothesized that the temperature range for cold stratification and germination would differ between these species. To examine tolerance ranges, seeds were stratified at 1, 5, and 9oC for 0 (fresh) and 12 weeks and then incubated at alternating temperatures of 15/6, 20/10, 25/15, and 30/15oC for 2 weeks. Seeds of *Asclepias* were collected from Missouri (38N), Illinois (41N), and Minnesota (44N); those of *Penstemon* from Missouri (38N) and Illinois (41N). Germination for fresh *Penstemon* seeds from both locations was low across the incubation range. In contrast, the incubation range at which high germination occurred for fresh *Asclepias* seeds varied: none from Missouri, 30/15C from Illinois, and 20/10-30/15oC from Minnesota. Stratification at 1C caused the most dormancy loss (compared to 5 and 9oC) across the broadest set of temperatures in *Penstemon* seeds from both locations. In contrast, 1, 5, and 9oC caused the most dormancy loss in *Asclepias* seeds regardless of location. Tolerance ranges for dormancy loss and germination differed among populations of *Penstemon* and *Asclepias*. Moreover,

the tolerance range of *Penstemon* (with limited dispersal) was narrower than that of *Asclepias* (with wide dispersal).

P43 Catherine J. Cole, William Hutchinson, Howard S. Neufeld
Biology, Appalachian State University, Boone, NC

An Unusual Succulent in the Appalachian Understory: Leaf Morphology and Light Capture in *Sedum ternatum*

Sedum ternatum, a prostrate succulent native to Appalachian deciduous forests, is exceptional in that it thrives in the moist forest understory, yet exhibits a leaf morphology more typical of species in dry, high-light environments, including many others in the *Sedum* genus. The thick leaves of *S. ternatum,* with their small surface area and large, succulent cells, would seem ill adapted to efficient light harvesting in low light, in contrast with the broader, thinner leaves generally associated with shade plants. However, because its leaves persist throughout the winter, we hypothesize that *S. ternatum* functions as a sun plant in early spring before canopy emergence, and in autumn after canopy senescence, accomplishing much of its carbon gain during seasons of high light on the forest floor. We are currently measuring photosynthesis in the field over the course of an annual cycle, and conducting chemical analyses of leaf pigments. This poster will present data gathered to date, as well as the results of a greenhouse experiment demonstrating the striking plasticity of *S. ternatum* when grown for five months in different light levels. Compared to plants grown under a 90% shade cloth, plants grown in ambient greenhouse light exhibited significantly thicker leaves, more densely packed rosettes, shorter stems, and lower chlorophyll levels. This morphological contrast suggests an underlying genetic versatility allowing *S. ternatum* to effectively adapt to the wide range of light conditions characterizing the temperate forest understory throughout the year.

P44 Canceled.

P45 Melissa Green[1], Demetrius Geiger[1], Paige Henley[1], C. Neal McReynolds[2], Eric A. Albrecht[1], Thomas McElroy[1]
[1] Kennesaw State University; [2] Texas A&M International University

Molecular Analysis of Gut Content in the Striped Bark Scorpion *Centruroides vittatus*

The Striped Bark Scorpion, *Centruroides vittatus*, is distributed through the southwestern United States, and they are abundant in south Texas. *C. vittatus* is primarily nocturnal and can be found in vegetation, logs, and other cool and damp areas. They forage mostly for insects, such as crickets, centipedes, spiders, many other smaller insects. Cannibalism also occurs; typically larger scorpions will eat smaller scorpions. Once prey is captured, the scorpion uses its pinchers to clasp and compress the prey. The telson may be used to sting the prey and inject venom. The prey is drawn towards the scorpion's mouth and ingested. Venom composition can vary among individuals. Previous results from venom toxicity testing suggest that adult venom may be 1.8 fold more potent than juvenile venom. Thus some variation in venom composition may be explained by ontogenetic differences; however, understanding the effects of diet on venom composition for scorpions in the wild will require the ability to reliably detect what the scorpion has eaten. The objectives of this experiment were to determine if cricket DNA could be reliably recovered from the gut contents of scorpions, and to estimate gut retention time. Preliminary results indicate that we were able to recover cricket DNA from the gut content of scorpions for up 4 days after feeding. We will report our latest findings on DNA recovery and gut retention times. These data will help us refine our procedures so that our research can investigate the diet of scorpions in their natural environment.

P46 Katie Nelson, John Kilmer, Travis D. Marsico
Biological Sciences, Arkansas State University, Joneboro

Methyl Jasmonate Applied to Host Plants Reduces Invasive Herbivore Growth

It is increasingly understood that limitations in host plant defenses have a role in invasive insect herbivore establishment and spread. *Opuntia humifusa* has coevolved defenses such as increased mucilage production and programmed cell death to limit damage from the native cactus boring moth, *Melitara prodenialis*. The South American cactus moth, *Cactoblastis cactorum*, has a nearly identical larval stage as the native moth. Without a shared evolutionary history, however, the plants are virtually defenseless against *C. cactorum* herbivory. Recent research has shown that non-defending hosts can be signaled to defend against *C. cactorum* from neighboring defending plants. Our experiment was to examine the role of the jasmonic acid pathway in the induced defense response to the invasive *C. cactorum*. Using freshly hatched *C. cactorum* larvae, we exposed separate groups of *Opuntia humifusa* clones to different concentrations of methyl jasmonate, a volatile organic compound associated with defense pathways against chewing herbivores. After 23 days of feeding, the larvae were extracted from the plant and weighed. An ANOVA of larval weights indicated that larvae were significantly smaller when plants were exposed to 2.5 mM methyl jasmonate spray when compared to the control (R2 = 0.21; p*Opuntia* host plants leads to increased defense, causing reduced growth of *C. cactorum* larvae.

P47 Maddison S. Couch, Walter H. Smith
Natural Sciences, The University of Virginia's College at Wise

Potential Environmental Causes for Central Appalachias Thyroid Disorder Hotspot

A growing body of literature is suggesting that ecological impacts from historical land disturbance in coal-bearing portions of Appalachia have far- reaching effects on human health and physiology. Of particular interest are impacts on the physiology of the thyroid, since coal-bearing portions of Appalachia overlap with known hotspots of thyroid disorders, particularly the elevated incidence of goiters. We performed a multidimensional study to determine if and how environmental disturbance legacies may extend to impacts on human thyroid function in the Appalachian region. The first dimension of the study used phenolic assays to test first-order tributary streams and private wells for the presence of phenolic compounds in coal-bearing versus non-coal-bearing regions. Coal-derived phenols have been previously identified as triggering goitrogenesis *in vitro* by interfering with typical thyroid function and have been hypothesized as a potential cause of high goiter incidence in central Appalachia. The second dimension of the study involved a demographic survey of thyroid patients' health history and primary source of drinking water. Phenols were present in significantly higher amounts in coal-bearing, previously-mined tributary streams and in some private well water samples than in streams outside of the coalfields. Our demographic survey results reinforced these findings, concluding that residents who rely primarily on private, untreated water sources are at a higher risk of developing a thyroid disorder in central Appalachia than those who rely on treated, municipal water supplies. Our results identify a potential route of goitrogen exposure that may partially explain the source of this enigmatic thyroid disorder hotspot.

P48 Robert Carter[1], Thomas Warren[2]
[1] Biology, Jacksonville State University, AL; [2] Snead State Community College, Boaz, AL

Landscape Scale Plant Communities in Oak Mountain State Park, Alabama

Oak Mountain State Park near Birmingham, AL supports fire suppressed longleaf pine (*Pinus palustris*) communities on ridges and steep slopes. The understory of these sites lacks the species richness found in other mountain longleaf communities likely due to fire suppression. Even in a fire suppressed state, the sites do have species common in other mountain longleaf communities. Common species include *Dichanthelium* spp., *Chasmanthium sessiliflorum*, *Elephantopus tomentosus*, *Tephrosia virginiana*, *Pityopsis graminifolia*, *Vaccinium pallidum*, *Euphorbia corollata*, and *Piptochaetium avenaceum*. Absent are species common in Coastal Plain and most mountain longleaf communities such as *Solidago odora* and *Sorghastrum nutans*. Some of the sites support populations of the endangered Boynton's sand post oak (*Quercus boyntonii*). The results of this research should provide baseline data for the management of mountain longleaf pine communities at Oak Mountain.

P49 Angela Langevin E., Michael Madritch, Gary L. Walker
Biology, Appalachian State University, Boone, NC

Quantifying the Impact of Avian Guano as a Nutrient Input to Cliff - Face Ecosystems in Western North Carolina

Terrestrial cliff-face ecosystems are unique habitats that harbor diverse floral communities and an array of animal species. However, vital processes like nutrient cycling in cliff-face ecosystems remain poorly investigated. Cliff-face floral communities receive some of their required nitrogen (N) through atmospheric deposition, but few other nutrient-linkages have yet been explored. Seabirds are a well-established vector of nitrogen subsides between marine ecosystems and coastal cliffs. This study documents a similar nutrient transfer between highly productive forest ecosystems and nutrient-poor terrestrial cliffs. Common ravens (*Corvus corax*) and Peregrine falcons (*Falco peregrinus*) are vagile forest- dwelling raptor species that frequently nest on cliffs in the Southern Appalachians. Like seabirds, they excreted N-rich guano at cliff nest sites subsequently increasing nitrate (NO3 -) and ammonium (NH4 +) availability below nesting sites. We compared levels of available NO3 - and NH4 + on the cliff surface between paired vertical transects with and without nesting or roosting activity. To measure the community effects of a potential N subsidy, we compared vascular plant, bryophyte and lichen diversity between the paired transects. NO3 - and NH4 + levels were higher on transects with raptor nests or roosts than on the control transects (*ppXanthoria candelaria* (L.) Th. Fr., *Physcia caesia* (Hoffm.) Furnr., and *Caloplaca citrina* (Hoffm.) Th. Fr., that are commonly found below avian perches were identified on nest transects. *Xanthoria* and *Physcia* speciesare eutrophic lichens, and are often indicators of high N levels in ecosystems. Eutroph presence, community shifts and elevated N levels below nests are evidence that raptor guano provides a significant nutrient input to cliff faces. Our study is among the first to explore terrestrial raptor species as a vector of N subsidies to cliff-face ecosystems.

P50 Olivia F. Vito, Ben T. Pisano, Megan E. Budnik, Anna E. Nordseth, Heather P. Griscom
Biology, James Madison University, Harrisonburg, VA

The Effect of Slope Position and Gap Size on Chestnut Hybrid Performance Relative to Tulip Poplar and Chestnut Oak: Implications for Reintroduction

Optimal growing sites within the forest environment must be identified for successful reintroduction of American Chestnut hybrids. Understory light levels, slope position, aspect, soil type and competition may all affect chestnut performance with some factors having a more pronounced effect. We focused on how understory light levels and slope position affect growth and survival of tree seedlings. The experimental study was conducted in an oak-hickory secondary forest in the Ridge and Valley province of Virginia. In 2008, pure and hybrid chestnuts, tulip polar, and chestnut oak seedlings were planted in two gap sizes, 200 m2 (30-45% of full sunlight) and 800 m2 (60-75% of full sunlight) and on two slope positions (upper slope and mid-slope) for a 2 x 2 factorial design. Percent ground cover of *Rubus* spp. was estimated for each plot to see if there was an effect on growth. Height (cm) and diameter (mm) were recorded at the end of every growing season to quantify relative growth rate and seedling survival. After six years, treatment (a combination of gap size and slope position) had a significant effect on diameter (p=0.008) and survival (p0.05). Chestnut establishment was most successful in small gaps on upper slopes because of lower rodent predation (by girdling) and less competition or crushing from *Rubus* spp. Tulip poplar had significantly greater growth than chestnut in all treatment types; however, chestnut was most competitive in small, xeric plots. Therefore, the recommended locations for chestnut reintroduction within oak-hickory forests in Virginia are small gaps on upper slopes due to a combination of greater ability to compete with tulip poplar and less rodent predation.

P51 David Jacobs, Jim Graves
Masters Science in Environmental Science, Green Mountain College, Poultney, VT

Climate Change Vulnerability Assessment of the Ecological Systems of the Tennessee River Gorge

Climate patterns are currently affecting our natural resources by creating landscape level trends that are altering our forests and landscapes. These changes are presenting new and varying challenges for natural resource managers to grasp and understand as they attempt to make informed science based management decisions. Using a coarse filtered approach, the Tennessee River Gorge Trust is conducting a Climate Change Vulnerability Assessment on the Ecological Systems of the Tennessee River Gorge. We will use satellite imagery to identify the Ecological Systems. We will ground truth the result by conducting random plot surveys. We will then apply the data gleaned from our sources into climate models and create a dynamic working depiction of potential trends. The selected Ecological Systems as the benchmark for these trends due to the readily available data already in existence, and the ability to later link periphery species, both common and threatened, to these systems. At the conclusion of this assessment, land managers of the Tennessee River Gorge will have a better understanding of the potential trends associated with climate patterns and use that information to inform future decisions related to stewardship and land acquisition. Climate modeling is a field that is certainly growing and the projections will be treated as projections, not absolutes in the decision making process. The model and application of data will be subsequently monitored over time to ensure the best application is being applied to truly understand the ecological impacts on management decisions and the landscape itself.

P52 Daniel T. Talley, Gregory P. Lewis, Cook F. English
Biology, Furman University, Greenville, SC

Relationships Between Water Quality, Rural Land Covers, and Watershed Topography in the South Carolina Piedmont

Agricultural land cover can influence water quality of streams and rivers. Previous studies have demonstrated that nutrient and sediment runoff from row crops can degrade stream water quality. However, fewer studies have examined influence of pastureland on stream water quality. We examined the effects of pasture, row crop, and forest land covers on water quality in streams draining 42 rural watersheds (3-34 km2 in area) in the South Carolina piedmont under baseflow conditions. We placed watersheds into three land cover categories: mostly (>90%) forested, mixed forest/pasture, and mixed forest/pasture/row crop. Across watersheds, concentrations of most solutes correlated negatively with sample site elevation. Therefore, when testing for influences of land cover on water quality, we used analyses of covariance and partial correlation analyses to account for the influence of elevation. Watersheds with row crops had the highest turbidity and concentrations of nitrate and dissolved organic nitrogen, even though crops covered only 9% to 34% of the watershed areas. Among watersheds without crops, concentrations of TDN, nitrate, potassium, dissolved iron, and chloride correlated negatively with percent forest cover, while chloride and TDN concentrations correlated positively with percent pasture cover for watersheds in the forest/pasture group. However, turbidity was not correlated significantly with pasture cover. Our results suggest that crop cover has stronger effects on water quality than does pasture in the South Carolina piedmont. Additional research is needed to determine if the higher dissolved nitrogen concentrations in watersheds with crops stimulate growth of algae or other microbes in streams or downstream ecosystems.

P53 Johnathan M. Overcash, Erik C. Usher, Joel M. Gramling
Biology, The Citadel, Charleston, SC

Wetland Assessment of a Blackwater Swamp Along the Black River, Georgetown County, South Carolina

Wetlands are essential ecosystems in coastal South Carolina, although a history of logging and other anthropogenic impacts has affected hydrology and environmental quality. Recently, The Citadel acquired the 544 acre Faircloth Property along the Black River in Georgetown County, SC. The overall quality of the wetland tract was assessed through the presence of wetland indicator plant species and water quality samples. To evaluate the property, a latitude and longitude grid at 15 second intervals was overlaid on a map to plot unbiased locations to sample from within the 544 acres. After identifying the dominant plants at each point, the indicator status was determined for each plant species: obligate wetland, facultative wetland, facultative, facultative upland and obligate upland. Each plant species was assigned a numeric value (0-4) representing its wetland indicator status; where an upland species would be assigned a 0 and an obligate wetland species would receive a 4. For each point location the wetland scores of the observed dominant plant species were averaged into a single numerical score. This information was compared to a map of the property developed from the National Wetland Inventory (NWI). Qualitative comparative analysis of the mapped units to the point observations accurately reflects the observed hydrology. The predicted floristics for the property was less accurate. Water quality samples demonstrated a hydrologic gradient typical of a blackwater swamp. Overall we found that the NWI was a useful tool for predicting the hydrology at a given point, but less useful for predicting the observed plant community.

P54 Anastacia L. Marcus[1,2]
[1] Biology, Jacksonville State University, AL; [2] Art, Jacksonville State University, AL

Biological Illustration

Biological illustration presents accurate representations of the natural world. Prior to the development of photographic techniques, naturalists drew accurate pictures of species in natural settings to convey habitat and ecological preferences. Care was taken to depict color patterns and morphology accurately. Illustrations of diagnostic body parts were used to help scientists visualize the key characteristics of individuals so they could identify them properly. Animals, plants, and humans have been the focus of much biological illustration. Good illustration requires a keen eye for details, and motor skills to translate what is seen with the eye to a rendering on a page. Illustrations connect historic observations of organisms to the present day. Certain extinct species rendered by hand is the only way we are able to observe their existence.Biological illustration brings together the ecological processes requiring thousand of words of description into a single picture. Illustrations are drawn with pencil, ink, and then if appropriate the use of watercolor can be applied. Renderings done in pencil and ink can illustrate the scientific complexity of a species for understanding of a specimen in whole. Renderings can also take on a more artistic view with a species painted in their environment to understand their natural habitat. The illustration process starts with preparatory drawings, rough drafts for defining, and then use of ink and color to finish illustration to completion. The purpose of biological illustration is to help the scientific field clarify complicated concepts by art design.

P55 Nyssa R. Hunt
University of Tennessee at Chattanooga

Spatio-Temporal Analysis and Predictive Modeling of Rabies in Tennessee

As a prominent mammalian virus, Rhabdovirus, or more commonly known as Rabies, continues to hold its fearful reputation and calls for further research. Such studies have been performed in spatial and temporal scopes, throughout different countries and seasons. With this in mind, the activity of the virus in the state of Tennessee was considered, as a formal analysis of such aspects was not well advertised to have been performed. Using GIS softwares (ArcMap 10.2, Fragstats, and Circuitscape) and spatial data gained from the Tennessee Health, a spatiotemporal analysis was performed that mapped past ranges, displayed collective densities of all cases and specific species, and modeled possible spread in the southeastern region of Tennessee - particularly in the ridge and valley zone. The historical aspect displayed that domestic dogs and foxes held the most cases in past decades, while skunk cases have been on the rise yet have decreased in recent years. The map of densities yielded the fact that rabies has mostly been reported around larger cities, such as Memphis, Nashville, Chattanooga, Knoxville, and the Tri-Cities area. The predictive modeling displayed that physical barriers seem to prevent the disease from spreading as efficiently in this area than that of flatter regions. Overall, this analysis points to the need to consider landscape aspects and corridors in relation to virus spread.

P56 Jeremy W. Hooper[1], Christopher B. Mowry[2], Lawrence A. Wilson[3], Randal J. Hale[4]
[1] Biological and Environmental Sciences, University of Tennessee at Chattanooga; [2] Biology, Berry College, Rome, GA; [3] Environmental Sciences, Emory University, Atlanta, GA; [4] North River Geographic Systems, Athens, GA

Using Social Media and Web-Based Platforms to Collect Scientific Data on Human-Coyote (*Canis latrans)* Interactions in Metro Atlanta, GA, USA Human-coyote (*Canis latrans*) interactions appear to be increasing across North America. Such interactions have the potential to influence human perception and acceptance for coyotes, and, as a consequence, conservation and management efforts. Thus, information on the spatiotemporal characteristics and human dimensions of human-coyote interactions can lead to more targeted, resource efficient management efforts. The use of citizen scientists is allowing researchers to collect meaningful data with limited resources. Moreover, citizen science data can be collected through web-based platforms, including social media. We are currently using a web-based survey to gain a better understanding of the spatiotemporal characteristics of human-coyote interactions and the general perceptions of, and attitudes towards coyotes in metro Atlanta, GA. This has resulted in over 1,800 survey responses in 4 months (Oct. 2014 - Jan. 2015), showcasing the potential power of using web based platforms for a variety of science related efforts, including data collection and outreach. However, such a platform is not a simple means to an end. Researchers must consider potential biases and limitations, which will vary depending upon the question(s) being addressed. We intend to elaborate on our use of these platforms to provide a framework for other scientists to use.

P57 Carrie A. Radcliffe[1], Jennifer M. Cruse-Sanders[1], Lisa M. Kruse[2], Joanne E. Baggs[3]

[1] Science and Conservation, Atlanta Botanical Garden, Atlanta, GA; [2] Wildlife Resources Division (Nongame Conservation Section), Georgia Natural Resources, Social Circle, GA; [3] Southern Region, USDA Forest Service, Atlanta, GA

Georgia Plant Conservation Alliance Safeguarding Database - Tracking and Reporting Conservation Activities for Rare Plant Species

The Safeguarding Database was developed by Atlanta Botanical Garden in conjunction with Georgia's of Natural Resources, the State Botanical Garden of Georgia, and the Chattahoochee-Oconee National Forest. Created to document the efforts and success of the Georgia Plant Conservation Alliance, it is a repository for tabular and geographic data pertaining to collaborative plant conservation projects. The use of the Safeguarding Database is expanding throughout the Southeast to track collaborative safeguarding and restoration projects of Atlanta Botanical Garden and its partner organizations. This system supplements and provides critical updates to Biotics, which is used by state natural heritage programs to track sensitive species. These updates not only provide valuable information to our local and regional conservation partners - they also feed into NatureServe, the national system for rare species and ecosystem conservation planning, ranking, and status assessments. Information about *ex situ* collections, *in situ* reintroductions, and wild populations are standardized and updated in the Safeguarding Database. Repeated monitoring data, site and landscape level management events, ecosystem protection and threats, as well as partner contacts are integrated within this system. In addition to compiling information from multiple sources and generating reports that facilitate cohesive communication for high-profile restoration and recovery projects, it provides details relevant to habitats across the landscape that can serve as indicators for responses to climate change. Combined with the resources it catalogs, the Safeguarding Database is invaluable for biodiversity conservation in the Southeastern U.S., which may be especially vulnerable to environmental changes associated with the shifting global climate.

P58 Ceil C. Martinec[1], Jyotsna Sharma[2], Jonathan M. Miller[1], Paul M. Stewart[1], Stephen C. Landers[1]

[1] Biological and Environmental Sciences, Troy University, AL; [2] Biology, University of Texas at San Antonio

Multivariate Analysis of Nematode Communities in Northern Gulf of Mexico Continental Shelf Sediments Following the Deepwater Horizon Oil Spill

This study analyzed marine nematode communities at 49 - 361 m depths on the Gulf of Mexico (GOM) continental shelf. Sediment cores were collected in Fall 2012 from central Louisiana to Apalachicola, Florida and analyzed for trace metals, organic carbon, sediment granulometry, and nematode genera. Twenty-six genera not found in GOM checklists were documented in this study. The dominant genera were *Dorylaimopsis* (13.0%) and *Sabatieria* (8.1%). *Sabatieria* abundance correlated with select sediment characteristics, specifically medium sand (negative correlation, $p < 0.01$) and silt+clay percentages (positive correlation, $p = 0.01$). *Dorylaimopsis* did not correlate with sediment granulometry, whereas other dominant genera did, illustrating the complexity of these communities; thus, communities were examined with univariate and multivariate analyses.

Univariate correlations between non-metric multidimensional scaling coordinates and abiotic variables suggested that metals and grain size were most closely linked to nematode community structure. This was supported by biotic correlations with principal components from both metals and granulometry. BIO-ENV analysis revealed that Cu (r = 0.567) and a combination of Cu and Al (r = 0.560) had the highest rank correlations to nematode similarity data. These metals significantly correlated with other trace metals and were likely attributable to natural clay minerals. The highest non-metal correlation to nematode similarity data was a combination of very fine sand, silt+clay, and organic carbon percentages (r = 0.504), indicating that nematodes may prefer certain sediment grain sizes that are associated with varying levels of organic carbon and trace metals.

P59 Kala J. Quinn, Caryn D. Ross, Mark L. Fink, Sujan M. Henkanaththegedara
Biological & Environmental Sciences, Longwood University, Farmville, VA

Long-Term Population Dynamics and Trends of Common Wintering Birds in Central Virginia

Several studies have shown a steady decline of common breeding birds in the eastern United States including Virginia. However, the long-term population dynamics of common wintering birds are poorly understood, especially for the Piedmont region of Virginia. We studied the long-term population dynamics of 20 common wintering birds in central Piedmont using Christmas Bird Count data from five count circles (Darlington Heights, Lynchburg, Warren, Gordonsville & Lake Anna). Linear regression models revealed significant population declines ($p < 0.01$) for some species including for Northern Cardinal (*Cardinalis cardinalis*), Carolina Chickadee (*Poecile carolinensis*) and Mourning Dove (*Zenaida macroura*), and significant population increases ($p < 0.0001$) for Eastern Bluebird (*Sialia sialis*), Turkey Vulture (*Cathartes aura*) and Red-tailed Hawk (*Buteo jamaicensis*). Additional analyses comparing average bird densities between Pre- and Post-1980 suggested similar population trends. This information may be critical in conservation management of regional birds.

P60 Michael C. Elza, James B. McGraw
Biology, West Virginia University, Morgantown

Analysis of Wood Thrush (*Hylocichla mustelina*) Movement Patterns to Explain the Spatial Structure of American Ginseng (*Panax quinquefolius*) Populations

American ginseng is America's premier wild-harvested, medicinal plant that inhabits the forest understory of eastern deciduous forests. Recent research using camera-traps showed that birds, particularly wood thrushes, disperse ginseng seeds, regurgitating viable seeds 15 - 37 minutes after consuming the berries. We carried out two studies to examine the potential effect of thrushes on spatial dispersion patterns of ginseng. First, for 28 natural populations of ginseng we created a clustering index (number of subpopulations / total individuals in the population), in order to quantify to what degree populations were structured into spatially separated units. Second, to analyze how far wood thrushes could disperse seeds, two wood thrushes were outfitted with radio transmitters and tracked for multiple days. The mean dispersion index differed for populations with and without wood thrushes (F= 5.411, p= 0.028). Over the time period in which wood thrush retain ginseng in their guts, the seeds would be dispersed between a mean distance of 15.2 - 21.7 meters. The observed distances ranged from 0 - 96.6 meters. These distances are comparable to the inter-cluster distances for ginseng populations with wood thrushes, which had increased spacing in comparison to those without wood thrushes. As wood thrush and ginseng populations are both experiencing declines, it is imperative to understand the interaction between these two species to facilitate conservation. These findings highlight the genetic and structural impact that wood thrushes have on ginseng populations and influence the plants' ability to respond to disturbances such as climate change, deer browse, and over-harvesting.

P61 Justin A. Walley
Biological and Environmental Sciences, University of Tennessee at Chattanooga

Diet Analysis of Wintering Waterfowl in Agricultural and Natural Wetlands

The purpose of this study was to gain a better understanding whether there is a habitat preference among wintering waterfowl between agricultural or natural wetlands, and to see if there were differences in the diet of birds foraging in the different areas, as well as among species. Specimens were obtained from waterfowl hunters at various sites across the Southeast region. I removed the digestive tract from each specimen and then dried the contents in an oven at 50 degrees Celsius for one week. Once dried, I recorded the aggregate weight of each digestive sample's content, along with the species, sex, collection location, and time into an Excel spreadsheet. A total of 298 specimens were obtained over the winter waterfowl season in 2013-2014, and an additional 165 specimens so far in the 2014-2015 winter waterfowl season. With this information I am analyzing the diet of over 25 species of waterfowl across a geographic broad range, from Arkansas to North Carolina. This information will give waterfowl managers a greater understanding of waterfowl foraging during the winter months and also show if there is a habitat preference in different geographic regions. Comprehensive results will be presented on the first year data and preliminary results will be discussed concerning the second year's data.

P62 Erika M. Dietrick, Renee Fortner, Claudia L. Jolls
Biology, East Carolina University, Greenville, NC

Using Microscopy to Assess Embryo Development and Seed Viability in *Thalictrum cooleyi*

Thalictrum cooleyi Ahles (Cooley's meadowrue) is an endangered native species of the pine savanna ecosystem. Although it is threatened by loss of habitat, little is known of Cooley's meadowrue seed biology. A congener *T. mirable* has underdeveloped embryos that are physiologically dormant at maturity. We asked if embryo development and ultimately seed germination of Cooley's meadowrue would be affected by different pretreat- ment conditions. Seeds larger than 2.5 mg in mass were exposed to one of seven treatments, including warm, cold, or room temperatures and duration of exposure (8-14 wk). We examined four seeds from each group with stereo- and scanning electron microscopy (SEM) to compare sizes of seeds and embryos among treatments through time, 2-14 weeks after initiation. We used a Leica EZ4 HD stereo light microscope at 25x and FEI Quanta 200 SEM on low vacuum and back scattered electron mode at 20 KV and 0.45 Torr vacuum pressure. Both techniques have limitations, but SEM may better discern embryos. Independent of time and treatment, the embryo comprised approximately 14% of Cooley's meadowrue seed length. Low sample sizes limit our ability to comfortably draw conclusions about embryo development. Only 50% of 100 seeds appeared to have embryos, suggesting very low seed viability. We examined 2556 seeds for this and a related study; only 620 (24%) were large enough to suggest the presence of an embryo and endosperm. Limited seed numbers and viability are major challenges in working with this rare taxon.

P63 Deja F. Rivera, Cynthia C. Bennington
Stetson University

Acidic Soils Benefit Seedling Growth in Two Perennial Plant Species Native to the Florida Sandhill Ecosystem

Sandhill ecosystems have been impacted heavily by logging, farming, and development, making their restoration a priority for land managers in the southeast. The soils associated with intact, mature sandhills typically have a low pH, and plant species native to sandhills may perform poorly in restoration sites where pH is close to neutral and/or where the native soil microbial community has been altered. Using soil from a small sandhill restoration site on our campus, we asked whether seedling establishment of narrowleaf silkgrass *(Pityopsis graminifolia*) and Florida paintbrush (*Carphephorus corymbosus*) is affected by soil pH, and also whether *C. corymbosus* establishment is affected by soil microbial composition. We germinated seeds of each species in petri dishes maintained under 24-hour light. Once germinated, 44 seedlings of *P. graminifolia* were transplanted to soil that had been collected from our restoration site, half of which was acidified to a pH of 4.5, while the other half served as a control (pH = 6.8). For *C. corymbosus*, 118 seedlings were similarly transplanted, but seedlings were evenly divided amongst treatments in a 2 x 2 factorial design with pH and native sandhill microbes as the two factors. After five weeks, we measured survival, number of leaves, and the average length of the longest leaf. Neither survival nor leaf number was affected by treatment(s) in either species. Low pH, however, resulted in significantly longer leaves in both species. Our results demonstrate the importance of soil properties in ecosystem restoration.

P64 John C. Levengood, Kaitlyn Hanley, David C. Rostal.
Biology, Georgia Southern University, Statesboro

Annual Variation and Timing of Reproduction in *Gopherus polyphemus* from 1994 to 2014

Climate change and other environmental aberrations in the past twenty years have adversely affected many reptilian species across the world, causing alarm for threatened and endangered species viability in a rapidly changing climactic system. These climactic changes are hypothesized to have caused varied rainfall totals and temperatures on the Fort Stewart US Army Installation sand hill. Reproduction variables including clutch size, timing of nesting and hatching success in the gopher tortoise are linked to rainfall and temperature. Temperature change linked to overall climate instability has been connected to changed rainfall totals, which presents a challenge to tortoise populations in the southeastern United States. The focus of this study is to compare rainfall and temperature data to nesting time and clutch size in order to determine if there is a distinct link between climactic variation, tortoise nesting time and clutch size. Data from 1994 to 2014 on clutch size, present number of reproductive females, and the time of nesting will be compared to annual rainfall and temperature data.

P65 Rachel E. Mowbray, H. Dawn Wilkins
Biological Sciences, University of Tennessee at Martin

Nest Site Characteristics and Spatial Dispersion of Osprey Nests at Reelfoot Lake, Tennessee

Osprey (*Pandion haliaetus*) nests show clumped dispersion in coastal populations. Two hypotheses have been suggested: information center hypothesis and nest-site hypothesis. The information center hypothesis suggests that individuals may gain information about the location and quality of fishing spots by watching their neighbors, which may increase their breeding success. The nest-site hypothesis suggests that dispersion patterns reflect resource constraints, such as nest site availability. Reelfoot Lake has a large inland population of Osprey. Our goals were to describe nest site characteristics and determine spatial dispersion of nests in Upper Blue Basin, Buck Basin, and Middle Basin. To characterize nest sites, we recorded tree diameter, nest height, tree height, tree species, and distance to the nearest neighboring tree. Nests were located near the top of cypress trees over water with the nearest neighboring tree approximately 14 m away. The average height of nests was 6.77 m. To determine spatial dispersion, we mapped the location of each nest site to calculate the area of each basin and the distance to the closest neighboring nest site. Using the Donnelly Modification of the Clark and Evans Test for Spatial Pattern, we determined that osprey nests showed clumped dispersion in Middle and Upper Blue basins, but random dispersion in Buck Basin. Since Ospreys build large nests that require substantial support, they are likely constrained by availability of appropriate nesting sites. Observations during the breeding season will help determine if Osprey are gaining information that may increase nesting success as predicted by the information center hypothesis.

P66 Justin Seibert, Andy Miller, P. Brent Nichols
Spokane Tribal Fisheries

Drift Dynamics of Post-Hatch White Sturgeon and Estimation of Spawning in the Roosevelt Reach of the Columbia River During 2012-2014

The subpopulation of White Sturgeon *Acipenser transmontanus* in the Columbia River between Grand Coulee Dam (Washington) and Hugh Keenleyside Dam (British Columbia) has experienced chronic recruitment failure for nearly 40 years. Past research has documented viable gametes that successfully hatch and begin larval drift. To understand why recruitment is limiting, larval drift dynamics must be understood. Post- hatch Sturgeon were collected nightly via benthic icthyoplankton nets during 2012-2014. Sturgeon were staged in the field and assigned to three overall stages: early-stage-free-embryo (EFE; stages 36-39); mid-stage-free-embryo (MFE; stages 40-43); and late-stage free-embryo (LFE; stage 44+). Based on larval developmental stage during collection, spawning in 2012 was estimated to occur between June 29th and August 13th; June 10th and July 15th in 2013 and June 19th to July 10th in 2014. Peaks in estimated spawning during all three years coincided with a descending hydrograph and water temperatures that ranged from 13.2-17.1oC. Post-Hatch White Sturgeon capture included 2,071 in 2012 (10% EFE, 9.4% MFE and 80.6% LFE), 4,321 (43.7% EFE, 25.2% MFE and 31.1% LFE) in 2013, and 13,656 (18.7% EFE, 25% MFE and 56.2% LFE) in 2014. Power peaking from upstream dams and raising of Lake Roosevelt to full pool was occurring during larval drift in all years. Ultimately, reservoir operations during larval drift could be limiting White Sturgeon recruitment.

P67 Anita K. Rose, James F. Rosson, Jr.
USDA Forest Service, Southern Research Station, Knoxville, TN

Longleaf Pine Resources in South Carolina: Changes in Spatial Extent and Community Structure Over the Last Two Decades

Longleaf pine (*Pinus palustris*) is important because it is a keystone species in a unique ecosystem, one that is vital to the survival of many plants and animals, such as the red-cockaded woodpecker. We used USDA Forest Service, Forest Inventory and Analysis (FIA) data collected across South Carolina to characterize the current status of longleaf pine in today's forests. As of 2013, there were 5,278,719 ha of forest land across the state of South Carolina. Longleaf pine was present, to some degree, on 409,760 ha (8%) of this forest area. It accounted for at least 50% of the basal area in nearly one-half of the stands where it occurred. The number of live stems (>2.53 cm d.b.h.) of this species was at a 50-year high in 2013, at 207.5 million trees (39 stems per ha across all forest land; 506 stems per ha on plots where it occurred). Between 2001 and 2013, the number of stems of longleaf nearly doubled, from 104.4 million trees to 207.5 million trees. Significant increases were noted in both natural and planted stands. Nearly one-half of live trees were in the smallest size class (2.5-7.4 cm d.b.h.). Longleaf pine ranked 9th overall, across the State accounting for 2.4% of the volume. Growth of longleaf pine averaged 682,375 cubic meters per year. Removals averaged 332,029 cubic meters per year, and mortality averaged 91,997 cubic meters per year. The significant increases in this species over the short term are a testament to the planting efforts that have been taking place across the State.

P68 Selimah Harmonm, John E. Quinn
Biology, Furman University, Greenville, SC

An Assessment of an Altered Soundscape along an Urban-Rural Gradient

The scope and scale of landscape change in the last 100 years is broadly recognized. Yet one often-overlooked measure of change in this discussion is the disruption of the soundscape, principally the increase inanthropogenic noise and its effects on both human and natural systems. Thus it is essential that we better quantify and understand the impact of this change on ecosystem state and function to better implement effective and efficient mitigation strategies. In this poster we present quantitative and qualitative measures of soundscape variation along an urban-rural gradient in Upstate South Carolina. Specifically we document how acoustic diversity varies across this gradient and how individual species adapt. Lastly, we suggest measures by which planners and practitioners can address these changes.

P69 Mary F. Feely[1], David U. Unger[1], Paul K. Keenlance[2], Joe J. Jacquot[2]
[1] Biology, Maryville College, Maryville,TN; [2] Biology, Grand Valley State University, Grand Rapids, MI

American Marten *(Martes americana)* Prey Base Species Composition Within the Manistee National Forest of Michigan

After extirpation in the early 1900's, the American marten (*Martes americana*) was reintroduced to the Manistee National Forest (MNF) of the Lower Peninsula of Michigan in 1986 (Clark et al.1987). Since reintroduction, marten in the MNF have been studied but the population does not appear to be expanding (Sanders 2014). Small mammals make up a significant portion of marten diet and marten adapt foraging to small mammal availability (Buskirk et al. 1996). Thus, the distribution, abundance, and diversity of small mammals as they relate to habitat type in marten range is valuable information for forest managers. Small pitfall traps and medium and large Sherman traps were utilized to examine multiple trap use in the capture of small mammals. The objectives of this study were to 1) determine if differences exist in the small mammal prey base between habitat types in known marten habitat and 2) determine if using a variety of traps provides a more complete representation of species diversity than using one form of trap. Traps were placed in four habitat types that the American marten were known to reside in within the MNF; deciduous, coniferous, mixed-oak and conifer-deciduous. Marten home-range data was examined and deciduous stands were the second highest in marten use at 26% after conifer (47%) suggesting that marten may be following the highest prey base availability and diversity of larger small mammals. Conservation should be aimed towards older and complex deciduous habitats where we found the highest small mammal diversity, abundance, and evenness.

P70 Philip R. Gould[1], Jordan D. Troisi[2], Kristen K. Cecala[1]
[1] Biology, University of the South, Sewanee, TN; [2] Psychology, University of the South, Sewanee, TN

Drivers of Land-Management Preferences in the Southeast

People's preferences can provide relevant information on what should be integrated into the existing land-management practices of different regions. With an understanding of stakeholders' views, planners are able to construct future land management practices that reconcile private goals and public preferences. Integrated objectives are important for land managers to create natural areas that satisfy the needs and desires of regional communities. Previous studies have identified occupation, proximity to nature, and socio-political views as factors that influence land- conservation attitudes of surrounding communities. These results suggest that the public values a range of services provided by natural areas. Our objective was to identify drivers of land-management preferences in communities in southeastern Tennessee. We designed a comprehensive mail survey delivered to 1000 residents in three counties along an urban-rural gradient. Results suggest that people who reside closer to natural areas value a broader range of land-uses than people who reside further from natural areas that prefer more natural land-uses. Future land managers should consider the various priorities and preferences of the communities they serve as they design management that also supports the public good and maximizes the value of natural areas.

P71 Katelyn C. Walters, Heather P. Griscom
James Madison University

The Effect of Slope Aspect on the Efficiency of Treating Eastern Hemlock (*Tsuga canadensis*) Trees with Imidacloprid for the Suppression of the Invasive Hemlock Woolly Adelgid (*Adelges tsugae*)

Eastern hemlock (*Tsuga canadensis*) is a foundation tree species native to the eastern United States including Shenandoah National Park in the southern Appalachian Mountains. This species is severely threatened by an invasive insect, the Hemlock Woolly Adelgid (*Adelges tsugae*). Hemlock trees are a shade-tolerant species that retains a dense needle canopy year-round creating a unique microclimate that provides habitat for both terrestrial and aquatic species. The loss of these trees has negative implications for many native species and the overall function of forest ecosystems. This survey aims to assess the effect of slope aspect (southwest vs. northeast), which is correlated with variations in soil moisture and organic matter. Soil characteristics can affect the efficiency of imidacloprid insecticide application on infected hemlock trees. Branch samples will be collected from treated hemlock trees at three sites to quantify adelgid density, seed cone production and imidacloprid residue. Soil samples will also be collected to correlate soil moisture and soil organic matter with hemlock health. The prediction is that the southwestern aspects will contain less soil moisture and have a lower percentage of organic matter. These soil factors will be correlated with lower levels of imidacloprid residues, higher adelgid densities, decreased hemlock health and increased hemlock reproduction in response to stress. The ultimate goal of this survey is to provide management recommendations for the preservation of the 20,000 Eastern hemlock trees in Shenandoah National Park.

P72 Gina L. Lowry, H. Dawn Wilkins
Biological Sciences, University of Tennessee at Martin

Use of Nest Boxes Located at the Edge as Compared to Within a Tree Line on a Farm in Northwest Tennessee

The availability of cavities, formed naturally or by primary cavity excavators, can influence species richness and abundance of secondary cavity users. For many species nest boxes can readily substitute for natural cavities. Landscape features may influence where birds choose to nest. Some species may reduce energy expenditures by feeding near nesting sites. Based on these observation, we predict that Eastern Bluebirds (*Sialia sialis*), which forage in open habitats, may be more likely to nest at the edge while Carolina Chickadees (*Poecile carolinensis*) and Tufted Titmice (*Baeolophus bicolor*), which forage in more forested habitats, may prefer to nest within the tree line. Our goal was to compare the nesting activity of these three species in PVC nest boxes located at the edge as compared to within the tree line. We placed and monitored 20 pairs of PVC nest boxes. Within each pair, Box A was located at the edge while Box B was 5 m behind within the tree line. Monitoring took place once a week during the peak of breeding season. Nests or nest starts were found in 35% of the boxes, with 17.5% successfully fledging young. Of the seven successful nests, four fledged Carolina Chickadee, two fledged Eastern Bluebirds, and one fledged Tufted Titmice. Five of the successful nests were in Box A, while two were in Box B. Further observations are needed to determine if different species show preferences between the two possible nest locations. Nesting success may have been impacted by vegetation growth around the nest boxes.

P73 Edward D. Mills
Biology, Wingate University, NC

Spectral Characteristics of Harmonics in the A-Call of Hatchling Chinese Blue-Breasted Quail (*Coturnix chinensis*)

Chinese Blue-breasted Quail (*Coturnix chinensis*) produce a vocally-rich A-shaped call immediately after hatching. The A-call is believed to be a contact call that maintains the cohesiveness of the foraging precocial family group. The call's fundamental frequency (~3700 Hz) is enriched by a harmonic stack (9000, 14,000 and 18,600 Hz) of similar duration. Harmonic frequencies are important because they are produced at lower amplitudes than fundamental frequencies and sound degradation can serve as distance cues for parents and offspring. Vocalizations were digitally recorded immediately after the hatchlings were removed from the incubator and placed in a brooder. Nine spectral properties of these harmonics were measured to form a baseline of information to examine family cohesiveness during the juvenile period. These measurements include call length, sound frequencies produced (Hz), energy (average and aggregate entropy) and call decibels (average and maximum power, dB).

P74 Samuel P. Hull, Brady P. Donovan, Sujan M. Henkanaththegedara
Biological & Environmental Sciences, Longwood University, Farmville, VA

Rapid Body Shape Divergence of Endangered Mohave Tui Chub (*Siphateles bicolor mohavensis*) and Potential Conservation Implications

Establishing new habitats for rare species by translocating individuals from a source habitat to a new refuge habitat is a standard practice in conservation management of endangered fish. Phenotype management stresses the importance of matching the potential refuge habitats with native source habitats when translocating protected species species. Failure to finding suitable habitats may result in rapid divergence of phenotype (e.g. body shape) of translocated populations compared to the source populations. Endangered Mohave tui chub (*Siphateles bicolor mohavensis*) have been extensively translocated to man-made habitats for recovery purposes. We studied body shape of tui chubs collected from the parental population and three other translocated populations in man-made habitats. We have established 9 body shape landmarks and measured fish (N = 115) for 13 morphometric measurements. We compared body shapes using a series of One-way ANOVAs ran on 13 morphometric measurements and we ran a NMDS to visualize collective response of body shape divergence. Collectively, our results suggest that two translocated fish populations rapidly diverged to produce a more robust body

shape with a short and deep caudal peduncle. Finding refuge habitats similar to the native source habitat may be critical in conserving the original phenotype of this endangered fish.

P75 Jaina S. Gandhi, Kristen K. Cecala
Biology, University of the South, Sewanee, TN

Interactive Effects of Temperature and a Glyphosate-Based Herbicide on Stream Salamander Anti-Predator Behavior

Land-use change has been implicated as the primary driver of amphibian declines. In particular, agriculture is widespread and creates multiple stressors in adjacent stream habitats. Herbicide runoff and riparian clearing are two potential stressors for stream organisms. Both the presence of herbicide and riparian clearing are known to impact amphibian survival and success. Behavioral shifts in response to these stressors may be responsible for these observed negative effects of agriculture on amphibian populations. Our objective was to assess the impact of low concentrations of a widely-used herbicide (glyphosate) and water temperature on wide-spread larval stream salamander behaviors known to alter survival such as predator avoidance and movement frequency and speed. Both temperature and glyphosate concentrations changed amphibian movement behaviors but not predator avoidance. Temperature negatively influenced movement frequency, and glyphosate concentration was negatively correlated with escape distance. We conclude that glyphosate has larger impacts at warmer temperatures and recommend that practitioners avoid applying glyphosate to fields with deforested riparian zones.

P76 Kate C. Donlon[1], John B. Jensen[2], Glenn A. Marvin[3], Thomas C. McElroy[1]
[1] Ecology, Evolution and Organismal Biology, Kennesaw State University, GA; [2] Wildlife Resources Division, Georgia Natural Resources, Forsyth, GA; [3] Biology, University of North Alabama, Florence

Identification of Polymorphic Loci for a Rare Plethodontid Salamander (*Plethodon petraeus*) by Cross-Species Amplification

Pigeon Mountain salamanders (*Plethodon petraeus*) exist in a small range and are protected as a rare species by the state of Georgia and listed as vulnerable by the IUCN. The distribution of this species correlates with rocky outcrops and cave openings patchily distributed within a 15 km area on the eastern flank of Pigeon Mountain in Northwest Georgia. Because small populations are at a greater risk of extinction, a genetic assessment of the species will significantly aid in conservation planning. However, no microsatellite markers have been developed for this species. We screened 27 microsatellite primers developed in the Western Slimy salamander (*Plethodon albagula*) for cross-amplification in *P. petraeus*. We have had successful cross-amplification for some loci and detected some polymorphic loci. We will present data on the loci assayed in this study and compare our findings to other cross-amplification studies performed for these loci. These newly identified polymorphic microsatellites will be valuable in the assessment of this rare species' genetic structure, genetic diversity and gene flow.

P77 Mark J. Dillard, Thomas P. Wilson
Biological and Environmental Sciences, Chattanooga, TN

The Spatial Ecology of the Eastern Box Turtle in Urban and Fragmented Landscapes of Southeast Tennessee

The landscape throughout the range of the box turtle (*Terrapene carolina carolina*) has changed drastically over the last few centuries. Consequently, populations appear to be in an overall state of decline. Habitats are fragmented and the microclimates are altered when roads, telephone and power lines transect them or when they are clear-cut. In this study, the spatial ecology and seasonal movement patterns of the box turtle in contrasting habitat and management types are investigated. Home range size, daily movement patterns, and habitat use areas were investigated to determine how box turtles use fragmented or anthropogenic disturbed habitats. We monitored a total of 15 radio-tagged turtles (3 males and 3 females) from August 2013 to January 2015 and (8 males and 1 female) from May 2014 to January 2015. Turtles were located at least two times per week throughout the active seasons and bi-weekly during the winter months. Home range sizes averaged 3.69 - 3.08 ha using minimum convex polygon analysis. The average distance moved per relocation in a straight line distance was 38.79 11.83 m. The average net distance moved throughout the season by all turtles in both study years was 1,054.07 - 754.53 m. During both monitoring seasons, turtles were located at sites with moderate to heavy canopy cover, suggesting that canopy cover may be an important attribute for box turtles when selecting suitable habitat and thermoregulation or other life history needs.

P78 Reuben Hilliard, Chelsea Harris, Joshua F. Hashemi, Paula C. Jackson
Ecology, Evolution and Organismal Biology, Kennesaw State University, GA

Developing a Research Method to Evaluate the Effect of Drought on Two Riparian Tree Species, With and Without Mycorrhizae

Riparian zones function as a natural buffer against erosion in river and stream banks, filter downstream pollution, and provide increased habitat complexity. Due to development, logging, and expanding agriculture, many riparian zones have been destroyed or depleted. This research is part of a larger study looking at the ecology and physiology of *Salix nigra* Marshall (Black Willow) and *Platanus occidentalis* L.(American Sycamore) and their use in riparian restoration. For this part of the research we focused on developing a greenhouse research method to evaluate the effect of drought on both riparian tree species with and without mycorrhizae. For this, we looked at: 1) running a bioassay to determine mycorrhizal spore viability; 2) finding an appropriate statistical design for our greenhouse setup; 3) determining anatomical and physiological measurements; 4) establishing the statistical methods to analyze results; 5) finding a method to stain and quantify mycorrhizal colonization.For our experimental design we found that 1) spores tested were not viable after >1 year storage; 2) a randomized complete block design be used for our greenhouse setup; 3) Anatomical and physiological measurements to include: total length of the plant, stem diameter, biomass, leaf area, mycorrhizal colonization, and gas exchange using a LI-COR LI-6400; 4) light curves will be compared using a factorial design (23), in a three-way analysis of variance with repeated measures (ANOVAR); 5) after staining, mycorrhizal colonization will be quantified using the root piece method, results will be analyzed using non-parametric methods such as the Mann-Whitney U test.

P79 Joshua G. Stonecipher, Lisa M. Krueger
Biological Sciences, University of Tennessee at Martin

Effects of Pine Needles on Pine Rockland Grass Seed Germination Due to Altered pH and Light Levels

Pine needles have been shown to exhibit allelopathic interactions with some grass species, as well as alter soil pH and light levels. However, the effects of pine needles on seed germination success for pine rockland species is still unclear. Pine rocklands are a globally imperiled ecosystem in south Florida. A previous study showed that mechanical scraping combined with native seed sowing was effective in reestablishing native grass species in a disturbed pine rockland. Since many grass seeds have plumose attachments designed for wind dispersal, a thin pine needle cover was used to keep seeds from becoming airborne during the study. If future restoration efforts involve the use of pine needles to facilitate native seed sowing, understanding the effects pine needles have on seed germination success is essential. We are examining the effect of pine needles on seed germination in four pine rockland grasses by subjecting seeds to five treatments designed to alter pH, light levels, or both: watering with deionized distilled water (18 MΩ) with or without a covering of cut pine needles or with a covering of cellulose seed testing paper cut into 1mm wide strips to imitate pine needles, watering with a pine needle extract, or watering with a citric acid dipotassium hydrogen phosphate buffer solution (pH 4.0). For each species and treatment, we are monitoring % seed germination, germination rates, and pH. Further observation will determine if differences in germination performance exist between treatments and whether those differences are due to changes in light level or pH.

P80 Matthew M. Howell, Devon V. Wasche, John F. Moeller
Biology, Wofford College, Spartanburg, SC

Identifying Chemosensory Cues Used During Oviposition by Bean Beetles, *Callosobruchus maculatus*

In choice experiments, female bean beetles (*Callosobruchus maculates)* have shown a preference for adzuki beans (*Vigna angularis*) over mung beans (*Vigna radiata*) during oviposition. Preference is likely influenced by several sensory cues from the beans. Beetle preference switched to mung beans (Matched pairs, $p < 0.009$) when tested with adzuki beans that exhibited observable differences in seed coats (e.g. dull vs. shiny). This observation suggests variation in chemosensory cues is a factor influencing differences in oviposition choice. Artificial substrates coated in specific compounds such as fatty acids have significantly altered oviposition behavior (Parr *et al.* 1998). Accordingly, we attempted to remove the organic compounds on the seed coat of our varieties of beans using acetone washes (1 hour) to characterize their chemical composition and to examine the ability of the seed coat extracts to influence oviposition. There was a significant increase in oviposition on artificial glass beads coated with the extracts compared to untreated beads (Student's t-test, $p < 0.0001$). Results from gas chromatography and mass spectrometry verified differences in the chemical profiles between different adzuki batches. Tentative results support the hypothesis that differences in the chemical nature of the seed coat of bean varieties are influencing oviposition choice of female *C. maculates*. The specific organic compound(s) that may be influencing these behavioral differences remains to be characterized. In future experiments, we hope to study the sensory neural pathways in *C. maculates* once we identify the behaviorally relevant chemical differences between these particular bean varieties.

P81 Sieu K. Tran, Paul Guy Melvin
Natural Sciences, Clayton State University, Morrow, GA

Evaluating the Effect of Substrate Complexity on *Cenchritis muricatus* Size and Population Distribution in San Salvador, Bahamas

The knobby periwinkle (*Cenchritus muricatus*) is a marine snail that is commonly found throughout the Caribbean islands. It inhabits the supralittoral zones of rocky shores, at times up to 14 meters above mean sea level, and on a variety of supralittoral substrate types. These substrates can vary dramatically in their complexity and include volcanic rock walls, sedimentary rock outcrops, boulders, and pebble beaches. Previous studies have proposed that periwinkle body size, population densities, and population distribution are affected by environmental conditions, but have produced mixed results. The purpose of this study was to evaluate the relationship between substrate complexity and periwinkle size and distribution on the island of San Salvador in the Bahamas. Substrate complexity was determined by calculating rugosity, a quantifiable measurement of surface topography. Periwinkle size was determined by measuring the width of the shell, the height of the shell, and the mass of the animal. Sites were evaluated encompassing different terrain types found on the island. The results of our study indicate that there is a correlation between periwinkle size and substrate complexity and between periwinkle population density and substrate complexity.

P82 Tom Fink, Alina Suedbeck, Amelia Shore, Kevin Adams
East Carolina University, Biology

How Lepidopteran Pupal Spiracles are Really Made: The Lamellae

The external lamellae of pupal spiracles are often easily noticed by eye or a stereo microscope.Despite their importance, the pupal spiracle lamellar structure have been inadequately studied and described. The only way to be sure of the true lamellar structure, involves imaging the spiracles in the Scanning Electron Microscope from external and internal views, cross-sectional views, and often through imaging halves of the spiracles teased apart. Stereo views through anaglyphs are often necessary to see how lamellae and lamellar projections relate to other lamellae. The same spiracle is often imaged many times, at many tilt angles and after many progressive dissection and imaging steps. Low vacuum mode of the Quanta 200 SEM facilitates progressive dissections since we do not have to coat specimens. We will present the results of observations from over 20 species, both local and exotic. Exotic species specimens were courtesy of the Magic Wings Butterfly House and Insectarium at the Museum of Life and Science in Durham, North Carolina, Dr. Ulrich Hartmond, director. In all species observed to date, lamellar complexity increases from internal to external views and both views are often very different. Lamellae are often more like lamellar plates and lamellae may be fused together (e.g. male Bagworm pupae). Black Swallowtail pupae are unusual in that lamellae of the two halves are different.

P83 Caleb M. Ardizzone, William H. Dees
Biology and Health Sciences, McNeese State University, Lake Charles, LA

Adult Mosquitoes in a Residential Park: A Four-Year Survey, Including Notes on Potential Mosquito-Borne Disease Risks

A seasonal longitudinal survey of adult mosquitoes is underway at a residential 24-acre woodland park. The park is separated into two distinct areas: one is an open area with playground equipment, picnic tables, open shelters, a small conference center, exhibits, wetland ponds, and concrete walking paths with benches; the other is a preserved forest with nature trails. The mosquito survey was initiated in summer 2011. We use Centers for Disease Control and Prevention (CDC) light traps baited with CO2 to collect mosquitoes. Mosquitoes are collected in the open area near the preserved forest in each of the four seasons: spring, summer, fall, and winter. Meteorological data are recorded during each trap night. To date, the predominant species collected (i.e. >50 in one trap night) are *Aedes atlanticus*, *Ae. taeniorhynchus*, *Ae. vexans*, *Coquillettidia perturbans*, *Culex nigripalpus*, *Cx. salinarius*, and *Psorophora columbiae*. *Uranotaenia* spp. were collected only in the summer and fall. *Psorophora* spp. were collected only in the spring, summer, and fall. *Culiseta inornata* was collected only in the winter. Information obtained in this study can be used to determine potential health risks associated with nuisance and disease vector mosquito species.

P84 Benjamin C. Hunt[1], Caroline L. Rowan[1], Dylan E. Skipper[1], Kiera A. Stevenson[1], Will Hemminger[2], Peter Van Zandt[1]
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The Effect of Birmingham's Urban Heat Island on Moth Phenology

Studies show that increased temperatures often lead to earlier phenology in ectotherms, such as plants and insects. In urban environments, average temperatures are often 1-3oC higher because anthropogenic structures such as buildings and pavement absorb heat during the day and re- radiate it throughout the evening. This urban heat island (UHI) effect can mimic global temperature increases that are predicted to occur over the next 85 years. In this study, we recorded temperatures hourly using temperature loggers and collected moths from urban, intermediate, and rural environments for 4 months to determine if the temperature differences created between sites by the UHI could cause advanced moth phenology. We evaluated our prediction by following 14 focal species which were abundant at all 3 sites. Nighttime low temperatures were higher, and five of the focal species emerged earlier at the urban site. However, not all species responded similarly, which could be helpful in identifying patterns of moth responses to global warming.

P85 Kristen E. Reiter, Matthew S. Lehnert
Biological Sciences, Kent State University at Stark, North Canton, OH

Hydrophobic Characterization of Butterfly Proboscises: Butterflies with Nectar Feeding Habits Have a More Hydrophobic Landscape

The feeding habits of butterflies and moths (Lepidoptera) are sometimes categorized into two feeding guilds, flower visitors (nectar feeders) and non-flower visitors (sap and rotting fruit feeders). The structural configuration of the proboscis tip of non-flower visiting butterflies (brush-like) has an adaptive value in facilitating the acquisition of viscous fluids from porous surfaces; however, the adaptive value of smooth tipped proboscises of flower visiting butterflies is understudied. The purpose of this study was to quantify the overall hydrophobicity of the distal region (i.e., drinking region) of proboscises of flower visiting and non-flower visiting butterflies and provide evidence for the potential adaptive value of a smooth proboscis. We used Nile red to stain the hydrophobic structures on proboscises of butterfly species from both feeding guilds. Proboscises were imaged on a confocal microscope and the percent area of red was quantified using Lenseye color analysis software. Our results indicate that smooth proboscises are more hydrophobic than the brushy proboscises of non-flower visiting butterflies. We suggest that the hydrophobic nature of smooth proboscises might aid in the retrieval of nectar from thin floral corollas by having less adhesive surface properties that could stick to the flower structures.

P86 Bert Crawford, Catherine P. Mulvane, Shorook Attar, Matthew S. Lehnert
Biological Sciences, Kent State University at Stark, North Canton, OH

The Relationship Between the Color of Butterfly Mouthparts and Feeding Habits

Butterflies use a proboscis to feed on nectar, rotting fruit, and a variety of other fluids. The substrates from which butterflies feed also differ. The horizontal surface of rotting fruit or tree sap (relative to butterfly body position), for instance, requires the proboscis to bend at the distal tip region; this positional configuration might not be necessary for flower feeding. Assuming that proboscis flexibility relates to color (an indicator of cuticle hardness), we hypothesized that proboscis color might differ among butterflies of surface-feeding and floral-feeding habits. The colors of three positional and functional regions were analyzed

on five species representing surface feeding (sap feeders) or flower visiting (nectar feeders) using Lenseye color analysis software. Surface feeding butterflies have a lighter proboscis in the mid-region where we would expect bending to take place when feeding from flat surfaces; however, there were no significant differences in color of the other studied proboscis regions among species. The data suggests that proboscis color could be a tool used for predicting the feeding habits of unstudied moths and butterflies.

P87 Gabrielle Madriz, Marc A. Milne
Biology, University of Indianapolis, IN

Using Scanning Electron Microscopy to Aid in the Identification of Some of the Smallest Spiders in the World

Spiders of the subfamily Erigoninae (Family: Linyphiidae) are some of the smallest in the world, with total body length averaging approximately 2 mm. Due to their small size and a lack of sufficient taxonomic keys, female erigoninae are very difficult to identify to species. Most spiders, including erigonines, are identified at the species level by examining the reproductive parts. We photographed the reproductive parts of several North American erigonine specimens using scanning electron microscopy (SEM) in order to better visualize the structures (when compared to visual light microscopy) so that we may aid other arachnologists accurately identify female erigonine spiders.

P88 Joshua York[1], Elizabeth Brown[1], Hugh Smith[1], Bruce Harrison[2], Carmony Hartwig[1]
[1] Biology, Catawba College, Salisbury, NC; [2] Western Carolina University, Cullowhee, NC

Disease Vector Status of Mosquito Species from the Fred Stanback Jr. Ecological Preserve at Catawba College, Salisbury, North Carolina

The Fred Stanback Jr. Ecological Preserve (FSJEP) comprises a 68 ha flood plain forest and adjacent mesic upland forest located on the Catawba College campus in the central piedmont of North Carolina. Current research efforts to elucidate mosquito species diversity and invasive species status within the FSJEP identified the presence of 28 mosquito species in our 2014 (April-September) collections. Of the 28 species collected in the 2014 season, 26 have been confirmed as positive carriers of West Nile virus (WNv) by the Centers for Disease Control and Prevention, and 14 are potential vectors for members of the Bunyaviridae, specifically Jamestown Canyon (JCv) and La Crosse viruses (LACv). Due to the high incidence of potential disease vectors of medically significant human infections in FSJEP populations we performed RT-PCR based virus surveillance of pooled mosquito samples using established methods. Here we report the WNv, JCv and LACv infection status of our potential vector populations and discuss future surveillance measures in the FSJEP.

P89 Elizabeth Brown[1], Hugh Smith[1], Joshua York[1], Bruce Harrison[2], Carmony Hartwig[1]
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Morphological and Molecular Identification of Mosquito Diversity in the Fred Stanback Jr. Ecological Preserve at Catawba College, Salisbury, North Carolina

The Fred Stanback Jr. Ecological Preserve (FSJEP), located in the central piedmont, is a 68 Ha natural area bracketed by the Catawba College campus, a riparian greenway, and residential areas. Prior to 2013, the current species diversity of mosquito populations in the FSJEP was largely unknown, primarily due to a twenty year lapse in surveillance. In order to continue our investigation of species richness, relative abundance, and invasive species establishment we expanded our 2013 survey of mosquito populations from four to seven collection locations in April - September 2014. Samples were identified morphologically and compared with previous collections in 1996 (Harrison and colleagues) and our 2013 reference collections. Currently we have morphologically identified 28 mosquito taxa, including 2 species previously unreported in the FSJEP. Ongoing efforts to confirm species identity through an established DNA barcoding method for the *Culicidae* will further enhance our understanding of mosquito diversity in the FSJEP.

P90 Gabrielle Rivest, Angela Montalvo, Darwin Jorgensen
Biology, Roanoke College, Salem, VA

Immune Response to Acute Bacterial Infection in the American Lobster: Characterization by Organ Culture and Confocal Microscopy

American lobsters mount an immune response to bacterial infection by releasing hemocytes (which engulf bacterial cells) into their hemolymph. In the open circulatory system of lobsters, hemolymph issues from the arterial network and bathes tissue cells directly before being collected into the venous system, which terminates in the infrabranchial sinus located just upstream from the gill circulation. Previous research suggests that hemocytes that have engulfed bacteria embolize in the tissues. The gills have been suggested to be particularly important in lobsters' immune response to infection but other organs and tissues appear to be involved as well. In our research, we wished to characterize timing of the immune response by sampling hemolymph at time intervals after acute bacterial challenge. Both hemocyte and bacterial hemolymph concentrations were determined on these samples. The bacterium used, *Vibrio campbellii*, is bioengineered to 1) be resistant to the antibiotics kanamycin and chloramphenicol (allowing us to isolate the effect of *V. campbellii* alone), and 2) express green fluorescent protein (allowing us to visualize distribution of emboli in the gills three-dimensionally). We characterized the role of organs and tissues in the immune response by two means 1) tissue/organ culture and 2) confocal microscopy. While we focus our attention on several different tissues/organs, we are particularly interested in characterizing hemocyte sequestration by the gills. Our results suggest that the gills are important in the immune response but that other organs play a significant role in the response as well.

P91 Erika Scocco[1], Wayne Gardner[2]
[1] Biology, Wingate University, NC; [2] Entomology, University of Georgia, Research Experiment Station, Griffin, GA

A Preliminary Analysis of the Molecular Characterization and Quantification of Endemic *Beauveria bassiana* (Balsamo) Vuillemin Populations within Kudzu Soil

Beauveria bassiana is an entomopathogen endemic to soils in the United States that cause natural epizootics in insect populations. The GHA strain of this fungus has been commercially formulated to control insect pest populations. One such insect pest that this fungus could control is the kudzu bug, *Megacopta cribraria*. *M. cribraria* is an invasive insect of kudzu and agronomic crops with no known natural enemies. However, one report indicated that a kudzu bug was naturally infected with *B. bassiana* in Georgia. This suggests a natural epizootic could be occurring in kudzu patches in North Carolina. Thus, this study aims to quantify *B. bassiana* in soil samples of kudzu bug infested kudzu. Genomic sequencing will provide strain specific characterization to determine species and pathogenic strains. Preliminary findings suggest low populations of *B. bassiana* in the soil ecosystem, which were recovered on Doberski and Tribe media. Therefore, addition of propagules to these endemic areas would increase infective propagules, thus, increasing infection and control of the kudzu bug.

P92 Caleb M. Ardizzone[1], Janie E. Theriot[1], Kathryn M. Leonards[1], Allison R. Fusilier[1], Omar E. Christian[2], Cecilia W. Richmond[3], Jill Hightower[4], William H. Dees1, Janet R. Woolman[3]

[1] Biology and Health Sciences, McNeese State University, Lake Charles, LA; [2] Chemistry and Physics, McNeese State University, Lake Charles, LA; [3] Louisiana Environmental Research Center, McNeese State University, Lake Charles, LA; [4] Calcasieu Parish Mosquito and Rodent Control, Lake Charles, LA

Screening Botanical Components for Potential Mosquito Toxicants

We are investigating if components and/or derivatives (e.g., extracts) of plants native to Louisiana alter the behavior and development of medically important arthropods (e.g., mosquitoes and nuisance flies). Information obtained from these investigations may lead to innovative area- wide pest management methodologies as well as novel personal protective measures against biting arthropods. Current studies focus on the effects of botanical components on mosquito mortality. We evaluated the effects of freshly-cut plant parts from eight plant families on female *Aedes aegypti* mosquitoes. Plant families included: Apiaceae, Apocynaceae, Asteraceae, Euphorbiaceae, Lamiaceae, Lythraceae, Malvaceae, and Verbenaceae. Standard plastic Petri dishes were used to hold mosquitoes and cut plant parts. We recorded percent mortality at 24 and 48 h. Mosquitoes exposed to fresh-cut flowers/petals, buds, leaves, stems, and seeds from Apiaceae, Asteraceae and Lamiaceae exhibited over 50% mortality when compared with the controls. Genera of interest include: *Chrysanthemum*, *Eryngium*, *Eupatorium*, *Rudbeckia*, *Monarda*, and *Pycnanthemum*. Mosquitoes exposed to different parts of a chrysanthemum plant (flowers, buds, leaves and stems) exhibited 100% mortality in 24 h. Mosquitoes exposed to cut buds of *Pycnanthemum muticum*, *P. tenuifolium*, and *Monarda fistulosa* as well as crushed seeds of *M. fistulosa* exhibited 100% mortality in 24 h.

P93 William H. Dees[1], Desmond H. Foley[2], David B. Pecor[2], Douglas A. Burkett[2], Leopoldo M. Rueda[2], Richard C. Wilkerson[2], Caleb M. Ardizzone[1], Allison R. Fusilier[1]

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Vectormap - an Online Repository for Biosurveillance Data and Data Management Tools

With world-wide vector biosurveillance efforts by governments, institutions and citizen scientists to monitor and forecast vector-borne disease risks, there is a need for an easily accessible spatial data repository enabling users to dynamically view the factors influencing risks of vector-borne diseases. VectorMap (www.vectormap.org) is an online repository for biosurveillance data that houses data management tools for uploading and managing surveillance information as well as spatial data critical for assessing disease risks. VectorMap is a web-based resource for reviewing and depositing collection records of mosquitoes, sand flies, ticks, fleas, mites, animal hosts, and disease pathogens from around the world. This resource contains distribution models of many components associated with vector-borne diseases, including ecological niche and disease risk models related to vector ecology. Users have access to a plethora of information including 450-plus ecological niche models for vector species world-wide, climate data, slide presentations on current vector-borne disease topics, and other resources, including links to the Armed Forces Pest Management Board, Centers for Disease Control and

Prevention, World Health Organization, and Walter Reed Biosystematics Unit (WRBU). The VectorMap Team at WRBU provides tools and support for publishing accurate and precise location data, vector identification and associated environmental data, and pathogen testing results, and contributes to global knowledge of vector-borne disease threats by collaborating with individual researchers and institutions around the world. For questions regarding VectorMap or if you wish to have your surveillance data (georeferenced/non-georeferenced data) posted to VectorMap, please email the VectorMap Team at mosquitomap@si.edu.

P94 Janee Muetterties, Patrice Ludwig
Biology, James Madison University, Harrisonburg, VA

Offspring Survival and Phenotype Depends on Resource Quality in the Dung Beetle *Onthophagus taurus*

The phenotype of organisms is often determined by the genetics of the organism and the environment in which those traits are expressed. The phenotype of the dung beetle, *Onthophagus taurus*, is heavily based on the environment. Adults construct brood balls to provision the offspring. The size of the brood ball affects the body size of all beetles and the presence or absence of horns in the males. These horns determine the mating strategy for the males; horned males guard tunnels, hornless males sneak matings with females. The quality of the dung, therefore, can have a large impact on the phenotype of the offspring and therefore the mating strategies employed. We compared the quality of horse versus cow dung on the presences or absence of and size of the brood balls. Many pairs of beetles failed to construct brood balls. Brood balls made of horse dung failed to produce live offspring.

P95 Jordan A. Weesner, William L. Kuenzinger, Joaquin Goyret
Biological Sciences, University of Tennessee at Martin

Do Naive *Manduca sexta* Use Chromatic Signals to Evaluate Nectar Sources?

While searching for flowers, insect pollinators mostly use vision and olfaction. Visually, objects may be detected through chromatic contrast (color) or achromatic contrast (brightness). Adult *Manduca sexta* are large moths that hover as hummingbirds in front of flowers while searching for nectar with their 8-centimeters-long proboscis. In a previous study, we found that *M. sexta* showed an innate preference toward dark blue artificial flowers (feeders) over white ones. However, those experiments were performed with a white background, where dark blue feeders offered a higher achromatic contrast than white feeders. We will be conducting an experiment in which we will offer blue and white feeders against a dark background as well as a white background to test the following alternative hypotheses: H1: Flower naive *M. sexta* utilize chromatic signals to evaluate potential nectar sources.H2: Flower naive *M. sexta* utilize achromatic signals to evaluate potential nectar sources. Our critical predictions are that under H1, moths will show a bias toward blue feeders independently of the background. Under the alternative H2, moths will show a bias toward the blue feeders against the white background, while they will prefer the white feeders against the dark background.Finally, because illumination levels physiologically affect the availability of chromatic and achromatic signals, and *M. sexta* is a crepuscular/nocturnal animal that experiences illuminances that range across six orders of magnitude, we also plan to investigate their visual innate preferences under different ambient illuminations.

P96 Richard Yi, Riccardo Fiorillo, Sairam Tangirala, Joseph Ametepe, Christopher Brown
Biology, Georgia Gwinnett College

Does Preservation Affect the Strength of Snail Shells? a Test of Three Methods

Aquatic snails are an incredibly diverse group of molluscs. Because a snail's shell is its primary method of defense, researchers are often interested in the strength and shape of the shell as adaptations to avoid predation. Snail shells consist of a complex matrix of organic and inorganic materials whose properties may be affected by preservation method. To our knowledge, no studies have investigated the effects of preservation method on shell strength. We hypothesize that certain common preservation methods affect the shells strength and investigate the effects of three such methods on snail strength. We compare the strengths of snails stored in alcohol, frozen, and dried to that of live snails. *Physa* and *Pseudosuccinea* spp. were collected in a pond located on Georgia Gwinnett College's campus in Lawrenceville, GA. Following capture, snails were either immediately crushed, using a PASCO economy force sensor (Roseville, CA) or preserved in one of the three treatments and crushed after one week of preservation. Shell length, width, and wet mass were measured before crushing. Preliminary results will be presented.

P97 John Kilmer, Travis D. Marsico
Biological Sciences, Arkansas State University, Joneboro

Chemical Defenses of *Opuntia humifusa* in Response to *Cactoblastis cactorum* Herbivory

The South American cactus moth, *Cactoblastis cactorum* (Berg), began its invasion of the southeastern US in 1989 by feeding on naive prickly pear cacti (*Opuntia*). This invasive herbivore has had negative impacts on *Opuntia* populations in Florida and has spread along the Atlantic and Gulf Coasts, now threatening to expand into cactus-rich regions in Texas and Mexico. The herbivore has encountered little resistance from the cactus populations, largely due to the plant's inability to respond to feeding by this insect. Volatile-induced defense signaling of *O. humifusa* by a coevolved cactus-boring moth has been shown to reduce success of the invasive moth. Known *Opuntia* defenses against native cactus moth include mucilage production and programmed cell death; however, the signaling to neighboring plants does not elicit the same level of induced physical defense. We are testing the hypothesis that the reduction in *C. cactorum* larval performance is a result of elevated chemical defenses. By using high performance thin layer chromatography to profile phenolic and terpenoid production in *Opuntia humifusa* host plants, we will determine changes to the chemical component of the induced defense. Increased knowledge of *Opuntia* chemical defenses could lead to more effective methods of controlling the range expansion of *C. cactorum.*

P98 Aahana Bajracharya, Sonakchhi Shrestha, Anika Tabassum, Barry K. Rhoades
Neuroscience, Wesleyan College

Electroretinograms in the Parasitoid Wasp *Nasonia vitripennis*

Nasonia vitripennis is a tiny parasitoid wasp of fly puparia. Methods were developed for recording the electroretinogram (ERG) from the compound eyes of jewel wasps in response to light flash stimuli. Each wasp was secured in a pipette tip by a variation of the "fly pooter" method developed for *Drosophila*. Light stimuli generated by a high-intensity LED were passed through a fiber-optic light pipe. Glass capillary microelectrodes were placed against the surface of the eye (live) and inserted into the thorax (reference). ERG responses were recorded via a DC differential amplifier and digitally saved for display and analysis. ERG recordings from female wild-type wasps demonstrate the slow negative-going photoreceptor response and onset/offset transients reflecting activation of the underlying laminar layer, as seen in other insects. Response amplitude varying predictably with stimulus intensity, shows both dark and light accommodation, and manifests flicker-fusion effects.The *Nasonia* visual system is of interest for several reasons. Males are flightless and may successfully mate before eclosing from the host fly puparium. Males and females therefore face very different visual behavioral requirements and this may be reflected in functional dimorphism of the visual system itself. Eye pigment mutants in *Drosophila* have shown ERG differences and superficially similar eye pigment mutant strains have been established for *N. vitripennis*. Furthermore, the genome of *N. vitripennis* has been fully sequenced within the past two years. This suggests that jewel wasps may become a model organism for studying the development and sexual differentiation in the insect visual system.

P99 Ramhari Thapa, Jennifer R. Mandel, Randall J. Bayer
The University of Memphis, Memphis, TN

Reconstruction of Phylogenetic Relationship in *Antennaria* (Asteraceae) Using Data from Hundreds of Loci

The phylogenetic relationships among amphimictic, sexually reproducing, *Antennaria* (Asteraceae) species are poorly understood. *Antennaria* is a genus of dioecious, perennial herbs with a broad distribution occurring in both the northern and southern hemispheres. Previous work using morphology-based cladistic approaches was unable to provide phylogenetic resolution in the group. Indeed molecular work utilizing data from nuclear ribosomal DNA internal transcribed spacers (ITS) did not produce a phylogenetic tree with high support. Therefore, we employed a novel target enrichment method coupled with next generation sequencing (NGS) to gather phylogenetic information from hundreds of nuclear loci. We performed this targeted enrichment and sequencing using a set of custom capture probes designed to work in species across the entire Asteraceae family. We sequenced species of *Antennaria*, as well as several outgroup taxa, and used a series of bioinformatic and phylogenetic programs to produce a well-supported phylogenetic tree for the group. The successful reconstruction of the known phylogenetic relationships across the genus is a valuable tool and provides a framework for future evolutionary studies including species diversification, and the origination of polyploidy in *Antennaria*.

P100 Lauren M. Lyon, Timothy J. Gaudin
Biological & Environmental Sciences, University of Tennessee at Chattanooga

Cranial Osteology of *Holmesina floridanus* (Mammalia, Xenarthra, Cingulata, Pampatheriidae) from the Pliocene of Florida

Holmesina floridanus is an extinct relative of modern armadillos from the Pliocene epoch (~3 mya). This species belongs to a small and poorly studied group of animals called pampatheres, which were giant herbivorous armadillos. Only six genera of pampatheres are known from a relatively small number of fossil remains. The Haile Quarry in central Florida (Alachua Co.) is a particularly noteworthy fossil locality, because it has produced multiple complete skulls, skeletons, and carapaces of *H. floridanus*. Most of the *H. floridanus* specimens used in this study are from Haile, which yielded eight complete or nearly complete skulls, including a juvenile. The goal of our study is to describe the cranial osteology of *Holmesina floridanus*, which would be the first ever detailed skull description of a pampathere. The features present in *H. floridanus* are compared to the features found in other pampatheres, glyptodonts (the sister taxon to pampatheres), and the extant yellow armadillo (*Euphractus sexcinctus*). We have already identified several novel derived skull features that are unique to pampatheres (e.g., the presence of a very rugose and robust pterygoid bone), as well as several new features that link pampatheres to other cingulate taxa (e.g., large rugose knobs on the descending process of the jugal bone in pampatheres is reminiscent of the extended descending process present in glyptodonts). At this point in time, the anterior 2/3 of skull has been described, and work on the remaining portion of the skull is still ongoing.

P101 Tin T. Nguyen, Thu Doan, Kendall D. Hyatt, Craig D. Byron
Biology, Mercer University, Macon, GA

Compact Bone Cellularity of the First Metatarsal in a Mouse Model for Pedal Grasping

It has been observed that mice raised among arboreal substrates made up of thin branches had a more robust first metatarsal (Mt1) compared to those in terrestrial habitats. This robusticity confers greater compressive and bending strength resistance, probably as an example of bone functional adaptation in response to hallucal grasping and pedal inversion. The current study was designed to test the hypothesis that changes to the Mt1 were due to increased osteocytes. Image processing software, ImageJ, was used to evaluate the Mt1 mid-shaft cross-sections and count total osteocyte lacunae present in each slice. Thirty CD-1/ICR mice were raised from weaning to adulthood in either an arboreal or terrestrial environment. At 4-6 months of age Mt1 were isolated and micro-CT scans were obtained at the University of Ghent (Belgium). Using ImageJ, the files were cleaned and a macro was created to batch process and count the amount of osteocytes located at proximal, mid-shaft, and distal slices of each Mt1. It was found that there were no significant differences between the two, and thus our research hypothesis was rejected. This result suggests that the bone functional adaptation previously observed in response to hallucal grasping and arboreality relates to cross-sectional geometry but not differences in osteocyte hyperplasia.

P102 Victor A. Garcia, Thu Doan, Tin Nguyen, Kendall Hyatt, Craig Byron
Biology, Mercer University, Macon, GA

Comparing Mouse Hand and Foot Bones in Regards to the Morphomechanical Effects of Climbing

Manual and pedal prehension is an essential feature for arboreal locomotion, especially for small mammals needing balance on narrow supports. Specifically, grasping with an opposable hallux is a common feature found in many organisms occupying this niche. For animals that do not possess morphological specializations, however, the bone functional adaptation that accompanies habituation to such environments gives insight into the multi-evolutionary stages of fine-branch arboreality. Such is the case when comparing 30 mice that were placed in either terrestrial or arboreal habitats. Climbing mice routinely use a pedal grasp that relies on an opposable hallux. *FIJI*, an image processing software built around *ImageJ*, was utilized to correlate this behavior with bone functional adaptation. Mid-diaphysis cross-sectional geometry of metatarsal and metacarpal image stacks recorded using micro-CT scanning technology available from the University of Ghent (Belgium) were analyzed. Cross-sectional area (CSA) and polar section modulus (Zpol) serve as proxies for compressive and bending strength, respectively. These measurements were taken at proximal, mid-shaft, and distal regions of hand and foot bones. For first and third metacarpals, and third metatarsals, the mice showed no significant difference between the arboreal and terrestrial habitats. The first metatarsal displayed a larger CSA and Zpol in climbers indicating greater resistance to compressive and bending loads along the Mt1 diaphysis. This data supports the hypothesis that a more robust metatarsal represents an initial transition towards becoming adapted for fine-branch arboreality. '

P103 Thu Doan, Tin T. Nguyen, Kendall D. Hyatt, Craig D. Byron
Biology, Mercer University, Macon, GA

The Morphomechanical Effects of Climbing on Mouse Tarsal Bones

In this study tarsals (talus and calcaneus) were compared between two groups of mice. These bones are of interest because they facilitate pedal inversion while mice grasp and balancing above narrow substrates. The growth of these bones may be affected by the mechanical loads experienced during this activity. Thirty mice were placed in two different habitats (arboreal or terrestrial) at three weeks old and raised there until 4-6 months of age. The talus and calcaneus were isolated for high resolution micro CT scanning at Duke University. Using ImageJ and Amira image analysis software, geometric properties such as cross-sectional area (CSA) and polar section modulus (Zpol) were examined at the talar neck midshaft as well as a cross section at the proximal calcaneus. These regions of interest may sustain mechanical loading analogous to a beam experiencing bending. Using this rationale, CSA relates to compressive strength while Zpol relates to bending strength. It was hypothesized that arboreal mice would show greater values for CSA and Zpol at each location due to the increased mechanical demands of pedal inversion and hallucal grasping on narrow branches. This hypothesis was rejected. However, some length parameters were observed to be significantly shorter in climber tarsals. We conclude that regular use of inverted ankle postures may be associated with shorter ankle bones but this may not represent bone functional adaptation.

P104 Madeline K. Strom[1], Luis A. Ebensperger[2], Rodrigo Vasquez[3], Enrique Bazin[3], Megan R. Taig[1], Loren D. Hayes[1]
[1] Biological and Environmental Sciences, University of Tennessee at Chattanooga; [2] Departamento de Ecología, Pontificia Universidad Católica de Chile, Santiago, Chile; [3] Departmenta de Ciencias Ecológicas, Universidad de Chile, Santiago, Chile

Habitat Specific Fitness Consequences of Sociality in *Octodon degus*

Theory predicts that social group living - a form of sociality in which individuals live in relatively long-lasting, stable groups - should persist if individuals living together gain greater net benefits compared to individuals living alone. To fully understand the adaptive significance of sociality, it is crucial that we examine the relationship between group size and composition and individual reproductive success within and between populations. The objective of this study is to describe the adaptive significance of sociality in the degu (*Octodon degus*), a caviomorph rodent endemic to central Chile. We are comparing the slopes of sociality-direct fitness regressions from two degu populations (Bosque Fray Jorge National Park; 7140'W, 30 38'S and Estaci Experimental Rinconada de Maip ; 3323'S, 7031'W). These sites differ in food abundance, vegetative cover and predation risk. We expected that the costs and benefits of group-living are very different in these populations. Ten years of study in Rinconada suggest that degus experience negative or neutral fitness consequences with increasing group size. In the first year of the study at Fray Jorge, conditions were sufficiently extreme that regardless of group size, no females experienced any reproductive success. We will present preliminary results and hypotheses for a subsequent field season. Funding: NSF IRES, ASM GIAR, UTC PSRA

P105 Margo E. Morton[1], Brian J. Shelburne[1], Richard S. Phillips[2]
[1] Mathematics and Computer Science, Wittenberg University, Springfield, OH; [2] Biology, Wittenberg University, Springfield, OH

Identification of *Peromyscus maniculatus* and *P. leucopus* Using Photo Analysis Algorithm

Efficient methods of distinguishing sister taxa in areas of sympatry are important for testing theories of niche partitioning, character displacement, and hybridization. *Peromyscus leucopus* and *P. maniculatus* are sympatric in many areas of the eastern U.S., however previous methods of morphological identification have not matched the accuracy of genetic analysis. Although genetic analysis may serve as the most accurate speciation technique, it remains costly and time consuming. Computer analysis allows additional rigor in morphological identification, so we developed an algorithm in Java to distinguish these species. The user can import a photo of a *Peromyscus* mouse, with the full body and tail shown, then run the 4-point analysis of fur color, tail to body ratio, ear to body ratio, and dorsal-ventral tail gradient. Logistic regression is applied to these traits to achieve a species classification. Using a data set of 48 species-identified mice, this program accurately classifies 95% of *P. leucopus* and 90% of *P. maniculatus* photos. With additional data and statistical optimization, we believe that these results can be improved. These results are promising because they have lowered the implicit bias in morphological identification. This program has many applications in character displacement studies in areas with and without hybridization.

P106 Nikolai M. Hay[1], Christopher Ulrey[2], Gary Kauffman[3], Marshall Ellis[4], Zack Murrell[1], Matt C. Estep[1]
[1] Appalachian State University; [2] National Park Service; [3] US Forest Service; [4] North Carolina State Parks

The Genetic Structure of Populations, Conservation and Natural History of *Geum radiatum* and the Implications for Its Future Survival on a Changing Earth

Geum radiatum is a high-elevation endemic, federally endangered herb with an extremely narrow range. Little is known about *G. radiatum*'s genetics, population interactions, and the long and complicated history of reintroductions, introductions, and augmentations that have occurred through conservation efforts. This study will aim at constructing a history of augmentations and reintroductions that identifies where plants are from, when those plants were relocated, and the current genetic structure of populations using microsatellite markers. We will address evolutionary questions of genetic diversity, gene flow, genetic drift, and assess the genetic difference between *G. radiatum* and *G. peckii.* The microsatellite markers have been screened against a small number of individuals from different populations and have been found to amplify across all sampled populations.The project is currently ongoing, so preliminary data will be presented. This information will provide a greater understanding of the genetic sustainability of *G. radiatum* and what kind of conservation efforts will most help this imperiled species survive.

P107 Jessica Padgett, Stacy Taylor-Bennetts
Biological Sciences, Georgia Regents University, Augusta

Metal Tolerance and Accumulation in a Rare Plant Species, *Pediomelum piedmontanum* (Fabaceae)

Pediomelum piedmontanum, "Dixie Mt. Breadroot," is a rareplant species with only three known populations, one on serpentine in Georgia and two on phyllite in South Carolina. Serpentine [$Mg_3Si_2O_5$] refers to a mineral and a soil, typically containing high levels of heavy metals. We hypothesize that local adaptations to edaphic metals may provide insight into the limited distribution of this species. We have previously shown that the serpentine population is tolerant from 10-50 µM NiSO4. Our current study investigates Zn tolerance and accumulation in this population. To test for zinc and increased nickel tolerance, seedlings were transplanted into one of following hydroponic solutions: 50 µM ZnSO4, 100 µM ZnSO4 or 100 µM NiSO4. Seedlings enriched with 50 µM ZnSO4 showed zinc tolerance with increased shoot and root growth whereas growth was significantly less than controls in 100 µM ZnSO4 and 100 µM NiSO4 solutions. Zn accumulation from field and experimental leaf samples was determined using the zincon colorimetric test. Zn concentrations in leaves from the field were significantly lower than other legume species. Zn concentrations were greater in the roots than in the shoots in plants propagated with Zn enrichment, which is not unusual since this species has a large taproot. However, to find Zn tolerance up to 50 µM ZnSO4 from a serpentine population in the Southeastern U.S. is a unique discovery. From growth and survivorship studies, it appears that this population has an atypical requirement for Zn and Mg, which will be the focus of future study.

P108

Shannon Kahn, Scott Harrison
Biology, Georgia Southern University, Statesboro

Divergence of Insect and Vertebrate Specific Toxin Genes Between Two Species of Widow Spider *Latrodectus geometricus* and *Latrodectus tredecimguttatus*

The brown widow spider, *Latrodectus geometricus*, is an introduced species to the southern United States. All species of widow spiders produce venom that is used against both predator and prey. These venoms are composed of several different protein toxins, some of which are taxa specific in their effect. Previous research has shown that positive selection pressures drive the evolution of venom of snakes and snails. The study presented here was designed to analyze the nucleotide and amino acid differences between Brown and Black widow spiders at two toxin genes. The purpose of the investigation was two-fold: 1) to characterize the nucleotide and amino acid divergence in insect specific latroinsectotoxin between the Brown widow and Mediterranean Black widow spiders, and 2) compare levels of divergence to that of vertebrate spedific a-latrotoxin and a non-toxin gene, Cytochrome Oxidase I (COI). We found between species nucleotide divergence to be similar at all three genes, while amino acid divergence was 2.3 to 3.2 times higher in the toxin genes relative to the non-toxin gene (COI). Amino acid divergence between species was 10% higher for latroinsectotoxin than a-latrotoxin.

P109

Samantha Reese[1], Fengjie Sun[2]
[1] School of Science and Technology, Georgia Gwinnett College, Lawrenceville; [2] Science and Technology, Georgia Gwinnett College, Lawrenceville

A Phylogenetic Study of Small RNA Tpke11 Using Secondary Structures

Recent genome-wide studies have shown that small RNA (sRNA) molecules possess structural, regulatory, and catalytic functions. The sRNA molecules are widespread in a variety of organisms and located in intergenic regions of their genomes. However, most of these sRNA-encoding genes are still uncharacterized and their cellular roles are unknown. In this study, we apply both the bioinformatics and award-winning phylogenetic methods to study the evolutionary history of the molecular structures in a small RNA family Tpke11. We use both geometrical and statistical data to generate trees of molecules to reveal the phylogenetic history of three domains of life (Eukarya, Bacteria, and Archaea) and trees of RNA substructures to show the evolutionary history of the major molecular domains in these sRNA molecules. This study is important for expanding our understanding of this

unique gene family and also demonstrates a successful application of the phylogenetic analysis of RNA structural evidence in support of the existing tree of life.

P110 Davisha Patel, Kendall Hyatt, Craig Byron
Biology, Mercer University, Macon, GA

Tail Use and Its Relationship to Arboreality in a Mouse Model System

Five lab mice were trained for fine branch arboreality and used to test tail use as means of enhancing stability on different diameter wires. Braided stainless steel lock-wire was used at 2.3 and 4.3 mm diameter thicknesses. Four trials were recorded for each mouse on each substrate (4 x 5 x 2 = 40) for a total of 40 bouts of branch walking. Within each bout, three points on the tail were tracked with a line point placed every ten frames at the base, midpoint, and tail tip. To analyze tail motion, ImageJ with the MtrackJ plugin and R software for statistical computing were used. Using these recorded trials tail motion is presented as movement distance of the three trackways (vertical oscillations) and movement forcefulness of the tail tip (the angle vector product). It is hypothesized that distal regions of the tail will show greater motion than more proximal regions and that thinner branch sizes also correspond to greater tail motion. Unsurprisingly, the results support the hypothesis that the tip is where most of the tail motion occurs. The hypothesis that thinner branches correspond to greater tail motion was not clearly supported. Furthermore, thin substrates corresponded to greater interindividual variation in both metrics for tail motion. We conclude that tail motion is used to enhance angular momentum about the animal's center of mass in order to promote arboreal stability.

P111 Christopher Wagner, Gina Botsko, Cindy Vigueira
Biology, High Point University, NC

Comparative Genetics of Parallel De-Domestication Events in Weedy Red Rice (*Oryza sativa*)

Red rice is an aggressive, weedy form of cultivated rice (*Oryza sativa*) that infests crop fields and is a primary factor limiting rice productivity in the U.S. and worldwide. As the weedy relative of a genomic model species, red rice is supremely suited to serve as a model for understanding the genetic and evolutionary mechanisms by which weediness evolves. Previous work has focused on the evolution of weediness in red rice from the southern U.S. that is genetically distinct from red rice found in California and Korea. Because these two regions have independent de- domestication events, we will be able to examine what genetic changes are required for weedy rice to take hold in an agro-ecosystem using comparative genetics. Three candidate genes that are involved in weedy traits have already been identified and sequenced in crop, wild, and weedy rice. Comparative genetics approaches have allowed for a better understanding of what weedy traits have evolved in independent weedy rice populations and what genetic mechanisms underlie the evolution of these weedy traits.

P112 C. Kabryn Mattison, David A. Beamer
Natural Science, Nash Community College, Rocky Mount, NC.

Past, Present, Future: Hybridization Between Two Dusky Salamander Lineages

The evolutionary relationship between Northern Dusky (*Desmognathus fuscus*) and Mountain Dusky Salamanders (*Desmognathus carolinesis*) has been very challenging to understand, even for many experts. Populations of these species can be found close to one another, but have never been located sympatrically. Recent phylogenetic reconstructions of Mitochondrial DNA demonstrate that many *D. fuscus* populations are characterized by mtDNA haplotypes belonging to *D. carolinesis*. This suggests that hybridization once occurred between these populations. In order to test if contemporaneous hybridization can occur between these species, I collected males and females from both species and performed a sexual incompatibility mating trial. Only intraspecific pairings that resulted in the deposition of a spermatophore were considered successful. Once the trials were complete, a Stalker Index of Sexual Incompatibility of "1" was calculated, this value indicates complete sexual isolation between the populations *D. fuscus* and *D. carolinesis* that I tested.

P113 Kayla A. Gomez, C. Kabryn Mattison, David A. Beamer
Natural Science, Nash Community College, Rocky Mount, NC

Phylogenetic Perspective of a Contact Zone Between *Desmognathus fuscus* and *Desmognathus carolinesis*

Recent phylogenetic reconstructions have detected the presence of Carolina Mountain Dusky salamander (*Desmognathus carolinesis*) mtDNA in populations of Northern Dusky salamanders (*Desmognathus fuscus*). Populations of Northern Dusky salamanders containing Carolina Mountain Dusky mtDNA have been found several hundred kilometers away from any known populations of Carolina Mountain Duskies. This suggests that hybridization between these two species occurred in the distant past. Currently, nothing is known about the interactions of these two species where they occur in close proximity of one another. Here, we present a phylogenetic perspective of populations of Carolina Mountain Duskies and Northern Dusky salamanders from an area where they occur within ~1 km of one another.

P114 M. Thilina R. Fernando, Chris Herlihy, Jeffrey Walck
Biology, Middle Tennessee State University, Murfreesboro

What Maintains the Strong Geographic Pattern of Flower Color Polymorphism in *Leavenworthia stylosa*?

Many plants exhibit variation in flower color, and in some species this variation differs geographically. Geographic variation in flower color could be due to local adaptation, variation in the abundance of pollinators and/or variation in the color preference of pollinators. Our study species *Leavenworthia stylosa*, which is endemic to cedar glades in middle Tennessee, has two main flower colors: yellow and white. We determined if local adaptation to abiotic factors or differences in pollinator abundance or color preference played a role in maintaining flower color polymorphism. Pollinator identity, abundance and preference were observed and plant survival and reproduction were recorded in a reciprocal transplant experiment, and pollinators were observed in two populations where both flower colors occur. We found variation in pollinator abundance among sites and variation in the color preference of pollinators; however, this did not occur in a way that could maintain the color polymorphism. Some pollinators showed assortative movement: 80, 54, and 46% of the transitions by butterflies, bee flies, and solitary bees were between white flowers. Both colors produced more flowers in their own color sites than in the other color sites. White plants had slightly reduced survival in yellow sites and the yellow plants had significantly reduced fruit production in white sites. Thus, pollinator-mediated selection on flower color was not observed in these populations. Although some evidence of local adaptation was found, it appears unlikely to play a strong role in the maintenance of the flower color polymorphism in *L. stylosa*.

P115 Alejandra Garcia, Joel R. McNeal
Ecology, Evolution, and Organismal Biology, Kennesaw State University, GA

Examining Differences in Host Specificity Across Closely Related Parasitic Plant Species in the Genus *Cuscuta*

Cuscuta pentagona, C.campestris and *C.harperi* are closely related parasitic plant species that inhabit different ecological niches and display varying levels of host specificity in nature. Expansins, plant proteins involved in loosening of cell walls, are expressed in the zone of *Cuscuta* attachment to the host (haustoria) and may be more diverse in species with an ability to successfully invade a broader range of host species. The diversity of alpha expansin genes expressed in each parasite species when it is invading the host will be determined by mining transcriptome data from the haustorial region of each species. Efficiency of each of the three different *Cuscuta* species in finding and making a successful connection to the host's vasculature will also be compared in greenhouse experiments using *Arabidopsis* and Alfalfa as hosts.

P116 Caitlyn R. McMullan, Courtney L. Vaeth, Melba D. Horton
Biology, University of North Georgia, Dahlonega

Lipid Production of Algae from Lake Lanier Waters for Biofuel Utilization

The pressure of finding a reliable alternative fuel source to replace petroleum is increasing at a staggering rate. Furthermore, biofuels are gaining more spotlight as the impending oil crisis and the extreme consequences of climate change become more evident than ever before. This study aims to explore the potential of lipid production of algae naturally occurring in the waters of Lake Lanier for biofuel utilization. It is hypothesized that various species will produce varying amount of lipid. Different species of algae collected from Lake Lanier were identified and the mixture was used for lipid extraction. Monocultures of two of the most common species found in the lake were obtained commercially; the chlorophyte, *Scenedesmus dimorphus* and the charophyte, *Spirogyra*, and the lipid contents were also extracted for comparison. In order to obtain relatively the same amount of biomass for extraction, *S. dimorphus* was cultivated in flasks using Bristol medium in a controlled chamber (37C; 12:12 LD cycles). Approximately four grams of wet weight biomass were used to extract the lipid following the method of Bligh and Dyer (1959) with some modifications. Results showed that the mixture of algae showed highest amount of lipid (61.2%), followed by (*Spirogyra*) (1.2%), and lowest amount obtained from (*S. dimorphus*) (0.2%) supporting the experimental hypothesis. Further analysis on the type of lipid composition from each extract will soon be conducted to determine which of the species or algal mixture will have better potential for biofuel generation.

P117 Thomas E. Gordon, Joshua B. Jones, Terry D. Richardson
Biology, University of North Alabama, Florence

Spatial Distribution, Size-Frequency, and Population Dynamics of *Bellamya japonica* in a North Alabama Pond

Bellamya (=*Cipangopaludina) japonica*, Japanese Mystery Snail, is a non-indigenous invasive species (NIS) from Asia, appearing in North America in the late 1800's. The occurrence of *B. japonica* in a pond in Muscle Shoals, Colbert County, Alabama is the first record of this species in the Tennessee River watershed. The spatial distribution, abundance and, size-frequency distribution of *B. japonica* across segregated sections in a lentic system was examined during 2014-15. Snails were sampled monthly by randomly choosing 15 locations from among thirty established positions throughout the pond and were grouped into twelve locations based upon depth and proximity to other samples.

Population densities varied seasonally and spatially throughout the pond. Near shore in the central area of the pond had the highest density at 106.8 (21.36 SE) snails/m2 while the deepest areas at the north and south ends contained no individuals. Mean population density for the entire pond was 49.1 (8.27) snails/m2. Peak monthly densities for the pond were found in May at 44.1 (11.69) snails/m2 and minimum densities of 1.4 (1.42) snails/m2 found in April). Average shell length was 42.87 (2.30) mm and size-frequency data suggest that the population is an older population with a high mortality rate for juveniles. Distribution of snails throughout the pond suggests that environmental factors like DO2 or food availability may be differentially affecting population densities at various locations.

P118 Jada M. Isenhower, Michael M. Gangloff
Biology, Appalachian State University, Boone, NC

Genetic Associations of Freshwater Mussels in the Upper Tallapoosa River Drainage

The Tallapoosa River is a major tributary to the Mobile River in northeastern Alabama and northwestern Georgia. The Mobile River Basin is a freshwater biodiversity hotspot and each of its other four major tributaries (Black Warrior, Cahaba, Coosa and Tombigbee rivers) historically supported an average of 45 freshwater mussel species. By comparison the Tallapoosa Drainage is relatively species poor supporting only 15 mussel taxa including one putatively endemic species, *Quadrula archeri*, one federally listed species (*Hamiota altilis*) and what may be an undescribed *Pleurobema*. Preliminary genetic data of Tallapoosa Drainage *Elliptio arca* populations indicate they are more closely related to *Elliptio pullata* in the Apalachicola Basin than to Mobile Basin *E. arca*. Analysis of the mitochondrial NDI gene showed, for the majority of comparisons, *E. arca* and *E. pullata* from the Apalachicola Basin. In contrast, Tallapoosa *H. altilis* exhibit relatively low genetic differences (~1.0- 1.7%) consistent with recent gene flow between populations in other Mobile Basin streams. Ongoing research will examine genetic differences between other mussel taxa in the Tallapoosa and other nearby drainages. We will also use more fine-scale markers including microsatellites to examine drainage linkages and divergence times between the Tallapoosa Drainage and other nearby drainages to provide a more complete picture of this drainage's freshwater mussel diversity.

P119 Marvin W. Fawley, Karen P. Fawley
School of Mathematical and Natural Sciences, University of Arkansas at Monticello

Characterization of Algal Strains from the Class Eustigmatophyceae Isolated from Arkansas

The Eustigmatophyceae are a little-known class of unicellular algae related to the Xanthophyceae, Chrysophyceae, diatoms and brown algae. Until very recently it was thought that the class was not very diverse and the organisms were rarely encountered in nature. Some members of the class are under intense study for biofuels and polyunsaturated fatty acid production. Although the Eustigmatophyceae are green, the presence of a large red, yellow, or orange lipid body in the cytoplasm makes them fairly easy to distinguish from green algae (Chlorophyta) and yellow-green algae (Xanthophyceae). Most of the known members of the Eustigmatophyceae are small (less than 10 micrometers), spherical or elliptical organisms with very simple morphologies. Some of these algae have sculpted or ornamented cell walls, but most are smooth-walled. We have isolated 3 strains of Eustigmatophyceae from plankton samples from eutrophic Lake Chicot (Chicot County), and 1 strain each from a shale seep in Middle Fork Barrens Natural Area (Saline County), the shore of Lake Monticello (Drew County), a small oligotrophic pond (Drew County), and a sphagnum pool in Warren Prairie Natural Area (Drew County). Characterization of these strains using DNA sequence analysis and light microscopy revealed that the strain from Middle Fork Barrens Natural Area is a member of the common soil genus *Eustigmatos*. However, the other 6 strains are all likely new taxa.

P120 Sarah G. MacDonald, Erin L. Quinlan
School of Science and Technology, Georgia Gwinnett College, Lawrenceville

Environmental Variables Impacting the Presence and Growth of the Non-Native Bivalve, *Corbicula fluminea*

Corbicula fluminea is a non-native species of freshwater clam found throughout the United States, including the Southeast. Stream conditions can contribute to the growth and survival rate of *C. fluminea*. These conditions can differ based on location of other bodies of water in relation to the stream as well as the prevalence of environmental stressors such as acid rain. Several streams throughout Gwinnett County, GA, USA were examined for the presence of *C. fluminea*, and two infested sites were chosen to determine a quick aging method based on shell length and weight. This method can be performed in the field to yield instant data on the age of the clams, as opposed to traditional staining methods for aging. The data was analyzed using ANCOVA to compare the growth curves of each site. Overall, the study suggests that there is a pH threshold for *C. fluminea* success in southeastern streams, and other environmental conditions including pH, temperature, and upstream conditions significantly impact ($p<0.05$) the growth patterns (length, weight, longevity) of this invasive species.

P121 Trisha K. Cardillo, Erin L. Quinlan
School of Science and Technology, Georgia Gwinnett College, Lawrenceville

Using Size Averaging to Evaluate Heavy Metal Accumulation in Shells of Asiatic Clams (*Corbicula fluminea*) as Biomarkers for Environmental Toxicity

Bivalves accumulate metals in their shells at significantly higher levels than in their muscle tissue, and therefore these organisms have been utilized as biomarkers for assessing metal contamination in various ecosystems. The objective of this study was to explore the potential for a non- native bivalve, *Corbicula fluminea*, as an indicator of long-term metal exposure. Sample watersheds in Gwinnett County, GA, USA were selected based on streams previously identified as sites of industrial effluent releases of copper, lead, chromium, and cadmium (USEPA, CDC). *C. fluminea* were categorized by their size (mass, length, width, and mass to length ratio), and metals were quantified using atomic absorption spectroscopy. Metal accumulation, growth rates, and shell size were analyzed by ANCOVA and Pearson's correlation coefficients. Statistical results suggests *C. fluminea* may be used as a biomarker for heavy metal exposure in streams.

P122 Tiffany N. Lutz[1], Jon M. Davenport[2], Winsor H. Lowe[2]
[1] Biology, Rutgers the State University of New Jersey, Camden, New Jersey; [2] Biological Sciences, University of Montana, Missoula

Competitive Effects of Native and Nonnative Fish on Larval Salamander Behavior and Growth

Spring salamander (*Gyrinophilus porphyriticus*) larvae are confined to streams until metamorphosis into adults. This confinement can result in intense competitive interactions with other stream organisms, including both native and nonnative species. We conducted a study in artificial streams to examine the competitive effects of a native fish, *Salvelinus fontinalis*, and non-native fish, *Lepomis gibbosus,* on growth and behavior of larval *G.*

porphyriticus and survival of a shared prey, larval *Eurycea bislineata*. To separate exploitative and interference mechanisms of competition, we deployed four fish treatments with each fish species either free-swimming or absent with fish chemical cues. A control treatment had *G*. *porphyriticus* alone. We hypothesized that competitive interactions would be strongest with the free-swimming native competitor and weakest with the chemical cues of the nonnative competitor. *G. porphyriticus* avoided areas with either fish competitor and growth was reduced in all fish treatments relative to the no-fish controls. *Eurycea bislineata* survival was low in all treatments, but was reduced the greatest in free-swimming *S. fontinalis* treatments. These results demonstrate that larval *G*. *porphyriticus* willalter their behavior to reduce encounters with both native and nonnative fish competitors, thereby compromising growth. Interestingly, the free-swimming *L. gibbosus* effects on *E. bislineata* survival were not statistically different from *G. porphyriticus* alone, suggesting that the nonnative fishmay be an inefficient predator, or may avoid *E. bislineata* completely. Overall, our findings show that competitive interactions between fish (native and nonnative) and salamanders can be complex and warrants further investigation.

P123 David Haines, Ellen Winant, William Ensign
Ecology, Evolution and Organismal Biology, Kennesaw State University, GA

Habitat Associations of Three Species of Pleurocerid Snail in an Etowah River Tributary

The pleurocerid snails *Elima carinifera, E. carinocostata*, and *E. modesta* co-occur in small streams in the lower Etowah River basin. Observations suggest there may be differences in the microhabitat occupied by the three species as well as ontogenetic shifts in habitat utilization. In this study, we investigate these potential differences in habitat utilization in Two Run Creek, an Etowah River tributary in Bartow County, Georgia. Sample points in Two Run Creek were randomly selected along a zig-zag transect. At each point velocity, depth, and substrate characteristics were recorded and snails collected. Snails were returned to the lab, identified, and aperture width recorded. Initial results indicate that *E. carinocostata* was the dominant species at the study site (59% of individuals) followed by *E. modesta* (27% of individuals) and *E. carinifera* (13%). Adult *Elimia* comprised the majority of snails (88% of individuals). Snails were most abundant on bedrock substrates and abundance declined with decreasing substrate particle size.

P124 Leah Davis, William Ensign
Ecology, Evolution and Organismal Biology, Kennesaw State University, GA

Wastewater Treatment Plant Effluent and Its Effects on Fish Diet

Wastewater treatment plants release treated discharge (effluent) into rivers and other bodies of water. The sewage effluent from the wastewater treatment plant can alter the abiotic and biotic components of the stream by altering the nutrients available. In particular, the invertebrate communities on which fish feed could potentially be altered. This study will compare two impacted streams in Georgia, Lawrence and Weaver Creek, with a more pristine stream, Raccoon Creek. Four species of fishes have been collected from each of these streams: Redbreast Sunfish (*Lepomis auritus*), Alabama Hogsucker (*Hypentelium etowanum*), Creek Chub (*Semotilus atromaculatus*), and Blackbanded Darter (*Percina nigrofasciata*). Stomachs will be removed and gut contents identified and enumerated. The hypothesis for this study is that sewage effluent will have an effect on the trophic structure of streams impacted by the effluent, altering the food resources available for fishes. Since Raccoon Creek is unaffected by sewage effluent, diets of each fish species from Raccoon Creek will be treated as a control group. The prediction is the streams affected by sewage effluent will display a diet that deviates from the diet of the fishes from Raccoon Creek.

P125 Nicole R. Lynch, Joseph M. Dirnberger
Ecology, Evolution, and Organismal Biology, Kennesaw State University, GA

Do Eastern Mosquitofish (*Gambusia holbrooki*) Take Advantage of the "Cheerios Effect" to Consume Small Planktonic Prey?

While the Eastern Mosquitofish (*Gambusia holbrooki*) is clearly adapted for surface feeding, numerous studies indicate that it is quite capable of consuming zooplankton. In this study, mosquitofish inhabiting macrophyte-dominated shallows consumed a wide size range of prey from large insect larvae to small microcrustaceans. Presence of microcrustaceans in suspended traps indicated that most are planktonic, and electivities based on gut analysis were positive for many, suggesting a potential for mosquitofish to alter plankton assemblages. However, prey items that are known to aggregate at the air-water interface (e.g. terrestrial insects and ephippial eggs) had the greatest electivities, suggesting that planktonic prey might be consumed not from the water column but when caught in the surface tension. Preliminary data from lab and field observations indicate that small cladocerans (numerically most dominant in mosquitofish guts) were preferentially caught in the surface tension. The Cheerios effect (the tendency for objects sitting on liquid surfaces to clump together) is documented in this study for plankton on the air-water interface, and can explain extreme variability among individual mosquitofish in number of prey consumed. Because mosquitofish are abundant and widely distributed, the physics of plankton entrapment in the surface tension is potentially important in understanding their impact on zooplankton assemblages, and in assessing energy transfer between pelagic and littoral zones.

P126 Rachel Schomaker, Gabriel Herrick
Biology, Florida Southern College, Lakeland

Effect of Nutrient Concentrations on Growth and Competitive Interactions in the Floating Aquatic Plant *Salvinia minima*

Nitrogen and phosphorus are nutrients that influence the growth and survival of many plants and animals in freshwater ecosystems by limiting primary productivity. Aquatic plants play a role in nutrient cycling and improving water quality by removing nitrogen and phosphorus from the water. One such aquatic plant is *Salvinia minima*, an invasive aquatic fern that inhabits freshwater habitats in Florida and other subtropical and tropical areas around the globe. Previous studies have shown that *S. minima* has the potential to suppress growth of other native aquatic ferns and native duckweed species when grown concurrently with conditions containing high nutrient levels and can compete with the other species for both space and nutrients. We test the hypothesis that nutrient levels affect the growth of *S. minima,* and predict that elevated nutrient levels will increase biomass and total number of *S. minima*. Further, for future studies, we postulate that nutrient levels affect competitive interactions between the invasive *S. minima* and *Azolla caroliniana* as well as between *S. minima* and *Lemna spp.;* thus, we expect to see competition between the different vegetative species change when nutrient levels are experimentally elevated.

P127 Mary Ann McBrayer, Kimberly A. Hays
Natural Sciences, Dalton State College, GA

Acute Toxicity Effects of Yarrow (*Achillea millifolium*) Essential Oils on *Daphnia magna*

Yarrow (*Achillea millifolium*) essential oils are reported to have larvicidal properties against the mosquito (*Aedes aegypti*). Synthetic insecticides, including organophosphates, are often used as larvicides and can be extremely toxic to non-target organisms. Establishing an environmentally safe alternative is critical for aquatic ecosystems. Our study will test and compare the acute toxicity effects of four Yarrow (*Achillea millifolium*) essential oils on the water flea (*Daphnia magna*). Four different commercial brands of *A. millifolium* essential oils will be tested, Nature's Oil, Nature's Kiss, Eden's Garden, and Artisan Aromatics. All four brands are marketed as 100% pure Yarrow (*A. millifolium*) essential oils; however, there are currently no labeling regulations on essential oil manufacturing companies. Preliminary toxicity tests were done using standard EPA protocols to establish appropriate dosing levels for later tests. At this time the results of the acute toxicity tests are preliminary; however, they suggest that 1, 10 and 100 ppm are appropriate levels at which to begin our study. More tests and replicates will be done to establish an accurate LC50 for *A. millifolium* oils on *D. magna.* Until further studies have been conducted on the toxicity effects of Yarrow essential oils on non-target organisms, it remains inconclusive that *A. millifolium* essential oils are effective alternatives to current synthetic insecticides that target mosquitos.

P128 Elizabeth G. Dobbins, Kristin A. Bakkegard
Biological and Environmental Sciences, Samford University, Birmingham, AL

Negative Effects of Rock Vane Installation on Local Macroinvertebrate Populations in Shades Creek, Jefferson County, AL

Shades Creek is a major tributary of the Cahaba River, one of eight international biodiversity hotspot recognized by the Nature Conservancy. Upper Shade Creek flows through light industrial and suburban areas of Jefferson County and is a 303d listed stream for sediment and E. Coli. To reduce local erosion, rock vanes were installed in a 400 m stretch of Shades Creek in 2010. We collected macroinvertebrates before the construction of the vanes and every subsequent year in the fall. The installation of the vanes was successful in reducing erosion in a local zone, but significantly altered habitat by removing shade and homogenizing the creek structure. Over the 4 years since the installation of the vanes, there has been an increase the percent of sensitive taxa [Ephemeroptera, Plecoptera, and Trichoptera (% EPT)] in the upstream control region with little to no change in the percent of sand-loving chironomids or invasive *Corbicula fluminea*. In the region where the vanes were installed, however, the situation is dramatically different. The percent of chironomids doubled and the percent *C. Fluminea* quadrupled, while the % EPT was severely reduced. The hot, artificially pooled section of the creek near the vanes is a nursery for invasive and tolerant species. The devastating loss of tree canopy and habitat diversity clearly outweighs the benefits of reduced local erosion. Subsequent attempts at stream reengineering must recognized the importance of maintaining habitat structure and diversity.

P129 Danielle Satre, Susan Scrivner
Reinhardt University

Possible Bisphenol a Contamination in Natural Water Systems

Bisphenol A (BPA) is a chemical used in many common consumer products such as plastic containers, canned foods and drinks, sales receipts, and even dental sealants. BPA is so prevalent it can likely be found in every household in the US. There is a growing body of evidence suggesting BPA can act as an estrogen mimic, having adverse effects on the reproductive systems of wildlife and humans. Moreover, a number of these studies report adverse effects at very low concentrations. Because BPA is prevalent in our environment, it degrades when exposed to detergents and high temperatures, and it is not removed by wastewater treatment processes, it is possible that natural waterways have been contaminated. If waterways are contaminated this could affect a large number of species, especially those that are aquatic. In this study the authors investigated BPA contamination in two natural water systems in Cherokee County, Georgia.

P130 Morgan Cato, Stephanie Unkles, Kingsley Dunkley
Biology, Abraham Baldwin Agricultural College

Mercury Levels in Freshwater Fish in South Georgia (Tifton)

Increasing mercury (Hg) levels are implicated as one of the major environmental pollutants throughout the world and are a tremendous concern in the health and food industries. Consequently, fishes and its freshwater habitats are being evaluated and regulated continuously for toxic levels of Hg aimed at protecting human health, livestock and other sensitive life forms. The objective of this study was to evaluate the Hg levels of two species of fish in the southern region of Georgia, where many people rely on local ponds and lakes for fish as protein source. Catfish (*Ictalurus punctatus*) and bass (*Micropterus salmoides*) were obtained from a pond on the Abraham Baldwin Agricultural College campus and the University of Georgia aquacultural facility. Fillet samples were prepared and analyzed at the University of Georgia Agricultural and Environmental laboratory using the Cold Vapor Atomic Absorption Spectroscopy method. Our results indicated that Hg was detected in all samples (ranging from 3.6 - 76.8 ppb Hg); however, current levels of total Hg in both species of catfish and bass were significantly lower than the mercury levels of the World Health Organization Safety Limit (500 ppb Hg) as well as the US Environmental Protection Agency (300 ppb Hg) Tissue Residue Criterion. Although our results provide basic information for the consumer in this area, to validate the findings, further testing is needed for Hg and other target chemicals in fillet samples and fish habitats. Nevertheless, our results suggest that these two species of fish pose no health risk to human consumption.

P131 Kimberly Couch, Molly Klinepeter, Gabriel Herrick
Biology, Florida Southern College, Lakeland

The Effect of Varying Nutrient Levels on the Growth of *Lemna valdiviana*

Like many aquatic plant species, the growth and development of *Lemna valdiviana,* a duckweed species native to Florida, is dependent upon the levels of nitrogen and phosphorous in the water. Recently, Florida's of Environmental Protection proposed a numeric nutrient criteria to assess the nutrient levels in the water and the responses of aquatic fauna to determine if a particular water way is considered impacted or not. We predict that increasing nutrient levels of phosphorous and nitrogen to the limits set by Florida's numeric nutrient criteria will result in an increased growth of *L. valdiviana*. In this experiment, we expose four replicates of *L. valdiviana* to three different nutrient treatments: high, low, and tap water (control). The high and low nutrient level treatments correspond to the upper and lower limits of the numeric nutrient criteria of 2.24 mg/L nitrogen, 0.496 mg/L phosphorous and 0.42 mg/L nitrogen, 0.093 mg/L phosphorous, respectively. The amount of growth of the species being exposed to each treatment is determined by measuring biomass, percent coverage of each container, and number of plants in each container. Data from this experiment support the hypothesis that increased levels of nitrogen and phosphorous in a particular water way will result in an increased growth of *L. valdiviana*. Different nutrient levels affect various ecological interactions, such as competition among species, so we plan to further test the hypothesis that nutrient levels affect competitive interactions between native and invasive species of aquatic plants.

P132 Joshua B. Jones, Thomas E. Gordon, Terry D. Richardson
Biology, University of North Alabama, Florence

Life History of the Japanese Mystery Snail, *Bellamya japonica* in a North Alabama Pond

Bellamya (= Cipangopaludina) japonica, is an aquatic freshwater viviparid snail endemic to Asia, and a non-indigenous invasive species (NIS) in North America since the 1800's. However, few studies assessing the ecology and life history of the species are available from the southeastern US. This study investigated the life history of *B. japonica* using monthly samples obtained from a pond in Northwest Alabama. This is the first reported appearance of this NIS in the Tennessee River drainage in Alabama. An Eckman grab was used to collect 15 randomly selected samples from the lake each month. Snails from each sample had sex determined and all relevant measurements recorded to the nearest mm. Shell measurements were then used to estimate shell volume (SV) in mL. Females were subsequently dissected and embryos counted. Significantly more females than males were observed, with an overall ratio of 3.1:1. Males differentiate and are identifiable at an overall SV of 0.48 mL; however, females did not contain embryos until they reached 8.62 mL. Embryos per mL SV (emb/mL) was lowest at 1.58 emb/mL in April followed by increase through December, reaching 3.32 emb/mL. It appears the snails begin reproduction in mid-winter with January water temperatures of 7.8oC (0.683 SE). *Bellamya japonica* appears to accumulate and hold embryos through the summer and fall commencing release in mid-winter with peak reproduction occurring around April-May coincident with senescence of older adults.

P133 Thomas A. Hess, Lori Tolley-Jordan
Biology, Jacksonville State University, AL

A Preliminary Survey of Macroinvertebrate Assemblages in Streams With and Without Fish in the Bankhead National Forest, Alabama

Little is known about how benthic invertebrate communities in streams differ in the presence or absence of fish due to natural barriers such as waterfalls. To address this question two, high gradient streams with waterfalls that separate fish and fishless reaches were sampled in November, 2014 in the Bankhead National Forest, Alabama. In one stream, macroinvertebrates were collected below a waterfall in a reach with fish while in the second stream, invertebrates were collected above a waterfall in a reach without fish. In both streams, invertebrates were collected by taking three surber samples from two representative habitat types. Family richness, evenness (Simpsons Reciprocal Index), and similarity in community assemblage (Jaccards Similarity Index) were calculated to determine differences in community structure between fish and fishless streams. In the fishless stream reach, 3,274 individuals/m2 from 17 families were collected, while in the stream reach with fish, 4,078 individuals/m2 from 11 families were collected. The stream reach without fish had lower diversity (SRI=2.67) than the reach with fish (SRI=4.10), with a 56% overlap in community assemblage. Although these results suggest that the fish and fishless stream reaches differ in diversity, we caution that these are preliminary results. Future efforts will include more streams, finer taxonomic resolution, and drift samples to better elucidate differences in macroinvertebrate assemblages between fish and fishless stream reaches.

P134 Mason O. Murphy[1], Mickey Agha[2], Thomas A. Maigret[1], Michael E. Dorcas[3], Steven J. Price[2]
[1] Biology, University of Kentucky, Lexington; [2] Forestry, University of Kentucky, Lexington; [3] Biology, Davidson College, NC

The Effects of Urbanization on Body Size of Larval Stream Salamanders

Body size is a key measure of fitness within a population. Furthermore, animal body sizes in urban areas are often found to be different from surrounding rural areas, which may impact overall population fitness's between urban and rural areas. We examined changes in larval body size in urban and non-urbanized catchments in two stream dwelling salamander species, the two-lined salamander (*Eurycea cirrigera*) and the dusky salamander (*Desmognathus fuscus*). Specifically, we utilized a before-after control-impact (BACI) study design which allowed for the assessment of differences in larval body size between multiple control and impacted sites, over a five year period. We found a significant decrease in larval body size in both species at the impacted sites in the first year after urbanization, followed by general increases in body size in years 3-5. Using generalized linear mixed effects models, we also found support that body size variations caused by urbanization are significantly linked to changes in abundances. Both *E. cirrigera* and *D. fuscus* are well known for their ability to persist in urbanized streams; our data suggest that despite overall lower abundances in urban streams, persistence may be due to increases in body size and subsequent post-metamorphic benefits.

P135 Angel R. Gosnell, Brandi Windham, Lindsey Richardson, Daniel T. Talley, Greg P. Lewis, Dennis C. Haney
Biology, Furman University, Greenville, SC

Differences in Stream Habitat Quality and Fish Population Parameters Across Rural Land Covers Within the South Carolina Piedmont

The impacts of agricultural, pastured, and forested land covers were assessed by examining relationships between land-use types against a suite of parameters associated with their indigenous stream systems. Stream quality was hypothesized to be highest in forested streams and most degraded by streams draining row crop agriculture. To examine this hypothesis, water, sediment and fish were collected from 39 small streams located in the Savannah, Saluda and Enoree River Basins of the SC Piedmont. Local habitat quality at each site was assessed using the Quality Habitat Evaluation Index and several simple geomorphological measures. Additionally, a variety of land cover measurements within the watershed of each sample site were determined using GIS methodology. Significant differences in sediment characteristics (e.g., median skewness), stream water chemistry (e.g., dissolved oxygen, $NO3$, and $NH4$), geomorphology (e.g., stream depth, riparian land cover scores, and entrenchment ratios) and land cover measurements (total relief and slope index) were found between the three land covers using correlational analyses and ANOVA. However, while several measured parameters supported the hypothesis that forested land covers were superior to pastured and agricultural land covers in habitat quality, others did not. For example, forested sites possessed the highest riparian scores and the lowest levels of ammonia, but forested and agricultural sites did not differ in Index of Biotic Integrity and entrenchment ratios. Furthermore, fish associated parameters (e.g., abundance, richness, and diversity) typically did not differ across land covers. This suggests that historical land use associated with intensive agriculture may still be affecting this region.

P136 James Rayburn[1], Steven Gardner[1], Donna Perygin[2]
[1]Biology Department Jacksonville State University; [2]Physical and Earth Sciences Department Jacksonville State University

Teratogenic Effects of Three Phthalates to Developing *Xenopus laevis* Embryos

Due to their large use as plasticizers since the 1930's, as well as their ability to leach off of the plastics themselves, phthalates have become ubiquitous in the environment. As a

result, many organisms including humans may be at health risk from exposure to them. Di-n-ethyl, Di-n- propyl, and Di-n-butyl phthalate were tested three times each to determine any toxic or teratogenic effects to developing Xenopus *laevis* embryos using standard Frog Embryo Teratogenesis Assay-Xenopus (FETAX). Xenopus *laevis* was used as it is a standardized model species that allows for estimation of teratogenicity of chemicals and mixtures. Adult Xenopus were injected with HGC and allowed to breed for twelve hours, after which, eggs were collected and jelly coats were removed using L-cysteine at a pH of 8. Eggs were then sorted under a microscope with 20 sorted eggs being placed into petri dishes containing 8 mL of test solution beginning with controls and ending with high concentrations. After 96 hours, probit analysis was used to calculate LC50 and EC50 values as well as the teratogenic index (96-hour LC50/96-hour EC50) for each compound. Teratogenic indexes were 1.25, 0.95, and 1.56 for Di-n-ethyl, Di-n-propyl, and Di-n-butyl phthalate, respectively, showing that teratogenicity decreases moving from a two to three carbon chain, with the fourth carbon chain increasing in teratogenicity.

P137 S. Keith Thompson[1], Gary J. Burtle[2], Carrie R. Crabtree[1]
[1] School of Science & Mathematics, Abraham Baldwin Agricultural College, Tifton, GA; [2] Animal & Dairy Science, University of Georgia - Tifton Campus

Monitoring of a Largemouth Bass Population for Its Potential to Produce Trophy Fish in Lake Henry

Lake Henry, located in Tifton, Georgia, contains a fish population that is being monitored for its potential to support trophy quality largemouth bass. Operation and management of the lake was conducted to enhance the quality of fish for this purpose. To evaluate the quantity and quality of the fish multiple hook and line samples were performed on a variety of days and weather conditions. Additional information was gathered from local fisherman who frequently visited the lake. The data gathered included what species was caught, approximate length, and approximate weight of the fish caught. Fish species caught included largemouth bass and crappie. The bass caught during the hook and line samples ranged from 0.5 lb. to 6 lbs. in weight and 12.5 in to 21.5 in length. Relative weights of the bass caught were calculated and ranged from 0.5 to 0.9, with an average of 0.74. From the data gathered on the fish populations in Lake Henry it was concluded that the management of the lake will need to continue to be monitored and managed in order to develop the trophy quality fish desired. The population of largemouth bass in Lake Henry appears to be above the level that would allow growth to trophy size. Heavier fishing pressure and selective removal of largemouth bass is needed to allow enough forage for a trophy bass population.

P138 Rob Hopkins
Wildlife and Fish Conservation and Management Program, University of Rio Grande, OH

Understanding the Role of Climate Factors in the Establishment of Introduced Fish Populations

Much research has aimed to estimate the bioclimatic envelope and assess the potential for rapid niche evolution in invasive species. In this study, we test for climate niche shifts in introduced populations of six species of cool-water fishes (Yellow Perch, Northern Pike, Walleye, Brook Trout, Rainbow Trout, and Lake Trout) in North America. Our results indicate significant niche differentiation has occurred in all species when comparing climate variables between native and introduced populations using univariate and multivariate analyses. In general, the trend is for introduced populations to occur in warmer, dryer climates with less seasonal variation in temperature compared to native ranges. Additional review of the data indicates a possible role of reservoirs in facilitating the niche shift as approximately half of all introduced populations are located in reservoirs. In conclusion, we suspect that shifts to climates with lower environmental selection pressures coupled with the hydrologic and thermal refugia offered by reservoirs are facilitating the establishment of populations outside of the native climate niche.

P139 Aaron Chase, Nicholas LaBon, Emily K. Prince
Biological Sciences, Georgia Regents University, Augusta

Is *Microcystis aeruginosa* Chemically Defended Against a Freshwater Rotifer?

Blooms of toxic cyanobacteria are a threat to human health. The cyanobacterium *Microcystis aeruginosa* produces several microcystins, non- ribosomal peptides that are hepatotoxins in mammals. Microcystins are hypothesized to defend *M. aeruginosa* against zooplankton grazers, however, tests of this hypothesis have produced mixed results. Here we clarify interactions between *M. aeruginosa* and the rotifer *Brachionus calyciflorus*, a common grazer in freshwater systems. We found that *B. calyciflorus* fed *M. aeruginosa* as a sole diet did not survive, however, when *M. aeruginosa* was part of a mixed diet rotifers survived and reproduced better than when fed a control food. The results were the same whether a toxic or non-toxic strain of *M. aeruginosa* was used. Rotifers fed only *M. aeruginsoa* stopped eating, suggesting that rotifers may starve when *M. aeruginosa* is the only food. However, in a mixed diet, rotifers consumed *M. aeruginosa* in proportion to the amount offered in the diet. A direct test of microcystin coated on food indicated that the toxin did not decrease rotifer survival or egg production, even at concentrations higher than found in *M. aeruginosa*. Interestingly, when extracts of *M. aeruginosa* cells were coated on control food, rotifers died significantly sooner than those fed food coated with a solvent control. Results suggest *M. aeruginosa* is not a good food for rotifers, but microcystin is not the cause. Instead, *M. aeruginosa* may produce an unknown compound unpalatable to rotifers. This study provides insight into dynamics of planktonic communities, and may offer strategies to manage cyanobacterial blooms.

P140 Kyle Kilpatrick II, John Hutson III, Skylar Melton, J. Bennett Anthony, Lauren Turbyfill, John Hains
Biological Sciences, Clemson University, SC

Ecology and Biology of *Bellamya japonica*, a New Invasive Species in the Savannah River Basin

Bellamya japonica, the Japanese mystery snail, is a new invasive species to Lake Hartwell, and this is the only reported occurrence in the Savannah River Basin although it is widespread in other parts of the United States. We performed analysis of the dimensions of snails captured from Lake Hartwell, to determine the relationship between mass, volume, and shell length. The data showed a predictable positive linear relationship between the three dimensions. As part of a mark-recapture effort to track their dispersal, after we measured the snails, we tagged them and re- released them into the lake at a defined location. On subsequent trips we took note of the distance of marked snails from the origin point where we had released them. During the course of the study, few of the snails had moved from the origin, indicating that *B. japonica* does not meet a critical assumption of the mark-recapture method. We also continued study of fecundity rates with weekly observations to determine the seasonal effects. These results indicated that warmer temperatures were the prime period for the snails to breed and reproduce, while cooler temperatures resulted in low fecundity. We have just begun another study to determine if protecting the shells with a polymer would improve their growth and survival compared to unprotected specimens. Here we describe the experimental rationale and design of this new field experiment to further describe the response of this new invasive species in its new environment.

P141 Andrea Sanchez, Sydney Welch, Abbie Tomba
Biology, University of Mary Washington, Fredericksburg, VA

Identification of Alarm Cue in the Crayfish *Cambarus acuminatus*

Chemical signals are a vital aspect of crayfish interactions. Crayfish use chemical signals to find food, mates and avoid danger. Alarm cues are conspecific damage released chemicals found in crayfish hemolymph that signal a predation event. Previous research shows that several crayfish species decrease locomotion in the presence of hemolymph. Limited research has been done to identify this molecule. The goal of this experiment is to confirm the presence of an alarm cue in *Cambarus acuminatus,* and identify the size of the molecule. A paired design was used to determine if *C. acuminatus* responds to alarm cues. Crayfish were collected from Horsepen Run (Stafford Co. VA). Ten individuals were each exposed to two treatments (food odor alone, and food odor with hemolymph). Food odor increases crayfish's locomotion. A water control was injected prior to each treatment. Crayfish were videotaped for two minutes after control and treatment addition. Then, time that walking legs were moving was measured. To determine the size of the molecule, similar trials were conducted expect except crayfish were treated with food odor mixed with hemolymph that was either > 30 kDa, 30 >10 kDa, or <10 kDa in size. When treated with food odor the crayfish showed a significantly greater mean change in movement (treatment - control; 39 ± 7.96 sec ± SE), than when the hemolymph was present (-25.6 ± 9.40, $p<0.0004$). Indicating that crayfish decrease movement in response to the hemolymph. We hypothesize that the alarm cue is found in the hemolymph and is smaller than10 kDa.

P142 Carolyn Lanza, Margaret Lund, Jenna Pruett, Michelle Voytko, John Hains
Biological Sciences, Clemson University, SC

A Comparison of Potential Mixes in Two Southeastern Lakes: Lake Jocassee, SC and Carters Lake, GA

The specific hydrodynamics of lakes, especially mixing frequency and depth, strongly influence all aspects of lake habitats and ecological relationships. While large deep lakes in the Southeastern USA tend to be warm monomictic lakes, there are examples of exceptional lakes, usually due to exceptional depth or morphometry. The biotic habitats of these lakes are strongly dependent on atmospheric contact and vertical transport of nutrients. Hydrodynamics controls both of these factors. Carters Lake is an example of one such exception as it qualifies as a meromictic lake (with a layer of deep water which never completely mixes). It displays both thermal and chemical characteristics of classical meromixis with a well-defined (in chemical terms) monimolimnion.Lake Jocassee is also a large, very deep lake and we are investigating its potential for meromixis as well, although historic data suggests that it has usually behaved as a warm monomictic lake with occasional years in which it did not mix completely. The thermal structure of those exceptional years, other factors remaining constant, provides clues to the factors controlling the mixing behavior.We are investigating the potential factors that might influence or control its mixing potential. Our initial investigation is based on morphometry which is complex. We compare this and selected historical data from Lake Jocassee to the known characteristics of Carters Lake. In this manner we will formulate further working hypotheses and potential ways to test them.This poster presents the initial comparisons of these two Southeastern reservoirs and their physical characteristics and mixing dynamics.

P143 Richard V. Trone, David R. Chalcraft
Biology and Center for Biodiversity, East Carolina University, Greenville, NC

Physiological Responses of Anuran Larvae to Predation Cues

Predators are known to cause prey to alter their morphology, life history or behavior in ways that reduce the likelihood of the prey being consumed by the predator. Seldom considered, however, are the consequences of predators on internal morphology (e.g., gut length) or physiology that may have important consequences for prey growth. We conducted an experiment where we ascertained whether predators induced changes in prey gut length or physiology. We found that tadpoles raised with predators had shorter guts but rearing environment had no effect on the metabolic rate of tadpoles or their body mass or survival. We also ascertained whether tadpoles alter their metabolic rate in response to visual and/or chemical cues from predators. Chemical cues from predators caused tadpoles that were not raised with predators to alter their metabolic rate but did not alter the metabolic rate of tadpoles raised with predators. Smaller tadpoles reared without predators reduced their metabolic rate by 45% in response to chemical cues while larger tadpoles reared without predators enhanced their metabolic rate by 370% in response to chemical cues. Chemical cues caused the metabolic rate of tadpoles reared with predators to be 76% lower than that observed in tadpoles reared without predators. Visual cues did not influence the metabolic rate of any tadpoles nor did it influence the effect of chemical cues on metabolic rate. Our results suggest that the tradeoff between costly predator defenses and growth may at least partially originate in prey physiology but further investigation is needed.

P144 Paul V. Cupp, Jr.
Biological Sciences, Eastern Kentucky University, Richmond

Territorial Defense by Male‐Female Pairs in Green Salamanders, *Aneides aeneus*

Previous studies of green salamanders, *Aneides aeneus*, have shown that resident males exclude intruding males from territories and resident females exclude intruding females (Cupp 1980, Cupp unpubl. data). This study addresses the question, will male-female pairs cooperate in defending against intruding males, or will resident males play a more significant role in territorial defense. Territorial and aggressive behavior of male-female pairs of green salamanders, *Aneides aeneus,* from southeastern Kentuckywere studied during late spring, summer, and fall. When male *A. aeneus* were placed into lab chambers or rock crevices containing resident male-female pairs, resident males responded aggressively while females did not. In 18 trials, resident males won 16 encounters, usually exhibiting overt aggression in chasing intruders from the chamber or crevice. Aggressive behaviors used during these encounters, primarily by resident males, included snapping, snout-pressing, biting, and bite-holds. In five cases, intruding males attempted to initiate courtship behavior with resident females. Females showed little or no aggression, usually remaining off to the side away from the aggressive activity. The lack of aggression of females toward males may be related to the stronger jaw musculature and elongated premaxillary teeth of males that could potentially damage eggs of gravid females. Males are the aggressors and defenders against intruding males.

P145 Kaitlin Norman, Carlos D. Camp
Piedmont College, Demorest, GA

A Test of Avoidance by an Aquatic Salamander (*Desmognathus folkertsi*) of Chemical Cues from an Aquatic Predator (*Nerodia sipedon*)

Chemical communication among different species is an important factor in animal behavior. For example, the detection of chemical cues left by a predator can enable a potential prey organism to avoid being eaten. One study showed that terrestrial, plethodontid salamanders (*Plethodon cinereus*) avoid the fecal material of predacious, terrestrial snakes (*Thamnophis sirtalis*), a behavior enhanced when the snakes have been eating salamanders. We asked the question, is this behavior specifically adaptive in terrestrial salamanders, or is it a plesiomorphic trait shard with stream-dwelling relatives that live in habitats in which avoidance of fecal cues might not be advantageous? To answer this question, we tested whether aquatic plethodontids *Desmognathus folkertsi*) avoid chemical cues in the fecal residue of aquatic snakes (*Nerodia sipedon*). We predicted that if avoidance is present in *Desmognathus folkertsi*, then the behavior is likely inherited as a plesiomorphic trait. However, if the behavior is absent, it may indicate that avoidance is specifically adaptive in terrestrial species. Salamanders were placed on 150 cm-diameter filter paper treated with (1) feces of *N. sipedon* fed *D. folkertsi*, (2) feces of *N. sipedon* fed fish, or (3) distilled water (control). With approximately 30 replicates for each treatment, we used survival analysis to compare the time it took for a salamander to exit the filter paper. There was not a significant difference among treatments, which suggests that avoidance may be specifically adaptive in terrestrial salamanders. However, more testing of both terrestrial and aquatic species is necessary to support this hypothesis.

P146 Erica B. Burton, Kelsey L. Hutson, Tom A. Blanchard
Biological Sciences, University of Tennessee at Martin

Differences in Habitat Use Among Species of Aquatic Snakes in the Reelfoot Lake Area of Northwestern Tennessee

Nine species of watersnake in the genus *Nerodia* are native to North America (Gibbons and Dorcas, 2004) and five of those occur in Tennessee (Neimiller, Graham, and Miller, 2013). All five of Tennessee's watersnake species are commonly observed in the Reelfoot Lake area. Although several studies of habitat use in these animals have been published, few address large-scale differences in habitat use among species where they occur together. Published information on watersnakes that occur in Tennessee suggests that all five species are habitat generalists and occur in habitats such as cypress swamps, bayous, lakes, streams, and ditches. However, personal observations of watersnakes at Reelfoot Lake suggest that some of the five species are more restrictive in their habitat use. The purpose of this study was to determine if meso-scale habitat use is different among the five species of watersnake that occur at Reelfoot Lake. We collected data from May - October of 2014 and from March - present in 2015. A variety of habitat types were carefully searched by boat or on foot, and snakes were captured if possible, identified, marked, and released at the site of capture. A location for each animal was recorded with a hand-held GPS unit and a variety of habitat variables were obtained. Our preliminary results suggest that some species of watersnake in the Reelfoot Lake area are generalist, whereas others are more restrictive in their habitat use.

P147 Kaitlyn E. Hanley, David C. Rostal
Biology, Georgia Southern University, Statesboro

Twenty Year Comparison of Reproduction of *Gopherus polyphemus* and Habitat Characteristics Between Two Sites with Differing Fire Management Plans

The effects of fire on *Gopherus polyphemus* populations in a sandhill habitat, specifically their reproductive success, has not been extensively studied in Georgia. Here we present data on a long term comparison of the reproduction and population structure under different management: long term active fire management verses a limited management approach. Reproductive output, population structure and habitat quality were compared at multiple intervals over a 20 year period (1994 to 2014). The project took place at: Fort Stewart Army Reserve (FSAR) which is managed aggressively for tortoises and George L Smith State Park (GLS) which only recently has received some management for its tortoise population. Female tortoises at FSAR are significantly larger than females at GLS. Clutch size was not significantly different between the two study sites (mean clutch size 5.375 + 1.41 eggs at GLS and 6.231 + 2.49 eggs at FSAR) in 2014 however sample sizes were extremely small and more data is needed. Clutch size at GLS had increased from 4.52 to 5.38 since 1996. The linear regression of clutch size and carapace length shows no correlation for either GLS or FSAR (r2=.0073, .586 respectively), in fact tortoises at GLS are showing a negative relationship between clutch size and female size. Habitat results were similar to the 1996 study. Tortoises at both sites are selecting habitat with low canopy and available ground forage however tortoises at FSAR are able to find more favorable available habitat throughout their range.

P148 Canceled.

P149 Glenn D. Stokes, William S. Birkhead
Biology, Columbus State University, GA

Status of the Alligator Snapping Turtle (*Macrochelys temminckii*) in Upatoi Creek on Ft. Benning, Muscogee County, Georgia

The Alligator Snapping Turtle (*Macrochelys temminckii*) suffered a dramatic decrease in population abundance as a result of heavy commercial harvesting during the 1970's and 1980's. Populations are reported to be in recovery but it is still listed as "threatened" in Georgia. In an effort to document the possible recovery in the eastern edge of its distribution a mark and recapture project was conducted in Upatoi Creek on the Ft. Benning Military Installation in west-central Georgia. Specimens were captured using 4-foot hoop net traps baited with fish during October and November of 2012, 2013 and 2014. In the first year of the study 21 adult animals were trapped, weighed, marked, measured and released. In 2013 trapping was made difficult by record rains and creek flooding that made access to the trap sites difficulty resulting in only three turtles being trapped, two were recaptures and one an unmarked juvenile. In 2014 four adults were captured, one of which was a recapture. The sex ratio of all captures was close to 1:1 (13 females; 12 males; 1 juvenile). Mean mass was 15.0 kg (SD=0.57 kg) for adult females and 24.5 kg (SD=1.33 kg) for adult males. Of note was the near absence of juveniles and subadults. This may be due to an evident and persistent wild hog problem on the installation.

P150 Diane E. McColl[1], Kyle Oliveira[1], Sarah A. Smiley[2], Terence M. Farrell[1]
[1] Biology, Stetson University, Deland, FL; [2] Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus

Pigmy Rattlesnake Predation on Ground Skinks and Florida Blue Centipedes: Prey Behavior Influences Predator Success

Sit and wait predators, including rattlesnakes, depend on prey movement and carelessness to capture prey. Field studies indicate that ground skinks and scolopendrid centipedes are two common prey items for pigmy rattlesnakes. We conducted laboratory trials in which field-captured centipedes (*Hemiscolopendra marginata*), skinks (*Scincella lateralis*), and pigmy rattlesnakes (*Sistrurus miliarius*) were placed in behavioral arenas to determine rates of predator success. Centipedes were consumed in 65.4% of trials while skinks were consumed in only 37.5% of trials. In the trials that resulted in prey consumption the time to the first successful predatory strike was significantly shorter with centipedes than with skinks. These differences in skink and centipede trials were largely the result of greater distances moved and reduced wariness in centipedes. We ran subsequent experiments to investigate which sensory cues (olfactory or visual) prey use to assess risk posed by a predator. Both skink and centipede movement and shelter use were quantified in the presence and absences of snake odor cues. Skinks behaved similarly in the presence and absence of rattlesnake odors suggesting they use visual rather than olfactory cues to avoid rattlesnakes. Centipedes were unresponsive to both snake odor cues and visual cues resulting in greater susceptibility to rattlesnake predation. Pigmy rattlesnake success in foraging is a result of both their foraging tactics and the centipedes' vulnerability.

P151 Christopher R. Peterson[1], Matthew W. H. Chatfield[2]
[1] University of Tennessee; [2] Unity College

Comparison of Bait Types in the Capture of Aquatic Herpetofauna

Poor detectability and low capture rate are frequent concerns for studies of herpetological ecology, particularly for aquatic or semi-aquatic species. Funnel traps are a commonly used passive sampling method in these studies. Prior work has demonstrated that both food and light can serve as baits to increase trap effectiveness, but the relative quality of these two methods has not been assessed. The objective of this study was to compare the effectiveness of glow stick and food baited aquatic funnel traps for capturing reptiles and amphibians. We sampled 5 locations in southern Mississippi and Louisiana for 4 summer field seasons using traps baited with glow sticks, cat food, or nothing. Catch was counted at the order level; differences in capture diversity and composition among site and bait type were examined analyzed with a Bray-Curtis distance principle coordinates analysis, and differences in capture effectiveness were evaluated with a hierarchical Bayesian model. Differences in capture effectiveness mirrored differences in capture diversity among baits and sites, suggesting that studies using a single bait type may not accurately sample community herpetofauna composition.

P152 Kevin R. Messenger, Yong Wang
Biological and Environmental Sciences, Alabama A&M University, Huntsville

Biodiversity and Movement Patterns of Snakes in the Carolina Sandhills National Wildlife Refuge

We studied the effect of abiotic and biotic factors in predicting snake activity with special reference to making species surveys more efficient. Understanding the interaction of variables can enhance the efficiency and accuracy of ecological surveys. We studied nocturnal activity of snakes in SC over a 7-year period; snakes were surveyed on 502 nights, yielding 2097 snakes of 27 species. After temperature, the effect of moon phase was a very strong predictor of snake activity. An intricate relationship between snake activity and moon phase and timing was evident. The average number of snakes encountered during large moons, was significantly lower than during small moons (one-tailed t-test, $p=0.03$). However, the data revealed a significant burst of activity in which snakes crossed more frequently just prior to an impending large moon rising that is not present in smaller moons (1.42 snakes/hr vs 0.98 snakes/hr; two-tailed t-test $p<<0.001$). On large moons, snake activity remains high during this period of darkness or low light until the moon reaches its half-way position in the sky, when activity drops significantly (0.34 snakes/hr; two-tailed t-test $p<<0.001$). The correlation between moon phase and number of snakes detected became stronger if observations were restricted to the brightest half of the night. During small moons where there was little illumination, activity levels for the night may be high, but on a per hour basis, are actually low, thus making surveys less efficient. With proper knowledge of the moon's role in influencing activity, targeted surveys could be made much more efficient.

P153 Kevan Khaksarfard, Aleesha Mincey, Megan Pike, Brandon Comer
Georgia Regents University

Testing the effectiveness of Visible Implant Elastomer (VIE) markers in hylid tree frog mark-recapture studies

Mark-recapture studies are used to estimate the population size of wild-caught animals. Marking techniques vary greatly depending on the targeted organism (i.e. leg bands, ear tags, neck collars). Methods for marking amphibians include: toe clipping, and Passive Integrated Transponder (PIT) tagging. Use of toe clipping has decreased recently over animal welfare concerns. PIT tagging is a successful, but expensive method. We tested the effectiveness of Visible Implant Elastomer (VIE) markers in a study of hylid tree frogs. Ten PVC traps were used at a forested wetland at the McDuffie Public Fishing Area. PVC pipes (5 x 45 cm) were capped at one end and suspended from trees 1.5 m above ground. Traps were checked weekly from June-October 2012. Captured frogs were identified to species, categorized by age class and sex, and marked using VIE markers. Elastomer markers were injected using 5cc syringes into the hindlimb. Colors (red/blue) and legs (right/left) were alternated weekly. A total of 35 green tree frogs (*Hyla cinerea*) and 25 squirrel tree frogs (*H. squirella*) were captured. Of 9 recaptures, none were recaptured at the trap of original capture. No frogs were recaptured more that two weeks after being marked. Seven of eight were recaptured one week after marking.

P154 Annalee M. Tutterow, Natalie Haydt, Shannon E. Pittman, Michael E. Dorcas
Biology, Davidson College, NC

The status of an isolated bog turtle (*Glyptemys mulhenbergii*) population in North Carolina

Long-term population studies of threatened species allow scientists to determine the likelihood of a population's survival and develop conservation strategies. The bog turtle (*Glyptemys mulhenbergii*) is a small and cryptic species listed as federally threatened in the United States. From late April through July 2014, we monitored a bog turtle population in Gaston County, North Carolina. Sixty bog turtles have been marked at the Gaston Bog since 1991, but a 2007 study located only thirteen adult bog turtles. Ninety-three probing hours and 1,302 trapping hours yielded only six turtles in 2014. After evaluation of both active and passive search methods, we concluded that probing (active search method) was the most effective strategy to detect individuals in the population. Additionally, we utilized game cameras to identify possible threats to turtle survival, resulting in the documentation of both raccoons and cows in the bog. Overall, the recapture of five marked adult turtles and one marked juvenile suggests that the Gaston bog turtle population may be unable to recruit new members. No new adults have been captured in eight years. Both habitat management and predator removal may be necessary to preserve bog conditions and prevent local extirpation of this species.

P155 Emma R. Parker, Natalie Haydt, Shannon E. Pittman, Michael E. Dorcas
Biology, Davidson College, NC

Variations in Movement and Risk Taking Behaviors of Juvenile Burmese Pythons

Burmese pythons (*Python molurus bivittatus*) have rapidly spread northward in Southern Florida, negatively impacting natural ecosystems. Though previous research has provided information about adult Burmese python behavior, little is currently known about the movement behavior of neonatal and juvenile pythons. The dynamics of invasive spread are particularly sensitive to the movement behavior of the juvenile age class, which is often the primary disperser among animal species. Our study analyzed the effect of sex and clutch on risk-taking behavior and movement patterns of neonatal Burmese pythons collected from South Florida. Thirty-eight neonatal pythons from three clutches (22 females, 16 males) were released alone in a rectangular arena for 20 minutes. Basic movement patterns for each snake were recorded, as well as the amount of time it took each snake to leave a hide-box and enter the arena (latency time). Pythons' movement paths were analyzed and each snake's total distance moved, average turning angle distribution, and latency time (time that the snake's head first emerged from the hide-box) was recorded. Although no significant difference between sex and clutch was found for the pythons' average turning angle distributions and latency times, one clutch displayed a higher average total distance moved than either of the other two clutches (P=0.024). Out results suggest that behaviors impacting invasive spread, such as dispersal propensity, may be heritable and will provide information critical for dispersal models which may lead to more refined conservation strategies.

P156 Regis Burkhardt
Biology, University of South Alabama, Mobile, AL

Natural Occurrence of Viruses in Wild Reptile Populations

There are currently seventeen families of viruses known to infect reptiles. These viruses cause various symptoms including, edyma, papillomas, fibropapillomas, skin lesions, respiratory infections, and nasal discharge with mortality rates frequently being high. Research on reptile viruses has increased due to an increased interest in reptile immunology. Despite this, a majority of what is known about reptile viruses comes from captive reptiles with research on reptile viruses in wild populations being sparse. Viruses that have been recorded in wild reptile populations include for example ranaviruses in Eastern Box Turtles (*Terrapene carolina carolina*), paramyxoviruses in Fer-de-lance snakes (*Bothrox atrops*), and herpesviruses in green turtles (*Chelonia mydas*). Data on population dynamics of infected wild reptiles are limited as it is the information on how widespread virus infections are in natural populations and their consequences. This work provides a review on what is known about occurrence of virus infection, effects, and virus transmission in wild reptile populations. Virus infection data on wild populations will be compared to what is known for captive populations, with emphasis on how virus dynamics differ between wild and captive reptiles. Virus infections can result in dead of many individuals and decline of reptile populations, as in the case of fibropapilloma infection in *Cheloina mydas*.As more studies are done on reptile viruses in wild populations an increased awareness of the effects of these viruses will lead to better prevention and conservation of reptile populations.

P157 Jaina S. Gandhi, Lindsey A. Liles, Kristen K. Cecala
Biology, University of the South, Sewanee, TN

Do Closed Canopy Roads Inhibit Ambystomatid Salamander Movement?

Amphibians have biphasic life histories that require high-quality aquatic and upland habitat. Although large-scale forest conversion is known to alter upland distributions of adult amphibians, less is known about features that disconnect upland habitats from breeding sites. Landscape features such as typical, paved roads are habitat fragmentors for many amphibian species, but less is known about low-impact roads that are narrow and unpaved with low traffic rates and closed canopies. Our study sought to evaluate the impact of two low-impact roads surrounding an ephemeral wetland on the Cumberland Plateau on spotted salamander (*Ambystoma maculatum*) breeding migrations. We tested whether sala- manders will be less likely to enter the wetland from directions that require them to cross a low-impact road and whether climate conditions inter- act with the occurrence of low-impact roads to alter entry and exit timing of adult salamanders. Using a drift fence, we evaluated entry and exit timing and direction of adult salamanders as a proxy for upland habitat use. Although roads may serve to fragment populations of some amphibian species, nearby low-impact roads do not appear to affect near-wetland movement or upland habitat use by Ambystomatid salamanders.

P158 E. Davis Carter, Rachel M. Goodman, Kristian M. Hargadon, Edward Lowry
Hampden-Sydney College, Hampden-Sydney, VA

Survey of Ranavirus in Central Virginia Reptiles

Emerging pathogens within the genus Ranavirus (family Iridoviridae) are carried by and can be lethal to ectotherms including amphibians, fish, and reptiles. Impacts of this virus in reptiles are understudied, and surveillance data is lacking for most species of reptiles in the wild. We surveyed four species of reptiles for ranavirus in central Virginia: Eastern Box Turtles (*Terrapene carolina carolina*), Eastern Fence Lizards (*Sceloporus undulatus*), Common Five-lined Skinks (*Plestiodon fasciatus*), and Eastern Worm Snakes (*Carphophis amoenus*). Tissue samples were taken from animals captured in the wild, and DNA was extracted and tested for presence of ranavirus using quantitative PCR. Our study confirms the presence of ranavirus in wild populations of reptiles in central Virginia. While ranavirus has been previously found and confirmed as a cause of die-offs in Eastern Box Turtles, it has not been surveyed in any wild squamates to date. Ranavirus has been detected and suspected to cause mortality in captive animals and in several snake and lizard species being transported through the pet trade. Our study contributes to better understanding of the range and prevalence of this emerging wildlife disease in reptiles.

P159 Skyla L. Slemp, Conner Stanley, Melissa Blackburn, Jack Wayland, Walter H. Smith
Natural Sciences, The University of Virginia's College at Wise

Occupancy Modeling as a Strategy for Clarifying the Distribution of the Green Salamander (*Aneides aeneus*) in the Ridge and Valley of Virginia

Occupancy modeling is an effective tool for determining the distribution of elusive species, especially when habitat variables associated with the species' presence are not known. We used occupancy modeling to clarify microhabitat selection in the green salamander (*Aneides aeneus*), an uncommon and understudied cliff specialist with an uncertain status in the Ridge and Valley region of Virginia. Microclimate and habitat variables (crevice morphology, surrounding vegetation, and landscape configuration) were measured at 100 rock faces within an unusually-abundant population of green salamanders in Wise County, Virginia to produce an occupancy model for this species. Model results were then used to locate potentially new populations of the species in Southwest Virginia and validate the accuracy of the model. Model results were found to be reflective of the presence of *A. aeneus* in multiple cliff face habitats throughout the region when compared to randomly-selected, unoccupied sites, with 36 new populations identified by screening sites for habitat variables reflective of site occupancy. Further analyses determined that crevice depth and width were found to be the most important factors predicting crevice occupancy, along with the proximity of rock faces to trees and other midstory vegetation within the context of surrounding forests. Our results validate the aforementioned habitat model and provide a more targeted means to survey for this species, without relying on detailed vegetation surveys. Our model may also be extrapolated to similar areas to further improve the biogeography of this secretive species across its range.

P160 Thomas P. Wilson, Bradley Reynolds, Joe Simpson, Daniel Armstrong, Nyssa Hunt, Paul-Erik Bakland, Simone Madsen, Jeremy Hooper, Team Salamander
Biological and Environmental Sciences, University of Tennessee at Chattanooga

Ecology of Syntopic Ambystomatid Salamanders in an Isolated Wetland in Southeastern Tennessee: Population Characteristics, Threats, and Conservation Status

Long-term investigations are needed to adequately assess herpetofaunal community structure and dynamics, and habitat alteration remains the most critical threat to these communities. Herein, we report on a long term study investigating the population dynamics of two ambystomatid species. Specifically, we evaluated relative abundance, sex ratios, body sizes and catchability of amystomatid salamanders in an isolated wetland in Hamilton County, Tennessee. We used drift fencing in conjunction with pitfalls and random sampling to capture over 13,000 salamanders. Evenness was low among all study years due to large sample sizes of ambystomatid salamanders and a variable reproductive cycle. Body sizes of Ambystoma were larger in females, and sex ratios of all Ambystoma were significantly male-biased in all study years except one female-biased sample of Ambystoma opacum (2009). This study is the first wetland community assessment for the southeastern Tennessee region and provides baseline data for future comparisons regarding changes in community structure and dynamics.

P161 Iwo G. Gross[1], Yong Wang[1], Callie J. Schweitzer[2]
[1] Biological and Environmental Sciences, Alabama A&M University, Huntsville; [2] USDA Forest Service, Southern Research Station, Normal, AL

Habitat Use, Dispersal, Hibernation, and Survival of Maternal and Neonatal Copperheads (Crotalinae; *Agkistrodon*) in a Managed Southeastern Forest Landscape

Recent studies have identified the neonatal snake cohort as an important dispersal vector in several species. Unfortunately, the comprehensive examination of early-life characteristics in snakes is logistically challenging as a result of ineffective tracking techniques and low detection probabilities in wild populations. In this study, we will examine the activity patterns, overwintering habitat requirements, and survival of gravid female Copperheads (*Agkistrodon contortrix*) and their offspring that inhabit Bankhead National Forest in northern Alabama. Gravid snakes will be implanted with standard radiotransmitters and tracked continuously from early summer until hibernation. In advance of parturition (late August), gravid females will be placed in hardware cloth exclosures at their parturition sites until they give birth. Select neonates >4g will be tracked using harmonic direction finder (HDF) tags, which function by re-emitting incoming radio signals at a harmonic frequency that can be detected by a handheld transceiver and pinpointed using basic telemetry methods. These tags require no batteries, are lightweight (*ca.* 8 mg), and have a detection range appropriate for tracking small organisms. Macro- and microhabitat surveys will be conducted alongside tracking efforts of both age classes throughout the activity season. The simultaneous implementation of these methods will help us draw conclusions concerning vital snake nesting and overwintering habitat, and the variation in habitat use and survival across Copperhead age classes. Further application and development of the HDF system could address queries regarding the ecological role and characteristics of the neonatal snake cohort, and benefit future studies of rare, elusive, or endangered species.

P162 Lacy E. Rucker[1], Yong Wang[1], Callie J Schweitzer[2], Joseph Obenschain
[1] Biological and Environmental Sciences, Alabama A&M University, Huntsville; [2] US Forest Service, Southern Research Station, Huntsville, AL

The Effects of Forest Disturbance on the Oviposition Site Preference of Amphibians Found in Upland Hardwood Forests on the Mid-Cumberland Plateau in Southern Tennessee

Because of their sensitivity to habitat disturbance, amphibians' response to silviculture practices has gained interest among researchers and conservationists. The effects of these practices on adult egg deposition have yet to be fully explored, although the importance of this is germane to sustaining these animals. The purpose of this study is to evaluate the impact of forest disturbance, distance from a forest edge, and the effect of light intensity on the breeding pool preference of amphibians in upland hardwood forests on the mid-Cumberland Plateau of southern Tennessee. One of three silviculture treatments (control, shelterwood, and oak shelterwood) were applied to stands and replicated resulting in 14 research stands. A single pool array will be placed at distance of 10, 50, and 100 meters from the edge within treatment stands and replicated for a total of 42 pool arrays. Pool arrays will contain three artificial mesocosms; each pool will be assigned a screen to manipulate light intensity. Artificial pools will be monitored over two peak-breeding seasons from April to September. The amphibian population will be estimated using opportunistic encounter surveys, visual encounter surveys, coverboards, and dip-net surveys conducted every 7-10 days, and morphometric data will be recorded on all collected individuals. The results of this study will improve our understanding of forest disturbance on the community ecology of amphibians, and will also provide forest managers and private landowners the knowledge to help reduce negative impacts of forest management techniques on amphibian populations while managing for oak regeneration on the Cumberland Plateau.

P163 Lauren Bryant[1], Stanley Trauth[2], Kevin Gribbins[1]
[1] Biology, University of Indianapolis, Indianapolis, IN 46227; [2] Biological Sciences, Arkansas State University, Jonesboro, AK

Developmental Steps of Spermiogenesis Within the Testis of the Softshell Turtle, *Apalone spinifera*

Histological accounts of spermatogenesis are accumulating in reptiles; however the turtles still have largely been ignored as far as the ultra- structure of sperm development. The following study is only the forth complete study of spermiogenesis within a turtle species. *Apalone spinifera* were collected during the months of June, July, and September 2007. The reproductive tracts were removed, fixed in Trumps, and then the testes were processed for transmission electron microscopy. Spermiogenesis within the testes of *A. spinifera* appears very similar to that of the Chinese Soft-shelled turtle, *Pelodiscus sinensis*. This suggests that chelonian spermatozoa and the process of sperm development may be highly conserved in turtles. *A. spinifera* have deeply embedded intranuclear tubules that appear to form from the subacrosome granule, which are also seen in croco- dilians, the Tuatara, and other turtles. Unlike turtles, squamates' extranuclear perforatoria are found within the subacrosomal spaces of elongating spermatids. Furthermore many spermiogenic characters of *A. spinifera* are shared among most of the other non-squamate reptiles and include the extensive acrosome complex, granular condensation of chromatin, cytoplasmic droplet loss caudally, and concentric layers of cristae within the mitochondria. All of these shared characteristics of *A. spinifera* and other turtles suggest common morphological and possibly phylogenetic kinship within non-squamate reptiles. However, restraint must be maintained until more genera of turtles and other reptilian taxa are studied for spermiogenic characters to ensure trends seen currently within the literature also appear within other turtles and non-squamate reptiles.

P164 Sarah A. Smiley[1], Kort Braeutigam[2], Jeremiah Butler[2], H. Lisle Gibbs[1], Terence M. Farrell[2]

[1] Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus; [2] Biology, Stetson University, DeLand, FL

All Snakes Arent Equal: Significant Functional Differences in Venom of Individual Pigmy Rattlesnakes (*Sistrurus miliarius*)

Snake venom composition varies between species, populations, and individuals, yet the functional significance of this variation is poorly understood, especially at the level of individual snakes. We examined whether venom collected from 25 individual pigmy rattlesnakes (*Sistrurus miliarius*) from 7 different populations differed in its toxicity to a prey species - the brown anole (*Anolis sagrei*). We conducted toxicity tests in which lizards were injected with weight-adjusted dosages (close to the expected LD50) of venom from randomly chosen individual snakes or saline controls. Toxicity tests were conducted in a paired fashion (25 venom treatments plus saline controls injected on the same date) and totaled 300 venom-injected lizards and 31 saline-injected controls. Lizards were monitored out to 48 hours post-injection. Of the 300 venom- injected lizards, 100 died, resulting in a mortality rate of 33%. Lizard mortalities were not equally distributed among snakes. The number of kills per snake did not fit an expected random (Poisson) distribution (Chi-squared= 48.33, $p<0.0001$), but was bi-modal with some snake venoms being very lethal to lizards while others induced no mortality. Using a logistic regression, lizard mortality was significantly explained by venom concentration (Chi-squared=55.51, $p<0.0001$), population of snake origin (Chi-squared=58.71, $p<0.0001$), and individual snake nested within population (Chi-squared=82.14, $p<0.0001$). This work provides evidence that previously well-documented differences in venom composition between individuals and populations likely have functional consequences for the ability of snakes to capture prey.

P165 Tyler Glanz, Kevin Gribbins
Biology, University of Indianapolis, IN

The Ultrastructure of Spermiogenesis in the Anole, *Anolis sagrei*

Most studies examining squamate sperm development have focused on the ultrastructure of spermatozoa, with few studies specifically detailing the developmental stages of spermiogenesis. In this study, testes of adult male anoles, *Anolis sagrei*, were analyzed using transmission electron microscopy to investigate the stages of spermiogenesis in comparison with previously published spermatid development data within *Anolis lineatopus,* in order to identify if spermiogenesis is conserved within the family Dactyloidae. Spermiogenesis in these two lizards have similar ultrastructural features that follow the same general steps including acrosome development, nuclear condensation and elongation, and flagellar development. While much of spermiogenesis seems conserved across Dactyloidae, there are some key morphological differences between *A. sagrei* and *A. lineatopus*. During nuclear condensation and elongation there is less spiraling of the chromatin and during this stage of development smaller nuclear lacunae are observed within *A. sagrei* nuclei. *A. sagrei* spermatids also appear to have a more round basal plate at the base of its perforatorium. There additionally are numerous myelin figures present during acrosome granule formation and an underdeveloped manchette, which is not observed at all in *A. lineatopus* spermatids. Overall spermiogenesis in *A. sagrei* is similar to that of *A. lineatopus,* with most morphological ontogenies being similar to that of other saurians. Future studies will continue to focus on changes to spermatids at

the early stages of spermiogenesis and more detailed analysis of the acrosome within the elongating spermatid to access their relevance in phylogenetic analysis.

P166 Emily Benfield[1], Rajvee Vajani[1], Hannah Masengale[2], Alison Matheney[2], Carlos Camp[1], Jessica Wooten[2]
[1] Piedmont College; [2] Centre College

Testing for Character Displacement in the Larvae of Two Cryptic, Parapatric Species of Two-Lined Salamanders (*Eurycea bislineata* Complex)

Character displacement occurs when differences between similar species become exaggerated in zones of geographic overlap. We tested for possible character displacement in the larval forms of two cryptic species of Two-lined Salamander, *Eurycea cirrigera* and *E. wilderae*. These two species are distributed parapatrically with *E. cirrigera* occupying relatively low physiographic regions (e.g., Piedmont, Coastal Plain) in the southeastern US and *E. wilderae* occurring in the southern Appalachian Mountains. The two species occur sympatrically in the Appalachian foothills of northeastern Georgia, and morphological character displacement has been suggested to be present in adults. We collected specimens (20+ of each present species per site) from two allopatric locations for each species and compared them to specimens taken from two sympatric sites. Specimens from the sympatric sites were identified genetically using both mtDNA and nDNA markers. We measured standard length (SL) plus 15 additional morphological variables. We tested for morphometric differences among allopatric populations as well as between sympatric populations using MANCOVA. We also tested for differences between paired populations in color and spot number using Mann-Whitney. We detected significant differences among populations within species but no consistent differences between species. Moreover, we found no evidence of character displacement. However, we cannot fully rule out ecological character displacement in the larvae of these species because we did not test specifically for differences in head-shape variables that might be associated with competition for food.

P167 Kevin Gribbins, Tyler Glanz, Lauren Bryant
Biology, University of Indianapolis, IN

The Ultrastructure of Spermiogenesis within the Germinal Epithelium of the Horned Lizard, *Phrynosoma cornutum*

Currently, there is inadequate histological information for spermatid morphology in lizards and other reptiles. There are only ten species of lizard that have complete ultrastructural data for spermiogenesis, including several species of *Sceloporus*. These studies have shown that differences can be seen between spermatids within saurians of the same genus. We wanted to further test the hypothesis that differences exist in spermatid morphology between species within the same family. Therefore, we collected four *Phrynosoma cornutum* males from Arizona and Texas. Their testes were extracted and worked up with standard TEM techniques. Many of the characteristics of spermiogenesis within *P. cornutum* are conserved and very similar in morphology to other sceloporines. These similarities include the development of the acrosome, perforatorium, subacrosomal cone, nuclear rostrum, and epinuclear lucent zone. However, there were also several differences observed in *P. cornutum* spermatids that are distinctive from other lizards. They include a wider and more robust perforatorium and an epinuclear lucent zone that is thinner and elongated compared to other phyrnosomatid lizards. The shoulders of the flagellar nuclear fossa also have a unique shape compared to all sqamates studied to date. The present results corroborate previous studies and show that even though there is morphological conservation within saurian spermatids, character differences between species can be recognized. Further studies on spermiogenesis are required in order to

judge the relevance of these ontogenetic changes in terms of using them in amniotic spermatid/spermatozoal phylogenic analysis.

P168 Canceled.

P169 Kameron B. Blair, James Rayburn
Biology, Jacksonville State University, AL

Determination of Altered Toxic Effects of Acetaminophen by Caffeine Using Frog Embryo Teratogenesis Assay-Xenopus (FETAX)

Acetaminophen, commonly known as Tylenol, is a drug used to reduce pain and fever, with side effects being liver damage for long term use and nausea, diarrhea, and jaundice. Caffeine is a central nervous system stimulant that is found in chocolate, sodas, and coffee that have potential side effects including increased heart rate, diarrhea, dizziness, and insomnia. Recently, all drugs containing acetaminophen content over 325 mg were discontinued, because of the long-term liver damage that has been found in humans. Frog Embryo Teratogenesis Assay-Xenopus (FETAX) was used to determine the toxic effects that caffeine causes when added to acetaminophen. Two adult Xenopus were bred by the injection of HCG. The eggs were collected, dejellied (with L-cysteine), and sorted. Twenty normally developing embryos were placed into 20mm Petri dishes with 8mls of test solution. Four dishes were used for each treatment. The test was placed in an incubator for 96 hours at 24 degrees Celsius. One treatment was a control with FETAX solution. A second treatment was acetaminophen (160mg/L). Three concentrations of caffeine (10, 75, and 150) were tested with and without acetaminophen. Also, the three levels of caffeine were combined with the high level of acetaminophen for 3 additional treatments. The experiment was repeated 3 times. Malformations, length measurements, and mortality were recorded each time. Synergisms were found with malformation and mortality of the Xenopus embryos.

P170 Samuel Thomas, Timothy O. Menzel
Natural Sciences, Piedmont College, Demorest, GA

Effects of Stream Habitat Improvement Structures on Brook Trout Populations

Man-made wooden structures for stream habitat improvement are a commonly used tool in southern Appalachian brook trout conservation, but little is known about their overall impact on streams. The goal of this study was to better understand these impacts and their relationship with native brook trout populations. Data was obtained from the Georgia DNR, which collected both fish population and stream characteristic data from 2009 -2013 on 29 streams where man-made structures were added for habitat improvement. Each stream included a 100 meter treatment section and a 100 meter control section with no structures. We selected nine streams with four years of post-treatment data and compared treatment and control sections in two separate blocked MRPP tests (MRBP) to determine whether there was a relationship between treatment and fish populations or stream characteristics. Both MRBP yielded significant results, suggesting that man-made structures have an impact on both fish populations and stream characteristics. A Mantel test was then used to determine whether changes in fish populations were related to stream changes. The Mantel test statistic was not significant, suggesting that the changes in measured stream characteristics were not responsible for the changes in brook trout populations. The MRPP tests were then repeated unblocked to eliminate the possibility that the Mantel's insignificance was due to the inability to block that procedure. The unblocked MRPP also showed significance. Taken together, our results suggest that there is some unmeasured stream variable related to these structures which is driving changes in brook trout populations.

P171 Stephanie Bridges[1], Courtney Alley[1], Kevin Gribbins[2], D. Grant Willhite[1]
[1] Natural Sciences, Tennessee Wesleyan College, Athens, TN; [2] Biology, University of Indianapolis, Indianapolis, IN

Spermatogenesis and Androgen Receptor Expression in Two Salamanders, *Desmognathus conanti* and *Plethodon serratus*

Many studies have linked androgen receptor (AR) expression to stages of spermatogenesis in species such as reptiles, mammals, and amphibians. However, no such studies have been reported in salamanders. Androgens cause a variety of effects in target tissues such as male reproductive organs, brain tissue, and skeletal tissue. In this study we sought to determine the expression of AR in spermatogenic tissue in two species of lungless salamander, Desmognathus conanti and Plethodon serratus. We present here comparative annual spermatogenic cycles and evidence of cross-reactivity between anti-human AR antibody and AR from these two salamander species.

P172 Courtney Alley[1], Stephanie Bridges[1], Kevin Gribbins[2], D. Grant Willhite[1]
[1] Natural Sciences, Tennessee Wesleyan College, Athens, TN; [2] Biology, University of Indianapolis, Indianapolis, IN

Spermatogenesis and Western Blot Analysis of Testicular Estrogen Receptor Alpha in *Desmognathus conanti* and *Plethodon serratus*

The plethodontid salamander plays a pivotal role in the delicate balance of many ecosystems. However, populations of amphibians are under increasing threat due to environmental hazards such as toxins and hormone mimics polluting their environments. Determination of the cycle of spermatogenesis in lungless salamanders and subsequent analysis of the role of estrogen in this process will allow for future research on the effects that these environmental hazards pose to male reproduction. In this study we aimed to determine the annual spermatogenic cycle of two plethodontid salamanders and the role that estrogen receptor alpha in the process of spermatogenesis.

P173 Christopher S. Thigpen, Travis D. Marsico
Biological Sciences, Arkansas State University, Jonesboro, AK

A Case of Frugivory in a Green Tree Frog (*Anura: Hylidae*) from Northeastern Arkansas

An adult green tree frog (*Hyla cinerea*) was collected in mid-September 2014 from Jonesboro, Arkansas. The frog was measured, euthanized, and examined before being fixed in 10% neutral buffered formalin and placed into the Arkansas State University herpetological museum. The stomach was removed, cleared of its contents, and measured. The contents were placed into 10% neutral buffered formalin for 48 hours and transferred to 70% ethanol. Contents included the remains of a beetle and two fruits from unknown plants. The contents were photographed, measured, and identified to the lowest achievable taxonomic level. The beetle was identified as a spotted cucumber beetle (*Diabrotica undecimpuncta howardi* Barber [Coleoptera: Chrysomelidae]). The fruits were identified as *Persicaria* sp. (likely *P. punctata* (Elliot) Small; Polygonaceae) and an as-yet unidentified species of a grass (Poaceae). Fruits in the stomachs of frogs are rarely reported in the literature, but could represent possible mechanisms for seed dispersal in plants. It is unknown if frogs select to sometimes eat fruits or if fruits are a bi-product of animal prey capture or missed predation attempts. In any case, the goal of this report is to raise awareness of a poorly documented phenomenon in an effort to direct attention to this possible method of seed dispersal.

P174 Kelly E. Dunham, Alexis R. Harman, Birvaben P. Patel, Kelsey S. Stephenson, Shawn E. Krosnick
Biology, Tennessee Technological University, Cookeville, TN

New Occurrence Data for State and Globally Listed Plant Species in Tennessees Cumberland Plateau

The Hollister Herbarium (HTTU) at Tennessee Tech University has ca. 35,000 herbarium specimens, with greatest representation of species that occur in Tennessee and the southeastern United States. The collection is in the early stages of being databased, and prioritization is currently being directed at taxa of conservation interest. Species that occur within the Cumberland Plateau, Cumberland Mountains, and Eastern Highland Rim Ecoregions of Tennessee listed with a threat status of S1-S3, G1-G3, or SH (historical significance) were identified within the Tennessee Natural Heritage Program's 2012 Rare Plant List. These taxa were located within the collection, databased, and georeferenced using Specify herbarium management software. These data will provide new information regarding occurrences, habitat preferences, and historical distributions, all of which will aid in conservation efforts relating to these taxa.

P175 Mason Brock, Dwayne Estes
Biology, Austin Peay State University, Clarksville, TN

Flora and Vegetation of Riverscour Communities of Tennessees Caney Fork River

Riverscour communities are linear communities along rocky riparian zones of high-gradient rivers maintained by flooding. These grassland-like areas often support rare, endemic, disjunct, and undescribed species. The Caney Fork River of Tennessee, located in portions of Cumberland, Warren, and White counties, has significant areas of limestone and sandstone riverscour. While sandstone riverscour communities have received some study, limestone riverscour has been poorly documented. The objectives of this study are to document the vascular flora and community associations of Caney Fork riverscour. From 2012-2014, twenty collecting trips were made along the Caney Forkin order to document to flora using herbarium specimens. In total, 345 species have been collected from these sites representing 251 genera and 98 families. A 17% species overlap was found between the sandstone and limestone sections. Rare species found during this study include *Ceratophyllum echinatum, Phyllanthopsis phyllanthoides, Potamogeton tennesseensis, Solidago arenicola*, and *Vitis rupestris*. The vegetation communities of the Caney Fork are also described. This represents the first comprehensive flora conducted of the Caney Fork River.

P176 Hannah Small, Michael Schiebout
Biology, Union University, Jackson, TN

Taxonomic Assignment of a Disjunct Population of Sand Post Oaks

Taxonomy, the branch of biology dealing with naming and classification of organisms, is vital in determining the species present in a region. Morphological classification allows tentative grouping of organisms by specific physical characteristics, but can often be difficult based on phenotype alone. This is especially true when floral or fruit structures are not present on the specimen. Thus, genotyping is a useful tool to determine the species of a particular plant. Recently,a population of sand post oaks (*Quercus margaretta*) was identified in southeastern Tennessee. As the location of this population of sand post oaks is unusual and undocumented elsewhere in Tennessee, the objective of this research is to determine their relationship of this population to other oak species by analyzing the genotypic relatedness of the DNA coding and noncoding regions. Specifically the coding regions attempting to be isolated and amplified through PCR include *rbcL* and *matK*, along with *ITS2*, a noncoding intergenetic spacer. Current data indicates the successful amplification of *rbcl*, and *matK*. Successfully amplified genes will be sequenced and then analyzed for relatedness to other oak (*Quercus*) species.

P177 Canceled.

P178 Christopher Mausert-Mooney[1,2], Dwayne Estes[1,2]
[1] Biology, Austin Peay State University, Clarksville, TN; [2] BRIT, Ft. Worth, TX

A Floristic Inventory of the Scour Zones of the Big South Fork River in Kentucky and Tennessee

Un-impounded, high-energy rivers of the Cumberland Plateau are known to experience periodic catastrophic flooding events that can create zones of highly disturbed scour habitat home for a diverse and unique assemblage of plant species. The Big South Fork River is one of the largest remaining undammed rivers in the east and contains a majority of the remaining Cumberland Plateau riverscour habitat, which is recognized as a globally imperiled system. Prior floristic surveys of Cumberland Plateau rivers have revealed the rich floristic diversity of these systems and refuge they provide for rare, disjunct and endemic plant species. Besides some limited surveys by the National Parks Service, the diversity of species and plant communities in the main stem of the Big South Fork River scour have remained enigmatic. After one year of data collection, over 280 species have been collected in riverscour habitat along the BSFR, including 11 state or federally listed species. In addition to compiling a comprehensive plant checklist, this study attempts to identify and explain the biogeographical patterns observed and augment existing abiotic and plant community assemblage descriptions through analysis of data collected from permanent plots.

P179 Sydney N. Bunting, Matt C. Estep
Biology, Appalachian State University, Boone, NC

Testing Cucumber Varieties for Resistance to the Gummy Stem Blight (*Didymella byroniae*)

The Gummy Stem Blight (*Didymella byroniae*) is a fungal pathogen of cucumbers (*Cucumis sativus).* There are no known varieties of cucumbers that are resistant to GSB. The purpose of this research was to test for GSB resistance in ten different cultivars, planted in triplicates with both an experimental (exposed to GSB spores) and control group. Leaf counts were taken every two days and final plant length was taken to compare the growth patterns between different varieties of cucumber. The plants were compared to each other and ranked on a scale of 1-5 based off their healthiness. Results suggest that none of the varieties were resistant to the fungus but that some could still grow and produce fruit even though infected. Further studies will need to be done to see if these varieties are able to withstand the fungus to produce healthy fruit suitable for agricultural purposes.

P180 Wayne Barger
State Lands Division, Natural Heritage Section, AL-DCNR, Montgomery, AL

An Overview of the Vascular Floras Conducted on Alabamas Forever Wild Tracts

Alabama's Forever Wild program is a land acquisition program that has secured more than 246,000 acres of ecologically sensitive habitat since land purchasing began in late

1994. Floral inventories have been initiated on many of the properties to document plant species occurring on the Forever Wild Tracts. This poster will provide an overview of the findings for the vascular floras conducted on these tracts.

P181 Wayne Barger
State Lands Division, Natural Heritage Section, AL-DCNR, Montgomery, AL

New and Noteworthy Records for the Flora of Alabama

While performing plant surveys across the state of Alabama, many state records and other noteworthy taxa have been collected. Site descriptions, collection information, along with brief observational data for each species will be discussed.

P182 Judy A. Redden[1], Dwayne Estes[2]
[1] Dept for Biology and Center for Excellence in Field Biology, Austin Peay State University, Clarksville, TN; [2] Botanical Research Institute of Texas

A Floristic Ecological Survey of Seepage Fens in the Western Highland Rim of Tennessee

Seepage fens are botanically unique ecosystem in the Western Highland Rim, supporting a distinct array of rare and endangered species. These small sized communities are characterized by saturated soils with an open to semi-open canopy composed of such woody species such as alder (*Alnus serrulata*), silky willow (*Salix sericea*) , swamp dogwood (*Cornus amomum*), and spice bush (*Lindera benzoin*). Notable species found within the 14 state, federal and private study sites include the federally and state endangered Tennessee yellow-eyed grass (*Xyris tennesseensis*) and state listed Grass of Parnassus (*Parnassia grandiflora*). Herbaceous flora include black-eyed susan (*Rudbeckia sp*.), rushes (*Juncus sp.*), cinnamon fern (*Osumdastrum cinnamomeum*), and October ladies'-tresses (*Spiranthes ovalis*). Documented graminoid species include *Andropogon glomeratus* var. *pumilus,* and *Carex mitchelliana.* The objective of this study is to document the flora and plant communities of these rare ecosystems.

P183 Canceled.

P184 Tori G. Collins, Mac H. Alford
Biological Sciences, University of Southern Mississippi, Hattiesburg

Species Delimitation and Relationships of Native Yams (Dioscoreaceae: *Dioscorea*) in Eastern North America

Most taxonomic treatments currently recognize two to three species of native yams in eastern North America: *Diosocorea villosa*, *D. floridana*, and sometimes *D. quaternata*, a segregate of *D. villosa*. Earlier authors (e.g., J. K. Small) had recognized as many as five species (with *D. hirticaulis* and *D. glauca* also as segregates of *D. villosa*). Key morphological features in distinguishing these putative species are rhizome morphology (long and cord-like vs. thick and contorted), number of first leaves (1-3 vs. 4-7), and habitat (sandy, rocky, swampy). Unfortunately, these critical features are rarely collected and preserved on herbarium sheets, given the length and twining nature of these perennial vines. Instead, herbarium material often consists of the terminal *D. floridana* and a broadly circumscribed *D. villosa* were recovered as genetically distinct, but no variation was found in the *D. villosa* complex. Given these data, any boundaries within the *D. villosa* complex remain ambiguous. Combined with data from other studies, these DNA data were then used to infer relationships of the native U.S. species to other species in the genus.

P185 Andrew C. Fennell, Daniel M. McNair, Mac H. Alford
Biological Sciences, University of Southern Mississippi, Hattiesburg

Species Delimitation in the *Euphorbia corollata* (Euphorbiaceae) Complex of Eastern North America

As part of a project to document the vascular flora of Wayne County, Mississippi, an unusual *Euphorbia* of the *Euphorbia corollata* complex was encountered in mature hardwood forests in limestone regions. These specimens approximately match the type of *E. apocynifolia*, a species described by J. K. Small from the Apalachicola region of Florida but usually synonymized with *E. pubentissima*. Unlike typical *E. corollata* and *E. pubentissima*, this putative species has long petioles (usually 0.5-1.2 cm), oval leaves, short stature, differences in floral morphology, and a different phenology from nearby *E. pubentissima*. Additional collections and searches in regional herbaria reveal that this morphotype is found in limey or prairie regions of the Jackson Prairie of Mississippi. In order to further test species boundaries, plastid and nuclear DNA data were gathered for *E. corollata*, *E. pubentissima*, the putative new species, and several other species of *Euphorbia* subg. *Chamaesyce* sect. *Alectoroctonum*. Analyses of DNA data affirm the distinctiveness of *E. corollata* and *E. pubentissima* but are inconclusive regarding this morphotype, given the current sampling.

P186 Andrew S. Methven[1], Andrew N. Miller[2]
[1] Biological Sciences, Eastern Illinois University, Charleston, IL; [2] Illinois Natural History Survey, University of Illinois, Urbana-Champaign, IL

Evolutionary Relationships of the Clavarioid Mushroom Genus *Lentaria*

The genus *Lentaria* includes a group of clavarioid mushrooms most commonly collected on rotten wood and debris in late summer and fall in temperate and subtropical forests around the world. Although the habitat and macroscopic features of the basidiomes of *Lentaria* are similar to those found in taxa in subgenus *Lentoramaria* in the genus *Ramaria*, the microscopic features are similar to those found in taxa in subgenus *Ligulus* in the genus *Clavariadelphus* which features smooth, narrowly elongated basidiospores. While previous phylogenetic work has clearly defined the *Phallomycetidae*, resolution of the clavarioid members of the clade has remained elusive. The working hypothesis for this project is that the genus *Lentaria* is more closely aligned phylogenetically with subgenus *Ligulus* in *Clavariadelphus* rather than with *Ramaria*. Two nuclear ribosomal regions, the 28S large subunit (LSU) and the internal transcribed spacer (ITS), have been amplified, sequenced and analyzed in an evolutionary context to resolve the phylogenetic position of *Lentaria* relative to *Clavariadelphus* and *Ramaria* and provide a better understanding of the evolution of the clavarioid growth form within the *Phallomycetidae*.

P187 Kylie Bucalo[1], Jennifer Cruse Sanders[2], Alex Reynolds[3], Alvaro Perez[4], Kevin S. Burgess[1]
[1] Biology, Columbus State University, GA; [2] Research and Conservation, Atlanta Botanical Garden, Atlanta, GA; [3] The Lovett School, Atlanta, GA; [4] Escuela de Ciencias Biológicas, Pontificia Universidad Católica del Ecuador, Quito

Evaluating the Evolutionary and Genetic Relationships among Taxonomically Complex Genera in the Andean Orchids of Ecuador

With over 4000 orchid species, representing over 240 genera, Ecuador has the highest orchid species diversity in the world. Orchids can be found in many regions of the country, however the largest concentration of diversity is found at high elevations, in the Andean cloud forests of Ecuador. Present in these environments are orchid genera that are considered to be taxonomically complex, where traditional morphology based taxonomy has been challenged, or failed to discriminate between species well. As a phylogenetic tool DNA barcoding can solve some of these issues using standardized loci to delimitate species, identify ambiguous taxa, further define genera, and explore evolutionary relationships.The goal of this project is to evaluate the genetic and evolutionary relationships among the taxonomically complex genera found at the Siempre Verde Research Station in the Imbaburra region of Ecuador. Our research describes the development of a DNA barcode library of ~200 native tropical orchid species that is currently being used to compare DNA sequence barcodes among orchid taxa. As many Orchid taxa are under threat due to deforestation, resulting in a loss of orchid biodiversity, this project contributes to an immediate conservation need to research, identify, and document the endemic flora in Andean cloud forest habitats.

P188 Samantha J. Worthy[1], Jennifer Cruse-Sanders[2], Alex Reynolds[3], Alvaro Perez[4], Kevin S. Burgess[1]
[1] Biology, Columbus State University, GA; [2] Atlanta Botanical Garden, Atlanta, GA; [3] The Lovett School, Atlanta, GA; [4] Escuela de Ciencias Biológicas, Pontificia Universidad Católica del Ecuador, Quito

Evaluation of the Relation Between Phytochemical Composition and Genetic Diversity in Tropical Plant Species

Amazonia is known for its vast diversity of plant species as well as for its many indigenous groups. Currently, this region is at the forefront of a conservation crisis that includes the loss of tropical rainforest diversity as well as a cultural loss of indigenous knowledge, including the medicinal uses of plants. While a fundamental goal of conservation is to preserve genetic diversity within and among natural populations of potential economic worth, very little is known about the relation between genetic diversity and plants of medicinal value. Medicinal plants have high levels of phytochemicals that have evolved through a selective advantage to deter herbivores; the question remains as to whether selection for phytochemicals has had an effect on the maintenance of genetic diversity in tropical plant populations. The goal of this research was to investigate the relationship between genetic diversity and chemical composition in medicinal plant taxa. Specifically, my objectives were to 1) evaluate the magnitude of DNA barcode polymorphisms among medicinal Amazonian plant taxa, 2) determine the relation between genetic diversity and the presence/absence of phytochemicals previously identified in Amazonian plant taxa, and 3) investigate the evolutionary significance of this relationship and place these findings in the context of conservation genetics. Results showed that the mean number of polymorphisms was significantly higher among species containing phytochemicals. Results from this study can help tailor conservation efforts in the Amazonian rainforest where DNA barcoding could potentially be used as a predictive tool for medicinal plant exploration.

P189 Katie McDermott, William DeMott, Gabriel Herrick
Biology, Florida Southern College, Lakeland, FL

Effect of Nutrient Concentrations on Growth and Competitive Interactions in the Floating Aquatic Fern, *Azolla caroliniana*

Azolla caroliniana, the only native *Azolla* to Florida, is a free-floating aquatic fern found in sluggish freshwaters across the eastern United States and tropics. Populations of such floating plants, which acquire nutrients directly from the water, can be diversely effected by variations in nutrient levels, which are frequently used indicators of water quality. The state of Florida uses Numeric Nutrient Criteria (NNC) to create standards for levels of ionic nitrogen and phosphorus in water, based on region and specific type of water body, and

uses these standards, among others, to determine if lakes, streams and estuaries are impaired. Excessive nutrient levels in water facilitate overgrowth of plants and algae, and can disrupt the competitive balance of the ecosystem. We studied the effect of elevated phosphate and nitrate levels on the proliferation of *A. caroliniana* in monoculture, using NNC standard for unimpaired lakes and ponds. We raised plants in three treatment groups of varying nutrient concentrations: a low concentration that fell within the NNC parameter for nitrate and phosphate levels in lakes and ponds, a high concentration that exceeded those parameters, and an unknown concentration from unaltered tap water. We recorded plant growth weekly, taking measurements of total mass, individual count, and percent coverage of water surface for each culture. High concentration cultures yielded more individuals, with less mass and surface area than low concentration cultures. Although the high nutrient level supported a higher reproductive rate, it did so at the cost of stunted growth. With this evidence in mind, we will further study how elevated nutrient levels affect the competitive success of *A. caroliniana* in mixed culture with *Salvinia minima* (invasive) *and Lemna valdiviana*, floating plants with which it commonly competes in the wild.

P190 Michael Woods
Biological and Environmental Sciences, Troy University, AL

A Revision of the Asian Species of *Apios* (Fabaceae)

The revision of the Asian species of *Apios* is based on morphological analysis of herbarium specimens and plants grown in the greenhouse. The genus is herein recognized as consisting of three distinct species and one infraspecific taxon in Asia. *Apios carnea* was described by Wallich in 1830. It occurs from northwest Laos through south-central China and northwest through northeastern Myanmar, eastern India, Bhutan and southeastern Nepal in low moist forest borders to damp, rocky uplands that are often associated with limestone. *Apios fortunei* was described by Maximowicz in 1873. It occurs in southeastern China, Taiwan and Japan in sunny thickets and along forest borders. *Apios delavayi* was described by Franchet in 1890. It occurs in south-central and southeastern China in sunny, grassy areas to densely-shaded wooded areas. *Apios delavayi* var. *gracillima* was described as *A*. *gracillima* by Dunn in 1903. It occurs in the south-central Chinese province of Yunnan in densely-shaded wooded areas. Demarcation is based on both reproductive and vegetative characteristics, both within and between species. Dichotomous keys, descriptions and distribution maps are based on more than 400 specimens studied during this project. Illustrations are presented for each taxon.

P191 Martin L. Cipollini[1], N. Royce Dingley[1], Patrick N. Felch[1], Richard Ware[2], Christopher Hughes[3], Renee E. Carleton[1], Kathy B. Richardson[4], Brian Erb[5]
[1] Biology, Berry College, Mount Berry, GA; [2] Georgia Botanical Society, Rome, GA; [3] Brookwood Tree Consulting, Atlanta, GA; [4] Provost's Office, Berry College, Mount Berry, GA; [5] Business and Finance Office, Berry College, Mount Berry, GA

The Berry College Arboretum: Initial Tree Inventory and Near-Term Plans

Berry College is perhaps best known for its >10,000 ha campus — the largest college campus in the world and one harboring a wealth of biological resources. The college considers its campus to be an "outdoor laboratory" and it is utilized by a variety of academic and student enterprise programs. Among these natural resources is the large variety of trees that have been planted on the college's campus since the school was founded in 1902, accompanied by extensive natural and managed forests. In 2014, a project was initiated to inventory trees on the campus and to establish an arboretum. This presentation provides an update on the GIS-based mapping accomplished to date and plans for the further development of the arboretum as a resource for public education, outreach, and scientific study. The arboretum is managed by a college-wide committee and will be associated with two long-term conservation projects that utilize campus resources (Mountain Longleaf Pine and American Chestnut projects), as well as new projects involving the propagation and establishment of heirloom horticultural and regional tree species. So far, records have been collected for over 1400 trees on the main campus (diameter, total and bole heights, condition, notes) comprising over 100 species and horticultural varieties. Outreach materials will include a web page, a walking tour, publically accessible maps and data files, and a Facebook page. Tree data will be maintained in a format permitting exchange using Darwin Core standards. An early goal will be to establish the Berry College Arboretum as a Level I arboretum within the ArbNet community.

P192 Kartz E. Bibb, Diann Jordan, Kennedy Wekesa, Audrey Napier, Manoj Mishra
Alabama State University, Montgomery, AL

Integrating Innovative Teaching Strategies in Biological Sciences at Alabama State University

The Biological Science Faculty Members of Alabama State University have set priorities and visions foral improvement in STEM courses by conducting a workshop for faculty to examine how well they may or may not be integrating innovative teaching strategies that engage all students in Biological Sciences. Our short term goal is to have faculty of Biological Sciences incorporate at least one innovative strategy that they are not already implementing into at least one of the courses they teach. We were able to access strategies already being practiced by engaging faculty members in a Tools for Mapping Vision and Change Core Concepts and Competencies Survey. The courses that were surveyed include General Biology Parts I and II, Molecular Biology and Genetics, Undergraduate Research, Microbiology of Water and Wastewater, Bio-techniques and Instruments, Ecology, and Human Anatomy. Learning outcomes and objectives for various courses included, but were not limited to: Identification of Molecular Functions, Comprehension of DNA Structure, Student interests in Science and Medicine, Water in Piped Systems, Waterborne Diseases, Water Treatment, Lab Practicals, Understanding Ecological Functions and Applications, Anatomy of Human Systems, Comprehending Biological Passages, Answering Scientific Questions, Summarizing Scientific Concepts, Becoming Familiar with Scientific Vocabulary, Applying Science to Every Day Life and Exploring DNA Biotechnology. Most instructors implemented strategies for learning outcomes focused on Systems.

P193 Sarah Marshburn, Zack E. Murrell, Gary L. Walker, Dru Henson
Biology, Appalachian State University, Boone, NC

One Path to the Top of the Mountain: Efforts to Reform a Comprehensive Biology Curriculum

Four representatives of the Biology Department at Appalachian State University attended a 3-day Southeastern Regional Pulse (SERP) Institute in June, 2014. Inspired by new ideas and strategies, we asked the question: could we synthesize our thoughts into a model of a four-year curriculum for ***our*** Department? The intention was **NOT** to construct ***"the"*** model that would be adopted by our Department. Rather, we set out to design a model that would facilitate meaningful and productive conversations among our faculty. We are cognizant that a design task of this complexity and magnitude can be perceived as overwhelming—hampering rather than stimulating creative thought. Thus, we wanted to design a model to serve as an exemplar for how to turn a task that faculty members may feel is an exercise of trying to create within confines and limitations into an opportunity for innovation and advancement. We stepped outside of the architecture of our current curriculum and used a backward-design approach to construct this model. By merging our goals with our situational factors, we created the framework of a curriculum that we believe empowers the next generation of biologists, incorporates modern pedagogical concepts, better utilizes our resources, and better serves the needs of all vested parties.

P194 James A. Carpenter, John K. Dogbe, William A. Wallace, Kevin N. Pennington
Barton College, Wilson, NC

Better Methods, Better Results: Implementing an Action Plan at the Barton College School of Sciences

In June 2014, members of the Barton College School of Sciences attended the Southeast Regional PULSE Institute in Richmond, VA. While there, the team developed an action plan, Bartons Action for Revision of Curriculum in the Biology and Chemistry Programs (BARC), with the primary goals of faculty development leading to more inquiry-based learning, increasing course embedded research, and mapping of the curricula leading to connections and reinforcements of learning goals across courses. A 12 month action plan with specific steps to reach these goals was begun soon after returning from the Institute. Time and resources continue to be the primary, but surmountable, hurdles to achieving goals. Discussions with other School of Sciences faculty have generated full support of the Action Plan. Meetings between the Dean of the School of Sciences and the VPAA and the Academic Council have led to the consensus that classroom innovations that impact student surveys would not negatively impact performance reviews but instead would be valued and encouraged. The dean has recalculated course loads and plans future use of course releases to improve curricular revision and student contact. To date, seven faculty in the School of Sciences have been involved in implementation of the plan. Many students have been affected so far including seventy students in Biology 101 and students in the physics and organic chemistry classes. A faculty-led student research group has been formed, which gives students a chance to discuss work in progress. Progress on the plan will be evaluated in April 2015.

P195 Paul Melvin, Michelle Furlong, Jacqueline Jordan, Barbara Musolf Clayton
State University, Morrow, GA

Biology Engaged Learning Initiative for Excellence and Valuable Experiences at Clayton State University

As part of our commitment to the Southeast Regional Pulse Institute (SERP Institute), we developed an action plan to transform our biology curriculum to better align with that suggested in the document, Vision and Change in Biology. After identifying our strengths and areas needing improvement, we developed short, medium, and long term goals for our. In the short term, we will focus on our first year Principles of Biology sequence. To recruit students earlier into mentored research, we have added authentic course embedded research in the second semester of Principles of Biology Lab. Groups of 3 4 students undergo practice in how to generate hypotheses, design methods, analyze and present results and write about their findings within the context of the scientific literature for our model organism. The student groups are then guided through designing and carrying out an inquiry based experiment. The findings of this inquiry based experiment are then used by the groups to design their own experiment and they are given time to carry out their own designed experiment. In the lecture portion of the second semester Principles of Biology, we are using enhanced pedagogy to promote building Higher Order Cognitive Skills (HOCS). Ultimately, we expect to increase retention graduation and rate, student performance, enrollment, and acceptance into professional and graduate programs.

P196 J. Scott Stauble, Jr., Dorothy Wood, Gretel Guest, Lori Khan, Kara Battle, Kathy Zarilla
Durham Technical Community College, Durham, NC

That's EPIC! (Engaging Pedagogies in Classrooms): Metacognition as a Tool to Improve Science Learning

Students often report the grade they earned on an exam does not reflect the time and effort they spent studying for it. In an attempt to link student preparation more closely with the outcome, the Science Discipline at Durham Tech is undertaking the inclusion of metacognitive strategies to improve the quality of learning by our students, and, by extension, their overall grades. With support from our college, several science instructors are using metacognitive best practices to introduce students to methods designed to engage them in thinking about their thinking. After the grades are released from the first exam, each participating instructor will deliver a short presentation on metacognitive learning strategies to introduce their students to metacognition. Metacognitive strategies will be discussed in class and hopefully adopted as a study strategy by many of the students. The grades from the first exam will be compared to those from the second exam to see if there is an improvement. Metacognitive strategies will continue to be reinforced throughout the semester. Final grade distributions from courses receiving metacognitive strategy support will be compared with distributions from classes lacking a focus on metacognition to determine if the use of the strategies improved learning. Students in courses actively employing metacognitive strategies will be asked to reflect on their perceptions of their learning. Student perception, correlated with actual grade improvement, will guide future implementation of metacognitive strategies.

P197 Joseph Bidwell, Cerrone Foster, Anna Hiatt, Cecilia McIntosh, Rebecca Pyles
Biological Sciences, East Tennessee State University, Johnson City, TN

Progress on Implementing Transformative Approaches in Southern Appalachia

Over the last year the Faculty of Biological Sciences at East Tennessee State University have been evaluating core coursework for biology majors and working towards transforming teaching approaches to enhance the undergraduate learning experience and improve overall learning outcomes among our graduates. Our institution serves a large population of low-income and first generation college students living and working in Southern Appalachian region. The most important motivation behind transformation is to provide highly-qualified graduates who can contribute to the economic development and growth of the area. In focusing on traineeship and skills development of graduates, we adopted an action plan focused on students, faculty, and curriculum development. Under the leadership of the chair, productive and positive discourse on curricular goals among faculty has shaped well-defined core concepts and competencies we envision for our graduates. Several faculty are using research-based methods to improve the core curriculum and to infuse best teaching practices in the classroom. The strengths of our program lie in having demonstrated success in providing students with authentic research experiences in upper-level courses. We are working towards infusing these ideas and skills-development into the introductory core curriculum in hopes of increasing the number of undergraduates who pursue professional graduate degrees. Our hopes are that investing in transformative changes in the classrooms and providing high-quality educational opportunities will increase the time our students devote to STEM career development and ultimately result in large-scale economic development on the Southern Appalachian community.

P198 Chrisha L Dolan, Grant Pilkay, Christina Fitch, M. Cameron Harmon, Leroy Humphries
Fayetteville Technical Community College, NC

A Metacognitive Approach to Teaching Scientific Method and Writing to General Biology Students

The purpose of this research has been to foster student self-awareness of learning processes and to empower faculty to utilize engaging pedagogies. The project focus is familiarity, comprehension and evaluation of the scientific method, scientific writing, and experimental design. Students completed a pre- and post- activity metacognition survey to self-assess their familiarity and confidence with the scientific method and writing. The laboratory activity included a lesson on scientific method, writing, and a group evaluation and presentation of a peer-reviewed scholarly journal. The preliminary data shows a general trend toward a greater familiarity and comprehension following the lab exercise. The greatest improvement of confidence was seen in scientific method and writing familiarity, comprehension and recognition of writing types. While still an improvement, post-activity confidence in critical analysis and original development of experimental design was moderate. This self- assessment will allow the to evaluate students confidence in their understanding and abilities and pinpoint where instruction should increase focus. A semester-long active learning activity was embedded in which students completed a research project that culminated in submission of a scientific paper. A student subsample completed a final metacognition assessment following the culmination of the research project. This sub- sample showed a defined trend toward increased confidence in scientific method familiarity and experimental design analysis. Future goals include project continuation with improvements where necessary, introduction of a course wide final metacognition assessment following the research project and a content evaluation of student comprehension.

P199 Jung Choi, David Collard, Linda Green, Chrissy Spencer
Georgia Tech, Atlanta, GA

Advancing Academic and Scholarly Engagement in Biology

To serve our majors, minors, and students in the Introductory Biology lab sequence, Georgia Tech Biology prioritizes alignment of the Biology undergraduate experience with Vision and Change. Our priorities are to: 1) Mentor new and existing faculty to practice student-centered learning strategies 2) Engage students in metacognitive reflection and the practice of successful learning strategies 3) Motivate and equip students to initiate undergraduate research in the freshman and sophomore years. Our action plan to address these goals is well underway as we seek to improve retention in the major, increase student learning, increase student identification as scientists, increase opportunities to engage in research scholarship, and to increase collaboration among faculty.

P200 Michael J. Wolyniak, Edward Lowry, C. William Anderson, W.C. "Mike" McDermott
Hampden-Sydney College, VA

Vision and Change for Good Men and Good Citizens: Implementing Pedagogical Reform at Hampden-Sydney College

Hampden-Sydney College is a liberal arts college in central Virginia enrolling approximately 1100 men. The College both benefits and suffers from 238 years of tradition launched from its 1776 founding. While the College provides a solid liberal arts education to its students, it has often found the embrace of new innovations in teaching difficult. Here we describe our efforts to bring the principles of Vision and Change to the life sciences at Hampden-Sydney. Our central objectives are to provide authentic research experiences at each level of our curriculum, to collaborate with other to provide more interdisciplinary experiences to our students, and to work with other institutions to develop research networks in which students and faculty can collaborate on large-scale projects. As a key first step in our reform efforts, we are designing a new introductory biology laboratory experience that will integrate the major tenets of a biology survey course into a semester-long research project characterizing the fungal invaders of natural and commercial lines of hops. The data generated in this laboratory experience will provide an authentic research experience to our students while directly contributing to the research agendas of biology faculty. This new lab will be run alongside a traditional lab curriculum that focuses multiple smaller project modules. Pedagogical data will be collected as part of a long-term study on the benefits of an authentic research experience that addresses all major themes of a survey course as opposed to a model that only covers a single area of biology.

P201 Tim Bloss, Kyle Seifert, Joanna Mott, Judy Dilts
Biology, James Madison University, Harrisonburg, VA

New Horizons in Biology at James Madison University

The James Madison University Biology action plan lays the foundation for a comprehensive restructuring of the Biology Major experience, with the goals of enhancing student learning and increasing retention through the development of a modern biology curriculum that includes authentic research experiences. Our initial focus is on both the improvement of the first year experience of the major and the integration of metacognitive strategies throughout the major. To facilitate unifiedal engagement, our ideas were presented during an open forum that achieved buy-in from a vast majority of faculty. To encourage active participation in the process, 4VA summer funding was procured to compensate faculty for work on course redesign. Already developed is a freshman advising seminar with a strong metacognition component that all incoming biology majors will experience beginning Fall of 2015. To aid in the freshman year course redesign, visits to comparable universities with successful first year, research embedded experiences closely aligned with the best practices of Vision and Change have been scheduled for this year, and the baseline mapping data collected will be used to inform changes in the first - year curricular redesign. In addition, we plan to broaden the diversity of our major population through the establishment of an REU proposal strongly associated with the community college system throughout Virginia. Ultimately, the vision we established at PULSE in the summer of 2014 remains the same today: the development of a student-centered, engaged faculty implementing a relevant, research-embedded curriculum based on core competencies and metacognition.

P202 TD Maze, Mark J. Pilgrim, Jason P Lee
Lander University, Greenwood, SC

A Comprehensive Learning Action Plan (CLAP) for Lander University's Biology Program

A comprehensive action plan was created at the 2014 SERP Institute to transform our curriculum into one that: 1. aligns student learning outcomes (SLOs) and the curriculum with the recommendations from Vision & Change by AAAS, 2. prioritizes higher-order student-centered learning practices, and 3. enhances faculty development. Subsequently, our college Dean, a SERP participant, funded a faculty member to complete and submit the self-analysis rubric to PULSE. The SERP team led an off-campus retreat to present the action plan to the and to review the core concepts and competencies of the V&C document, led monthly Development Meetings with topics stressed during the SERP Institute, and created a library consisting of books and articles on best practices in teaching. A persistent lack of time for faculty to redesign courses or programs has been an obstacle and the university does not provide release time for faculty to engage in these activities. Despite this obstacle, our faculty members have been engaged in meaningful discussions about SLOs in their syllabi and five of our upper-level courses now involve course-embedded research (CER). The number of students making presentations, from independent research and CER, has increased dramatically from last year. Seventeen students will be presenting at our university-wide academic showcase, two students are presenting at the regional Upstate Research Symposium in Spartanburg, and two students are making presentations at the international Experimental Biology meeting in Boston. Another retreat is planned to discuss our progress and to reevaluate the action plan for possible enhancements.

P203 Kevin M. Drace, Lake Lambert, Katharine V. Northcutt, Linda L. Hensel, Virginia A. Young
Mercer University, Macon, Georgia

Save the Bears: Report on the Action Plan of Mercer University's Biology

During our week at SERP, we outlined four steps as part of our action plan for 2014-2015 and four steps for moving beyond the current academic year. We have completed or begun work on each of those steps, and we are confident that we will continue to build on our actions in the coming years. One major accomplishment was obtaining buy-in; to date, more than half of our members have modified teaching approaches in the classroom based on information we brought back from SERP. For example, many of us now include classroom sessions on metacognition as a method to improve student study skills and classroom performance. Dean Lambert and Dr. Hensel shared metacognition strategies with all of the colleges UNV 101 First Year Student Experience sections. Dr. Drace and Dr. Hensel implemented authentic research into the laboratory components of Introduction to Biology II and Genetics, respectively. Dr. Northcutt and Dr. Hensel reached out across campus to encourage multi- disciplinary approaches to teaching introductory biology, psychology, mathematics, and chemistry courses with authentic research experiences. Dr. Northcutt is planning an integrative course that couples Introduction to Biology I with Pre-calculus, Statistics, Physics, and Psychology, and this course will debut in 2015-2016. Dr. Hensel is collaborating with an organic chemist and a mathematician to offer an integrative course encompassing Introduction to Biology II, Organic Chemistry I, and Mathematical Modeling. Additional examples of steps we are taking to fulfill our action plan and plans for moving forward will be discussed.

P204 Loretta O. Adoghe, A. Viera, J. Morata, M. Neer, A. Leon
Miami Dade College, FL

SERP 2014 in Action at MDC

Representatives attended the SERP institute to discuss Miami Dade College's (MDC) participation in PULSEs mission toward advancing the reforms addressed in Vision and Change in Undergraduate Biology Education: A Call to Action [AAAS, 2011]. This resulted in: (1) The School of Science Dean charging science to complete the STEM Evaluation Rubric; (2) Collaborate with grassroots leaders to discuss evaluation and dissemination of results. Currently on-going; faculty have received the rubric and data will be discussed during spring retreat; (3) Establish Active-Learning Science task-force to develop initiatives to share with the academy. Currently ongoing; faculty have established active learning initiatives across the discipline e.g. students have researched news topics such as Ebola, analyzed data and presented to the campus community, incorporated flipped classroom model in Anatomy and Microbiology Hybrid courses, including instruction using Learning Catalytics, incorporating POGIL formative assessments in Microbiology classes, authentic research using PBL in laboratory courses, and research within learning communities integrating iPads; (4) Distribute Core Competency Rubric in Principles of Biology courses. This is an on-going; feedback from rubric is expected in spring 2015; (5) Explore existing partners and local institutions for research opportunities. Partnerships have been established, participants will continue explore this; (6) Leverage the Fall-term SACS visit to encourage change and re-direction if necessary; completed; (7) Initiate metacognition dialogue within through speaker facilitation. This has been accomplished; Dr. McGuire was invited to address the MDC community and efforts have been established to incorporate metacognition principals into student advisement and course development.

P205 Charles N. Horn, Valarie Burnett, Steven Lambert,
Dale Brown Newberry College, SC

Active Learning: A Strong PULSE at Newberry College

Newberry College is a small liberal arts college (1,050 undergraduate students), located in Central South Carolina. Our five full time faculty help to educate students within three concentrations of the biology major: environmental studies, forensics and secondary education. Our program population is predominantly white (72%) and male (52%). Our mission is to produce graduates who are actively engaged in lifelong learning, self-reflection, and possess critical thinking skills. As we push for program changes, we have recognized some challenges which include instructor time constraints, the need for additional faculty training, and that students may be poorly trained for college level work. Further, students are in need of better critical thinking skills, a feature which we recognize as a weakness of many students starting college. Thus, our priorities are to incorporate higher order cognitive skills and integrate course embedded research that will result in students having improved critical thinking skills and eventually participate in independent research. Toward an attempt to realize our goals we see the need to include all biology program faculty and severalal and college administrators in implementing our action plan. At theal level we have been involved in the writing of grant proposals to help with remedial science and math skills as well as incorporation of critical thinking and research skills into courses. We have also noticed our strengths (assessment is in place, and the targeting of core competencies) as well as weaknesses (pedagogical methods and faculty development).

P206 Maureen Scott, Ashley N. Haines, Regina A. Oyesanya, Larry Mattix
Norfolk State University, Norfolk, VA

From Classical to Modern Pedagogy: A Case Study

Norfolk State University is a 4 year, comprehensive, state university with ~6500 students, primarily African American. The University's Biology program is made up of 17 faculty members serving ~320 majors, many with an interest in medical, dental and veterinary fields. In light of the changes in standardized tests, such as the MCAT, and the emphasis on critical analysis and reasoning skills, our faculty has committed to updating our teaching techniques and curriculum. Our short-term goals include adding more course-based research to our laboratory courses, increasing student engagement with faculty and focusing our learning assessment techniques on higher-order cognitive skills (HOCS). To accomplish this, a research component was added to the Zoology, Microbiology and Embryology laboratories, building on those already in place for Botany and Molecular Biology. We have begun reviewing existing learning assessments as part of a project to prepare aal annual assessment test, designed to identify at-risk students. HOCS will be added to a database that can be accessed by all faculty, in hopes that this resource will encourage us to re- evaulate our exams and other testing materials. More significant changes to our overall are planned as we prepare for PULSE Ambassadors to visit our campus in May. We look forward to using the V&C Rubrics and Worksheets to meet our long-term goal of transitioning from a more classical biology curriculum, to one better suited to the needs of todays students and reflective of the recent research in the scholarship of teaching and learning.

P207 Gail P. Hollowell, Wendy H. Grillo, Amal M. Abu-Shakra, Mabel O. Royal
North Carolina Central University, Durham

Strengthening the PULSE of Our Majors: Infusion of a Course-Based Undergraduate Research Experience (CURE) into the Biology Curriculum

The Biology at NCCU with the support of Howard Hughes Medical Institute (HHMI) has created a mechanism for student success by integrating Course-based Undergraduate Research Experiences (CURE) into the curricula. This has been done by training new and current faculty in the development and delivery of engaging curricula. NCCU is the first liberal arts institution for African-American students (65% Pell-eligible; 30% First generation) with an average freshman retention rate of 70%. Our goals are to help science majors better apply scientific concepts, and enjoy early exposure to basic research techniques, and to improve first year retention rates from Biology I to Biology III. The sciences have the highest attrition rates of any major (NSF, 1996), and undergraduate research experiences have a strong impact on enhancing retention rates for those students who pursue an undergraduate science degree (Lopatto, 2004; Gregerman et al., 1998). Our CURE model is currently being implemented into 3 core biology classes using yeast as a common organism. We have adapted the modular concept within the course that begins with Module #1 that introduces scientific techniques and familiarize students with scientific equipment, followed by Module #2 that incorporates authentic research experiences. Each course has a different research question which is supported by a relevant experimental design, alongside peer led teaching and learning (PLTL) activities. Our PLTL communities that consist of a faculty member, a post-doctoral fellow, a graduate assistant, and an undergraduate assistant, enhance faculty teaching and ensure effective development and implementation of innovative curricula.

P208 Natalie Lenard, Dixie Gautreaux, Ratna Gupta, John Maloney, Daphne Oldendorf, Brian Rash, Dawn Simms
Our Lady of the Lake College, Baton Rouge, LA

CLARE: Consequential Learning Achieved by Research Experiences

Last year's SERP Institute Team established a priority to 'provide all students with evidence-based research opportunities throughout the curriculum to increase learning gains in the core competency of scientific inquiry.' While it is straightforward to address this competency within the biology curriculum, it is decidedly more difficult to provide such experiences for the health professions, health service administration, and liberal studies curricula. To these ends, 5 sciences faculty have infused or enhanced CUREs in courses primarily taken by health professions students (Chemical Fundamentals), biology students (General Chemistry Lab, Organic Chemistry Lab, Biology Research), and both groups (General Biology Lab, Microbiology Lab, Intro to Scientific Research). This included a total of 210 students in the fall semester of 2014. Examples of inquiry- based experiences included 1) a LabQuest-based activity titled 'Acid-Base Properties of Household Products' in Chemical Fundamentals, 2) a two- lab project wherein students tested enzymatic presence, structure, and/or functional properties in food products in General Biology Lab,

3) a multi-lab project wherein students investigated the identity of an unknown organism in Microbiology Lab, and 4) student-generated hypotheses, and subsequent development of proposals for testing these hypotheses, in Intro to Scientific Research. Preliminary data indicate an increase in achieved student learning outcomes (i.e., 5% in Chemical Fundamentals) and overall improvement in student engagement. The spring semester will see additional CURE-based curriculum added to the Biology Research and Organic Chemistry Lab courses, including a total of approximately 181 students. Future endeavors include possible infusion of CUREs into Anatomy and Physiology Lab coursework.

P209 Vonda L. Reed, Paulette R. Dillard, Renata H. Dusenbury, Kimberly L. Raiford
Shaw University, Raleigh, NC

Shaw on a Mission Through Vision and Change

The mission of the Bachelor of Science Program in Biology at Shaw University is to teach high quality science courses; prepare students for entry into graduate or professional programs through comprehensive course requirements; and to provide academic and professional enrichment for students who desire to pursue careers in biological sciences. The priorities of the program are to improve student retention and graduation rates and increase the number of underrepresented students who pursue post-graduate studies. The specific aims identified to address our strategic priorities are to: 1) enhance student cognitive and metacognitive skills and 2) strengthen core competencies within the classroom. To achieve these aims, our team initially utilized the PULSE Vision & Change and STEM Evaluation rubrics to perform an assessment of our current status as a baseline. The next step of the plan is to gain support of a key stakeholder, the Director of First Year Studies at Shaw University. With the unanimous support of another stakeholder, the biology faculty, the Biology Curriculum Map was revised by aligning the Program Learning Outcomes and Student Learning Outcomes of all courses within the program to reflect the BioCore Guide. Interdisciplinary teams were formed and HIPS activities, such as weekly seminars, learning communities, collaborative assignments, undergraduate research, and an amended Senior Capstone course were initiated. Baseline data and the assessment plan will be used at the end of the 2015 academic year to evaluate our progress.

P210 James B. Stukes, Judith D. Salley, Ashley E. Knowell, Shanora G. Brown
South Carolina State University, Orangeburg

Curls to Cures: Transformingal Modalities One Lesson at a Time

The call for reform outlined in Vision and Change framed a new vision and priorities for transformation in the of Biological and Physical Sciences at South Carolina State University to include faculty development, authentic course-based research and pedagogical strategies. The purpose of this pilot study was to infuse new pedagogical strategies, Course-based Undergraduate Research Experiences (CUREs), into an introductory and junior level Biology course for majors. The SC State SERP team invented Course-based Undergraduate Research Lessons (CURLs), as a mini-CURE as the faculty workload did not allow time for full planning and implementation of a CURE. This adapted pilot study reports on the outcome of our CURLs to CUREs model. In June 2014, the team implemented its first CURL entitled The SC State Health Education and Research Training Scholars (HEARTS) workshop for 10 rising high-school sophomore minority females. The HEARTS were effectively educated on the interdependence of biomedical research, its application to clinical diagnosis, treatment and ethics. The second series of CURLs were piloted Fall 2014, and introduced research methodology, critical thinking and general biology concepts to 157 students. Preliminary surveys indicated CURLs positively changed the attitudes of faculty to implement new teaching strategies, motivated and engaged students to experience CURLS. When compared to traditional lecture and lab report format, students gained a better understanding of Biology concepts, conducting research and reporting technical data. Future plans include additional training and resource development for implementation of the first CUREs in the freshman level Introductory Zoology and junior level Microbiology courses.

P211 Christopher M. Finelli, Joseph A. Covi, D. Ann Pabst, Martin H. Posey, Amanda Southwood Williard
Biology and Marine Biology, University of North Carolina Wilmington, Wilmington, NC

Taking the PULSE at UNCW: A Plan for Curriculum Review and Change

The University of North Carolina Wilmington is a comprehensive university that serves 13,000 undergraduate and 1,600 graduate students. We have a strong emphasis on undergraduate education, especially with respect to engaging students in applied learning outside of the classroom. The of Biology and Marine Biology is a campus leader in teaching and research, with undergraduate and masters degrees in both biology and marine biology and a PhD in marine biology. Participation by our faculty in the PULSE-SERP Institute is motivated by a strong desire to bring into the classroom the rigorous and active student experience that is found in the applied learning setting. The timing of this participation is especially fortuitous, as the university has adopted applied learning as the central component of its Quality Enhancement Plan as part of its accreditation with SACS-COC, and the faculty has embarked on a strategic planning process that includes a review of our curriculum. We initiated a discussion of Vision and Change, as well as best teaching practices, at our retreat in August. Currently, all faculty members are engaged in an ongoing discussion teaching practice that is parallel to our discussion of curricula. To encourage the adoption of scientific teaching and student-centered learning in the classroom, we have invited national experts to present workshops focusing on scientific teaching and metacognition. We are also engaged in several proposals to the National Science Foundation to facilitate this transformation at the level and throughout the university.

P212 Nova Arnold, Kacy Gregory, Bethany Breakhall, Lindsay Calderon
Biological Sciences, Eastern Kentucky University, Richmond, KY

Nicotine-Induced Breast Cancer Cell Migration and Invasion Phenotype Is Mediated by Ca2+–Independent Phospholipase A2β

Ca2+-independent Phospholipase A2β (iPLA2) is a member of the phospholipase A2 superfamily has been linked to the regulation of a variety of cellular signaling pathways and functions. This is in part due to the catalytic activity of iPLA2 β-cleaving glycerophospholipids at the *sn*-2 position causing the release of free fatty acids including arachidonic acid and 2-lysophospholipid. However, the ability of iPLA2 to mediate breast cancer cellular functioning including proliferation and migration remains unknown. Our central hypothesis is that suppression of iPLA2 reduces nicotine- induced breast cancer metastasis through attenuating MMP-9 (Matrix Metalloprotease-9) secretion. Our in-vivo preliminary data shows that iPLA2 is overexpressed in 4TI stage four breast cancer tumors grown in-vivo for 2 weeks and nicotine (5mg/kg/day) significantly increased growth at 2 weeks and 4 weeks. Additionally, we found Bromoenol lactone, 3uM (BEL) an inhibitor of iPLA2 significantly attenuated nicotine-induced breast cancer cell proliferation. Further, we found that BEL significantly decreased nicotine-induced breast cancer cell migration (gap closure) utilizing a scratch assay. Through the use of gel zymography we elucidated that BEL attenuates nicotine-induced matrix metallopreotease-9 secretion, which, is an important contributor to cancer cell metastasis and the initiation of angiogenesis. Taken together, our in-vivo and in-vitro results indicate that iPLA2 is an important regulator of nicotine-induced breast cancer tumor growth, cell migration, and proliferation. Much work is still to be done in future studies to fully elucidate the full capacity of iPLA2 in mediating breast cancer tumerogenicity, angiogenesis, and its invasive nature.

P213 Joshua L. Watson, Matt C. Estep
Biology, Appalachian State University, Boone, NC

A Comparison of the Efficiency in Finding Genes Between Sequences Enriched for Hypo- Methylated Regions and Whole-Genome Shotgun Sequence in Bread Wheat

Bread wheat (*Triticum aestivum*) has a roughly 16Gbp hexaploid genome, resulting from a hybridization event between tetraploid emmer wheat (*Triticum dicoccoides*) and diploid goat grass (*Aegilops tauschii*). This large plant genome is composed of at least 80% transposable elements (TE's), making the transcriptionally active areas (genes) difficult to locate. Epigenetic methylation of DNA is a common indicator of low transcriptional activity and is used to silence TE's within a genome. Using restriction enzymes that are sensitive to methylation (HpaII and XXX), Illumina sequencing libraries were constructed that are enriched for hypomethylated regions of the wheat cultivar "chinese spring". The resulting sequence data (roughly 4.5 Gb) was assembled into contigs with AbySS using *k*-values of 36, 50, and 64. Resulting contigs were then annotated for gene content using Blastx and Blast2GO. Our findings were then compared to un-enriched sequences to access the gene enrichment potential of our selection strategy. We will determine if enriching for hypo-methylated regions with partial restriction yields more identifiable genes than a whole-genome shotgun sequence of the bread wheat genome.

P214 Kevin G. Loftis, Lacey Thompson, Bonny B. Millimaki
Biology, Lipscomb University, Nashville, TN

Expression Pattern of *Tdp2* and *Top2b* in *Danio rerio*

Topoisomerase (TOPO) enzymes create double stranded breaks in the DNA to relieve torsional strain that is created during transcription and DNA replication. Occasionally, TOPO enzymes remain bound to the DNA and require another enzyme, Tyrosyl DNA phosphodiesterase (TDP), to remove them, allowing completion of the DNA repair process. In addition to their role in DNA repair, both TOPO and TDP have isoforms that have been implicated in the development of the nervous system. One isoform of TOPO, TOPII is necessary for neural development; however, the role that it plays in the developmental process of neurons remains unclear. TDP2 has been implicated in regulating normal transcriptional levels of neural specific genes within the murine brain. Because both TOPII and TDP2 play a role in neural development, and TOPII interacts with TDP2 in DNA repair, as described above, we want to know if these proteins function together in neural development. Our lab is utilizing zebrafish as a model system to examine the role of TopII and Tdp2, the zebrafish isoforms of TOPII and TDP2, in neural development. We have developed an anti-sense RNA probe for both TopII and Tdp2 and examined the location of their expression via in situ hybridization. We have observed localized expression of Tdp2 in the brain consistent with its role in neural development. Exploring which tissues express these genes can further our understanding of their functions.

P215 Kadilee Adams, Bonny Millimaki
Biology, Lipscomb University, Nashville, TN

Inhibition of Topoisomerase2 with HU-331 Results in Axonal Pathfinding Defects in *Danio rerio*

Topoisomerases (TOPO) are vital DNA repair enzymes that function to relieve torsional strain induced during replication and transcription. Recent studies have indicated that TOP2, one of the vertebrate isoforms of TOPO2, is necessary for proper neural development, however TOP2's role in neural development remains unclear. In order to better elucidate the effect TOP2 has on the development of neurons, we treated zebrafish embryos with a catalytic inhibitor of TOP2, HU-331, during the peak times of neural development, 12-24 hours post fertilization. To examine embryonic behavior we performed a startle response assay. Control embryos responded to a stimulus by quickly swimming away in a straight line. Those treated with HU-331 had a delayed, weak response and some swam in a circular pattern. Staining of the axons in the brain with anti-acetylated tubulin or anti-3A10 antibodies revealed that a pair of commissural neurons, Mauthner neurons, have aberrant axon pattern in treated embryos when compared to control embryos. This suggests that the role of TOPO2 in neural development is to aid in proper axonal pathfinding.

P216 Canceled.

P217 Sunada K. Khadka, Holly, B-T. Boettger-Tong
Biology, Wesleyan College, Macon, GA

Effect of All Trans Retinoic Acid on Collagen Deposition in the Extracellular Matrix of Uterine Smooth Muscle Cells

The Extra Cellular Matrix (ECM) supports and facilitates structural and biochemical homeostasis for tissues and cells. Collagen is one of the structural proteins of the ECM that plays an integral role in maintaining tissue integrity, cell attachment and differentiation. However, defects in the expression of ECM proteins can result in pathology. Leiomyomas are benign tumors of myometrial smooth muscle in the uterus that are characterized by a disrupted and disorganized deposition of ECM with an increased expression of collagen that alters smooth muscle cell contractility. Previous studies have established All Trans Retinoic Acid (ATRA), a natural derivative of vitamin A, as having an antiproliferative effect on smooth muscle cells. The aim of this study is to determine if ATRA treatment also alters the levels of collagen produced by these cells. A Fast Green Sirius Red based collagen assay was performed to assess collagen production by control and treated smooth muscle cells. Collagen levels were quantified by determining the absorbance on a UV-VIS spectrophotometer at 540 nm. The data indicate that collagen levels are influenced by ATRA treatment.

P218 Soniya Bastola, Wanda T. Schroeder
Wesleyan College, Macon, Georgia

Hormonal Regulation of Involucrin Protein in Immature Mouse Vaginal Epithelium

Involucrin is a soluble cytoplasmic protein synthesized in epidermis and vaginal epithelia and is the major component of the protein envelope formed in these cells during the normal differentiation process. The cornified envelope is formed by cross-linking of involucrin and other cytoplasmic proteins by the calcium-dependent enzyme transglutaminase-1 (TGase-1). In hormone-responsive epithelia, such as the vaginal epithelium of the mouse, differentiation is controlled hormonally by estrogen and progesterone. While sexually mature mice express involucrin in vaginal epithelium, immature mice lack involucrin expression. The estrogen-dependent expression pattern of involucrin has been established by injection of exogenous estrogen into immature mice. However, the effect of progesterone, another hormone important for normal differentiation and maintenance of hormonally-responsive epithelia, has not been examined. In the current project, immature mice (20-days old) were injected with estradiol, progesterone, estradiol and progesterone, or vehicle control. At time points of 6, 12, 18, 24, and 48 hours post-injection, the mice were sacrificed and the vagina excised. Excised tissues were frozen in liquid nitrogen, sectioned and stained with anti-involucrin antibody to examine the effect of progesterone on vaginal expression of the involucrin protein. Preliminary data suggested that estrogen-dependent expression of involucrin was delayed in mice injected with a combination of estradiol and progesterone. This study will aid in the understanding of the normal differentiation process in hormonally responsive epithelial tissues.

P219 Andrew J. Patterson, Margaret J. Kovach, Manuel Bernal Mejia
Biology, University of Tennessee at Chattanooga, Chattanooga, TN

In Vitro Characterization of a Nanofiber-Based Bone Repair Device

Bone tissue engineering aims to replace contemporary treatment methods used to repair defects in bones. Electrospun nanofiber scaffolds, impregnated with osteogenic cells and growth factors, can be used to supplement normal bone repair and remodeling process. The nanofiber scaffold mimics the 3-D extracellular matrix of bone and provides a suitable environment for osteogenic cells to secrete bone matrix. The objective of this study was to evaluate the biocompatibility of nanofiber scaffolds comprised of poly(lactic-co-glycolic acid)(PLGA), hydroxyapatite (HA), and collagen in support of growth and differentiation of the human mesenchymal and osteoblastic cell lines HEPM and hFOB 1.19. Cellular viability and proliferation was measured as a function of metabolic ATP production in a two week time course assay. Confocal microscopy evaluated migration of the cells into the nanofiber matrix. Finally, RT-PCR examined expression of molecular markers for osteoblast differentiation including *OCN*, *ALP* and *IBSP*. Growth curves demonstrated a characteristic pattern of active proliferation early on followed by a dramatic decline in cellular viability and reduced proliferation. We hypothesize this transition to correlate with osteoblast differentiation. While this growth pattern was observed for all nanofiber compositions tested, the nanofibers containing PLGA, HA, and collagen achieved 24.1% more ATP production at the peak of proliferation and 110% more ATP at the conclusion of the time course assay than nanofibers containing only HA. Preliminary confocal microscopy indicates cellular adherence and migration into the nanofiber scaffold. Future studies will include evaluation of primary human osteoblasts, as well as a separate study using a rabbit model.

P220 Julian L. Gendreau Plant
Biology, University of Georgia, Athens

The Role of GATA Transcription Factors in Arabidopsis Embryo Development

The GATA transcription factor HANABA TARANU (HAN) is a known regulator of flower, shoot apical meristem, and more recently embryo development. Recent unpublished work has found that the GATA transcription factor HAN functions redundantly with two closely related GATA factors, HAN LIKE 1 (HANL1) and HAN LIKE 2 (HANL2) in embryo development. Knockouts for HAN, HANL1, and HANL2 together produce embryos with striking defects, they fail to form a shoot or root and accumulate abnormally enlarged cells around their periphery, eventually arresting. My research is aimed at understanding whether other members of the GATA family of transcription factors might also play a role in embryogenesis. I have conducted gene swap experiments in which the following eight factors, GATA29, GATA16, GATA17, GATA17-LIKE, GATA22, GATA21, GATA23, and GATA1, were placed under the control of the HAN promoter and expressed in triple mutants. Preliminary results indicate that GATA29 rescues the triple mutant phenotype, and is biochemically equivalent to other HAN genes, we are currently conducting experiments to identify whether these factors play a role in embryogenesis.

P221 tCaitlin Cato[1], Hongliang Wang[2], Karen R Harris-Shultz[2], Kingsley Dunkley[1], William Anderson[2], Xinzhi Ni[2], Joseph Knoll[2]
[1] Biology, Abraham Baldwin Agricultural College; [2] USDA-ARS, Coastal Plains Experiment Station, Tifton, GA

Identification and Mapping of a Single Recessive Gene That Confers Resistance to the White Sugarcane Aphid in Sorghum

Known for its resilience in arid environments, sorghum (*Sorghum bicolor*) is a multi-functioning staple food crop grown around the world. Sorghum produces grain, sugar and cellulose-material that can be used for: livestock feed, human consumption, ethanol production, and building materials. Despite its drought and heat resistance, sorghum still succumbs to fungal, insect, bacterial, and viral damage. White sugarcane aphids *(Melanaphis sacchari)* are prevalent in the southeastern United States and are rapidly spreading north. The white sugarcane aphid recently switched hosts from sugarcane to sorghum and heavily impacts sorghum yields. Aphids are grass-feeding insects that produce a sugary substance called honeydew, which enables the growth of sooty mold on plants. The mold further reduces yields by reducing the amount of sunlight available to plant leaves and clog harvest equipment. The utilization of hybrid sorghum with resistance to the sugarcane aphid would be desirable. A previous study identified a dominant gene (RMESI) that confers resistance to sugarcane aphid in a grain sorghum line. In this study, a sweet sorghum line was identified, Entry 22, that has resistance to the white sugarcane aphid. Crosses with this line with susceptible line AN109 and the development of an F2 population revealed that the resistance is conferred by a single recessive gene. Experiments are currently undergoing to determine if linkage exists between RMESI and the newly identified recessive resistance gene.

P222 Amber D. Dyson, Andrew C. Bellemer
Biology, Appalachian State University, Boone, NC

A Genetic Screen for RNA Processing Genes That Control Sensory Neuron Function in *Drosophila melanogaster*

Approximately 100 million Americans are affected by chronic pain, generating costs of up to $600 billion per year, according to the Institute of Medicine. The need for safer, more effective clinical interventions poses a significant hurdle in addressing this pervasive problem. To this end, researchers seek to identify mechanisms governing molecular signaling pathways in sensory neurons. We are using the larvae of *Drosophila melanogaster* as a model organism for identifying genes that control sensory neuron function by measuring nocifensive escape locomotion (NEL), which is adistinct and quantifiable behavioral response to noxious stimuli in *Drosophila*. Additionally, *Drosophila* are particularly amenable to genetic manipulation using the GAL4/UAS system for cell-specific expression. Recent studies have indicated that the mRNAs transcribed from several genes involved in sensing pain are alternatively spliced to control their function. RNA processing is also integral in sensory neuron development and morphology. We are conducting a cell-specific RNA interference (RNAi) screen in which we systematically knock down RNA-processing genes in nociceptor neurons of *Drosophila* larvae and test for changes in nocifensive behavior relative to wild-type larvae. We have compiled a list of 119 putative RNA-processing genes and obtained fly lines targeting each of these for

RNAi knockdown. We have successfully tested 50 of these and found that 6 of them (12%) show a potential defect in NEL behavior. Once the initial screen is complete, we will further characterize the best candidates through morphological analysis of sensory neurons and RT-PCR analysis of identified splicing targets.

P223 Kevin S. Stewart, David M. Donnell
Biology, The Citadel, Charleston, SC

Assembling a Larval Transcriptome of the Parasitoid Wasp *Copidosoma floridanum*

The polyembryonic wasp *Copidosoma floridanum* parasitizes the eggs of the caterpillar *Trichoplusia ni*. The resulting wasp brood consists of thousands of genetically identical yet caste-differentiated larvae. These larvae appear to go unnoticed by the host immune system even as the host is consumed by the wasp larvae. To facilitate our investigation of the genetic mechanisms utilized by *Copidosoma* in the processes of caste differentiation and host immune system evasion, we obtained 1.2 Gb of RNA sequence data from one of the larval castes. Efficient assembly of such a large amount of data requires substantial computing power and bioinformatics knowledge often out of reach of smaller labs. However, using a personal laptop and an allocation on the XSEDE supercomputer Blacklight, we were able to implement the Trinity suite of programs to obtain a de novo assembly of the larval transcriptome and to determine expression levels and establish gene ontology for each of the resulting transcripts. This research demonstrates the potential for small laboratories to undertake large-scale transcriptome projects.

P224 Jonathan B. Anderson, Barbara E. Musolf
Natural Sciences, Clayton State University, Morrow, GA

Behavioral and Biomolecular Characterization of Anxiety in Crayfish, *Procambarus clarkii*

The aim of this study was the quantification of the behavioral and biochemical characteristics of stressed and minimally stressed crayfish, *Procambarus clarkia*, to better classify and understand anxiety-like behaviors. Behavioral distinctions were examined between crayfish of the two experimental groups through the use of an ethogram quantifying aggressive, submissive, escape, and exploratory behaviors. Additionally, the location of 5-hydroxytryptamine (serotonin) and 5-HT1a along the crayfish CNS, which has been shown to be affected by stress and anxiety in mammals, was qualitatively examined through the use of a modified Immunohistochemical protocol. The results of the behavioral study suggest that crayfish subjected to an initial period of stress exhibit a higher occurrence of aggressive behaviors, such as meral spread and flexing postures as well as pinching with the chelipeds, than those of the corresponding low stress group upon the introduction of a secondary stressor. This aggressive behavior was reduced in the high stress group following the injection of the anxiolytic Paroxetine, but little to no change occurred in the low stress group. There are evident variations in the locations of serotonin and 5-HT1a receptors along the CNS among the different experimental groups.

P225 Brandon Snider, Andrew Murray, Kevin Battersby, Alex Cozad, Matt Estep
Biology, Appalachian State University, Boone, NC

MoTEf: A Bioinformatics Pipeline for Annotating Retrotransposon Structures

Transposable elements, particularly the LTR retrotransposons (Class I elements), are a major component of all eukaryotic genomes, and have consequentially shaped the evolutionary history of these genomes and the organisms to which they belong. To better understand the evolutionary history of the different groups of Class I transposable elements and the effects of this evolutionary history on genome structure, we sought to generate a hand-curated database of LTR retrotransposons found within the grasses (Poaceae), including their structural motifs.The goal of the project is to construct a Perl-based pipeline for annotating the Class I elements and their structures, with compatible outputs for a variety of genome annotation programs (Apollo, WebApollo, GeneTools, and Geneious). The pipeline software will read in next generation sequences in a FASTA format and compare them to known transposable element structures. The annotation output will then be generated with additional files, as needed for a high quality manual review of the annotation. Thus the pipeline reduces the amount of time required to compare and annotate important structural sequences, but does so in a way that is open to high quality manual annotation. Consequentially, the software will allow for the rapid construction of a well organized database of LTR Retrotransposons with reliable, hand-annotated structure maps, which we intend to use in further projects. This pipeline is part of a larger project designed to facilitate high throughput identification and annotation of transposable elements using next-generation sequences from novel grass genomes.

P226 Nadav Topaz, Jonathan Winkjer, Cori Moore, Rosalyn Price, Tsai-Tien Tseng
Molecular and Cellular Biology, Kennesaw State University, GA

Understanding Voltage-Gated Ion Channels Via Bioinformatic Analyses

The voltage-gated ion channels (VIC) is a superfamily of energy-independent transmembrane transporters with selectivity towards potassium, calcium and sodium ions. In excitable tissues, they are responsible for transmission and propagation of signals. Most recently, VICs are also implicated in the proliferation of cancer cells. While individual members of this superfamily are selective towards one of the above three ions, they have a wide variety of topologies, as a result of multiple duplication and fusion events. Fine-tuning of the kinetics and biogenesis is carried out by auxiliary subunits, which form a complex with the pore-forming principal unit in the membrane. Our study focuses on the molecular evolution of pore-forming subunits and their auxiliary subunits. We reconstructed the path of evolution, including fusion and duplication events, to find that fusion between voltage-sensing domain and pore helices occurred prior to the divergence between the three kingdoms of life. We further expanded previous findings by mining newly sequenced homologues in databases to aid in future annotation efforts. The degree of sequence similarity and path of evolution are demonstrated by structural analyses, multiple sequence alignments and phylogenetic trees. We also incorporated many sequences of potassium channels from metagenomic data to more accurately depict the history of evolution of this superfamily. For auxiliary subunits, the inclusion of certain homologues, such as ones from pea aphid and silkworm, has allowed us to conclude that many of these auxiliary subunits arose prior to the presence of higher eukaryotes.

P227 Jacob Prock, Katelyn Herman, Shivam Patel, Craig Byron
Biology, Mercer University, Macon, GA

Using Herpes Simplex Virus as a Transneuronal Tracer of Somatosensory Pathways from Oral Tissues in a Mouse Model

The somatic sensory innervation of oral tissues in *Mus musculus* was studied by employing the neurotropic tendencies of herpes simplex virus type 1 strain H129 recombinants 772 (EGFP) and 424 (mRFP). Both H129 recombinants were successfully cultured using the African green monkey kidney epithelial cell line, Vero. Using harvested viral stocks, a titer of 107 was determined by plaque assay. The periodontal ligament (PDL) below the upper and lower incisors was inoculated with H129 recombinant 772 and the buccal epithelium from the oral cavity was inoculated with H129 recombinant 424. Specimens were allowed varying incubation periods before being euthanized, then perfused, and fixed using intravenous paraformaldehyde (PFA). Brain sections were counterstained using Hoechst 33342, Trihydrochloride, Trihydrate and visualized using fluorescent microscopy in order to identify regions of viral accumulation. Results are expected to show viral accumulation in the primary and secondary somatosensory cortices in locations previously shown to display activity related to lower jaw innervation. Such results have implications for improved treatment of periodontitis and other diseases associated with degenerative oral tissues such as the periodontal ligament and cranial sutures.

P228 Viachaslau Katliarou, Chris Murdock
Biology, Jacksonville State University, Jacksonville, AL

Generation of Full-Length, Normalized cDNA Libraries for the Venom Glands of the Timber Rattlesnake (*Crotalus horridus*) and Copperhead (*Agkistrodon contortrix*)

Snake venoms are an exquisitely complex mixture of many different enzymes, carbohydrates, lipids and biologically active peptides. They tend to belong to relatively small, stable protein families. Different venomous snake taxa employ different combinations of mechanisms and no single species employs them all. There are differences between venoms of juveniles and adults, and even among different geographic regions. The primary function of snake venom is to immobilize, paralyze, kill and digest prey. In spite of the harmful effects of snake venom, it has an important place in scientific research and medicine, given that some venom components including disintegrins, phospholipase A2 (PLA2), metalloproteinase and other components have importance in the treatment of thrombosis, arthritis, cancer, strokes, heart attacks and many other diseases. In our research we are creating normalized cDNA libraries from venom gland tissues of both *Crotalus horridus* and *Agkistrodon contortrix*. One limitation to generating cDNA libraries has been the significant variation in concentration of different transcripts within cells. Normalized cDNA libraries attempt to control this by reducing the presence of highly expressed transcripts so that abundances are equalized. Therefore, normalization increases gene discovery rate by bringing frequency of each transcript in the library to a narrow range. In our research we are utilizing a duplex-specific nuclease normalization technique. The normalized cDNA is subsequently amplified by PCR and used for the construction of normalized cDNA libraries for the venom gland tissues. These data may serve as a foundation for comparative transcriptome studies for these two species of pit vipers.

P229 Thomas M. Shoemaker, Linda M. Niedziela
Biology, Elon University, NC

Gene Expression of *Danio rerio* Gill and Skin Atpase Gene *zatp 1a.1a.5* Is Altered by Exposure to Oil Dispersant

With the high frequency of oil spill accidents, the application of large volumes of dispersant formulations is potentially harmful to the marine environment. Previous research in our lab established that the gene expression of Na+/K+ ATPases in *Danio rerio* were affected by the presence of oil dispersants; however, the dose response needed further clarification. In order to better understand and quantify the effect of dispersant on isoform *zatp 1a.1a.5*, *D. rerio* were exposed to six concentrations of Dispersit ranging from 0.05 to 1.0 ppm for 24 hours. After harvesting gill and skin tissue samples and converting mRNA to cDNA, quantitative real-time PCR was performed in order to compare the amount of mRNA present in each treatment to the solvent control. A significant difference between the control and experimental groups supporting a concentration dependent effect was found when analyzing the data with two-way ANOVA. The shape of the response is silimar between gill and skin but the strength of the response differs. These results will help determine the toxicological effects of oil dispersants commonly used to clean up oil spills, and hopefully contribute to the development of non-toxic alternatives.

P230 Timothy R. Demers, Linda M. Niedziela
Biology, Elon University, NC

Oil Dispersant Disrupts *zatp 1a.1a.1* Atpase Expression within the Skin and Gills of Zebrafish (*Danio rerio*)

Currently approved surfactant-based oil dispersants are deemed safe due to low mortality in aquatic life. However sublethal doses can impair key processes that affect survivability. ATPase enzymes are essential in maintaining osmoregulatory and electrolyte homeostasis. However, dispersants can disrupt ATPase function causing ionic and osmotic imbalances in the cell. Structural and functional miscues of dispersant-ATPase interactions have been proposed but not analyzed in detail. The current study expands upon previous research in our lab in order to better understand the alteration of expression seen in quantitative PCR (qPCR) analysis. Adult zebrafish (*Danio rerio*) were exposed to six concentrations of Dispersit ranging from 0.05 to 1 ppm for 24 and 48 hr. Gill and skin samples were collected and mRNA converted into cDNA before qPCR of ATPase isoform *zatp 1a.1a.1* was performed. An initial increase in ATPase expression was observed at low concentrations followed by a rapid decrease. The initial increase is thought to stem from pressure on the system to upregulate ATPase to cope with impairment by oil dispersants. However, at high doses cells may no longer be able to compensate and transcription decreases. These results contribute to our understanding of the mechanism of oil dispersant toxicity at the molecular level of the zebrafish.

P231 Vandna Gahlot, Elias Fernandez
BCMB, University of Teneessee

Structure‐Function Studies on Nuclear Receptors

Nuclear hormone receptors (NRs) are multi-domain, ligand-mediated transcriptional factors which bind specific DNA response elements. These are conserved modular proteins composed of an N-terminal (NTD)/activation function-1 domain (AF-1), DNA binding domain (DBD) that recognizes and binds specific DNA response elements (DREs) and a C-terminal ligand binding domain (LBD), regulates transcriptional activities and act as receptor for hormonal ligands. These regulatory interactions make nuclear receptors potential targets for pharmaceutical development. The AF-1 domain is believed to be unstructured, but it is known to have critically important roles in transcriptional activation and multiple protein-protein interactions with co-regulatory proteins. These interactions have been associated with induced structural changes in NTD of NRs. The multi-domain NRs exhibit an inter- and intra-domain allosteric communication in the presence or absence of the co-regulatory proteins. Our goal is to understand the regulatory mechanism of NRs. We focus on the unstructured AF-1 NTD and its role in communication between different domains, using the thyroid receptor (TR). We are characterizing the interactions of NRs with the ligand-dependent and -independent co-factors molecules (co-activators and DNAs). Preliminary 1) binding assays using steady-state intrinsic tryptophan fluorescence quenching indicates that DNA-binding to the DBD can induce a conformational change in the AF-1 and 2) structural analysis using analytical ultra- centrifugation (AUC) indicate that ligand dependent assembly of co-activator binding to NR heterodimer complex with retinoid x receptor (RXR) is affected by the ligand bound state of the NRs. Long-term goals include structure determination by X-ray crystallography and small angle X-ray and neutron scattering.

P232 Gabrielle J. Valles, Melissa M. Fox
Wingate University

Development of an Immunohistochemical Staining Protocol to Evaluate AMPK Protein Expression Patterns in Primary Canine Cancers

Metformin, an AMPK activator, is an anti-diabetic agent that has gained attention in the oncology field due to preclinical findings that suggest anti- tumor effects. The possibility of prescribing metformin as a preventative or therapeutic cancer agent abounds in the medical field and is currently being investigated in clinical trials for the prevention of breast cancer recurrence. Due to these positive implications, the use of metformin as an anti-tumor agent has also been gaining ground in the veterinary setting. The use metformin as a substitute for traditional chemotherapy is exciting since it is inexpensive, has been proven safe for veterinary use, and confers few, if any, side effects. Metformin is believed to inhibit tumor progression through a metabolic protein called AMP-activated protein kinase (AMPK). This protein has two enzymatic isoforms, AMPKa1 and AMPKa2. Previous work in human breast cancer has identified that AMPKa2 gene expression is required in order to reap the full benefits of metformin therapy. The expression pattern of AMPK in veterinary tumors is currently unknown and elucidation of this phenotype will be critical in determining suitable candidates for treatment. There are no commercially available antibodies against canine AMPK to perform this work, however preliminary investigations show sufficient sequence homology between the human and canine proteins to yield successful cross reactivity. The purpose of this study is to develop an immunohistochemical staining protocol using antibodies generated against human AMPK protein to evaluate AMPKa2 expression patterns in primary canine cancers.

P233 Breanna R. Lee, Carol A. Hurney
Biology, James Madison University, Harrisonburg, VA

Hoxc12 and Hox13 Expression in Embryonic and Post-Embryonic *Hemidactylium scutatum* Tails

The salamander *Hemidactylium scutatum* adds axial tail segments throughout its life, both embryonically and post embryonically. This is uncommon, as most vertebrates stop adding axial tail segments at the end of embryonic development. The mechanism that causes continual addition of vertebral segments is unknown, but may shed light on vertebral development in vertebrates. During embryonic development, Hox proteins act sequentially to initiate signaling cascades in several tissues, primarily somites and their derivatives. Segmentation and segmental identity is controlled via these cascades along the anterior-posterior axis with Hoxc12 and Hox13 paralogues expressed most posteriorly in all vertebrates. Hoxc12 and Hox13 paralogues are suspected to be involved in vertebral segmentation throughout the life cycle of *H. scutatum*. Through the use of RT-PCR techniques, Hoxc12 and Hox13 paralogues were cloned and sequenced from *H. scutatum* tissues and the expression of Hox13 in larval, juvenile, and adult tail tissues was explored. Ultimately these studies will help determine if Hoxc12 and Hox13 paralogues play a role in post-embryonic tail development.

P234 David W. Cobb, Monique Singhal, Amy M. Wiles
Biology, Mercer University, Macon, GA

Identifying *Saccharomyces cerevisiae* Genes Required to Maintain Viability During Sulfur Starvation: A Genomic Analysis

Sulfur is critical to the maintenance of life on a cellular level, but sulfur-containing compounds are not always readily available to the cell for metabolism. Like all organisms, *Saccharomyces cerevisiae* has had to adapt to nutrient deficits in its environment, including the limited availability of sulfur. In order to determine the roles of individual genes in responses to sulfur starvation, a knockout library of the *S. cerevisiae* genome was screened to determine genes affecting cell viability in a low-sulfur environment. Growth assay data were used to statistically rank genes, first via differences of Z-scores compared to control data and second by a quantile normalization method followed by M-value calculations. The highest ranking genes from the lists generated by each statistical method were deemed most likely to effect yeast survival in a sulfur-deficient environment and were selected for further study. Finally, the pathways and ontologies of genes found to be essential for viability in the limited- sulfur environment will be discussed. Genomic studies of *S. cerevisiae* as a model organism are often used to gain an understanding of the genetics of more complex eukaryotic cells; therefore, elucidation of the yeast responses to sulfur starvation on a molecular level can shed light on the responses of other organisms to limited sulfur conditions.

P235 James B. Hayes, Jr., Lauren E. Heusinkveld, Erin E. McClelland, David E. Nelson
Biology, Middle Tennessee State University, Murfreesboro

Modulation of Macrophage Inflammatory NF-Kb Signaling by Intracellular *Cryptococcus neoformans*

Cryptococcus neoformans (*Cn*) is a facultative intracellular pathogen capable of causing life-threatening meningitis in immunocompromised persons. This incredibly common yeast is present worldwide in soil and bird excrement, and has been found to infect roughly 70% of individuals under the age of 5 living in urban environments. *Cn* is known to alter cell fate and suppress the inflammatory function of macrophages. However, the precise molecular mechanisms by which intracellular *Cn* achieve such results is unknown. By using single cell imaging techniques, we have monitored the effect of intracellular *Cn* proliferation on the temporal dynamics of the NF-kB signaling pathway as well as the expression of downstream pro-inflammatory genes, such as TNF-a. At low burden (defined as macrophages containing 1-3 ingested *Cn* organisms), *Cn* impaired the ability of macrophages to respond to secondary pro-inflammatory stimuli (i.e. bacterial lipopolysaccharide) by delaying translocation of NF-kB to the nucleus. At high burden (>4 *Cn* per macrophage), *Cn* induced spontaneous nuclear translocation of NF-kB, which did not necessarily increase expression of NF-kB dependent genes. These contrasting effects of intracellular *Cn* at low and high burden suggest the existence of two different mechanisms through which *Cn* alters inflammatory NF-kB signaling. These results shed light on how intracellular *Cn* modulates macrophage function, and perhaps more importantly, may increase overall understanding of the intricate relationship between this pathogen and its host.

P236 Jessica L. Moore
Biology, Western Carolina University, Cullowhee, NC

Genomic Annotation and Analysis of the Draft Sequence of the Pathogenic Microorganism, *Elizabethkingia meningoseptica*

Elizabethkingia meningoseptica is a gram negative, rod shaped bacillus that can cause meningitis-like symptoms in immunocompromised individuals. *Elizabethkingia* is a genus within the Flavobacteriaceae family of Bacteroides, consisting of three species: *Elizabethkingia meningoseptica*, *Elizabethkingia anophelis* and *Elizabethkingia miricola*. *Elizabethkingia meningoseptica* exhibits multiple drug- resistance as does *Elizabethkingia anophelis,* which is found in the gut of the malaria vector, *Anopholes gambiae.* A draft genome sequence of *Elizabethkingia meningoseptica* was published in July 2013 as a joint effort between the National Institute of Technology and Evaluation in Tokyo, Japan and Oklahoma State University. The Oklahoma State University draft genome sequence has the designation *Elizabethkingia meningoseptica* ATCC 13253 [Taxon ID 1216967], with 115 contigs that cover 3,796,928 base pairs and 3370 total protein sequences. This genomic sequence was minimally analyzed when submitted to NCBI, with very little manual annotation. The purpose of this project is to manually annotate the genome of *Elizabethkingia meningoseptica* ATCC 13253, and to gain insight into the molecular basis for pathogenesis of this and related species. We have taken a comparative genomics approach in which syntenic blocks are identified and analyzed between the *Elizabethkingia meningoseptica ATCC* 13253, and the draft genome sequences of four closely related organisms; *Elizabethkingia meningoseptica 502*, *Elizabethkingia meningoseptica KuYH*, *Elizabethkingia anophelis Ag1* and *Elizabethkingia miricola*. Studying conserved blocks of genes between the various strains and species of *Elizabethkingia* allows for more consistent gene annotation, identification of functional operons, as well as locating key differences between different species, such as chromosome rearrangements, gene duplications and pseudogenes.

P237 Maria Hosseinipour, Lucia P. Creek
Pathology, Microbiology, Immunology, University of South Carolina School of Medicine, Columbia, SC

Functional Role of the Homeobox Transcription Factor SIX1 in HPV16-Mediated Transformation of Human Keratinocytes

The SIX1 protein is part of the SIX family of homeodomain-containing transcription factors. SIX1 has a critical role in the expansion of progenitor cells during embryogenesis but is no longer expressed when mammary cells begin to differentiate. The overexpression of SIX1 occurs in many adult human cancers.SIX1 has been shown to be associated with tumorigenesis, promoting malignant transformation and metastasis. The mechanisms that promote tumor onset and progression are still unknown, especially in cervical cancer. We would like to study the role of SIX1 as a regulator of growth and transformation in HPV16-transformed human keratinocytes, which we have demonstrated express high levels of SIX1 RNA and protein. We will test the hypothesis that SIX1 expression is required for the maintenance of growth, survival, differentiation resistance and invasiveness in HPV16-mediated transformation. HPV16 is the most common high-risk oncogenic papillomavirus that contributes to cervical carcinogenesis. HPV16-mediated transformation requires the continuous expression of the viral oncoproteins E6 and E7. These proteins bind to and promote the degradation of the p53 and Rb tumor suppressor proteins, respectively. We have studied the effects of suppressing SIX1 by a short hairpin RNA (shRNA) approach where we have shown to knockdown SIX1 to variable degrees. We investigated whether decreased expression of SIX1 affected cell proliferation and/or E6/E7 expression by performing cell proliferation assays and Real-Time PCR for E6 and E7. We examined p53 and Rb protein levels by ELISA. Decreased SIX1 expression resulted in slower proliferation rates, and had variable effects on E6/E7 expression. Since we were not able to consistently suppress SIX1 expression, we argue that SIX1 expression is vital to cell survival. These studies will give us valuable insight into the complex pathways affected by SIX1 and the functional significance of its inappropriate expression in cancers, particularly those due to HPV.

P238 Chris Murdock, Emily Powell, LaJoyce Debro
Biology, Jacksonville State University, AL

Comparative Genomics of Two Novel Mycobacteriophages Isolated from a Cave System in Alabama

The objective of the reported study was to isolate and compare novel mycobacteriophages from a cave system in north Alabama. Soil samples were recovered from sites within Cathedral Caverns State Park in Marshall County, AL. Samples were enriched such that culture conditions favored the growth of mycobacteria, and thus infection by mycobacteriophages as well. Multiple mycobacteriophages were isolated and purified from these samples taken within this cave system. Two previously undescribed mycobacteriophages, CaptainTrips and MinionDave, were isolated and purified from soils collected at the edge of an underground stream system located within the cave. Further, genomic DNA was isolated from both viruses and subsequently sequenced. In reference to CaptainTrips, genome annotation analysis revealed 103 protein encoding genes, though no tRNA genes were identified. Similarly, MinionDave also appeared to contain 103 genes within its genome. Both viruses appear to belong to the F1 cluster of mycobacteriophages and appear to possess a gene that had previously been described from a Streptomyces bacteriophage and could be involved in site-specific integration into a *Streptomyces* sp. host. Therefore, it is possible that both CaptainTrips and MinionDave may be able to infect a range of bacterial hosts. Three additional viruses were found in the soil where CaptainTrips and MinionDave were isolated and are currently being studied (e.g., DNA isolation and electron microscopy). Further, the native bacteria communities of these cave soil samples are being studied using 16S rRNA sequencing for culture-independent analysis of diversity, in an attempt to identify natural hosts for these viruses.

P239 Jeremy Kitchen, Neville Forlemu, James M. Nolan
School of Science and Technology, Georgia Gwinnett College, Lawrenceville

Characterization of the RNase A Active Site by Phage Panning

We used the "Phage Panning" technique to identify peptide sequences that bind to a protein target. A library of bacteriophages, each expressing a different segment of seven random amino acids at the beginning of the capsid protein on its exterior was allowed to bind to the immobilized target protein; in this case the RNAse A enzyme was immobilized on small petri plates. Plates were washed to remove non-binding phage and actively bound phage were eluted by washing with an RNAse inhibitor, which binds at the active site of the enzyme. The eluted phage were propagated by replication in the host bacteria and the process was repeated for three rounds to select for sequences that bind the RNAse A active site with highest affinity. Individual phage plaques from the last round of purification were amplified and used to prepare DNA samples for sequence analysis. We are analyzing the predicted amino acid sequences of active molecules for common features in order to develop hypotheses about how these proteins may interact with their target. In addition to experiments, the proposed project will use autodock molecular docking software to predict interaction affinities, identify the binding domains and interaction mechanism between RNase A and sample peptide sequences. This project was performed as a lab module of the Advanced Biochemistry course at Georgia Gwinnett College during the Fall 2014 and Spring 2015 semesters.

P240 Canceled.

P241 Un Ji Byeoun, Austin Menzmer, Ana Jimenez, Alex Pervis, Timothy Trott
Biology & Allied Health, Southern Adventist University, Collegedale, TN

Proline-Rich Protein (PRP) Genes in Non-Crop Angiosperms of Southeastern Tennessee

Plant cell walls are composed of a highly cross-linked network of cellulose, complex carbohydrates, lignin, and several categories of structural proteins. One class of structural proteins are the Proline-rich proteins, or PRP's. PRP's are characterized by recurring variations of the consensus sequence PPVYK. PRP genes have been identified in crop plants such as soybeans, maize, rice, as well as the model plant system *Arabidopsis thaliana*. The expression patterns of all PRP genes examined has suggested a unique role for the encoded proteins in remodeling the cell wall in a way that conveys unique functional characteristics to these cell types. It is the aim of this research to increase knowledge of the sequence diversity present in PRP genes across a wide sampling of non-crop angiosperms native to southeastern Tennessee. For our research, plant leaves were collected, and DNA was extracted using commercially available products. Polymerase chain reaction (PCR) using primers designed against known PRP sequences was used to identify similar sequences in DNA from collected plants. PCR fragments were analyzed by DNA gel electrophoresis and reactions containing unique bands were sequenced. Using this approach we have been able to identify sequences bearing high levels of identity to *AtPRP3*, one of four PRP's previously identified in *Arabidopsis thaliana*. Continuing research is centered on expanding our database of PRP sequences in a variety of regional plants.

P242 Rosemary H. Kelley, Michael Terribilini
Biology, Elon University, NC

Computational Analysis of Aggregation of FUS and TDP-43 Proteins Involved in Amyotrophic Lateral Sclerosis

Amyotrophic lateral sclerosis (ALS) is a progressive neurodegenerative disease thought to be caused by protein aggregation. ALS affects nerve cells in the brain and spinal cord causing patients to lose the ability to initiate or control muscle movement, resulting in fatal paralysis. Recent research in the pathology and genetics of ALS has revealed the involvement of two distinct RNA-binding proteins, FUS and TDP-43, implying that abnormal RNA metabolism is a key event leading to neurodegeneration. These RNA-binding proteins are unique due to the presence of prion-like domains, which indicates their potential to form harmful aggregates. However, while it is clear that both of these proteins play a role in ALS, the mechanisms by which each protein contributes to neurodegeneration are not clear. Using various software, we generated structural models of FUS and TDP-43 and several potential homodimer conformations. We then used molecular dynamic simulations to evaluate the energetics of these conformations. This analysis allows us to compare certain aspects of the different dimer conformations, such as the location of the prion-like domains and RNA-binding domains, ultimately revealing specific mechanisms by which FUS and TDP-43 may aggregate. In the future, computational modeling can describe the possible time course of aggregate formation - ultimately providing a causal link between aggregate formation and onset of disease.

P243 Maxwell Marlowe[1], Christopher Beavers[1], Gretchen E. Potts[2], Margaret J. Kovach[1], Ethan A. Carver[1]
[1] Biological and Environmental Sciences, University of Tennessee at Chattanooga; [2] Chemistry, University of Tennessee at Chattanooga

Effects of Alkaloids Found in Electronic Cigarette Refill Solutions on Cell Growth and Gene Expression

E-cigarettes (e-cigarettes) have become increasingly popular in the past decade and are marketed as smoking cessation aids. However, these products are not well regulated or researched. A number of toxic compounds have been discovered in refill solutions. However, the long-term effects of e-cigarette use are still largely unknown. Nicotine is one of the primary components within e-cigarette refill solutions. Nevertheless, other tobacco alkaloids are present including; cotinine, myosmine and anabasine. These compounds are not disclosed on the refill packets. This study uses known amounts of tobacco alkaloids to test of the effects of these chemicals on the growth of human cells in a culture system. All alkaloids, either singly or in pairs, decreased cell growth in culture. Next, e-cigarette refill solutions subjected to high performance liquid chromatography to quantify the alkaloids present. We studied the growth of cells exposed to these refill solutions. Interestingly, fluids with flavor additives restricted growth more extensively than other refill solutions, regardless of alkaloid concentrations. The chemicals associated with flavorings are not routinely disclosed by the manufacturer. Based on these results, we believe that exposure to tobacco alkaloids and flavorings adversely change growth rates and alter gene expression patterns in the cell cultures. Currently we are initiating experiments to analyze gene expression variations between control and exposed cultures. These changes in gene expression may be linked to the development of tobacco- related diseases in humans. Overall, this project illustrates the need for research on refill solutions, and the need for better labeling and regulation of refill solutions.

P244 William N. Setzer, Chelsea N. Powers
Chemistry, University of Alabama in Huntsville, Huntsville, AL

A Molecular Docking Study of Phytochemical Estrogen Mimics from Dietary Herbal Supplements

In this study, 568 phytochemicals found in 17 of the most popular herbal supplements sold in the United States were built and docked with two isoforms of the estrogen receptor, ERa and ER(a total of 27 different protein crystal structures). The docking results revealed six strongly docking compounds in *Echinacea*, three from milk thistle (*Silybum marianum*), three from *Gingko biloba*, one from *Sambucus nigra*, none from maca (*Lepidium meyenii*), five from chaste tree (*Vitex agnus-castus*), two from fenugreek (*Trigonella foenum-graecum*), and two from *Rhodiola rosea*. Notably, of the most popular herbal supplements for women, there were numerous compounds that docked strongly with the estrogen receptor: Licorice (*Glycyrrhiza glabra*) had a total of 26 compounds strongly docking to the estrogen receptor, 15 with wild yam (*Dioscorea villosa*), 11 from black cohosh (*Actaea racemosa*), eight from muira puama (*Ptychopetalum olacoides* or *P. uncinatum*), eight from red clover (*Trifolium pratense*), three from damiana (*Turnera aphrodisiaca* or *T. diffusa*), and three from dong quai (*Angelica sinensis*). Of possible concern were the compounds from men's herbal supplements that exhibited strong docking to the estrogen receptor: *Gingko biloba* had three compounds, gotu kola (*Centella asiatica*) had two, muira puama (*Ptychopetalum olacoides* or *P. uncinatum*) had eight, and *Tribulus terrestris* had six compounds. This molecular docking study revealed that almost all popular herbal supplements contain phytochemical components that may bind to the human estrogen receptor and exhibit selective estrogen receptor modulation. As such, these herbal supplements may cause unwanted side effects related to estrogenic activity.

P245 Bo Peng[2], Catherine E. Hueston[1], Qingyun Li[2], Pelin C. Volkan[3]
[1] Neurobiology, Duke University, Durham, NC; [2] Biology, Duke University, Durham, NC; [3] Duke Institute for Brain Sciences, Duke University, Durham, NC

The Conserved Chromatin Remodeling Protein *Alhambra* Regulates Olfactory Sensory Neuron Differentiation in *Drosophila melanogaster*

Understanding how neurons acquire distinct identities is a central question in developmental biology. The olfactory system of *Drosophila melanogaster* is an excellent model to answer questions about neuronal identity due to its small yet highly diverse system of olfactory receptor neurons (ORNs). Although the specific expression patterns of ORNs are well characterized, little is known regarding how diverse ORN identities originate from a small number of neuronal precursors. Here we show that the highly conserved chromatin remodeling protein *Alhambra* in *Drosophila* is required for correct expression of a subset of ORN identities in adult and pupal flies. *Alhambra* appears to be expressed in affected ORNs during pupal development; specifically during the time period of odorant receptor expression, the key marker of ORN identity. To confirm these results and expand our understanding of the endogenous Alhambra protein, we present a plan to tag *Alhambra* with GFP using the CRISPR/Cas 9 system. With this new technology, not only can we directly visualize the presence or absence of endogenous *Alhambra,* but we can also perform future biochemical analysis. This work implicates chromatin modification in identity specification in ORNs, and may contribute to sensory plasticity in fly courtship behavior.

P246 Raquel R. Hand, Rebecca D. Moody, Carly R. Albritton, Faith K. Allen, Victoria L. Andino, Tatyana E. Foster, Ashlei N. Grant, Chamika M. Jeffrey, Joshua D. May, Anika H. McIntyre, Amanda J. Nivens, Jerrurod Paul Jr., Angelin S. Shajan, Bridget N. Smith, Kayla R. Thornell, Kathleen S. Hughes
Biology, Columbus State University, Columbus, GA

Effects of Acrylamide and Caffeine on Nerve Activity in *Procambarus zonangulus* and *Lumbricus terrestris*

We examined the effects of acrylamide and caffeine on the nerve activity of *Procambarus zonangulus* and *Lumbricus terrestris*. As a neurotoxin, acrylamide affects neurobiology including axonal transport, synapses, and the sodium-potassium ATPase pump. Caffeine is a psychostimulant and also affects oxygen levels and pH in aquatic environments. Although both chemicals are identified as contaminants in the southeast, little is known about their effects on invertebrate nerve activity. We hypothesized that invertebrates would have (i) lower nerve activity following acrylamide exposure and (ii) higher nerve activity following caffeine exposure (compared to control groups). Both invertebrate groups were exposed to acrylamide (0 mM, 0.5 mM, or 2.5 mM) for seven days. *L. terrestris* groups were exposed to 0 mM, 2.5 mM, or 5.0 mM caffeine in the soil for five days, and *P. zonangulus* groups were exposed to 0 mM, 5.0 mM, or 10 mM caffeine in the water for five days. Nerve activity amplitude was recorded with BSL Pro 3.7 software utilizing a Biopac nerve chamber for the earthworm and a suction electrode for the crayfish. Representative amplitude results from six *L. terrestris* trials and four *P. zonangulus* trials were analyzed using one-way ANOVA. There was no significant difference found in the nerve activities across the treatments. Thus, deleterious effects of the chemicals under these treatment conditions do not seem to be associated with changes in nerve activity.

P247 David M. Donnell, Kevin S. Stewart
Biology, The Citadel, Charleston, SC

De-Novo Transcriptome Sequencing and Analysis of *Copidosoma floridanum*

*Copidosoma floridanum*is a parasitic wasp which lays a couple of eggs in the catterpillar *Trichoplusia ni*. The eggs then rapidly divide and grow into larvae, creating gigantic broods of larvae which parasitize the catterpillar for nutrients. The larvae fully develop and then break out of the catterpillar. *Copidosoma*larvae perform unique operations while parasitizing the host that make it subject to research. The eggs all begin with the same DNA, but through signalling the larvae develop into castes of fertile larvae which will become adults, and sterile soldier larvae which protect the fertile larvae and will never become adults. Also, previous research points to a series of protein products secreted from the extra-embryonic membrane of the larvae which may help fight the caterpillar immune system. In order to identify the mechanisms involved with caste differentiation and immune system evasion, our team set up an RNA sequencing pipeline to create and analyze the transcriptome of the *Copidosoma* larvae. De-Novo Transcriptome assembly (RNA assembly without a reference genome) requires a lot of computing power and bioinformatics knowledge usually out of the reach of smaller labs. However, utilizing a personal laptop and an allocation to the XSEDE supercomputer Blacklight our team produced a transcriptome of the L1 stage larvae of *Copidosoma floridanum* as well as a gene ontology and an expression count of the RNA in the transcriptome. This information will aid future research into the mechanisms of development for *Copidosoma floridanum*.

P248 Adam J Ramsey, Jennifer R Mandel
Biological Sciences, University of Memphis, Memphis, TN

Genetic Diversity and Gene Flow in Crop and Wild Carrot

Queen Anne's Lace (QAL; *Daucus carota* ssp. *carota*) is a non-native, generally invasive biennial weed that has been present in North America since the early colonial period. Since its introduction it has spread across the continent and contributes to the $120 billion in economic losses caused by invasive species in the United States each year. Its crop relative (ssp. *sativus*) is grown and harvested within a few months for root production or allowed to flower after two years of growth for seed production. Despite being biennial, individuals of any age may flower (called bolters) and hybridize with QAL. These bolters may disperse pollen to, or receive pollen from, adjacent wild populations, the results of which are white, deformed roots in the crop and introgression of possibly beneficial alleles into the wild. Economically, crop-wild hybrids are wasteful, yet little is known about how this introgression affects wild population structure and genetic diversity. This project investigated genetic diversity and gene flow in QAL populations of various distances to crop fields in two locations: Nantucket, Massachusetts (an island off Cape Cod) and Sequim, Washington (on the Olympic Peninsula). We used nuclear and chloroplast markers to calculate levels of genetic diversity and population structure across populations to test the hypothesis that QAL populations closer to crops have experienced higher levels of introgression than those farther from crops. Results from this project reveal levels of crop-wild gene flow in carrot while future plans are to investigate the ecological consequences of this gene flow.

P249 Jasmin E. Jones, Marlee B. Marsh
Division of Business, Mathematics and Sciences, Columbia College, SC

Determining the Presence of the Aryl Hydrocarbon Receptor (Ahr) in *Fundulus heteroclitus* Liver Tissues from the Belle Baruch Marine Sanctuary at Hobcaw Barony (Georgetown, South Carolina)

Fish innate immune responses are routinely evaluated as indicators of immune function and immunotoxicant exposure. *Fundulus heteroclitus,* an estuarine fish commonly used as a model in immunotoxicological studies, were collected from the North Inlet of Belle Baruch Marine Sanctuary in Georgetown, SC. In order to analyze the fish, an antibody specific for the Aryl hydrocarbon receptor (AhR) will be used as a biomarker. Biomarkers of exposure reflect the presence of toxic compounds in the environment and the value of each biomarker depends on its specificity, sensitivity, simplicity, and stability (Arrellano-Aguilar *et al.,* 2009). In this leg of a longer scientific project, I will be examining Ah receptors (AhRs) and their presence in fish who are found in a marine sanctuary to provide baseline data. Ah receptors are cytoplasmic proteins that bind certain aryl hydrocarbons, translocate to the nucleus, and activate transcription of particular DNA segments. AhRs are identified by their high-affinity for binding to several carcinogenic or teratogenic environmental chemicals. It has been suggested in a previous experiment that AhRs, and especially AhR2, may be recurring targets for selection during local adaptation of fish to dioxin-like aromatic hydrocarbon contaminants, although the specific molecular changes may vary among independently adapting populations or species (Reitzel *et al.,* 2014). Later studies in the project will examine fish from contaminated sites and compare to our data. The samples of the *Fundulus heteroclitus* are currently being processed with all experimentation expected to be completed by early March.

P250 Michael Judge, Annkatrin Rose
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Redundancy and Functional Divergence of a Small Gene Family in *Arabidopsis thaliana*

Gene duplication events are thought to be major drivers of diversity in angiosperm lineages. For most duplicated genes, one of the paralogs is quickly lost to fractionation or pseudogenization. Alternatively, random mutations in one or both paralogs sometimes allow them to develop new or specialized roles. We hypothesize a current shift from redundancy to subfunctionalization between the paralogs AtFLIP4-1 and AtFLIP4-2 (Filament-like Protein 4), two uncharacterized coiled-coil proteins in *Arabidopsis thaliana*. Phenotypes differ for single knock-out mutants (flip4-1 plants are sickly with low fertility; flip4-2 plants are indistinguishable from the wild-type). Furthermore, FLIP4-1 is highly expressed in sperm and pollen while localization of FLIP4-2 to the chloroplast has been observed in green protoplast culture. On the other hand, double knock-out mutants appear to be inviable, suggesting a redundant and vital FLIP4 function. To explore potential genetic interactions between the genes and their product functions, reverse-transcription quantitative polymerase chain reaction (RT-qPCR) is being used to quantify the expression of both genes throughout the development of the plant. Detailed expression profiles in wild-type plants will test for subfunctionalization, while those from single knock-out mutants should reveal putative redundancy or compensation interactions in the expression of the genes. More broadly, the results of this study will provide insight into the fates of preserved genes after duplication.

P251 Emelin Garcia, Marlee Marsh
Columbia College, Columbia, SC

Examination of Innate Immune Activity in the Gills of *Fundulus heteroclitus*

In this study the immune response to parasites in the gills of Fundulus heteroclitus were examined. Fish innate immune responses are routinely evaluated as indicators of immune function and status following exposure to pathogens, biological response modifiers, immunotoxicants, and nutritional regimes. Fifty of these small killifish organisms from the North Inlet Estuary at Hobcaw Barony in Georgetown, South Carolina, were collected and examined for parasites. Most parasites were visibly found in the mesentery and gastrointestinal tract. However, it was not certain whether many parasites were present in the gills since they were not visible to the naked eye. Therefore, abnormalities were noted on the specimens before the tissues were embedded and cut. Parasite prevalence and intensity of infection will be calculated. It is known that monogean parasites are commonly found in the gills, but they have not been determined to be present just yet. Recently, we developed two monoclonal antibodies (mAb) that are useful in identifying fish innate immune cells. mAb M24-2 recognizes lysozyme in several species of fish and has been used in comparative immunological studies. Lysozyme is found in macrophages and neutrophils and is one of several humoral and cellular factors associated with innate immunity in all vertebrates. mAb 2C11 recognizes eosinophilic granular cells (EGCs) in fish. It is thought that these cells are similar to the mammalian eosinophil; therefore it is also believed that EGCs have an anti-parasitic function. The purpose of this study is to use the M24-2 and 2C11 antibodies to examine cellular profiles of parasite-infected and uninfected gills of the Fundulus heteroclitus collected. The increased activation of the immune system due to parasite infection will be analyzed. The experiment and data collection is currently in process and will be completed by March.

P252 Andrew W. Siv[1], Layla V. Norbash[2], Daniel J. Shults[3], Steven J. Symes[3], David K. Giles[1]
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Exogenous Fatty Acids Affect Phospholipid Structure, Membrane Remodeling, Biofilm Formation and Susceptibility to Environmental Stress in *Vibrio vulnificus*

Vibrio vulnificus, a motile gram-negative pathogenic bacterium, is a causative agent of skin-wound and food-borne infection as a result of ingestion or exposure to contaminated water and seafood. *V. vulnificus* infection causes life-threatening consequences of septicemia and/or necrosis to individuals, especially those who are immunocompromised. The danger of *V. vulnificus* is its ability to thrive in warm seawaters and in raw seafood, and its pathogenesis is aided through possession of a capsular polysaccharide and ability to form biofilm. *Vibrio* species are known to be capable of fatty acid assimilation from environmental sources, an ability that may have an effect on its pathogenic lifestyle. The current study connects *V. vulnificus* exposure to exogenous fatty acids with modification in bacterial membrane phospholipid structure, membrane permeability, response to environmental stresses, and biofilm formation. Phospholipids extracted from *V. vulnificus* grown in the presence and absence of various polyunsaturated fatty acids (PUFAs) were analyzed by thin layer chromatography. The phospholipid profiles were different, indicating structural changes. Exposure to PUFAs caused significant changes to membrane permeability as assessed by a hydrophobic compound uptake assay. Analysis of phospholipids by ultra-performance liquid chromatography/mass spectrometry (UPLC/MS) indicated the formation of new phospholipids predicted to contain an acyl chain matching the exogenously supplied PUFA. Exposure to certain fatty acids also affected stress survival as judged by minimum inhibitory concentration (MIC) assays for hydrogen peroxide (H2O2) and the antimicrobial peptide polymyxin B. Significantly, PUFAs influenced biofilm formation, causing both increases and decreases depending on the fatty acid added.

P253 Elena L. Brown, Mai H. Tran, Joong W. Park
Biological and Environmental Sciences, Troy University, Troy, AL

Bacterial Response to the Elk River Chemical Spill in West Virginia

In January 2014, up to 7,500 gallons of 4-methylcyclohexanmethanol (MCHM), a chemical used for coal purification, leaked into Elk River in West Virginia. However, there is scant research on the chemical properties and its toxicity to human and the environments. One of the main concerns involves the MCHM's potential as an inducer for microbial growth, either pathogenic or biodegrading species. This research proposes to identify microbial species in the MCHM-treated sediments. We hypothesize that there are bacteria that thrive in sediments containing MCHM. In order to test our hypothesis, bacterial DNAs were extracted and analyzed using molecular-based techniques, including PCR-DGGE and DNA sequencing. The results of this research can help develop biodegradation strategies for future MCHM-spills and establish safety regulations in handling this chemical.

P254 Anna R. Moravec[1], Daniel J. Shults[1], Steven J. Symes[1], Manuel F. Santiago[1], David K. Giles[2]
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Membrane Remodeling Via Utilization of Exogenous Polyunsaturated Fatty Acids (Pufas) Modifies Virulence Phenotypes in *Vibrio cholerae* and *Vibrio parahaemolyticus*

Key to bacterial survival is membrane lipid homeostasis, specifically the ability to alter its lipid composition according to environmental changes or stressors. Modifying acyl chain length and saturation of bacterial phospholipids changes membrane characteristics, potentially affecting pathogenesis and virulence. The current study sought to explore the polyunsaturated fatty acid (PUFA) uptake capabilities and phenotypic consequences in *Vibrio cholerae* and *Vibrio parahaemolyticus*. Thin layer chromatography of isolated phospholipids from cultures grown in the presence of PUFAs indicated structural changes. A crystal violet (CV) uptake test revealed fatty acid-dependent changes in permeability of up to 20% in *V. cholerae* and 40% in *V. parahaemolyticus*. A combination of high performance liquid chromatography/gas chromatography (HPLC/GC) and ultra performance liquid chromatography/mass spectrometry (UPLC/MS) confirmed bacterial production of new phospholipid species containing acquired PUFAs. To determine the ramifications of phospholipid remodeling, cultures were grown with fatty acids prior to the introduction of peroxide, lactic acid, and antibiotic stress. Although susceptibility to lactic acid was unaffected, *V. parahaemolyticus* displayed increased sensitivity to oxidative stress for all PUFAs, while exposure to docosahexaenoic acid (22:6) enhanced resilience of *V. cholerae.* Resistance of *V. parahaemolyticus* to the antimicrobial peptide polymixin B was reduced. Biofilm assays revealed a diminished capacity for biofilm formation in *V. cholerae* and elevated activity in *V. parahaemolyticus* for all PUFAs except 22:6 and 18:3. These results implicate fatty acids as important resources for bacterial membrane remodeling that may affect environmental persistence and host virulence in *Vibrio* species.

P255 Ethan C. Givan[1], Kimberly L. Cook[2], Ritchie D. Taylor[3]
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Escherichia coli Strain Diversity: Implications for Its Use as a Pathogen Surrogate

Contamination of food and water by pathogens is a substantial public health issue in the United States. One of the challenges in protecting the public against water and foodborne illnesses is understanding the routes of contamination. *Escherichia coli* is widely used as a fecal indicator bacteria (FIB) and as a pathogen surrogate for water quality and food safety research. A key step in using *E. coli* as a pathogen surrogate is to understand how this organism varies in the environment relative to pathogens so that the most representative surrogate can be selected. Research is needed to understand the strain level differences in *E. coli* isolates, so that selections of strains that behave similar to pathogens can be made. In this study, 63 *E. coli* isolates were selected from a pool of 1,346 isolates taken from animal and surface water sources. These 63 environmental *E.coli* isolates, the produce associated pathogens *Salmonella typhimurium* and *E. coli* O157:H7, and a common quality control *E.coli* strain were evaluated for phenotypic characteristics including biofilm formation, curli expression, and growth rates. These characteristics are thought to play major roles in the ability of pathogens to survive and persist in the soil and on plant surfaces. Results from these assays showed high strain level differences in *E. coli* from different sources and growth conditions. This data exemplifies the diversity in isolates from environmental sources, that growth environments affect the behaviors of *E. coli* strains, and that current *E. coli* quality control strains may not be appropriate indicators of pathogens.

P256 V. Douglas Landers, Cameron D. MacQuarrie, Amanda D. Williams
Biology, Lipscomb University, Nashville, TN

Determining the Potential Role of NF-kb in Immunoproteasome Subunit Expression Induced by TNF-α

Immunoproteasomes are a special form of proteasomes present during a viral infection that differ from constitutive proteasomes by the subunits LMP2, LMP7 and MECL1. These subunits alter the cleavage properties of the proteasome to make it more efficient at cleaving viral antigens for loading onto the MHCI molecule for antigen presentation. We hypothesized that TNF-α, a cytokine known to play a role in the immune response during viral infections, is activating transcription factor NF-kB, which is leading to activation of immunoproteasomes. In order to test our hypothesis, JAWSII murine dendritic cells were treated with TNF-α, and then we measured levels of both immunoproteasome subunits and NF-kB by western blot. We found that NF-kB expression levels peaked well after the expression levels of the immunoproteasome subunits started to decrease. This suggests that NF-kB is not the transcription factor responsible for the activation of the immunoproteasome and another cellular pathway is responsible for their activation

P257 Beth Dudash, Lisa Ann Blankinship, Rosmely Hernandez
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Development of a Multiplex PCR for the Detection of KPC-Positive Bacteria Isolated from Clinical Sputum Samples

Antibiotic resistance is a well-known problem within the healthcare setting. Bacteria are known to pass antibiotic resistance genes from one species to another via conjugation. Antibiotic resistance can also be acquired via transduction or transformation. These mechanisms create and increase the prevalence of multi-drug resistant pathogens. Kirby Bauer is the common method of testing antibiotic resistance but requires multiple days and costly consumables to complete the test. PCR detection of pathogens and antibiotic resistance genes would decrease costs in testing and patients could be prescribed effective drug therapy in a shorter time. This project sought to create a multiplex PCR that amplifies antibiotic resistance genes and a region of the 16S rDNA of bacteria. To date, a PCR reaction that includes the KPC1 gene and the 16S rDNA region has been developed. Primers and PCR reactions for additional classes of antibiotic resistance genes are being developed. Each PCR reaction is tested against bacteria isolated from a clinical sputum sample of known antibiotic resistance profile. If successful, a multiplex PCR reaction that detects predominant antibiotic resistance patterns would be of great value to clinical microbiology and reference laboratories in saving time and expense in sample processing.

P258 Priscilla C. Barger[1], Mark R. Liles[2], Joseph C. Newton[1]
[1] Pathobiology, Auburn University College of Veterinary Medicine, Auburn, AL; [2] Biological Sciences, Auburn University, Auburn, AL

Differential Production and Secretion of Potentially Toxigenic Ecps from an Epidemic Strain of *Aeromonas hydrophila*

Aeromonas hydrophila is a bacterial pathogen ubiquitous in aquatic ecosystems and has traditionally been considered a secondary pathogen of fish. In 2009 a new, highly-virulent strain of *A. hydrophila* was responsible for widespread outbreaks of motile aeromonad septicemia in Alabama catfish production ponds. The bacterium continues to cause significant losses in the Southeastern catfish industry. This epidemic strain, referred to as virulent *Aeromonas hydrophila* (VAh), shows significant genetic variation from the traditional *A. hydrophila* and is capable of producing disease as the primary pathogen, resulting in rapid and devastating mortality in catfish production ponds. Experimental infections by intramuscular or intraperitoneal injection in channel catfish result in death within hours with only minor gross and histologic lesions, suggesting a toxin-mediated mode of pathogenicity. Natural VAh infections occur only during summer, suggesting production and secretion of potentially toxigenic extracellular proteins (ECPs) may be in direct relation to environmental temperature. In order to determine the role of ECPs in pathogenicity, and to evaluate the potential environmental factors affecting ECP production, secretory profiles of VAh cultured under different conditions were compared. Comparison of VAh secretomes by PAGE of culture supernatants found variability in ECP profiles based on complexity of media, culture conditions, and culture temperature. Furthermore, injection of concentrated cell-free supernatant resulted in rapid mortality, mimicking previous whole-cell bacterial challenges. These findings suggest that the rapid mortality associated with VAh outbreaks may be due, in part, to increased toxin production as a response to nutrient availability and/or seasonal temperature fluctuations.

P259 Jordan L. Hartman, Amy L. Rangel, Hannah M. White, C. Brian Odom
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Antimicrobial Profiles and Properties of Sanguinarine and Chelerethryne Obtained from Two Different Species of *Papaveraceae*

Two plants in the Papaveraceae, common bloodroot, *Sanguinaria canadensis* and Chinese plume poppy, *Macleaya cordata*, contain similar metabolite profiles regarding alkaloid biosynthesis and content. Primarily, the compounds of commercial and medical interests found in these plants are sanguinarine and chelerethryne, which are found in the rhizomes of *Sanguinaria* and the seed capsules of *Macleaya*. Extracts from both species were prepared, chemically profiled and tested for their antimicrobial activity.

P260 Layth M. Awartani, Christine M. Stracey, Melanie J. Lee-Brown
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A Survey of the Bacterial Microflora Present in the Feces of Nine Day-Old Loggerhead Shrike (*Lanius ludovicianus*) Nestlings

There are few studies on non-domesticated avian gut flora and even less research on the microbial populations of nestling fecal sacs. Of the few studies, most focus on zoonotic bacteria or the health of commercially important domestic avian species. This study examines the culturable gut microbes from the fecal sacs of nine-day old Loggerhead Shrike (*Lanius ludovicianus*) nestlings. Loggerhead Shrikesare migratory passerines (perching birds) and top-level predators. Their diet consists of arthropods, amphibians, reptiles, small mammals, and other birds. Their populations have fallen sharply over the past half-century and they are now classified as a Tier I at-risk species in the U.S. and critically endangered in Canada. Variation in the gut flora, based on diet, nesting time, and food availability, may influence the health and condition of the nestlings at fledging. Fecal sacs were collected from four different nests over a four month period in Antelope Island State Park located in the Great Salt Lake, Utah in the summer of 2014. This study compares the culturable composition, species richness, and overall abundance of bacteria in the nestling fecal samples.

P261 Neely M. Wood, Ralph C. Bishop, Min-Ken Liao
Biology, Furman University, Greenville, SC

Bacteria Biodiversity from Soil of Different Land Managements at Furman University

There are at least three different soil management practices on the Furman University campus: chemically managed (lawn on the Furman Mall), organically managed (Furman farm), and no management (untreated forested area). Based on the assumption that different land managements, or lack thereof, would create different ecosystems, we hypothesized that the bacterial communities in the soil of these land managements would be different. We isolated soil bacteria from different land managements and selected 6-10 isolates that are morphologically distinct to represent each site for further analysis. We amplified and sequenced the 16S rRNA gene of these representatives and taxonomically identified them to the genus level then categorized them at the family level. For each soil type, we concluded, then, that the family *Bacillaceae* was most prominent, followed by *Paenibacillaceae*, *Flavobacteriaceae*, and *Pseudamonaceae* for the forested area, the organically managed area, and the chemically managed area, respectively. Concurrently, we performed double restriction enzyme digests (HinP1I and MspI) on the 16S rRNA gene of the remaining bacterial isolates for a quick comparison of bacterial community diversity in different soil types. Our preliminary results based on double digest data of at least 15 individual isolates per site showed no significant difference in relative diversity. However, based on the sequencing analysis results and the Simpson's diversity tests, the soil bacteria community in the forested area was the most diverse, followed by the organically managed soil and, lastly, the chemically managed soil. More soil samples will be collected and analyzed in summer 2015.

P262 R. Clayton Bishop, Neely M. Wood, Min-Ken Liao
Biology, Furman University, Greenville, SC

Tetracycline Resistant Bacterial Communities in Soils of Different Land Managements at Furman University

This study was to examine the diversity of the tetracycline resistant (tetr) bacterial community in soils of three different land managements on campus: soil that is chemically managed (Furman Mall), organically managed (Furman farm), and unmanaged (forested area). We focused on tetr bacteria because it has been shown that soil microbes are a reservoir of tetracycline resistance genes. We hypothesized that the diversity of the tetr bacterial community in the organically managed soil of Furman farm would be the greatest and that the soil of the chemically managed Furman Mall would be the lowest. We isolated 50 tetracycline resistant bacteria from the sites of different land management. The 16S rRNA gene from each of these isolates was amplified and sequenced, and the sequences were used to identify these isolates to the family level. The Simpson's diversity index result suggested that the tetr bacterial community in the organically managed soil had the highest diversity, followed by the chemically managed soil, and the unmanaged soil. We also studied the prevalence of tetr genes in soils of different land managements. We hypothesized that a higher diversity in tetr genes would be present in soil that was chemically managed. We extracted the total DNA from each soil sample and used multiplex PCR to identify the tetracycline resistance genes, if present. Our results showed that in all sites the most common tetracycline resistance gene was *tet*(A). More samples will be collected and analyzed to draw a more concrete conclusion in the future.

P263 Jennifer Bailey, Nicolas Rios
Biology, Armstrong State University, Savannah, GA

Nitrogen-Fixing Bacteria in Scale Insects and Mealy Bugs Infesting Ghost Orchids

Herbivorous insects, such as mealy bugs and scale insects, feed on plants which are a poor source of nitrogen. Nitrogen is essential for the synthesis of proteins and nucleic acids. To compensate, some herbivorous insects have evolved a mutualistic relationship with intestinal endosymbionts that supply the insect with fixed nitrogen. These bacterial endosymbionts perform nitrogen fixation which involves converting N2 gas from the atmosphere to ammonia (NH3). Excess ammonia is then absorbed by the host for growth and maintenance. The objective for this project is to determine whether specific herbivorous insects harbor nitrogen fixing bacteria. We are currently screening mealy bugs and scale insects collected from Florida Panther National Wildlife Refuge in Summer 2014. Rare ghost orchids harbor these insects and are known to have infestations. However, it is unknown whether these insects possess nitrogen fixing bacteria. DNA extractions of mealy bugs and scale insects will be screened by PCR for the *nif*H gene. *nif*H gene encodes for nitrogenase, a key enzyme for nitrogen fixation that is specific to nitrogen fixing bacteria. Amplified *nif*H genes will be sequenced and compared to those detected within others insects possessing nitrogen fixing endosymbionts. This experiment will help determine whether a symbiosis exists between mealy bugs/scale insects and nitrogen fixers.

P264 Jennifer M. Goodman, Jeffrey Thomas, Joanna Katsanos
Biology, Queens University of Charlotte, NC

Microfloral Community Differences on the Talons of Birds of Prey

In this study, an analysis was done of the bacterial flora found on the talons of four taxonomically differing raptors; the Cooper's Hawk, the Red Shoulder Hawk, the Screech

Owl, and the Black Vulture. The swabs taken from each raptor's talons were then streaked on a nutrient agar plate and incubated at 37oC. The morphology, color, and size of each distinctly formed colony was documented prior to gram staining, selective and differential plating, and enterotube inoculation. The results showed that bacterial community structure varied across raptor species in composition, structure, and density.

P265 Marc J. Muraski[1], Daniel P. Christen[2], Melanie Lee-Brown[1]
[1] Biology, Guilford College, Greensboro, NC; [2] Chemistry, Guilford College, Greensboro, NC

Pseudomonas aeruginosa Biofilm Disruption Via Yayurea a&B Quorum Quenching

Antibiotic-resistant pathogenic bacteria are a major health concern. Antibiotic resistance is conferred through many different mechanisms such as cleavage or modification of the antibiotic, antibiotic export or genetic alteration of the antibiotic target. Biofilm formation can decrease the efficacy of antimicrobials by preventing them from penetrating the thick polysaccharide layer to reach the target cells. The formation of a biofilm requires both the accumulation of cells and the production of the extracellular matrix. The density dependent, cell-cell communication required for this to happen is referred to as quorum sensing. This research explores new methods of inhibiting biofilm formation via quorum quenching as an approach to increasing the efficacy of current antibiotic treatments. Quorum quenching involves binding or down-regulating quorum-sensing receptors. Two compounds (yayurea A and B) produced by Staphylococcus delphini are quorum quenchers. In this study, yayurea A and B were chemically synthesized and tested for their ability to disrupt quorum sensing; both their abilities to prevent the formation of new biofilms and also to disrupt established biofilms. Preliminary assessment of cytotoxicity was performed in *C. elegans*.

P266 Stephanie S. Momeni[1], Jennifer Whiddon[2], Stephen A. Moser[2], Noel K. Childers[3]
[1] Biology, University of Alabama at Birmingham; [2] Pathology, University of Alabama at Birmingham; [3] Pediatric Dentistry, University of Alabama at Birmingham

Repetitive Extragenic Palindromic PCR (Rep-PCR) of Oral Streptococci Using DiversiLab™

Mitis salivarius with bacitracin (MSB, Gold's) is a selective media commonly used for the isolation of *Streptococcus mutans* (Sm), an organism associated with dental caries. This media is currently being used in a large-scale epidemiological study to genotype Sm using repetitive extragenic palindromic PCR (rep-PCR). During quality control, several non-Sm isolates were found. The purpose of this study was to identify non-Sm isolate species by PCR for 16s rDNA sequencing and to establish a rep-PCR genotype library for these background bacteria isolated from MSB. Overall, 400 isolates failed validation by PCR with Sm specific primers; 92 had rep-PCR data completed and were selected for this study. Identification was performed by real-time PCR using published 16s sequence specific primers. Amplicons (466 base-pairs) were purified, sequenced and identity determined by BLAST search. Rep-PCR was performed as previously described and dendrograms were generated using DiversiLab web-based tools. A total of 53 rep-PCR genotypes are reported for 10 different bacteria/bacterial groups. The majority of isolates were identified as *S. sobrinus* (n=48), *S. gordonii* (n=28), *S. sanguinis* (n=11), *S. constellatus* (n=9) and *S. anginosus* (n=7). The number of rep-PCR genotypes found for these bacteria were 9, 15, 10, 6, and 6 respectively.This study supports reports that oral streptococci besides Sm can be isolated from MSB. This is the first known study to classify oral streptococci besides Sm using rep-PCR. The diversity of rep-PCR genotypes reported in this study will provide a reference for other labs seeking to classify oral streptococci using a rep-PCR approach.

P267 Heath A. McLean, Kevin M. Pitz
Biological Sciences, University of Tennessee at Martin

Isolation and Characterization of Novel Yeast Strains from West Tennessee

Yeasts are used in many industrial, commercial, and scientific applications. Isolating and characterizing novel strains of yeasts could benefit one or more of these areas. We have isolated candidate yeast strains from environmental samples collected in and around The University of Tennessee at Martin in west Tennessee through enrichment using malt-based media. This work has yielded 4 candidate yeast strains for identification and characterization. We used the ITS (Internal Transcribed Spacer) region (rRNA) for generic, species, and strain identification. Herein, we present the results of molecular and microbiological analyses characterizing these strains.

P268 Dominique Clark, Elrica Brown, Angel Garcia, Ashley King, Jonathan Moore, Bianca Garner
Biology, Tougaloo College, MS

Bacillus amyloliquefaciens Response to Iron Limitation

Bacillus amyloliquefaciens is a biocontrol agent whose genome has recently be sequenced. Within the genome, we have identified genes associated with iron acquisition, including bacillibactin production. We questioned how iron restriction would impact the physiology of *B. amyloliquefaciens.* Iron limitation in the growth medium resulted in a decrease in growth yields. Iron limitation was confirmed by the presence of catechol, which was not detected when cells were grown in the presence of iron. Spore production was also decreased under iron limitation, as was biofilm formation. These initial studies suggest the importance of iron for *B. amyloliquefaciens*. Further studies are required to elucidate the mechanisms governed by iron availability.

P269 Angel Garcia, Elrica Brown, Dominique Clark, Jonathan Moore, Ashley King, Bianca Garner
Biology, Tougaloo College, MS

Iron Impact on Biofilm Formation in *Bacillus cereus* Group Microbes

Biofilms are an important physiological state observed in numerous microbes. Biofilm formation has been demonstrated in numerous organisms, including members of the *Bacillus cereus* group of organisms. This diverse group includes, in addition to the human pathogen *B. cereus*, the insect pathogen *Bacillus thuringiensis* and the zoonotic pathogen *Bacillus anthracis*. While iron has been demonstrated to alter the expression of iron acquisition genes, we questioned whether iron limitation would alter biofilm formation in these strains. Multiple ATCC strains of both *B. cereus* and *B. thuringiensis* were cultured under iron restriction using a defined minimal medium. Iron restriction had no impact on the formation of biofilms in the *B. cereus* strains tested. Biofilms were formed under iron-limited growth in minimal medium for both *B. thuringiensis* ATCC 10792 and *B. thuringiensis* ATCC 33679 grown in vinyl plates at 30g/mL) to cultures resulted in a statistically significant decrease in biofilms for both strains. While a similar pattern could not be detected when strains were cultured in polysterene wells, transferrin decreased biofilm formation in *B. thuringiensis* ATCC 33679 when samples were incubated in glass tubes. Elucidation of role of iron in this process may provide additional insight into the complex regulatory mechanisms that govern physiology in the *B. thuringiensis.*

P270 Joshua J. Doughty
Biology, Queens Universty of Charlotte, Charlotte, NC

Comparing Microbial Colonies on Different Birds of Prey

The first 24-hours of care are the most crucial in the survival of the birds of prey in rehabilitation centers. Within that time-frame the birds die from their immediate injuries or infections that have had time to grow out of control. Nosocomial infections from basic procedures, as well as infections from various dangerous microbes are common in rehabilitation patients. Swab samples were taken from various taxonomic groups of raptors, incubated and then analyzed with enterotubes to determine the different species of microbes. Analyses of feather and intestinal swabs show that there are signs of dangerous spore forming microorganisms playing roles in infections. These tests resulted in the identification of multiple species of spore forming microorganisms. Two of the species found are multi-drug resistant, mutate quickly as well as have high mortality and morbidity rates. Other species found vary in the severity of possible infections, though one particular microorganism, *Strenotrophomonas maltophilia*, is known to be able to infect humans. Further studies on this matter could lead to the betterment of care for birds of prey and the safety of the caregivers.

P271 Jessica L. Allement, Jack O'Brien
Biology, University of South Alabama, Mobile, AL

Ecological Interactions Between Trematodes and *Cerithidea pliculosa*

Parasites play an important role in the natural history and ecology of ecosystems. Trematodes are especially interesting in this regard because they castrate their snail hosts. We report here part of an ongoing study examining the relationships among a community of trematode parasites and their intermediate host, the horn snail, *Cerithidea pliculosa* (Mollusca: Gastropoda) in Airport Marsh on Dauphin Island, AL. This salt marsh is an estuary located at the southern end of the Mobile-Tensaw Delta. The trematodes use birds, fish, and mammals such as raccoons as definitive hosts. We intend to identify the species of trematodes infecting horn snails in the habitat. Bi-weekly collections and tethering of snails in the field and observations of cercariae in the laboratory are being conducted. Size-frequency plots reveal that large snails are much more likely to be parasitized than small individuals. Previous work (Rothschild 1938, 1941) using another trematode host association has shown that infected hosts grow faster than uninfected snails. We are investigating whether the correlation between infection and increased growth rate also occurs in *C. pliculosa*. Currently we are following a cohort of host snails over time and are accumulating seasonal prevalence data by trematode species. These data will help determine whether there is a succession or repeatable sequence of trematode species in one host and, if so, does competitive dominance occur among the trematode species within an individual host. This research is important to this region and provides insight into the fascinating and unique world of ecological parasitology.

P272 Lindsey J. Boyle[1], Skylar R. Hopkins[2], Lisa K. Belden[2], Jeremy M. Wojdak[3]
[1] Biology, The College of William and Mary, Williamsburg, VA; [2] Biology, Virginia Tech, Blacksburg, VA; [3] Biology, Radford University, VA

The Effects of Variable Parasite Densities on Growth Rates, Feeding Rates and Mortality in the Snail *Helisoma trivolvis*

Trematodes (i.e. flatworms) are common parasites of many freshwater invertebrates and vertebrates. The aquatic snail *Helisoma trivolvis* acts as both first and second intermediate hosts in the life cycles of several trematode species. Previous research has focused on

the fitness costs of snails infected as first intermediate hosts, where infection can lead to host castration and death. However, relatively little research has been conducted on the fitness costs for snails infected as second intermediate hosts of trematodes. We determined how the fitness costs (in terms of reduced growth, feeding, or survival) imposed by the trematode *Echinostoma trivolvis* on the snail *H. trivolvis* varied with parasite exposure and snail size. None of the snails greater than 5.5mm in diameter died during our experiment. Smaller snails experienced high mortality rates, but only when exposed to the highest parasite density treatments. Surprisingly, trematode infection did not affect the growth or feeding rates of snails, regardless of snail size. These results underline the context-specific nature of parasite-host interactions; Parasites may have no quantifiable effects on some hosts while causing high mortality rates at different exposure rates and host sizes.

P273 Luke Cunningham[1], Riccardo Fiorillo[2], William Ensign[1]
[1] Ecology, Evolution and Organismal Biology, Kennesaw State Univ., Kennesaw, GA; [2] School of Science and Technology, Georgia Gwinnett College, Lawrenceville, GA

Parasite Loads in *Lepomis spp.* from Streams with Varying Levels of Human Impact

Parasite populations are often overlooked when investigating ecosystem structure and function, but have recently been demonstrated to have a surprisingly large impact on the communities they inhabit. In particular, impacts associated with altered feeding behaviors of key consumers have been documented. *Posthodiplostomum minimum* is a digenetic trematode that uses 3 distinct hosts: snails in the genus *Physa*, fish in the genus *Lepomis*, and a waterbird (typically the great blue heron, *Ardea herodias*). *Lepomis* are often the numerically dominant species of fish in streams affected by urban and suburban development and parasite induced changes in their behavior may be important. The purpose of this study is to quantify the parasite load of *Posthodiplostomum minimum* in three *Lepomis* species (*L. auritis, L. cyanellus*, and *L. macrochirus*) in streams from watersheds with differing anthropogenic impacts. Fish for this study were collected with a backpack electroshocker during the summer, fixed in formalin, cleared, and then stored in ethanol. Preserved specimens were identified to species, measured (SL), dissected via blunt dissection and the heart, liver, gonads and intestines inspected for encysted *P. minimum* metacercaria. Cysts were removed, identified and counted under a dissecting microscope. Data analysis will focus on potential differences in parasite load among species and size classes across the varying level of human impacts in the study streams.

P274 Samantha B. Saylor[1], Chris S. Lantz[2], Tracy L. Deem[1]
[1] Bridgewater College, Bridgewater, VA; [2] James Madison University, Harrisonburg, VA

Mechanism for Malaria: A Look into the Possible Involvement of NK Cells, NKT Cells, Macrophages and Neutrophils

Malaria is one of the most severe public health problems worldwide, and it is a leading cause of death, especially in children and pregnant women in developing countries (CDC, 2012). Murine models of malaria infection have been used to understand malaria pathogenesis. In our laboratory we previously showed knocking out the hematopoietic growth factor, interleukin-3 (IL-3) during malarial infection with *Plasmodium berghei* NK65 extended the time of death of male mice, suggesting that IL-3 exacerbates disease (Auclair *et al.*2014). We hypothesized that the reason WT mice die faster may be due to an overwhelming recruitment of inflammatory cells that results in tissue damage. Therefore, we looked at recruitment of early inflammatory cells, namely NK cells, macrophages, and neutrophils as well as the expression of inflammatory cytokines. While we saw no difference in the number or percentage of NK cells in the spleen and blood by flow cytometry, there was a significant increase in the number of inflammatory macrophages and neutrophils in WT mice compared to KO mice. Furthermore, there was an increase early in inflammatory cytokines in WT mice. Taken together, these data suggest that WT mice do have an early, and possibly, an overwhelming inflammatory response.

P275 Lillian R. Neal, Marlee B. Marsh
Division of Business, Mathematics and Sciences, Columbia College, SC

Using Mab M24-2 (α Fish Lysozyme) to Examine the Host-Parasite Relationships in Livers from *Fundulus heteroclitus* from North Inlet Estuary (Hobcaw Barony) in Georgetown, South Carolina

Fish innate immune responses are routinely evaluated as indicators of immune function and status following exposure to pathogens, biological response modifiers, immunotoxicants, and nutritional regimes. Recently, we developed monoclonal antibody (mAb) M24-2 that recognizes lysozyme in several species of fish (E.g. *Fundulus heteroclitus*) used in comparative immunological studies. Lysozyme is found in macrophages and neutrophils and is one of several humoral and cellular factors associated with innate immunity in all vertebrates. The purpose of this study was to use mAb M24-2 to examine cellular profiles of immune cells in livers of parasite-infected and uninfected livers of 50 fish from Belle Baruch Marine Sanctuary in Hobcaw Barony (Georgetown, SC.) There are only a paucity of reagents available to examine the cellular mechanism of fish immune response and mAb M24-2 has been successful tool thus far. Furthermore, we hope to elucidate any direct role(s) of neutrophils and macrophages in fish immune responses to parasites. Data collection is still in progress and will be completed by March. In this study, we probe paraffin- embedded livers of *F. heteroclitus* and compare the lysozyme profiles of parasite-infected vs. uninfected individuals.

P276 Mara N. Reiss, Marlee B. Marsh
Division of Business, Mathematics and Sciences, Columbia College, SC

Probing the Entryway for Infection: An Examination of the GI Tracts of *Fundulus heteroclitus* for Immune Responses to Metacestodes

Fifty *Fundulus heteroclitus* from the North Inlet Estuary at Hobcaw Barony in Georgetown, South Carolina, were collected and examined for parasites. The predominant parasite found were metacestodes located in abdominal mesenteries and in the livers. *F. heteroclitus* acquire this parasite through their diet, and parasites must penetrate the gastrointestinal tract to establish infection. Fish innate immune responses are routinely evaluated as indicators of immune function and status following exposure to pathogens, biological response modifiers, immunotoxicants, and nutritional regimes. Recently, we developed two monoclonal antibodies (mAb) that are useful in identifying fish innate immune cells. mAb M24-2 recognizes lysozyme in several species of fish and has been used in comparative immunological studies. Lysozyme is found in macrophages and neutrophils and is one of several humoral and cellular factors associated with innate immunity in all vertebrates. mAb 2C11 recognizes eosinophilic granular cells in fish- a cell whose presumed function is similar to that of the mammalian eosinophil (anti-parasite). The purpose of this study is to use these antibodies to examine cellular profiles of immune cells in the gastrointestinal tract of parasite-infected and uninfected gastrointestinal tracts. The data collection is currently in progress and will conclude in early March.

P277 Tracy L. Deem[1], Erik M. Ehinger[2], Samantha B. Saylor[1], Andrew Shepherd[1], Chris S. Lantz[2]
[1] Bridgewater College; [2] James Madison University

Role of IL-3 in Immune Responses to *Plasmodium berghei* in a Murine Model of Malaria

Malaria is a potentially fatal disease caused by parasites of the genus *Plasmodium* and spread by the *Anopheles* mosquito. In 2012 there were 207 million cases contributing to 627,000 deaths worldwide (WHO, 2014). In a murine model, IL-3 was shown to decrease survival times compared to IL-3 KO mice (Auclair *et al*., 2013). A difference in survival was not due to differences in hemapoiesis; however, IFN-g levels were higher in the blood of WT mice early in infection. Other recent reports have shown malaria infection leads to increased plasmacytoid dendritic cell (pDC) activation and secretion of interferon (IFN)-a resulting in mast cell release of Flt-3 ligand (Flt-3L), which activates classical dendritic cells (cDC) to activate T cells. Since IL-3 has been shown to be involved in both mast cell and DC development, we hypothesized that IL-3 KO mice survive longer due to differences in DC activation, Flt-3L production, and T cell activation. Therefore, we used flow cytometry to quantify the percentage of DCs, T cells, and B cells in *Plasmodium berghei*-infected KO and WT mice and used an ELISA to measure splenic and serum levels of Flt3L. Our results show percentages of DCs and B cells are the same in both types of infected mice. However, Flt3L, the percentage of CD4+ T cells, and the amount of antibodies is higher in WT mice. Further investigation of DC co-stimulatory markers will determine if there are differences in DC and T cell activation that might account for longer survival in KO mice.

P278 Theresa Nguyen, Sydney Welch, Abbie Tomba
Biology, University of Mary Washington, Fredericksburg, VA

Molecular Identification of Digenetic Trematodes in the Rappahannock River Using Cytochrome C Oxidase (COI)

Digenetic trematodes are parasitic flatworms whose primary intermediate hosts are snails and definitive hosts are vertebrates. Larval trematodes castrate snail hosts, potentially affecting host populations within a community, as well as alter host interactions with freshwater ecosystems. Determining individual species would be invaluable in gaining a comprehensive understanding of trematode biodiversity and their ecological effects within the Rappahannock watershed. Due to their morphologically cryptic larval stages, molecular techniques are essential in identifying species within snails and determining specific lifecycles. The mitochondrial cytochrome c oxidase subunit 1 (COI) gene is highly conserved with low conspecific divergence, and serves as a DNA barcode to distinguish between closely related species. DNA was extracted from larval trematodes from snails previously collected within the Rappahannock and Little Rivers (Fredericksburg, and Hanover Co., VA). COI genes were then amplified using PCR with trematode specific primers, and sequences were obtained (ACGT, Inc.) and analyzed using Geneious. Interspecific comparisons were made through the construction of pairwise alignments and neighbor-joining phylogenetic trees. Out of the 26 samples digested, 15 were successfully amplified. Eight of these were sent for sequencing, 5 of which were sequenced successfully. COI genes from all 5 parasite samples were between 377-446 bp in length. The phylogenetic trees created suggest that samples N2 and N3 are a single species belonging to the order Echinostomida. N8 and N16 represent a species within the family Collyriclidae, as does N13. More sequencing is currently underway.

P279 Curt Skipper, Patrick Stokley, Sherry Herron
Center for Science and Mathematics Education, The University of Southern Mississippi, Hattiesburg, MS

An Investigation of Tree Biomass in the Great Smoky Mountains National Park

The purpose of this study was to determine carbon storage (biomass) in four forest types in the Great Smoky Mountains National Park: pine/oak, cove hardwood, northern hardwood, and spruce/fir. Based on the GLOBE Programs land cover protocols (www.globe.gov), and the University of New Hampshire's GLOBE Carbon Cycle Program (http://globecarboncycle.unh.edu/), we knew that species and circumference of tree would be the two most critical factors in determining biomass, but we also hypothesized that number of trees in a study site and the elevation of the site would impact biomass. We hypothesized that old growth forest would contain greater biomass than a young forest. We recorded tree circumference and tree species for every tree that had a circumference greater than 15 centimeters in each plots of 900 square meters. The circumference of a total of 219 trees represented by 22 different species, as well as forest type, elevation, and GPS coordinates for each plot, were recorded. Using SPSS to analyze the data, tree circumference was found to be the factor that explained the greatest variability in biomass (t = 19.729, p = 0.001, r2 = 67.9). We also found that old growth forests contained more biomass and carbon than younger forests ($x$old growth biomass = 21,469,292, $x$younger forests biomass = 12,790,900). These findings could be used to help us educate students on the importance of trees, especially the old growth trees. Also, we can encourage people to plant trees in cities and urban areas to help offset carbon emissions.

P280 Canceled.

P281 Brielle Bowerman, Emma Johnson, Shannon Pittman, Michael E. Dorcas
Biology, Davidson College, NC

Positive Impacts on Attitude Towards Conservation, the Environment, and Herpetofauna Through an Educational High School Program

Currently, lesser-known, yet important groups of animals such as amphibians and reptiles are experiencing global declines, which have the potential to harm ecosystems. Environmental education is integral to increasing awareness of the natural environment and to ensure continued and growing conservation practices to halt the declines. Reptile and amphibian education is crucial and allows for the development of an appreciation for conservation through an increased knowledge of species and their environments. To increase awareness and education, we created a 5-week program designed for high school students (Woodlawn School, Mooresville, NC) to increase students' knowledge of conservation, local herpetofauna, and common fieldwork skills. We gave five presentations about conservation and the major groups of herpetofauna and led a fieldwork day to implement a system of passive herpetofauna sampling techniques (coverboards and PVC pipes) on the school's property. To measure the impact on the students, we administered a survey before and after our program to test knowledge of herpetofauna, conservation, and current threats to the environment as well as perspective questions, which asked students to rank their feelings towards conservation and reptiles and amphibians. The average score on the content questions increased from 69% to 93% after our program, as well as trends for stronger connections to the environment, decreased fear of snakes, and increased knowledge and appreciation of herpetofauna. Our study shows that with enthusiastic, hands-on instruction, students can help develop an appreciation for herpetofauna, conservation, and the environment.

P282 Elexander N. Atkinson
Biology, Queens University, Charlotte, NC

C. elegans as a Model Organism for Undergraduate Labs and Research

Students seeking their bachelor's degree in a science field across the nation have a demanding workload and a lot of material to learn in four short years. This amount of material is constantly growing as advances in the sciences happen everyday. Biology majors are one of the primary groups that experience this continual growth in amount and depth of material. Many biology programs are using the same labs, techniques, equipment, procedures, and models from decades ago 1. It is apparent that there needs to be some innovation in the undergraduate biology programs on several levels. One of the main challenges facing these and their students is how to prepare them for graduate school or a career if they choose to pursue biology2. Exposing students to as many techniques, technologies, and model organisms as possible are effective ways to help bridge the information-understanding gap2, 3. 1'*Caenorhabditis elegans* is a widely used model organism that could be used to demonstrate many concepts to biology majors2. *C. elegans* is a small soil nematode that is a decomposer in the ecosystem, mainly eating small organic matter and microbes. *C. elegans* fits the description of a model organism almost perfectly as it is small (less than 1mm long), reproduces in the hundreds at a three to four day generation turnover, is easily manipulated and has a fully mapped genome2-4. This poster will serve as a starting point for undergraduate institutions interested in using *C. elegans* as a model organism for genetics, cell biology, and behavior in their curriculum. 1Woodin T, Carter V, Fletcher L. 2010. Vision and Change in Biology Undergraduate Education, A Call for Action—Initial Responses. *CBE Life Sci Educ*. 9 (2): 71-73.2Roy N. 2013. Using RNAi in *C. elegans* to Demonstrate Gene Knockdown Phenotypes in the Undergraduate Biology Lab Setting. *Bioscience: Journal of College Biology Teaching*. 39 (1): 16-20.3 Knight J, Smith K, Wood W. 2013. What's Downstream? A Set of Classroom Exercises to Help Students Understand Recessive Epistasis. *Journal of Microbiology and Biology Education*. 14 (2): 197-205.4 Aschner M, Au C, Benedetto A, Helmcke K, Leung M, Meyer J, Williams P.2008. *Caenorhabditis elegans*: An Emerging Model in Biomedical and Environmental Toxicology. *Toxicological Sciences*. 106(1): 5-28.

P283 Thomas P. Wilson, Bradley Reynolds, Paul-Erik Bakland, Nyssa Hunt, Mark Dillard, Joe Simpson, Jermey Hooper, Simone Madsen, Team Salamander
Biological and Environmental Sciences, University of Tennessee at Chattanooga

Team Salamander and Its Evolution in Becoming the Longest Running Group Studies Initiative at University of Tennessee at Chattanooga (UTC)

Since 2004, over 350 students have participated in the longest running group studies project at UTC, entitled "Team Salamander". Most curriculums are based on predetermined benchmarks that have to be met and the Team Salamander experience is no different. However, it is more than just a traditional syllabus based lecture/laboratory course. Rather, it is a hands-on-cooperative experience that forces students to become independent and forward-thinkers. Ultimately, we strive for them to become natural science practitioners and informed citizens, and several have followed the path to graduate or professional school. Team Salamander gets recharged and reinforced every time a former member becomes a medical doctor, lawyer, pharmacist, engineer, geologist, school teacher, environmental consultant or even an academic. No matter their individual path, the team has collectively contributed to UTC and Chattanooga. Specifically, they have contributed to the research and education efforts at UTC, Tennessee River Gorge Trust, City of Chattanooga, Hamilton County Public Schools, Hamilton County Parks and Recreation, Thrive 2055, Tennessee Aquarium, Challenger Center, Chattanooga Arboretum and Nature Center, and others. The team has organized wetland clean-ups, restorations and has been instrumental in starting a new UTC sanctioned club, entitled, "Wildlife-Zoology Club". They have also contributed materials to a new UTC course, entitled, "Amphibian Conservation", and have shared educational materials with interested parties using multimedia and the internet. The list goes on, but their greatest contribution has been educating others about the science and conservation issues involving amphibians and reptiles in the Southern Appalachians and in their own backyard.

P284 Brandon C. Reagan[1], Nina L. Shouse[1], Jeffrey K. Denny[2], Amy M. Wiles[1]
[1] Biology, Mercer University, Macon, GA; [2] Mathematics, Mercer University, Macon, GA

From Media to Model: Expanding the Mathematical Biology Experience in Undergraduate Education

Mathematical biology is a growing field that is often neglected at the undergraduate level due to a lack of bench-to-model exercises, instructor experience, and resources. This neglect results in a disconnect between undergraduate and graduate level education in the field of Mathematical Biology. Here we developed a bench-to-model teaching exercise for an upper-level mathematical modeling course. The goal was to introduce students to biological data collection as well as data analysis through mathematical modeling. An assay was designed to examine the effects of competition on the growth of *Escherichia coli* and *Serratia marcescens* grown in the same culture. The assay was developed using growth curves of the two species grown individually and in mixed cultures. After the assay was designed and protocols were written, the exercise was implemented in a classroom setting at Mercer University. Supplemental videos and a preparation exercise were created that demonstrated proper lab safety and aseptic techniques to students unfamiliar with bench research. After collecting biological data, the students defined parameters for the model using the data and applied them to a series of competition models that were used to observe trends in the growth of the two species. The models showed that *S. marcescens* out-competed *E. coli* under the conditions of the experiment. After completion of the lab experience and subsequent modeling, the students evaluated the effectiveness of this exercises. The positive responses and suggestions from the class were used to modify this exercise for future use.

P285 William H. Dees[1], Caleb M. Ardizzone[1], Janet R. Woolman[2], Hannah G. Fogg[2], Lyle J. Hardee[2], Sean M. Hicks[2], Cullen L. Haymon[2], Sandesh Thapa[2], Lacie C. Petticrew[2]
[1] Biology and Health Sciences, McNeese State University, Lake Charles, LA; [2] Office of Economic Development, McNeese State University, Lake Charles, LA

Innovation and Applications in Undergraduate Research

Through a partnership with the University of Maine, the McNeese State University Student Innovation Center offers Innovation Engineering classes to undergraduate students in every discipline and features technology to enhance creativity and bring ideas into reality. The Innovation Engineering curriculum, offered as a minor, is a groundbreaking program that provides a systematic approach to creativity and invention. The innovation engineering program is a data-driven, replicable model for developing and commercializing innovations with value in both established and new businesses. The fundamental concepts of the program include tools and methods for creating, communicating, and commercializing meaningfully unique ideas. Students learn how to employ these tools and methods in their fields of interest. These skills are essential to participation in the global economy and prepare students to lead the commercialization of new products, services and technologies. A team composed of students, faculty, and local professionals in biology, business, computer science, design art, engineering, innovation, and mathematics is conducting research and designing practical uses for both evolving and state-of-the-art technologies. Team members are, for example: (1) developing solutions for applied research using the Innovation Center's 3-D printing/scanning equipment, 3-D milling machine, 3-D printing pen and advanced development software, and (2) investigating a new technology acquired by the Innovation Center, Google Glass, to augment classroom learning, conduct research, explore surroundings, and develop new applications. Strategic use of emerging technologies, creativity tools, and applied innovation methods provides new avenues for attracting students and faculty to pursue creative contributions and engage in scholarship and research.

P286 William H. Dees[1], Janet R. Woolman[2], Lyle J. Hardee[2], Hannah G. Fogg[2], Justine A. Gunnell[2], Sean M. Hicks[2], Lacie C. Petticrew[2], Caleb M. Ardizzone[1]
[1] Biology and Health Sciences, McNeese State University, Lake Charles, LA; [2] Office of Economic Development, McNeese State University, Lake Charles, LA

Taking Undergraduate Research to the Next Level: The McNeese State University Student Innovation Laboratory

Within the last several years (2011-2015), the Student Innovation Center at McNeese State University (MSU) evolved from a conceptual idea to an actual center within the newly constructed multimillion dollar three-story Southwest Louisiana Entrepreneurial and Economic Development (SEED) Center. The SEED Center currently houses the MSU undergraduate scholar and research program, the MSU Student Innovation Center, the local chamber of commerce, and other economic development offices. The Student Innovation Center is located in three rooms on the ground floor of the SEED Center and is comprised of the Innovation Classroom, Innovation Lab, and Student Business Incubation Studio. The Innovation Lab is a transformative ecosystem with non-linear and writeable wall space, intentional design imagery, interactive technology, communication devices, a prototyping center, and idea creation tools designed to pioneer student invention through interdisciplinary collaboration. This learning environment connects undergraduate students to peers, faculty mentors, and interdisciplinary research opportunities. Through exploration, mentoring, technology, idea creation tools, and a relaxed environment, students are able to: (1) collaborate with students from other disciplines, (2) create and refine ideas, (3) pioneer invention, (4) prove and communicate a concept, (5) conduct patent searches and data mining, (6) forecast sales, (7) network with peers and local companies, (8) access faculty and peer mentoring, and (9) create working prototypes. Through new programs and activities, McNeese State University is leading an effort to create an environment that supports innovation in undergraduate research and gives students the tools they need to create and refine an idea and translate it into an opportunity.

P287 Janet R. Woolman[1], William H. Dees[2], Hannah G. Fogg[1], Lyle J. Hardee[1], Lacie C. Petticrew[1], Cullen L. Haymon[1], Joyce D. Patterson[3]
[1] Office of Economic Development, McNeese State University, Lake Charles, LA; [2] Biology and Health Sciences, McNeese State University, Lake Charles, LA; [3] McNeese Alumni Association, McNeese State University, Lake Charles, LA

Multidisciplinary Scholarship and Undergraduate Research at McNeese State University

Within the last seven years (2008-2015), the undergraduate research (UR) program at McNeese State University evolved from a small science event with a few undergraduate students selected from the College of Science presenting their research to today's current campus and University of Louisiana System-wide events. The current McNeese State University Alumni Association Undergraduate Scholar and Research Symposium engages all disciplines and all six colleges on campus - Business, Education, Engineering, Liberal Arts, Nursing, and Science. The McNeese Alumni Association has sponsored this symposium since its inception. This program continues to grow due to the overwhelming support by university administrators, alumni, students who continue to see the significance of engaging in their selected discipline, and devoted faculty members who recognize that UR programs can be both academically and professionally rewarding. By participating in the UR program, students have found discipline-related employment, built their portfolios for application to professional schools (e.g., graduate, medical and veterinary schools), enhanced their professional communication skills and self-confidence, and have become more involved in their selected disciplines. These successes, along with year-long faculty development initiatives in the principles and practices of mentorship, led to increased participation of faculty members from diverse disciplines engaging in UR mentorship and students from different disciplines actively learning about their field of study. This project will present growth strategies and best practices for sustainable UR engagement at a predominantly teaching institution. Future strategies include dedicated funding for student research, UR work-study activities, and transcript designations.

P288 James L Wood
Odum School of Ecology, University of Georgia, Athens

Evaluating the Impact of a Traditional Ecology Course on Students Perception of the Health of Their Environment, the Educational Value of Service-Learning, and Their Responsibilities to Ecosystem Health in an Urbanizing World

The world is becoming more urbanized, and an increasing proportion of people are living in cities. This phenomenon is having significant impacts on ecosystem health and global biodiversity. Using pre- and post-questionnaires, I surveyed 41 students in a traditional ecology course to investigate how the course influenced their perceptions about the environment and their role in an urbanizing landscape. The ecology course (Ecol 3500) is often taken as a general science requirement by biology, dental and pre-med students, and these students have diverse life experiences and motivations. The questionnaire was organized into six categories evaluating: students' perception of the health of the environment, the impact of urban areas on pollinators and birds, how the students' actions impact the environment, students' perceptions of service-learning and citizen science, students' feelings about the importance of community organizations and volunteering, and students' view of their responsibility to improve the environment. Interestingly, students view service-learning as important components of their educational experience and feel that they have some responsibility to volunteer with community organizations. This study is the first part in a larger project to evaluate the impact of a service-learning urban ecology course on students' perceptions of urban landscapes and their role in ecosystem health.

P289 Rebekah Ward, Christopher Brandon, Jennell Talley, Christopher Brown
School of Science & Technology, Georgia Gwinnett College, Lawrenceville, GA

The Challenges for a Completely Objective Assessment of Program Goals

When engaged in the assessment of specific program goals, the utmost objectivity is required. This will ensure that the most accurate image of student learning outcomes emerge from the data, be it quantitative or qualitative. At Georgia Gwinnett College, we have introduced a pilot program for the longitudinal assessment of core concepts as well as scientific writing skills in an attempt to refine our current assessment methods. In this pilot study, a cohort of professors volunteered to participate on the grading committee, and all student work evaluated was stripped of identifiers to maximize objectivity. Further, to minimize variability in the assessment of writing skills, collaboratively constructed rubrics for the short answer questions were created. Additionally, a pre-established lab report rubric to which students had access to prior to their submissions was also utilized. Participating faculty found the experience an excellent opportunity for professional development and self-reflection as educators. However despite the use of rubrics, there were still significant differences in evaluation of the same work between graders. This suggests that further steps must be taken in order to objectively assess some components of student learning.

Index of Presenters

FIFTY-EIGHTH ANNUAL MEETING
BETA BETA BETA
SOUTHEASTERN REGION

DISTRICTS 1 and 2

MEETING JOINTLY WITH THE SEVENTY-SIXTH ANNUAL MEETING OF THE ASSOCIATION OF SOUTHEASTERN BIOLOGISTS

hosted by

The University of Tennessee at Chattanooga
and the Tennessee Aquarium

Host Chapter: Tau Gamma, East Carolina University,
Greenville, NC

April 1-4, 2015
Chattanooga, Tennessee

DISTRICT I BROOKS AWARD SESSION
Rooms 9-10

*Paul Frye, and Constance Rogers-Lowery, Tau Eta, Catawba College. "The Effects of Increased levels of CO_2 on Photosynthesis and Respiration of *Favia fragum"*

Ocean acidification is a major factor contributing to global climate change, impacting ecosystems as diverse as coral reefs and kelp forests. The current study focuses on the effects of ocean acidification on coral physiology. The golfball coral, Favia fragum, were exposed to 380 ppm, 700 ppm (predicted atmospheric CO_2 level in 2100), and 1300 ppm atmospheric CO2 for 7 days. At that time, oxygen consumption at 26 and 32 degrees Celsius in both light and dark conditions were measured to calculate rates of photosynthesis and respiration, respectively. It is hypothesized that if there is an increase in CO2, then the coral's metabolism and respiration will decrease.

*Honorable mention winner of the District I Brooks award

Fürstenwerth, Finn, Taylor Spillman, Duncan Cameron, Jay Bolin, Tau Eta, Catawba College. "Is the Southern Blue Thread (Burmannia capitata) partially mycoheterotrophic?"

The Burmanniaceae contain several lineages of achlorophyllous mycoheterotrophic plants that may associate with arbuscular mycorrhizal fungi (AMF). Here we investigate the isotopic profile of a green and potentially mycoheterotrophic wetland plant in situ, *Burmannia capitata*, the Southern Blue Thread, and associated vegetation. We generated δ 13C and δ 15N stable isotope profiles of a population of *B. capitata* and adjacent reference plants from the Sand Hills Game Lands in Scotland County, North Carolina. The highest δ 15N values were observed in the *B. capitata* shoot, congruent with similar reports in other mycoheterotrophic plants. Reference vegetation shoot and root fractions (C3 and C4) were statistically indistinguishable, whereas *B. capitata* shoot and root fractions were statistically different from each other. Interestingly B. *capitata* is a C3 plant and the *B. capitata* root fraction resembled C4 reference vegetation. This may indicate that *B. capitata* has access to a carbon source with an isotopic signature different from C3 photosynthesis, and potentially a signal of mycoheterotrophic carbon gain. Glomeromycota specific AML1 and AML2 primers were used to amplify the 18S rRNA region of fungal symbionts from whole *B. capitata* root DNA extracts. We detected *Glomus* clade A specific DNA sequences in 3 out of 6 *Burmannia* root samples. Isotopic and DNA evidence is strongly suggestive of partial mycoheterotrophy in *B. capitata.*

*Smith, Kimberly; Pieter AP deHart, and Geoffrey Cox, Psi Omicron, Virginia Military Institute. "Redefining how biologists analyze data: Augmenting the two-dimensional proportional contribution model with a three-dimensional approach to enhance analysis of stable isotope data"

No abstract submitted.

*Second place winner of the District I Brooks award

Rooks, Sarah; Anna Watson-Selph; Bhabesh Dutta; Ron Gitaitis; Claudia Nischwitz; Stephen W. Mullis; Albert K. Culbreath; and Alex Csinos, Tau Delta Kappa, Abraham Baldwin Agricultural College. "Impact of Micronutrients on Tomato Spotted Wilt of Tobacco (*Nicotiana tabacum*) and Superoxide Dismutase and NPR1 genes"

In previous studies, levels of tomato spotted wilt (TSW) of tobacco (*Nicotiana tabacum*), caused by *TSW virus*, had a linear relationship to cations in the soil. In multi-year studies, predictive equations from soil analyses were developed with variables consisting of concentrations of Cu, Fe, Zn, and the Fe:Mn and Cu:Fe ratios. In year one the spatial distribution of TSWV-infected plants exhibited a severity gradient that matched the Cu:Fe soil gradient. In 2014, sites were surveyed at UGA's Bowen Farm; soil cation concentrations were analyzed and used as independent variables in predictive TSW models. Before tobacco planting, two sites were selected as high- and low-TSW risk areas based on model predictions. When rated for TSW prior to harvesting, plants at the low-risk site had 4.5% TSW severity compared to 33.1% disease severity at the high-risk site. Low-risk site plants had a 5.5-fold, 2.3-fold, and 625-fold increase in *MnSOD, FeSOD*, and *NPR1* gene expression, respectively, when compared to high-risk site plants. These results support our hypothesis that cations affect genes regulating systemic acquired resistance pathways and the detoxification of reactive oxygen species. Soil profiles of fields used with TSW predictive models could be part of management strategies to control TSW of tobacco.

Gordon, Natalee (Kayla Spenard, Irma Santoro). Psi Pi, Reinhardt University. "Is Drinking Beer Influenced By Genes?"

It is known that bitter taste receptors (TAS2Rs) dictate the consumption behavior of a wide range of food and beverages in humans, and there are many different forms due to genetic variability. This family of taste receptors is linked to diseases such as obesity, diabetes, and alcoholism. One gene in particular, *TAS2R38*, mediates the perception of bitter taste and three common single nucleotide polymorphisms (SNP) have been identified. These three polymorphisms have been linked with the ability to taste bitter compounds such as coffee and phenylthiocarbamide (PTC). This study focuses on beer consumption behavior in of-age undergraduate students on the Reinhardt University Campus. We're interested in determining a link between the inability to taste bitter, and a preference to drink beer. This study incorporates the collection of surveys on taste perception of student participants between the ages of 21-25, their ability to taste PTC paper, and an Allele-Specific SNP Genotyping analysis from cheek cell genomic DNA. Forty one samples are being analyzed from 30 males and 11 females primarily from Caucasians of Western European descent. Any correlation between survey answers, the ability to taste bitter using PTC paper, and the genotyping results will be presented.

Funk, C. Ronnie, May, Melanie, Blenda, Anna V.; Schwartz Charles E, Sigma Gamma, Erskine College. “Search for a Novel Molecular Basis of Split Hand Foot Malformation”

No abstract submitted.

*Giangiuli, Stephanie and Kevin Drace, Beta Omega, Mercer University. “The Comparison of *mer*A Isolated from Mercury Resistant Bacteria Isolated from Artisanal Gold Mining Sites in Mozambique and Ecuador”

The process of small-scale artisanal gold mining makes use of mercury amalgamation for the purpose of gold extraction and isolation. Unfortunately, improper disposal of mine tailings and poor mining techniques have led to the accumulation of mercury in the environments surrounding mining camps. Our lab is interested in the effect that this release of mercury may have on existing microbial populations in both Mozambique and Ecuador. Preliminary data suggest that areas of high mercury contamination may put selective pressure on bacteria to acquire mercury resistance. Bacteria that contain the *merA* gene synthesize the enzyme mercury reductase, which reduces toxic inorganic mercury to less harmful elemental mercury. Our hypothesis is that *merA* will be selected for in bacteria from artisanal gold mines around the world. We isolated and characterized mercury resistant strains from soil and sediment samples collected in Mozambique and Ecuador. Genetic material from these strains was isolated and we developed a PCR protocol to amplify part of the *merA* gene. These amplified products are being sequenced and analyzed for comparison in an effort to determine the effect mercury contamination has on the exchange of genetic material in the bacterial ecosystem surrounding the mines.

*First place winner of the District I Brooks award

*Smith, April and Jennifer Cannon, Kappa Kappa, Georgia Regents University. “The effects of perfluorooctanoic acid on cell viability and peroxisome proliferator-activated receptor gene expression in MCF-7 cells”

Perfluorooctanoic acid (PFOA) is an endocrine disrupting compound found in food, water, clothes, and other consumer products. It is known to accumulate in the environment and can be taken up through ingestion, inhalation, or skin contact. It has a half-life of nearly four years in humans. PFOA has been shown to bind and activate peroxisome proliferator-activated receptors (PPARs), which are transcription factors found in mammalian cells. PPARs regulate numerous cellular activities, including proliferation and differentiation. Activation of PPARs has been shown to positively regulate PPAR expression. This study aimed to examine the effects of PFOA on cell viability and on PPAR expression in MCF-7 breast cancer cells. Cells were treated for 24h and 48h with 100nM to 100μM PFOA and viability was determined using the CellTiter-Blue® Viability Assay. While there was no decline in viability at 24h with any of the PFOA treatments, there was a significant decrease in viability in cells treated with 100μM PFOA for 48h. At both the 24h and 48h time points, cell lysates were collected and RNA isolated using Ambion's RNaqueous®-Micro kit. Primers for PPARα, PPARβ, and PPARγ have been ordered and are being optimized for real-time RT-PCR to determine mRNA levels of those genes.

*Third place winner of the District I Brooks award

Denzongpa, Kunga, Sigma Phi, Guilford College. “Myths vs. Facts: Prenatal Health Care Awareness In Sikkim, India”

Prenatal care is a crucial aspect of women's health especially in developing countries like India, the world's second-most populous country. Lack of knowledge regarding proper prenatal care is common among the population of Sikkim, a state in North-Eastern India, where pregnant women and their families have inaccurate knowledge of care required during the prenatal stages. The government-funded hospital in this state shows substantial disparity in health care access and awareness provided to women compared to the state's private hospital. This study examines the qualitative differences in prenatal care that women receive in each type of medical facility in Sikkim. It also shows how education plays a vital role in healthy maternal and child care during the prenatal stages of pregnancy. Data were collected using field research methods including interviews of medical professionals, pregnant women, their husbands, and their parents. The interviews included questions regarding the care and information on prenatal health provided by each type of medical facility, and the patient's own knowledge on prenatal care. Results show the lack of government medical professionals' efforts in providing information on proper prenatal care. The high rate of illiteracy among patients in the government-funded hospital also plays a major role in how they perceived prenatal care. The study reveals the lack of awareness and access to quality prenatal care for many women in Sikkim, and gives insights on how to improve quality of care and public access to care and awareness

Brown, Caleb, Daniel Christen, Melanie Lee-Brown, Sigma Phi, Guilford College. “Using *S aurantiaca* Derived Natural Products for Quorum Quenching and Biofilm Disruption of *P. aeruginosa”*

Antibiotic resistance has become a major problem in recent times arising from both cellular modes of resistance and biofilm formation. The use of traditional antibiotics intrinsically accelerates the accumulation of resistance in bacterial populations because it increases selective pressure. This is a increasing a problem in healthcare settings where antibiotic resistant *Pseudomonas aeruginosa* infections are spreading rapidly. Quenching quorum sensing to prevent the density dependent expression of virulence factors has been proposed an alternative approach. A structural approach to identifying potential quorum quenchers of *P. aeruginosa* was used to identify test compounds. Natural products aurachin C and D from *Stigmatella aurantiaca* were synthesized utilizing a Conrad-Limpach cyclization and will be tested as quorum quenchers of *P. aeruginosa.* A *C. elegans* pathogenicity assay was developed to determine the virulence expression of *P. aeruginosa* over time. These compounds were additionally tested for their ability to inhibit biofilm formation by both exposing cultured *P. aeruginosa* biofilms to a solution of aurachin C or D and by introducing the solution into media before biofilm formation occurred.

DISTRICT I BROOKS AWARD SESSION
Rooms 16 and 17

Gallman, Kathryn; Grace, Michael; Emer, Sherri, Sigma Psi, Florida Institute of Technology. “Cellular Organization of the Micro-Retina, and Projections to the Brain in the Brahminy Blindsnake, *Ramphotyphlops braminus”*

No abstract submitted.

Clayton, Sean Margaux Usry, Robin White, Sydney Nazerian, Ryan Shanks, Steven Lloyd, Psi Rho, University of North Georgia. “Drug and sex specific alterations in dopamine receptor expression following adolescent exposure to methylphenidate”

The prevalence of ADHD medications correlates with the abuse of psychostimulants in adolescent populations including methylphenidate (MPD), the active ingredient in Ritalin®. MPD increases dopamine (DA) in synapses by blocking the DA transporter (DAT). DA and its receptors (D1-5) play essential roles in reward-motivated behavior, especially in the prefrontal cortex (PFC) and striatum (STR). We previously demonstrated that adolescent MPD exposure leads to long-term behavioral sensitization, a hallmark of addiction, but only in females. We hypothesized that alterations in DA signaling or handling underlies this observed behavior. Therefore, adolescent mice (P22) were treated with i.p. 10-mg/kg MPD or saline for 10 days, and RNA was isolated from the PFC and STR. RT-qPCR was used to quantify MPD-induced mRNA expression changes in D1-5, DAT and VMAT2. D2- 5, DAT, and VMAT2 expression was not altered by MPD ($p>.05$). D1 was down-regulated in the PFC and STR of MPD-treated animals, with female MPD-treated mice showing the greatest striatal D1 reduction (all comparisons $p<.05$). MPD-reduced D1 expression could alter DAergic signaling, contribute to altered plasticity, and/or result in increased addictive tendencies in females with important clinical implications in ADHD treatment and MPD

*Penrod, Louis, Sigma Psi, Florida Institute of Technology. “The influence of climate change on invasive and native fish performance”

Growing concerns about the consequences of climate change have revitalized research on the effects of temperature on organismal performance. In particular, the predicted poleward spread of tropical-invasive species as a consequence of rising global temperature is alarming. This paper investigates how temperature mitigates predator-prey interactions in aquatic ecosystems. To address this objective, two experiments were conducted. First, the effects of temperature on Ram-Suction Index (RSI), a measure of predator-prey interactions, were compared among three invasive and one native fish species. Second, the escape response of fish (*Gambusia*)- and shrimp (*Palaemonetes*)- prey was compared among different temperature conditions. High-speed videography revealed that temperature-induced variation in predator-prey interactions is predator-species specific. Certain invasive species changed their feeding mode from suction-feeding to ram-feeding according to temperature conditions. High-speed videography also revealed that environmental temperature induced a change in the escape response of prey. The shrimp-prey switched from an escape response involving multiple tail flips at low temperature to a single tail flip at high temperature conditions. It is proposed that attempts to elucidate the consequences of climate change on predator-prey interactions must include an investigation of the differential effects of temperature on the performance of predator and prey.

*Second place winner of the District I Brooks award

Nazerian, Sydney, Ryan A. Shanks, and Steven A. Lloyd, Psi Rho, University of North Georgia. “An exploratory analysis of methamphetamine-induced break down of the blood brain barrier in C57Bl/6J”

The blood brain barrier (BBB) is a system of brain capillary endothelial cells, pericytes, astrocytes, and nerve endings that maintain the homeostasis of the central nervous system by blocking the movement of molecules except relatively small molecules crossing cell membranes by means of lipid solubility (oxygen, carbon dioxide, ethanol, and steroid hormones) and those transported by specific transport systems. Matrix metalloproteinases (MMPs) are enzymes in the pericellular environment. Their activation is important in maintaining tissue homeostasis and synaptic physiology. Their role in neuronal plasticity is of interest in the context of addiction as they are thought to contribute to the development of behavioral sensitization to drugs such as methamphetamine (METH). Effects of METH are thought to depend on the drug’s similarity to dopamine (DA), which allows METH to enter DA axons and release DA from the synaptic vesicles. We hypothesize increased activity of MMPs contributes to many of the synaptic changes that result in formation of addiction pathways and may lead to the “leakiness” of the BBB. Here, we investigate the effect of high-dosage METH treatment BBB breakdown in the striatum and prefrontal cortex of adult C57Bl/6J mice given their role in reward, addiction, behavioral sensitization, and associated neural remodeling.

*Narzynski, Annette, Sigma Psi, Florida Institute of Technology. "Visual analysis of Lionfish (*Pterois volitans*)"

The spectacularly beautiful lionfish, popular in the aquarium trade, has successfully invaded the waters of the western Atlantic Ocean and now ranges throughout the Atlantic seaboard, the Gulf of Mexico, the Caribbean and northern South America. They are highly efficient predators with few natural enemies because of their venomous spines. As lionfish continue to spread and populations grow, they present an ever-increasing threat to sensitive reef ecosystems. Lionfish are visually-guided predators as suggested by their large eyes, but compared to other vertebrate species, including many other bony fishes, essentially nothing is known about the lionfish visual system. This study utilized the most common invasive lionfish in Florida, the red lionfish (Pterois volitans), in an investigation of the functional architecture of its retina. Using histology, immunofluorescence, and light and laser-scanning confocal microscopy, retinal structure was characterized and the distribution and relative number of rod and cone photoreceptors was assessed. Microspectrophotometry will be used to quantify the number and types of cones present to display their visual range. Results of this work will be used in conjunction with behavioral experiments to understand the relationship between neural organization and behavior in order to better understand the ecological effects of and hopefully control invasive lionfish populations.

*Honorable mention winner of the District I Brooks award

*White, Robin; Sean Clayton, Dr. Ryan Shanks, Dr. Steven Lloyd, Psi Rho, University of North Georgia. "The Effects of Chronic Adolescent Methylphenidate Abuse on Brain Derived Neurotrophic Factor (BDNF) Expression"

Methylphenidate (MPD), the active ingredient in Ritalin®, is a prescription psychostimulant often used and abused by adolescents. Our lab demonstrated that chronic adolescent MPD exposure induced cross-sensitization to methamphetamine in female and not male mice. These results demonstrate MPD-induced alterations in neuronal circuitry, indicative of addictive behavior, that persist into adulthood in a non-ADHD mouse. Brain derived neurotrophic factor (BDNF) is a growth factor known to play a role in facilitating synaptic plasticity in dopaminergic circuits through its receptor TrkB. Using the same adolescent dosing paradigm that induced behavioral cross-sensitization, we isolated total RNA on the final day of injections from the prefrontal cortex (PFC) and striatum (STR), which are two dopaminergic regions implicated in the addiction process. mRNA expression was measured with RT-qPCR using BDNF and TrkB specific primers. No alterations in TrkB were observed. In the PFC no alterations in BDNF were observed, but we observed an increase in males and a decrease in females in BDNF expression in the STR ($p<.05$). The sex-specific change in BDNF expression with stable TrkB expression implicates striatal BDNF in synaptic alterations leading to the observed MPD-induced psychomotor differences indicative of increased addiction susceptibility.

*Third place winner of the District I Brooks award

Zbasnik, Nathaniel, Sigma Psi, Florida Institute of Technology. “Divergent Feeding Biomechanics Reflects Divergent Feeding Ecology in Sympatric Fishes”

It is well known that sympatric species maintain divergent food habits (feeding ecology) in order to release each other from competing for limited food resources. Is ecological divergence consistent with functional or biomechanical divergence in sympatric fishes? This study investigates the ecological correlates of functional morphological divergence by comparing the trajectories of growth in key components of the feeding mechanism in two sympatric North American teleost fishes through ontogeny. Upon metamorphosis, two *Lepomis* species develop divergent food habits in North American lakes and ponds. The suction-feeding bluegill, *Lepomis macrochirus* feeds primarily on soft, elusive, and planktonic prey whereas the durophagous redear, *Lepomis microlophus* eats hard-shelled invertebrates such as clams. Growth trajectories established from scaling biomechanical metrics with body size revealed that the scaling coefficients (growth rate) of the Suction Index (SI), physiological cross-sectional area of the epaxialis muscle and the mechanical advantage of the neurocranial rotation mechanism differed between species. This variation in scaling coefficients is consistent with the contrasting diet between these sympatric species. It is proposed that the divergence in growth rate of functional morphological traits that is reflective of contrasting food habits contributes to the formation of organismal and ecological diversity in coexisting fishes.

Bhullar, Ashley and Chang-Story, Ashley. Rho Rho, Nova Southeastern University. “The effects of various concentrations of caffeinated and alcoholic dietary additives/beverages (caffeine tablets, energy drinks, alcoholic drinks, and ethanol) on gene expression in *Saccharomyces cerevisiae* (Baker’s Yeast)”

Especially while in college, young people are supplementing their diets with various additives including caffeine in the forms of pills and energy drinks, in addition to consuming alcoholic beverages. This project aims to investigate the effects of various concentrations (low, medium, and high) of various caffeinated and alcoholic dietary additives/beverages. Since yeast share approximately 30% of their genome with humans several conserved genes belonging to various functional groups (digestion, cell cycle, ion channel, molecular chaperone, kinases and transcription) were selectively targeted in this study. High, medium and low concentrations of caffeine tablets, energy drinks (Red Bull energy drink, Arizona Energy drink), ethanol, and alcoholic beverages (Bacardi rum and Bud Light beer) were administered to yeast cultures growing in typical YEPD media. These yeast cultures were allowed to grow for 42 hours to reach a density measure of approximately 1.2 at A_{660}. Then RNA was extracted, followed by cDNA preparation. The relative degree of expression of the selected genes belonging to the various functional groups was compared through the use of reverse transcriptase PCR. In this presentation, the results of the relative expression of selected digestion genes (SUC2, TDH1, GPT2, DAP1, and GIP2) exposed to the different treatments will be highlighted.

*Muraski, Marc, Sigma Phi, Guilford College. “Pseudomonas Aeruginosa Biofilm Disruption Via Yayurea A&B Quorum Quenching”

No abstract submitted.

*First place winner of the District I Brooks award

DISTRICT II BROOKS AWARD SESSION
Rooms 18 and 19

P. Van de Vuurst , K.A. Bakkegard, E. Dupal, Ph.D. & E.G. Dobbins, Ph.D.. Eta Nu, Samford University. “The Effects of Hiking and Mountain Bike Trails on Stream Ecosystems in Oak Mountain State Park in the Southern Appalachian Mountains”

Little is known about the effects of hiking and mountain biking trails on stream ecosystems. Oak Mountain State Park in Shelby Co, Alabama is a popular recreational location with both hiking and mountain biking trails. We studied the effects these trails on adjacent streams (within 10 m) by observing the deposition of inorganic sediment, the physical and chemical water quality characteristics, and both the salamander and macroinvertebrate populations over a one month period. We found that mountain bike trails significantly increased sediment deposition and turbidity in adjacent streams. In addition, mountain bike trails significantly reduced salamander population densities and macroinvertebrate richness, density, and percent EPT. Our results suggest a negative impact on stream ecosystems adjacent to mountain bike trails. Streams associated with hiking trails did not show a distinct difference from control streams. Further study is needed to determine the mechanism by which mountain bike trails effect streams, but our results implicate sediment. We recommend that future mountain bike trails be placed at least 10m from adjacent streams to protect these fragile ecosystems.

Hernandez, Rosmely and Tina Hubler, Beta Zeta, University of North Alabama. “Techniques for the Rapid Detection of KPC Gene Isolated from Bacteria found in Sputum Samples using PCR Amplification”

The emergence and spread of carbapenemase-producing bacteria has become a well-known problem in clinical settings. *Klebsiella pneumoniae* carbapenemase, KPC, is an enzyme able to provide bacteria with resistance to carbapenems and cephalosporins via hydrolysis of the antibiotic beta-lactam ring. It is of high importance to detect pathogenic organisms containing the KPC gene in order to provide the most effective antibiotic treatment. The purpose of this project was to develop a rapid detection method for the KPC gene using PCR amplification. PCR primers were designed using the coding sequence for the KPC gene. A KPC positive strain of *K. pneumoniae* was used as a positive control to test the effectiveness of the PCR amplification. Bacterial isolates obtained from clinical sputum samples and previously tested for their antibiotic resistance profiles will be subject to genomic and plasmid DNA isolation. The DNA isolated will be used to test for the presence of the KPC gene using PCR amplification. It is expected that this project will be successful in the rapid detection of KPC and will save time and money otherwise spent in antibiotic testing. In clinical settings, a correct antibiotic treatment regimen can be provided once the presence of a gene conferring antibiotic resistance has been confirmed.

*Moody, Rebecca, Mu Omicron, Columbus State University. “Effect of fluoxetine on proliferation and viability of cardiomyoblasts”

Serotonin has been shown to play a role within cellular division and differentiation during early heart development. Prenatal exposure to fluoxetine (Prozac), a selective serotonin re-uptake inhibitor that readily crosses the placenta during pregnancy, acts on nerve synapses by inhibiting the uptake of serotonin from the cleft. Disruption to early serotonin levels has been shown to result in decreased myocyte proliferation, decreased ventricle size, and myocellular disorganization; with dilated cardiomyopathy and an increase in postnatal mortality rates being consequences to this interruption. The effects of exposing *Rattus norvegicus* cardiomyoblasts to fluoxetine on the proliferation and viability of early heart muscle cells were examined. We hypothesized that exposure to fluoxetine would inhibit proper cellular development and result in a decrease in cellular proliferation and cellular viability. Cultured cardiomyoblasts were exposed to 0.3, 0.6, and 0.8 mg/L of fluoxetine once every two days for a week and assessed for viability and growth rate. There were no significant differences in cellular proliferation among the three exposure levels. Furthermore, cellular viability did not differ significantly across treatments. Average percentages of viable cells across the treatments (0.3, 0.6, and 0.8 mg/L, and the control) were 50.74, 65.97, 62.01, and 47.03, respectively.

*Honorable mention winner of the District II Brooks award

Harry, Brittany, Beta Phi, University of West Alabama, and Swayamjit Ray, Flor Acevedo, Shan Jin, Michelle Peiffer, Dawn S. Luthe, Gary Felton, Lambda Gamma Beta, The Pennsylvania State University. “Caterpillar saliva mediates herbivore defense gene expression in maize”

Understanding how plants defend themselves from pathogens and herbivores is essential in order to protect our food supply and develop highly disease-resistant plant species” (Chuang, W.-P., et al. New Phytologist, 2014). Corn earworm (Helicoverpa zea) herbivory to maize is economically damaging worldwide and results in many challenges for farmers and consumers. Caterpillars feeding on plants often leave ‘cues’ behind that activate defense mechanisms. This study looks at the oral secretion of saliva that is left behind recognizably as a ‘cue' on the leaf tissue. Caterpillar saliva is known to elicit plant defense response in several plants but the effect of H . zea saliva on corn defenses has not yet been reported. A series of experiments were conducted to test how corn earworm (H. zea) saliva affects defense gene expression in Zea mays (corn). In this study, we will examine this affect in three different genotypes of maize: B73 (susceptible to herbivory), Mp708 (resistant to herbivory) and Mc4050 (hybrid of maize). Techniques used in this project will include caterpillar spinneret ablation, RNA extraction, genomic DNA digestion, reverse transcriptase, quantitative real-time PCR, and One-Way ANOVA.

Hamm, Michael, Mu Omicron, Columbus State University. "Effect of Indole-3-Propionic Acid on *Saccharomyces cerevisiae* Lacking YFH1, A Homologue of the FXN Gene in Humans"

Friedreich's ataxia (FRDA) is a degenerative neuromuscular disease that affects roughly 1 in every 50,000 people in the United States. It has several symptoms, including loss of coordination, fatigue, and hypertrophic cardiomyopathy. FRDA is caused by inheriting two copies of a defective FXN gene, and it leads to decreased frataxin protein. Producing less frataxin results in mitochondrial dysfunction, along with production of reactive oxygen species and an increase in iron in the mitochondria. Yeast, such as *Saccharomyces cerevisiae*, have a homologue to the FXN gene of humans, called YDL120 (YFH1) and might be a good model for understanding FRDA in humans. The goals of this research are to assess oxidative stress in yeast cells that lack YFH1 compared to controls and to assess the ability of an anti-oxidant, indole-3-propionic acid, to reduce oxidative stress in these cells. Oxidative stress will be measured by the percentage of cells positive for reactive oxygen species. Preliminary results indicate that cells lacking YFH1 experience oxidative stress as indicated by slow growth on rich medium.

Lane, Haley, Mu Omicron, Columbus State University. "Center Pivot Irrigation and Upper Lethal Temperature for Freshwater Mussels"

Center pivot irrigation is used to boost agricultural production, but can reduce stream discharge and lead to increased pooling and water temperatures that threaten many stream organisms including freshwater mussels. These problems are exacerbated during droughts. I first established the impact of center pivot irrigation on stream discharge with an analysis of a 75-year time series of precipitation and stream discharge that spanned the initiation of center pivot irrigation. Second, I conducted an experiment to better understand the impact of reduced stream discharge on *Eliptio crassidens,* a common mussel in the basin, by monitoring survivorship at three different temperatures that were either held constant or were varied on a 48-hour cycle. We found that precipitation increased during the time series, but stream discharge declined after the start of center pivot irrigation. These results suggest that center pivot irrigation reduced stream discharge leading to greater chances of pooling and higher stream temperatures. Experimental results indicated mussel survivorship was much lower in tanks that reached 37°C compared to all other temperatures. Varying temperature did not alter survivorship. Therefore, mussel mortality will likely increase in streams that reach 37°C that could reduce mussel diversity and abundance.

*Rice, Alexus (Stefania, Guglielmi; Miriam, Steinitz-Kannan; Stuart, Oehrle), Mu Iota, Northern Kentucky University. "Removal of microcystins via bio-activated sand filtration systems"

In this study we investigated the efficacy of the removal of microcystin toxins in rapid virus incubated sand filtration systems with and without established biofilms. Sand samples, with established biofilms, were obtained from Greater Cincinnati Water Works (GCWW) and the Northern Kentucky Water District (NKWD). Columns prepared with the bio-activated sand from GCWW, NKWD, and sterilized sand were inoculated with water samples that tested positive for microcystins. The first filtration collected after six minutes, second filtration collected after one hour, and a final filtration collected after 24 hours in contact with the sand. After each collection period the water was expelled from the columns, and the eluent was analyzed for toxicity utilizing HPLC-MS. Results showed that the sand filters containing established biofilms removed microcystins significantly better than sterile sand filters.

*First place winner of the District II Brooks award

*Brittany Jones and Lindsey Walters, Mu Iota, Northern Kentucky University. "Nighttime inattentive bouts by incubating female Carolina chickadees (*Poecile carolinensis*)"

Incubating female birds must balance their time between maintaining the temperature of their eggs and foraging for their own food. Previous research has shown that incubating female birds leave their eggs occasionally during the day, but their behavior at night has not been investigated. We monitored incubating Carolina chickadees for more than 3,000 hours during the summers of 2012, 2013, and 2014 at St. Anne Convent in Melbourne, KY. We used iButtons to record the temperature of the nest every 2 minutes in order to determine whether these birds left their eggs at night. We also verified that the temperature data from the iButtons accurately portrayed the birds' behavior by observing nests with another method. In the summer of 2014, we recorded nocturnal incubation using night-vision cameras. We found that female chickadees left their eggs an average of 0.96 times each night from 10 PM to 2 AM and 1.16 times each night from 2 AM to 6 AM. Although it is clear that these birds do take incubation breaks, it is unclear why they would do this, as foraging would be difficult after dark.

*Second place winner of the District II Brooks award

Morgan, Aubri, Valario Johnson, Ethan Powell, Andrew Clarke, Brady Bouldin, Layton Avery, and Christi Magrath, Mu Epsilon, Troy University. "Impact of antibiotic agents on filament length and frequency and cellular clumping in *Saccharomyces cerevisiae"*

No abstract submitted.

Tran, Mai, and Joong-Wook Park, Mu Epsilon, Troy University. "Effect of Freshwater Exposure on Tarballs Bacterial Community"

Tarballs are remnants of petroleum found on the shoreline after oil spills or oil seeps. Many characteristics of tarballs resemble those of a biofilm-forming environment, making them a possibly favorable microcosm for bacteria. Much research has focus on oil-biodegrading microbial communities in marine tarballs. A study by Tao *et al.* in 2011 revealed that tarball samples collected on the Gulf coast contain an unusual accumulation of non-hydrocarbonoclastic bacteria *Vibrio vulnificus,* a human pathogen. This result further suggests the potential of tarballs as a reservoir for a variety of microbes. It has been observed that some of coastal tarballs float around and reach freshwater estuaries and lakes connected to the ocean. As no study has analyzed the microbial community in the freshwater tarballs, this study proposes to investigate the shift of bacterial community in marine tarballs collected on the Gulf coast after being exposed to freshwater. Total DNAs extracted from marine and freshwater tarballs will be analyzed using PCR-DGGE and DNA sequencing to identify dominant bacteria in the freshwater tarballs in comparison with those in the marine tarballs.

DISTRICT I JOHNSON AWARD SESSION POSTERS
EXHIBIT HALL C

Patel, Aayushi, Tau Gamma, East Carolina University. "Affect of Dominance Hierarchy Formation on Neurotransmitter Gene Expression in the Crayfish *Procambarus clarkia"*

Sociality has long been of interest to behavioral biologists. The red swamp crayfish, *Procambarus clarkii*, is a model species for studies of sociality with many similarities to vertebrate taxa, including humans. *P. clarkii* is known to form stable social systems in which large, aggressive males establish dominance over smaller, submissive competitors for food, territory, and mates. Past studies have demonstrated that neurotransmittors, such as dopamine and serotonin, play a role in dominance and subordinance, which are established between individual crayfish over time through series of behavioral interactions. However, investigations focusing on changes in the relative expression of neurotransmitter receptor proteins have not been attempted. Herein, we utilize next-generation sequencing technologies to determine whether changes in social status result in concomitant variations in neurotransmitter receptor gene expression, which would demonstrate a plastic genetic response to an individual's position in a social hierarchy.

Satre, Danielle and Susan Scrivner, Psi Pi, Reinhardt University. "Investigation of Bisphenol A contamination in Sharp Mountain Creek from a construction waste disposal site"

Bisphenol-A, also known as BPA, is a synthetic product used in the creation of many plastics, including PVC pipes and other materials used in the construction industry. BPA is a chemical of concern because it is an endocrine disrupter. This chemical has been shown to act as a hormone in the body and cause physiological abnormalities, especially in reproductive systems during specific periods of development. Furthermore, this chemical is prevalent in the environment and thereby could be affecting wildlife. Many studies have reported adverse effects in wildlife, particularly in aquatic organisms, at much lower concentrations than those deemed safe by the US Environmental Protection Agency. Even small effects on reproductive function in some species could reduce and eventually decimate their populations, therefore it is important to identify possible point sources of contamination and monitor our local waterways. In this study, an enzyme linked immunosorbant assay was used to determine BPA levels in water above and below a landfill used by construction companies. It was hypothesized that this landfill may be a source of BPA contamination in the stream. Researchers expect to detect BPA at greater concentrations below stream of the landfill than above stream.

Sidney Bedsole, Michael Reubens, Lucas Hopkins, Ritu Dalia and Tim W. Christensen. Tau Gamma East Carolina Univeristy. “Mutations in Drosophila Mcm10 Effect the Formation of Chromatin”

Mcm10 has been shown to be involved in both DNA replication and the establishment of chromatin states. To date most of the research on Mcm10 has focused on understanding its replicative roles, leading to speculation about Mcm10’s potential chromatic functions. As our understanding of epigenetics increases, the importance of chromatin formation on genome stability has become more apparent. For this reason, a thorough understanding of Mcm10’s function in the formation of chromatin may provide insight into mechanisms of oncogenesis, since aberrant Mcm10 expression has recently been observed in many types of cancers. This project focused on mapping the portions of Drosophila Mcm10’s C-terminal domain (CTD) involved in the establishment of endogenous chromatin states. To address this question, we have evaluated the impact of 20 different C-terminal point mutations on the formation of chromatin using three different experimental approaches. A white-mottled-4 position effect variegation (PEV) assay allowed us to evaluate the impact that the point mutations had on the formation of heterochromatin spectrophotometrically using the amount pigmentation in the adult eye. We were able to assess the packaging of DNA in endoreplicating tissue by evaluating the mass of DNA per unit volume in the nuclei of salivary glands from third instar wandering larvae. Furthermore, we were able to observe the presence of condensation defects in DAPI stained mitotic chromosomes present in the central nervous system of third instar wandering larvae. The data compiled from these investigations suggest that the CTD of Drosophila Mcm10 is important for proper packaging of DNA into chromatin in these different tissues. These results combined with the known replicative roles of Mcm10 provide support for the idea that Mcm10 mis-regulation is likely correlated with cancerous states; as stressed DNA replication and improper chromatin establishment can have serious impacts on genome stability and function. These results add to a growing body of evidence suggesting that Mcm10 serves multiple important functions both in and out of DNA replication in eukaryotes.

Hutcheson, Rebecca; Washida, Blackman; Priyancka, Naik, Hensel, Linda, Beta Omega, Mercer University. “Comparing transformation efficiency of UV damaged DNA in *Escherichia coli* and *Bacillus subtilis”*

Transformation mechanisms differ between gram positive (G^+) and gram negative (G^-) bacteria but many similar proteins and homologs are used in both. Little is known about the differences between G^+ and G^- when damaged DNA is transported and requires repair. We induced DNA damage in a plasmid by exposure to ultraviolet radiation. After the plasmid was treated with ultraviolet radiation, the damaged plasmid DNA was transformed into recA- strains of bacteria. The bacteria successfully transformed with GFP were quantified in both G^+ *B. subtilis* and G^- *E. coli* bacteria. Damage in the plasmid DNA showed enhanced transformation ability in G^+, but showed a decrease in transformation in the G^- bacteria. Several repair systems respond to UV-induced DNA damage; for example, the recA protein is involved in base-excision repair and SOS repair within the cell. By comparing the response in G^+ and G^- recA variants, we can begin to separate the effect of UV light on transformation itself from the cell’s ability to repair UV damage. Our results indicate that UV damaged DNA increases transformation in G^+ and that the damage has an effect on the ability of the cells to bind, knick, unwind, or uptake the DNA during transformation.

Burrow, Angela K., Chi Lambda, Georgia Gwinnett College. “Impacts of Restoration Treatment on Arthropod Biodiversity and Native Plants”

While urban development remains the primary threat to natural areas, competition from invasive plants can result in a loss of native plants, threatening biodiversity and drastically altering the ecosystem. Full restoration of a natural habitat involves a comprehensive approach of invasive removal followed by replanting with individual species determined to be both functional members of the community and beneficial components of the larger landscape. Limits imposed by time, funding, and volunteerism often require resource managers to rely on less intensive approaches. This project proposes to compare the effects of three restoration treatments on arthropod biodiversity and invasive plant re-colonization: 1) invasive plant removal only, 2) limited restoration planting, and 3) full restoration planting. We hypothesize that a full restoration will result in the greatest increase in arthropod biodiversity and least re-colonization by invasive plants. Furthermore, we hypothesize that removing invasive plants without replanting will have negative impacts while a single species native replanting will have limited beneficial effects. In 2014, pre-treatment, vegetation and arthropods were sampled in spring and fall. Following treatments, winter 2014, bi-annual sampling will re-occur for 3 years. The frequency, density, and abundance of invasive plant occurrence will be compared via t-tests. The arthropod orders of Hymenoptera and Hemiptera were selected for biodiversity analysis due to their close plant associations. Biodiversity will be calculated and compared for each plot using the Shannon diversity index. Species richness, vegetation and arthropod, will also be compared. These results will be used to provide recommendations to land managers regarding restoration methods.

Schmitt, Amanda and Joseph Oyugi, Tau Sigma, Gardner-Webb University. “The Habitat Preferences of Six-lined Racerunners (*Cnemidophorus sexlineatus)* at Broad River Greenway, NC”

We investigated microhabitat preferences of Six-Lined Racerunners (*Cnemidophorus sexlineatus*) within a wooded habitat in Broad River Greenway, North Carolina. We let *C. sexlineatus* reveal their perceptions of habitat quality by measuring how they allocate their activities across several scales of heterogeneity. We used frequency of occurrence and individual sizes as direct measure of thermal response and habitat choices (bare ground, dead leaves; and dead leaf coverage and shrubs). All individuals regardless of size preferred areas of dead leaf coverage and shrubs. The number of trees, logs, and rocks had no influence on individual size frequency distribution, but all individuals regardless of size preferred areas where there were logs and trees. There was high correlation between microhabitat and organism individual temperatures. Preference for dead leaf coverage and shrubs on the ground could be associated with abundant food resources, escape from heat and predators. Areas of logs and trees could provide shelter and escape routes from predators. Ectothermic temperature regulation by *C. sexlineatus* confirms the high correlation between individual body temperature and substrate. Overall, we have linked species activities to habitat heterogeneity and identified axes of environmental heterogeneity that promote species survival in its habitat.

Conway, Corianne, Sigma Psi, Florida Institute of Technology. “Variation in feeding-morphospace between pre- and post-metamorphic marine fishes”

Over five decades of research on post-metamorphic (i.e., juvenile- and adult-life history stages) fishes have resulted in our understanding of the diversity and evolution of fish-feeding systems. In contrast, we have a limited understanding of the feeding systems in pre-metamorphic (i.e., post-hatch larva stage) fishes. This study attempts to contribute to our understanding of the ontogeny of diversity in fish-feeding systems by contrasting the morphospace occupied by marine-fish larvae and conspecific post-larvae. Suction Index (SI), as well as key components of SI, including the physiological cross-sectional area of the epaxialis muscle and the mechanical advantage of the neurocranial rotation mechanism will be measured from fish larvae and post-larvae, and then subjected to a Principal Components Analysis (PCA) to generate the feeding morphospace. Factor loadings in the PCA will be used to identify which of the functional-morphological characters contribute to the variation in morphospace between the two life-history stages. It is hypothesized that the functional-morphological determinants of feeding performance, as well as the pattern of morphology-performance relationships in juvenile and adult fishes may be different from those of larval conspecifics.

Dunn, Stephanie L., Lauren M. Dehnart, Devanshi D. Patel, Kevin M. Andres, Virginia A. Young, Beta Omega, Mercer University. “Isolation and Identification of Bacteria Surviving in the Presence of the Long-term Antimicrobial Protect ’N Shield”

This is a continuation of previous years’ analysis of the efficacy of Protect ’N Shield on collegiate wrestling mats. In previous years, we monitored the efficacy of the long-term antimicrobial Protect ’N Shield and began the process of identifying three isolates able to survive in the presence of Protect ’N Shield. Given that Staphylococcus infections are a common occurrence among collegiate wrestlers, we selected colonies that visually resembled *Staphylococcus* species, and then performed biochemical tests to confirm the identity of the isolates. After identification based on biochemical tests, we tested for resistance to the cleaning agent Maxima 135 and to antibiotics to determine if the surviving bacteria represent a health concern to the wrestlers. The identification of the isolates based on biochemical tests and 16S rRNA gene sequencing will be discussed.

*Shadik, Courtney, Guaria Cardenes, and Mark Bush, Sigma Psi, Florida Institute of Technology. “Reconstruction of lake level changes using diatom assemblages in paleolake El Valle, Panama from 110 to 130ka”

Fossilized diatoms, highly siliceous photosynthetic microalgae, can be used to trace lake levels and eutrophication throughout time. A study of diatom species was performed on a sediment core from El Valle de Antón in western Panama. A sediment core of 55m was taken from this paleolake and sampled every 5cm.The present study focuses on the section from 45 to 54m in depth (110-130ka). Changes in the diatom assemblage composition were observed over 146 samples using standard protocols and 300 frustule counts. Abundance of planktonic species such as *Aulacoseira granulata* and *Achnanthidium duthiei* were found to be high in the lake showing the presence of a water body of significant depth. Nevertheless, there are periods around 120ka where benthic species rose in abundance. These periods of rising benthic abundance suggest lower lake levels. The lake level changes spanning 20,000 years of the Last Interglacial can correspond to fluctuations in precipitation and moisture availability in the area due to climatic changes.

*Second place winner of the District I Johnson award

Escobedo, Rene, Tau Gamma, East Carolina University. “Evaluating the chemotherapeutic potential of a novel J-series prostamide”

Effects of treatments on cancer is the second leading cause of death in the United States. Many of the chemotherapeutic agents and surgical procedures that eliminate cancer cells can cause severe adverse effects because they also cause damage to normal cells. Therefore, improved chemotherapeutic treatments are needed to reduce cancer mortality. For this reason, researchers have begun to study the use of cannabinoids, endocannabinoids, and their metabolites as anticancer agents. One such example is the endogenous cannabinoid neurotransmitter, arachidonoyl ethanolamide (AEA), which induces tumor cell death. AEA is metabolized by cyclooxygenase 2 (COX-2) to prostaglandin-ethanolamides. COX-2 is an enzyme that is overexpressed in many cancers including colon and non-melanoma skin cancer. Our group determined that the primary metabolite of AEA metabolism by COX-2 was the novel prostaglandin ethanolamide, 15-deoxy-Δ12,14 prostaglandin J2 –ethanolamide (15d-PGJ2-EA). The current study seeks to determine if 15d-PGJ2-EA is a potent agent that selectively induces death in tumor cells.

Boyd, Morgan, Tau Gamma, East Carolina University. “Effect of Endocrine-Disrupting Chemicals on Fetal Testes Morphology”

Studies have shown that testicular dysgenesis syndrome (TDS), which is the impairment of gonadal development and function, is increasing in prevalence. This syndrome includes cases of cryptorchidism, testicular cancer, abnormal spermatogenesis, and penile malformations like hypospadias, which is a congenital malformation where the external urethral opening is misplaced. It is hypothesized that TDS results from an irreversible developmental disorder that originates in the fetus, likely due to altered androgen signaling induced by endocrine disrupting chemicals. Fetal Leydig cells are interstitial cells within the testes that are the primary source of androgens, and therefore play an important role in the development of the genitalia. However, the link between altered fetal Leydig cell function and altered genitalia development is unclear. Androgen receptor antagonists, like vinclozolin can induce an increase in testosterone production because the binding of the chemical to the androgen receptors negates the negative feedback system that normally reduces testosterone production. However, the genitalia are not expected to respond to this increased testosterone due to vinclozolin’s anti-androgenic effects. Therefore, there will be a dis-coordination between testis function and genitalia development. To begin to understand the coordination between testis form and function and genital form and function I conducted a dose response experiment with the model anti-androgen vinclozolin, which is known to induce hypospadias. I hypothesize that fetal Leydig cells will be hypertrophic (more numerous), due to the increase in testosterone production, and that germ cells, seminiferous tubules, and Sertoli cells will show dose dependent effects. Specifically, we exposed pregnant dams (N=3) at embryonic days (E) 13.5-16.5 to either a corn oil control (0), 100, 125, or 150 (mg/kg). Embryos were dissected at E 18.5, testes removed, blood samples collected, and histological samples of the testes at E 18.5 were sectioned at 10µm and examined using ImageJ for morphological changes. Our findings will begin to characterize the link between the fetal testes function and genitalia development. Understanding how endocrine-disrupting chemicals break the linkages between these organs’ systems could lead to advances in the treatment and prevention of testicular digenesis syndrome.

Roberts, Lori, Melanie Lee-Brown, Sigma Phi, Guilford College. "Antimicrobial activity of Goldenseal (Hydrastis canadensis) against opportunistic, potentially pathogenic bacteria"

Antibiotic-resistant pathogenic bacteria are a major health concern. Antibiotic-resistant pathogenic bacteria have had an overwhelming increase and are continuing to rise. With the alarming rate in which multi-drug resistant (MDR) bacteria are rising, the scientific community is clambering to come up with new remedies, that the bacteria will have difficulty resisting. Some are turning to alternative treatments, including natural compounds. This study will encompass a broad, comprehensive analysis on the resistance/sensitivity of a broad range of important Gram-negative and Gram-positive bacterial species, using a natural compound called, Golden Seal (Hydrastis caradensis). The antibacterial activity of goldenseal extract(s) against bacterial species will be assessed. The microdilution method will be used. Determining the minimum inhibitory concentration (MICs), growth inhibition assays using 48-well plates, CFU/mL (colony forming units) and colony growth.

Perera, Pasangi, Williams Delaney (Michele, Malotky). Sigma Phi, Guilford College. "Epigenetic Changes Associated with Nicotine-Related Products and Effects on Addictiveness to Other Substances"

Hookah and e-cigarettes are being used more frequently throughout society as a "healthier alternative" to cigarettes; however, these substances still contain the addictive component, nicotine. Previous studies observed histone modifications and behavioral changes in model organisms following frequent exposure to nicotine. Our study focuses on exposing *Caenorhabditis elegans* to hookah and e-cigarette smoke to determine whether transgenerational histone modifications occur as seen in past studies. Once histone proteins have been analyzed, this study hopes to see if the organisms are susceptible to other addictive substances such as alcohol and kratom, a model for marijuana. Our results may give additional insight into the mechanisms affecting addiction and the impact that these epigenetic effects have on the likelihood of addiction in offspring.

Deanna Moquin and Michele Malotky. Sigma Phi, Guilford College. "Wise worms: effects of ginkgo biloba on learning and memory in *Caenorhabditis elegans"*

Ginkgo biloba is an herbal supplement traditionally used an alternative treatment to improve cognitive function. Scientific evidence regarding the efficacy of ginkgo is limited and inconclusive with the majority of studies focusing on human subjects with cognitive impairment. Few studies have examined the cognitive effects of ginkgo in healthy subjects. There is a clear need for basic animal models with improved experimental control and design to clarify ginkgo's efficacy. *C. elegans* is a model organism that is widely used as a research tool in the biomedical sciences. It shares many essential characteristics of human biology and has been used to study many processes including learning and memory. In the current study an associative learning assay was used to test the effects of ginkgo on *C. elegans* avoidance response to pathogenic bacteria.

Worms were treated with ginkgo during or after the training phase of the experiment and differences in the calculated learning indices between experimental and control groups were examined. This research will provide valuable insight on the use of *C. elegans* as a successful model to study the efficacy of ginkgo biloba on learning and memory and other cognitive processes.

*Everett, Aminda, Kalem Burns, Kolt Owenby and Nancy Eufemia Dalman, Psi Rho, University of North Georgia. "The effect of carbaryl and glyphosate pesticides on killifish (*Fundulus heteroclitus*) feeding behavior"

Neurotoxic pesticides may enter tidal creeks and disrupt food webs. The current study examined the effect of two pesticides, carbaryl (Sevin) and glyphosate (Round – up), on feeding in *Fundulus heteroclitus* (killifish), an important member of the salt marsh food web. Thirty fish were exposed to each pesticide at the LC50 (a concentration lethal to 50% of fish exposed for 96 hours) or half of the LC50 concentration for 24 hours, without food, prior to testing. Fish were individually placed in a t-maze and the time it took them to find and consume food was recorded. Shrimp pellets were placed in alternating arms of the t-maze for each trial. Fish exposed to pesticides were either unable to consume pellets or took significantly longer to ingest pellets than control fish. This occurred in fish exposed to both LC50 and half LC50 concentrations, although the effect was more pronounced at the higher concentrations. In a subsequent recovery control study, fish exposed to half LC50 concentrations were able to resume pre – exposure feedings rates within 5 days of toxicant removal. Based on these results, both carbaryl and glyphosate adversely affect the killifish's feeding ability, which can have consequences throughout the salt marsh food web.

*Honorable mention winner of the District I Johnson award

Henderson, Kyle, and Jay Bolin, Tau Eta, Catawba College. "Non-lethal predator avoidance by aquatic beetles to the red swamp crayfish (*Procambarus clarkii*)"

Community assembly has been shown to be influenced by non-lethal predator cues in many aquatic predator-prey systems. We experimentally evaluated the effect of the red swamp crayfish (*Procambarus clarkii*) on the community assembly of aquatic beetles using mesocosms. We established a gradient of *P. clarkii* presence in a randomized block design (control = 0; low = 1 crayfish; high =2 crayfish). Predators were separated visually and tactilely from colonizing aquatic beetles by caging and a vinyl screening. The study was conducted in a field habitat at Catawba College's Fred Stanback Jr. Ecological Preserve, located in the central piedmont of North Carolina. The total mean beetle abundance was significantly reduced in one and two crayfish density treatments ($P = 0.041$). A pilot predation study was conducted that demonstrated *P. clarkii* predation on *Acilius semisuculatus*, *Tropisternus blatchyi*, and *Tropisternus collaris*. This is the first report of predator avoidance of crayfish by aquatic beetles and suggests that community assembly of aquatic beetles can be influenced by a ubiquitous invasive species.

*Petilli, Beverly, and Richard Turner, Sigma Psi, Florida Institute of Technology. "Formation of compound plates in the skeleton of the sea urchin *Tripneustes gratilla"*

A sea urchin's body, or test, is composed of 20 columns of calcareous skeletal plates divided into alternating paired columns of ambulacral (bearing tube feet) and interambulacral regions. Plates are added to each column at the top of the test beneath an ocular plate. Ambulacral plates are compounded (fused) together in triplets, and the compound plate usually bears one large spine. It has been unclear how compound plates form from singular plates. In the present study, I examined the growing ambulacral regions near the ocular plates of the urchin *Tripneustes gratilla* by scanning electron microscopy. Fusion of compound plates occurs within even the youngest plates. A newly forming ambulacral plate fuses to the next older plate whether the new plate is part of that compound plate or is the first plate of a new compound plate. Neighboring young ambulacral plates are cemented by a calcareous "glue" that fills in the otherwise porous skeleton. The glue is not visible in fused sutures within older compound plates or in open sutures between adjacent older compound plates. The glue might form a temporary bond that prevents the developing plate from becoming displaced early in its formation

*First place winner of the District I Johnson award

Askey, Jessica, Alanna Natanson, Bryce Wesley, Amy Ciccolella, Kaitlin Lewis, Dane Kuppinger, Laura Watts, Beta Alpha, Salem College. "Coal Ash Impacts on Dan River Water and Soil Quality Including Elevated Chromium Levels"

On 8 February 2014, over 52,000 tons of coal ash were spilled from Duke Energy's Dan River power plant. Coal Ash contains a number of heavy metals and other contaminants which can negatively impact organisms and alter ecosystems. This study assessed whether water and soil quality impacts were present one year after the spill. Soil and water samples were collected from the river channel and bank above, at, and below the spill site. Chromium concentrations were significantly higher downstream from the spill site in both bank and channel samples and within bank samples at the spill site ($p<0.05$). Levels downstream were above EPA set limits of safety for aquatic life but below human toxicity thresholds. Soil nitrate levels were also significantly elevated downstream ($p<0.05$) but soil pH was not significantly different in downstream samples. No trend was observed in water Nitrate concentrations, dissolved Oxygen, turbidity, or total dissolved solids.

Burrus, Abagail, Dane Kuppinger, Beta Alpha, Salem College. "Exploring the Historic Flora of the Salem College Herbarium"

Herbaria play a crucial role in botany and many other fields by providing detailed insight into plant characteristics and morphology. They can also be used to measure changes within the regional flora over time, thereby aiding conservation efforts. This study investigated the herbarium specimens at Salem College dating from 1815 to 1900 (hereafter historical specimens or species) to determine whether the collection was acquired solely from within the surrounding Forsyth County region and indicate possible entrances into (or absences from) the modern flora of Forsyth County. 335 historical specimens were compared to 234 species present in Forsyth county today as documented by the specimen database maintained by UNC-Chapel Hill. 51 species were present in both sets of records. Of the 284 historical species not present in the modern flora, 145 are native to Forsyth County indicating the incomplete nature of digitized records. 18 of the historical species are introduced exotics, providing very early records for exotic species present in the United States. 4 of these exotic species have very restricted home ranges. 67 species within the historical collection are mostly native to the Northeastern United States, suggesting that the Moravian founders of the herbarium brought specimens with them from Pennsylvania.

DeCreny-Jackson, Jada, Laura Aleman, Cristal Jackson, Joelisa Khun, Nicholas Odorizzi, Taylor Rhodes, Juyoung Shin, Dane Kuppinger, Laura Watts, Beta Alpha, Salem College. “Assessing the Impact of Coal Ash Exposure on Soil Microbes in the Dan River”

On 8 February 2014, over 52,000 tons of coal ash were spilled from Duke Energy’s Dan River power plant. Coal ash contains a number of heavy metals which can be toxic to microbes. In spite of the toxic properties of coal ash, some bacterial genera have been found to develop resistance to the heavy metals present in it. This study assessed the overall viability of soil microbes extracted from the Dan River upstream, at, and downstream of the spill site. To assess the differences in culturable bacteria between the spill and reference sites, sediment samples were cultured on agar plates and counted. The mean absorbencies of soil samples collected at the spill and reference sites were also found to asses microbial density. Soil microbes downstream of the spill site exhibited an overall decrease in population density, yet there was an increase in culturable bacterial growth at the bank location downstream of the spill site. Dehydrogenase assays were also performed in order to evaluate the differences in microbial metabolic activity upstream, at, and downstream of the spill site. These studies demonstrated differences in microbial density and bacterial density in the sites exposed to coal ash versus the reference sites.

Lopez, Tara Jeremy Sheppard Dr. Aliya Donnell, Psi Pi, Reinhardt University. “A Preliminary Inventory of the Vascular Flora of the Reinhardt University Campus, Waleska, Georgia”

The present study documents the start of a first-ever comprehensive inventory of vascular plants on the campus of Reinhardt University in Waleska, Georgia. Reinhardt’s campus is located on a 162 ha property and encompasses a variety of plant community types, including wetlands, evergreen, hardwood and mixed forests. From January to late March 2015, specimens containing reproductive parts were collected once per week from natural (undeveloped) grounds on campus. Habitat, GPS coordinates and other pertinent information was recorded for each plant collected. Over 30 specimens, representing at least 20 species, were collected, pressed, and identified. Once identified, accepted names, authorities, and synonymies were confirmed using appropriate databases. Plants collected were also cross-referenced with current distributions, and any county records were documented. Voucher specimens will be deposited at the soon to be established Reinhardt University Herbarium.

Bolick, Christopher and Jay F. Bolin, Tau Eta, Catawba College. “Hybrid intermediacy in Ashe’s sumac (*Rhus ashei*) a hybrid of the federally endangered Michaux’s sumac (*Rhus michauxii*) and common smooth sumac (*Rhus glabra*)”

Ashe’s sumac (*Rhus ashei*) is a hybrid of the federally endangered Michaux’s sumac (*Rhus michauxii*) and common smooth sumac (*Rhus glabra*). We hypnotized that *R. ashei* would present intermediate traits in comparison to *R. michauxii* and *R. glabra*. Here we present data on the growth patterns and morphological characteristics of *R. michauxii*, *R. glabra,* and *R. ashei* including *rachis* trichrome density and plant height and width growth rates. We found significant evidence of hybrid intermediacy in regard to vertical growth rate within *R. ashei.* Our data shows an average vertical growth rate of 21.31 cm for *R. glabra*, 17.09 cm for *R. ashei*, and 14.00 cm for the endangered *R. michauxii* over an eight month period. Our data also determined that rachis trichome density within the hybrid R. ashei is highly variable with individual specimens yielding densities as high as 275 trichomes per cm and as low as 2 trichomes per cm. The mean densities for rachis trichome density of *R. ashei* is significantly different from that of *R. glabra* and *R. michauxii*. Our data yield a mean density of 60.68 trichomes per cm for *R. ashei*, 118.67 trichomes per cm for *R. michauxii*, and 0 trichomes per cm for *R. glabra* which is a non-pubescent species.

Teter, Christina, Tamara Johnstone-Yellin, Nu Upsilon, Bridgewater College. “The effect of deer exclosures on the fiber content of plants”

When deer selectively over-browse plants with low tannin content, it tends to reduce the amount of plant species present. This, in turn, affects the composition and distribution of the local fauna. We hypothesized that a deer exclosure would enable the enclosed plants to develop higher tannin levels, making them unpalatable to deer. As a consequence, the deer would no longer consume those plants once the exclosure was removed. This would ensure adequate diversity of both the flora and fauna. To test this hypothesis, we collected plant samples from corresponding exclosure and control plots and sorted them by functional group. We then performed sequential fiber analysis and analyzed the data. A majority of the corresponding samples were not statistically different. This may be because the exclosures have not been erected long enough to allow a significant difference in the fiber contents; however, some samples had higher fiber content in the exclosure while others were higher in the control. This may be due to variations in the fiber content of different species within the same functional group and a differential representation of these species in our exclosure and control samples. Regardless, further experimentation is required to enable a better conclusion.

Harshbarger, Alys, Nu Upsilon, Bridgewater College. “A Comparative Study of Normal Bacterial Flora of Pond Versus Aquarium Raised Channel Catfish (*Ictalurus punctatus*)”

The normal bacterial flora of Channel Catfish (*Ictalurus punctatus*) is of interest due to recent bacterial infections that have plagued southern states’ fish farms and increased fish mortality. There is little known about the bacterial flora present in pond raised versus aquarium raised catfish. Therefore, the purpose was to characterize, identify, and compare bacterial flora of catfish from both environments. The suspected outcome was that bacterial flora of pond raised catfish would differ from that of aquarium raised catfish. Channel catfish from both environments were collected, euthanized, and necropsied. Samples were obtained from intestinal fecal matter and a BIOLOG GEN III MicroPlate^{TM} was run to determine the types of bacteria isolated. Bacteria were also identified through comparison of physical characteristics of colonies to those of previous studies. The majority of the bacteria identified from the pond raised catfish were gram positive, while the majority of those identified from the aquarium raised catfish were gram negative. The results support the hypothesis that the bacterial flora differs in fish subjected to both environment.

McCabe, Jacqueline A. and Tracy L. Deem, Nu Upsilon, Bridgewater College. “The effect of vitamin D on weight gain and blood glucose levels in Type II diabetic mice”

Vitamin D supplementation has been shown to increase insulin secretion and improve glucose tolerance in Type II diabetic individuals but it is unclear if Vitamin D has an effect on weight gain. Given this, we examined the effects of Vitamin D supplementation on weight gain and blood glucose levels in mice fed a high-fat diet. At four weeks of age, mice were fed *ad lib* a 60 kcal% fat diet, and changes in weight and blood glucose were monitored. At six weeks of age, the experimental group (n=7) was administered 300 I.U. of Vitamin D_3 per week. Their percent weight gain and blood glucose levels were compared to the control group (n=8). Preliminary data suggest that Vitamin D supplementation may slow the increase in weight gain and help to lower blood glucose levels.

Alewine, Jacob, Sigma Gamma, Erskine College. “Post-translational modifications of Fun30 and its role in chromatin remodeling”

Packaging miles of chromosomal DNA requires hard work and energy from the cell. To aid in the highly ordered packaging of DNA and to regulate DNA metabolism, cells have evolved a special class of proteins called the ATP-dependent chromatin remodeling enzymes. A remodeling enzyme of particular interest is Fun30, which is similar to those in the SWR1/INO80 family (1). Conserved from yeast to human, Fun30 has been previously implicated in DNA repair (2-4), DNA replication (5), heterochromatin silencing (6-7) and transcription (10).

Powered by ATP hydrolysis, Fun 30 acts by "remodeling" the position of the nucleosome in cis or trans (10,11); however, the regulation for this activity is unknown. Evidence suggests that post-translational modifications, such as sumoylation, aid in the regulation of Fun30. SUMO (small ubiquitin-related modifier) proteins are often conjugated to proteins that are involved in transcription, chromosome segregation, and DNA repair (12). SUMO conjugation and ligation involve a complex pathway that includes "helper" proteins that bind SUMO to its substrate. As shown in Figure 1, SUMO protein matures, activates, and conjugates with the help of E1(Uba2/Aos1complex), E2 (Ubc9) and ATP. After conjugation, SUMO is ready for ligation to the substrate. E3 (Cst9, Mms21, Siz1 and Siz2 in yeast), an enzymatic protein, aids in the ligation process.

Thus, Post-translational modifications, such as sumoylation, regulate the chromatin remodeling function of Fun30, thus contributing to the mechanism in which Fun 30 slides nucleosomes rendering DNA for transcriptional repression.

Michael A. Dubuc, Zach I. Felix, Psi Pi, Reinhardt University. "Estimating the number of land snail species found in the state of Georgia"

We compiled a database of all records (total = 5234) from 9 museums for land snails collected in the state of Georgia. After updating the taxonomy of all records, we compiled a list of all unique species collected in Georgia. We believe that this is the first list of land snail species for the state and represents an important step towards learning about the ecology and diversity of this group in the region. We used these museum data to test the validity of a model we previously developed to predict the number of land snail species in Georgia. This model used maps in Hubricht's 1984 monograph on eastern land snail distributions and a set of rules based on ecoregional affinities to predict the likelihood of occurrence for species not yet documented in Georgia. We found that additional species have been documented in Georgia since the publication of Hubricht's work, and that these species were most often the ones our model predicted as "likely" to occur in Georgia. Our results indicated that there are still many species remaining to be documented within the Georgia state line.

Martinez Palomera Baez, Sebastian, and Nicolette Zahner, Sigma Psi, Florida Institute of Technology. "Urbanization Impacts on Anuran Species in Brevard County's Wetlands"

In Florida, increasing urbanization is leading to a steady loss of upland habitats. Urbanization causes an increase in pollution, habitat degradation, fragmentation, and a decrease in native species richness. Using anuran species' high frequency on the wetlands as an indicator of a healthy and rich habitat, the study aims to learn more about the wetlands richness by looking at the type of area, as well as the type and frequency of anuran species surrounding the site. This study used the presence of anuran species and chorusing events to estimate the impact of urbanization on wetlands in Brevard County. The study consisted on analyzing audio recordings to determine the quantity of different anuran species on different sites, calculating the percentage cover of woodlands, wetlands, and urbanized areas on 100m and 1000m radius buffers around the sites. Preliminary results suggest that wetlands within urbanized settings retain their recognized function of supporting biodiversity.

Kirtley, Adam; Dakota Pruitt and Joseph Shillinglaw, Sigma Pi, Charleston Southern University. “Pleistocene Fossil Terrestrial Vertebrates from South Carolina”

No abstract submitted.

Shore, Ashley, Tau Gamma, East Carolina University. “Spiracles:Structure and Function”

No abstract submitted.

Negron, Natalie, Rho Rho, Nova Southeastern University. “Creating a personal phylogenetic tree using mitochondrial, autosomal, and Y-DNA testing”
People have often been interested in their ancestral roots and the ability to document ancestry via the use of genetic tools has never been greater and more economical. The Human Genographic Project, under the guidance of Dr. Spencer Wells, has been established to document human ancestry by combining genetic testing with genealogy research to better understand the origins of human populations and their movements across the globe over time. The purpose of this study was to similarly employ the usage of genetic testing (via mitochondrial DNA and some autosomal markers) as well as genealogical records to uncover details regarding a specific individual's personal ancestry. For this study, the principal investigator examined her personal genetic ancestry. Previous research has shown that the investigator's mitochondrial DNA can be linked to Haplogroup L1 Subclade L1c1, which is one of the human subpopulations to have more recently migrated from Africa. By focusing on specific molecular markers that represent human ancestral migration patterns, the researcher gained a better understanding of the connections that reveal more direct and recent African ancestry along her Puerto Rican maternal lineage. Completion of this study resulted in the generation of a personal phylogenetic tree using both genetic and genealogical data.

*Hanley, Kaitlyn and David Rostal, Tau Kappa, Georgia Southern University. “Twenty Year Comparison of Reproduction of *Gopherus polyphemus* and Habitat Characteristics between Two Sites with Differing Fire Management Plans”

The effects of fire on *Gopherus polyphemus* populations in a sandhill habitat, specifically their reproductive success, has not been extensively studied in Georgia. Here we present data on a long term comparison of the reproduction and population structure under different management: long term active fire management verses a limited management approach. Reproductive output, population structure and habitat quality were compared at multiple intervals over a 20 year period (1994 to 2014). The project took place at: Fort Stewart Army

Reserve (FSAR) which is managed aggressively for tortoises and George L Smith State Park (GLS) which only recently has received some management for its tortoise population. Female tortoises at FSAR are significantly larger than females at GLS. Clutch size was not significantly different between the two study sites (mean clutch size 5.375 + 1.41 eggs at GLS and 6.231 + 2.49 eggs at FSAR) in 2014 however sample sizes were extremely small and more data is needed. Clutch size at GLS had increased from 4.52 to 5.38 since 1996. The linear regression of clutch size and carapace length shows no correlation for either GLS or FSAR (r^2=.0073, .586 respectively), in fact tortoises at GLS are showing a negative relationship between clutch size and female size. Habitat results were similar to the 1996 study. Tortoises at both sites are selecting habitat with low canopy and available ground forage however tortoises at FSAR are able to find more favorable available habitat throughout their range.

*Third place winner of the District I Johnson award

Luoma, Rachel and Zachary Stahlschmidt, Tau Kappa, Georgia Southern University. “The effects of digestion on innate immunity”

Following a meal, an animal can exhibit dramatic shifts in its physiology that can result in rapid growth of the gut and heart, as well as a massive (>40-fold) increase in metabolic rate associated with the energetic costs of processing a meal. However, little is known about the effects of digestion on an important physiological trait: immune function. Digesting animals may upregulate their immune systems due to increased microbial exposure from ingested food. Support for this hypothesis predicts that animals will exhibit greater immune function during digestion. Alternatively, digesting animals may downregulate their immune systems to devote energy to the breakdown of food. Support for this hypothesis predicts that animals will exhibit lower immune function during digestion. We tested our hypotheses by measuring two assays of innate immunity (the chief mechanism of host defense across taxa) on the blood plasma of corn snakes (*Pantherphis guttatus*) during and after meal digestion. We specifically measured hemoagglutination (antibody-mediated immune response resulting in agglutination of foreign red blood cells) and hemolysis (complement-mediated immune response resulting in lysis of foreign red blood cells) at two time points (1 and 7 day[s] post-feeding [dpf] to reflect digestive and non-digestive states, respectively). Hemoagglutination was higher at 1 dpf in partial support of our first hypothesis. Furthermore, females had higher lysis at 7 dpf than males. In sum, we demonstrate the effects of digestive state on innate immune function, further highlighting the myriad physiological responses that occur in response to food intake and digestion.

Allen, Daniel and William Irby, Tau Kappa, Georgia Southern University. “Carbon dioxide sensing in the pitcher-plant mosquito, *Wyeomyia smithii”*

The pitcher-plant mosquito, *Wyeomyia smithii*, utilizes carbon dioxide receptors primarily on their maxillary palps to seek potential hosts for blood meals. Three disjunct populations of *W. smithii* are being analyzed to test for differences in carbon dioxide sensitivity that would correlate to the varying levels of autogeny, ranging from the autogenous North Carolina population to the anautonenous Florida population, with the Georgia population exhibiting a shift over time from autogeny to anautogeny. Trials are being conducted using a Y-tube olfactometer to determine decision-making when exposed to varying carbon dioxide concentrations and normal air. Results are expected to demonstrate that the Florida population is most sensitive to carbon dioxide as they actively seek blood meals after laying the initial egg batch.

Alfred, Joanna, Logan Thomas, Christina Michaels and Richard W. Nelson, PhD, Psi Tau, Covenant College. “Bacterial expression of proteins involved in the control of gastrulation movements in Xenopus Laevis”

No abstract submitted.

DISTRICT II JOHNSON AWARD SESSION POSTERS
EXHIBIT HALL C

*Ware-Gilmore, Fhallon (Michelle Peiffer, Dr. Ketia Shumaker , Dr. Dawn Luthe, Dr. Gary Felton), Beta Phi, University of West Alabama. “Trichomes: The First Line of Defense Against Herbivores”

Pest insects have significant economic, environmental and social impacts on society. The cabbage looper, Trichoplusia ni, is a pest native to the United States. When herbivores initiate feeding on a host plant, they present "cues”, which the plant perceives and uses to help rapidly mobilize its defenses in response to the herbivore’s attack on the plant. This study was designed to determine if T. ni, is able to induce the production of leaf hairs or trichomes on newly forming leaves of tomato plants. In some plant species, herbivore attack or defoliation triggers the production of increased trichomes which act as defenses against herbivores. We will be answering two questions: 1) Does cabbage looper saliva induce trichomes?, 2) Does increased trichome density interfere with growth of cabbage loopers? These experiments were conducted to better understand the interaction between insects and plants to facilitate the development of new pest control systems.

*Third place winner of the District II Johnson award

Heidi Y. Knecht and James D. Daniels, Beta Nu, Huntingdon College. “Severe Winter Decimates Population of *Nephila clavipes* at Northern Range Margin”

A population of *Nephila clavipes* near Prattville, Alabama (N32.50°, W-86.43°) at the northern range margin of the species (Bakkegard and Davenport 2012) was monitored biweekly over three years (2012-2014). During the first two years the population was stable, and reproducing (pers obs). In 2014, we encountered no evidence of *Nephila clavipes* during our censuses. In 2013-2014 the winter was uncharacteristically severe; five snowfall events accompanied by consecutive days of subfreezing temperatures, and 3 nights with single digit lows distinguished 2013-2014 from the previous winter. We expect that the severity of the winter resulted in complete mortality within the monitored population. We calculated the Accumulated Winter Season Severity Index (AWSSI), (Bousted, et. al. 2013) in order to compare the winters of 2012-2013 and 2013-2014, as well as average temperatures at the site. The average AWSSI value for the site is 0 (zero) with no average lows below freezing and no snowfall events. The winter of 2012-2013 had a calculated AWSSI of 29 (no snowfall events, 3 nights in the low 20's Fahrenheit). The winter of 2013-2014 had a calculated AWSSI of 77 (5 snowfall events, 2 instances of consecutive days with continually subfreezing temperatures and 3 nights with single digit lows.)

McLane, Alyson; Mu Iota, Northern Kentucky University. "Survey of Bacterial Resistance in Recreational Water Sources in the Greater Cincinnati Area"

The greater Cincinnati/Northern Kentucky area contains many notable bodies of water which are used for a wide variety of leisure activities (i.e. fishing, swimming, canoeing, boating, etc.). However, many of these locations also receive runoff from sewage treatment plants, hospitals, and farms; despite advances in treatment methods, this runoff still contains traces of antibiotics excreted by humans and animals. The presence of antibiotics in the environment favors the growth of resistant bacteria and the spread of antibiotic resistant mechanisms. The spread of antibiotic resistance poses a threat to human health. Surveying the presence of resistant bacteria at recreational locations will provide a better understanding of the resistant strains that humans and animals come into contact with. Samples will be collected and screened for resistant bacteria using standardized values of kanamycin (30 μg/mL) and carbenicillin (100 μg/mL). Steps will be taken to identify the resistant strains of bacteria in order to better understand and manage resistant strains in the environment.

Mahan, Farrah, Kathleen Penney, Kristi Jones, Beta Nu, Huntingdon College. "Annotation of *Drosophila biarmipes* (contig 6) using *Drosophila melanogaster* as the reference species"

Comparative analysis of species can provide useful information on functionality, among various other things. Using multiple lines of data, we constructed a gene model that annotated *Drosophila biarmipes* (contig 6) using *Drosophila melanogaster* as the reference species. Our goal, in collaboration with the Genomics Education Partnership at Washington University, was to identify and annotate all genes of *D. biarmipes* dot chromosome contig 6. This was done using The Basic Local Alignment Search Tool (BLAST) and sequences were referenced using the GEP UCSC Genome Browser. Other various tools were used to retrieve *D. melanogaster* gene structure information, find exons smaller than 30 amino acids long, and verify our proposed gene model. Overall, *D. biarmipes* contig 6 had a total of 9 features, including 22 exons and 24 isoforms. RNAseq data, along with other gene predictors, predicted splice sites, and alignments, led to this information, along with our prediction that a nested gene lies within contig 6.4.

*Cox, Alyxandra N. Mu Iota, Northern Kentucky University. “Organic Extractions of Antimicrobial Compounds from Environmental Microbes”

New antibiotics are needed to prevent increasing morbidity and mortality caused by infections with antibiotic resistance microorganisms. Antimicrobial activity surveys of environmental microorganisms led to the discovery of many of the antibiotics currently in clinical use. A survey of soil samples taken from varies residential locations in the Cincinnati/Northern Kentucky region identified 15 bacterial species with the ability to inhibit the growth of *Escherichia coli* or *Candida albicans*. I Organic extractions were performed to isolate the active compounds. The activity of these extracts was determined using the Kirby-Bauer disk diffusion method.

*Second place winner of the District II Johnson award

Patel, Hinali,. Mu Omicron, Columbus State University. “Effects of Fumonisin B1 Mycotoxin on Neural Tube Development in Zebrafish (Danio rerio)”

Fumonisin B1 (FB1) is a mycotoxin that is produced by Fusarium, a mold commonly found on corn and in corn products. Consumption of contaminated corn products during pregnancy is associated with fetal neural tube defects in humans. The major goal of this research is to assess the utility of zebrafish as a model system for studying the effects of FB1 on neural tube development. Preliminary results indicate that FB1 increases embryonic mortality and delays hatching compared to controls. FB1-exposed and control embryos collected at various times before and after hatching are being examined histologically for evidence of neural tube defects.

*Boeck, Hailey M; Anna K. Hinson and Isaac M. Sleadd, Beta Zeta, University of North Alabama. “Cross-tolerance in the upside-down jellyfish Cassiopea xamachana"

Heat shock proteins (HSPs) are a family of proteins that are produced constitutively and as a result of stressful conditions. They perform chaperone functions, stabilizing new proteins by aiding them in correct folding and also by refolding proteins that are damaged by stress. It has been suggested that HSPs may afford cross-tolerance to certain marine organisms. To explore this possibility, we investigated a potential role for HSPs during cross-tolerance in the upside-down jellyfish *Cassiopea xamachana.* Animals exposed to acute heat stress (37 °C) and subsequent 24-hour recovery at 26 °C displayed increased salinity tolerance as measured by time to pulsing cessation and loss of responsiveness at 70 ppt. On average, heat-shocked *C. xamachana* survived 4.5 times longer than control animals following transfer to a hypersaline environment. To our knowledge, this is the first time cross-tolerance has been demonstrated in a true jellyfish. The above data are discussed in combination with protein-level analysis of HSP70 expression, with implications in ecophysiology and invasion biology.

*Honorable mention winner of the District II Johnson award

Millwood, Joshua and John McCall, Beta Phi, University of West Alabama. "Feeding habits of early juvenile sciaenid fishes of Santa Rosa Sound, FL"

The sciaenid fish spot, *Leiostomus xanthurus*, is found in great abundance as juveniles and adults in coastal waters along the Lower Atlantic and Gulf coasts. In many locales, early juvenile spot have been found to prey heavily on benthic meiofauna, and in some situations have been suggested to play a role in control of meiofaunal densities. Most of these studies have been conducted in muddy salt marsh habitats. Studies in Santa Rosa Sound, a coastal lagoon in extreme northwestern Florida, have revealed large densities of spot occurring in nearshore waters over relatively coarse sand habitats. Here we report the results of a preliminary analysis examining the feeding habits of spot in this system, as well as a comparison to meiofaunal communities in the area. Spot in Santa Rosa Sound were found to rely heavily on meiofaunal prey. The degree to which spot predation may impact meiofaunal densities remains to be determined.

Parrish, Essence and Dr. Brian Burnes, Beta Phi, The University of West Alabama. "Transfer of S. *aureus* from Gym Equipment to Hands"

A concern with *staphylococcus aureus* has emerged because of the possibility that fomites may play a significant role in the transferral of *S. aureus* to humans. Aside from health facilities, studies have found that relatively large numbers of *S.aureus* are also found on shared gym equipment in community fitness centers; however, whether *S.aureus* reaches the body on contact with the fitness center equipment remains unclear. The purpose of this study is to identify *S.aureus* equipment-to-body transfer in a small community fitness center. The users of the equipment were sampled were sampled for *S.aureus* before and after the equipment was used. A previous study at the same gym found that *S. aureus* was present on 84% of surfaces. This study further examines and confirms that fomites do lead to the transmission of potentially infectious Staphylococcal species.

Slattery, Elizabeth, Mu Iota, Northern Kentucky University. "Adaptation of a microbroth dilution assay to assess the activity of novel potential antimicrobials"

No abstract submitted.

Tran, Mai, Elena Brown, and Joong-Wook Park, Mu Epsilon, Troy University. “A’Bacterial Response to the Elk River Chemical Spill in West Virginia”

In January 2014, up to 7,500 gallons of 4-methylcyclohexanmethanol (MCHM), a chemical used for coal purification, leaked into Elk River in West Virginia. However, there is scant research on the chemical properties and its toxicity to human and the environments. One of the main concerns involves the MCHM's potential as an inducer for microbial growth, either pathogenic or biodegrading species. This research proposes to identify microbial species in the MCHM-treated sediments. We hypothesize that there are bacteria that thrive in sediments containing MCHM. In order to test our hypothesis, bacterial DNAs were extracted and analyzed using molecular-based techniques, including PCR-DGGE and DNA sequencing. The results of this research can help develop biodegradation strategies for future MCHM-spills and establish safety regulations in handling this chemical.

*Duke, J., K. Ichikawa, J. Pittman, M. W. Morris, and S. Liu , Mu Epsilon, Troy University. “Assessment of extracts prepared from native St. John's wort species (*Hypericum* spp.) on anxiety/depression-related behaviors and neural pathways in zebrafish (*Danio rerio*)”

Several species of St. John’s wort (*Hypericum* spp.) native to the southeastern United States (*H. fasciculatum, H. microsepalum, H. punctatum, H. cistifolium,* and *H. prolificum*) are being investigated as potential sources of chemical compounds with antidepressant properties that are already well known in the Eurasian *H. perforatum*. Hypericin, hyperforin, rutin, and quercetin are among the *psychiatrically* beneficial compounds previously identified in *H. perforatum* that could hypothetically be present in American species of *Hypericum*. The purpose of this study is to test for possible antidepressant effects of extracts prepared from *Hypericum* species in zebrafish (*Danio rerio*). Extracts were prepared from dried material of native St. John’s wort species collected at anthesis and subsequently administered to zebrafish, which were pharmacologically-induced to model depression. Preliminary test results show positive behavioral effects using a Novel Tank Diving Test, and changes in dopamine, serotonin, and norepinephrine levels were noted using an enzyme-linked immunosorbent *assay* (*ELISA*). Detection of bioactive compounds is currently being conducted through High Performance Liquid Chromatography (HPLC). The preliminary results from this study highlight the potential efficacy of species of compounds extracted from native species of St. John’s wort (*Hypericum* spp.) commonly found in the southeastern United States.

*First place winner of the District II Johnson award

Guglielmi, Stefania, Mu Iota, Northern Kentucky University. “Removal of microcystins via bioactive sand filtration systems”

No abstract submitted.

Byars, Gary R. Jr., Lauren King, Mu Omicron, Columbus State University. "The Effect of Antimicrobial Peptides on Acinetobacter baumannii"

Acinetobacter baumannii is a primarily opportunistic pathogen responsible for a large proportion of hospital-acquired infections and infections among military personnel. Despite unclear virulence mechanisms, the mortality rate associated with A. baumannii infections is often very high due to multidrug-resistance (MDR). Because antibiotic treatment is often ineffective, our research is currently focused on alternative treatments including antimicrobial peptides similar to ones produced by the innate immune system and found in human white blood cells that have been shown to have lethal effects on some MDR bacteria. We examined the planktonic antibiotic resistance and biofilm formation of clinical isolates of A. baumannii using standard assays. All clinical isolates were multiply-drug resistant and variable biofilm formation was observed in all of the strains. Antibiotic resistance and biofilm formation are key factors in virulence and, in future studies, we will examine the effects of antimicrobial peptides on these virulence factors as well as on intracellular survival. By elucidating these complex virulence mechanisms, new treatments and more effective treatments could be found.

Smoot, Tamara, Brian Burnes, Beta Phi, University of West Alabama. "Exposure to Candida in a college environment"

No abstract submitted.

Shajan, Angelin, Mu Omicron, Columbus State University. "The effects of curcumin on the expression of p53 and Bcl-2 proteins in the human breast carcinoma cell line MDA-MB 468"

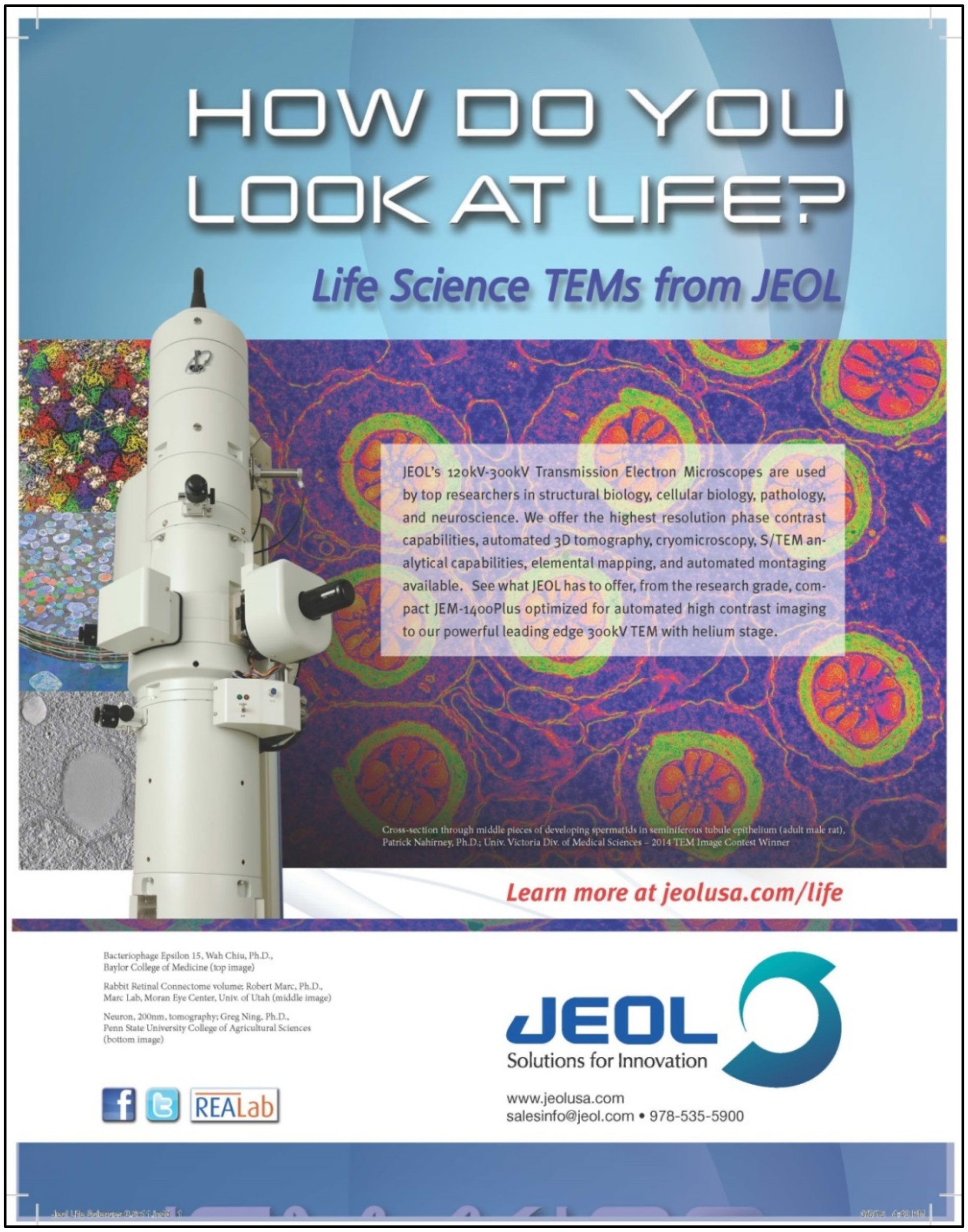
We studied the effects of curcumin on the proliferation and viability of MDA-MB-468 breast cancer cells and its effects on the expression of Bcl-2 and p53 proteins in these cells. Based on previous studies, we predict a dose-dependent increase in p53 (tumor suppressor) expression, and a decrease in Bcl-2 (anti-apoptotic oncoprotein) expression. Briefly, MDA-MB-468 cells were seeded into 12-well plates at 2.0×10^4 cells/well and allowed to grow for 72 hrs. Cells were treated with curcumin at 0, 25, 50 and 100 µM in triplicate at time zero and cultured for another 24 hours. All data were obtained using a Muse Cell Analyzer. Proliferation and viability data were determined using the Annexin V and Dead Cell Kit and p53 expression was determined using the Multi-Colored DNA Damage Kit. We found a dose-dependent decrease in viability at 50 and 100 µM concentrations. We also found a dose-dependent increase in the number of cells experiencing late apoptosis/death and phosphorylated ATM activity at 50 and 100 µM concentrations which correspond to p53 activation. As a result of these data, further studies are ongoing to investigate the mechanisms by which curcumin induces these apoptotic effects using the Bcl-2 Activation Dual Detection Kit.

Tran, Lina, Tulane University, Elizabeth Hayes and Keith Whiteneck, Eta Nu, Samford University. "Using Sanger and next generation sequencing to investigate the macro- and microbiota of a pond connected to Oak Mountain Lake, Shelby County, AL"

The often overlooked, freshwater eukaryotic microbial communities play dynamic roles in the ecosystem, including bacterial control, nutrient cycling, and energy transfer. To address this oversight, we undertook a molecular survey of the suspended biota of a small pond connected to Oak Mountain Lake in Shelby County, AL. DNA was extracted from water samples from five pond sites and 18S rDNA was amplified using standard eukaryotic primers. Sanger sequencing of sixteen cloned segments followed by BLAST searches identified 8 of the operational taxonomic units (OTUs) present in the pond. A preliminary model summarizing microbial loop interactions was constructed. Bar-coded 18S rDNA amplicons were submitted to Virginia Bioinformatics Institute for next generation sequencing (Illumina sequencing). Preliminary UniFrac ordination analysis suggested that two aspects of microhabitat (vegetation density and sample depth in the pond) may be correlated with OTU diversity. The implications and limitations of these results are discussed.

Givens, Jordan L. and Isaac Sleadd, Beta Zeta, University of North Alabama. "Heat-shock protein expression during temperature and salinity stress in the Antarctic nemertean worm *Parborlasia corrugatus"*

In recent years the Antarctic Peninsula has experienced a dramatic increase in annual temperature. The coastal marine environment has previously been extremely cold and stable, and consequently the majority of Antarctic species appear to have lost the ability to elicit a heat-shock response, thus making them ill-equipped to deal with elevated temperatures. The cold-adapted nemertean worm *Parborlasia corrugatus* is an important benthic scavenger and predator found throughout Antarctica and the Antarctic Peninsula. To our knowledge, no research has been conducted to characterize *P. corrugatus*'s cellular response to heat and salinity stress and as a result it is unclear the effect that global climate change will have on these ecologically significant organisms. The goal of this study was to investigate Hsp70 expression using western blotting. Specimens were collected from the Ross Sea and experiments were conducted at McMurdo Station, Antarctica. Animals were exposed to acute heat stress (10°C) or salinity stress (28ppt or 24ppt) and protein levels of Hsp70--a crucial molecular chaperone--were determined. Here, we present our findings and discuss their implications in the context of global climate change.



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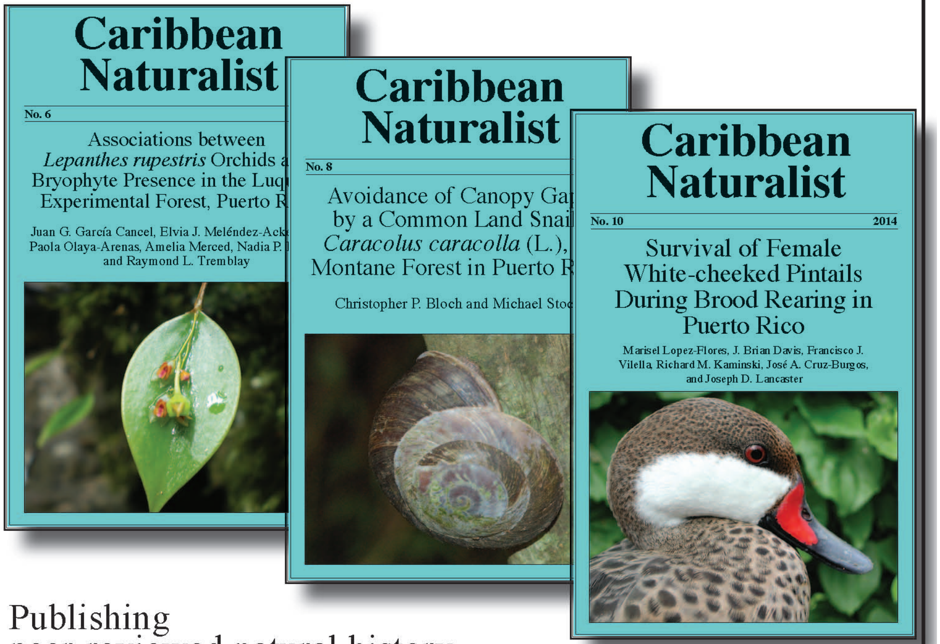

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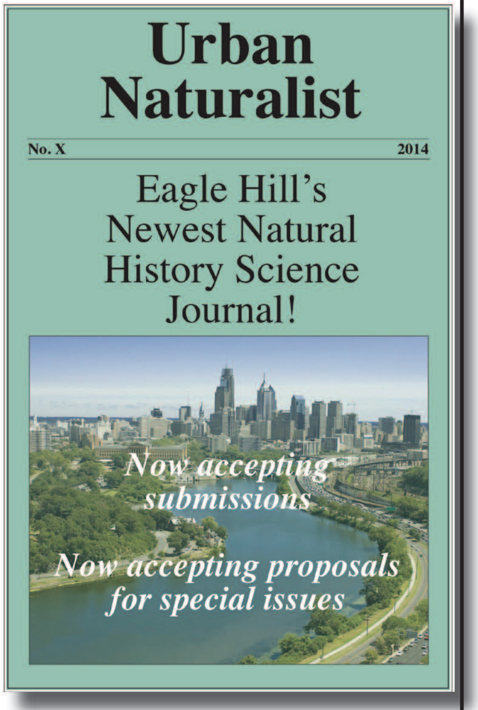

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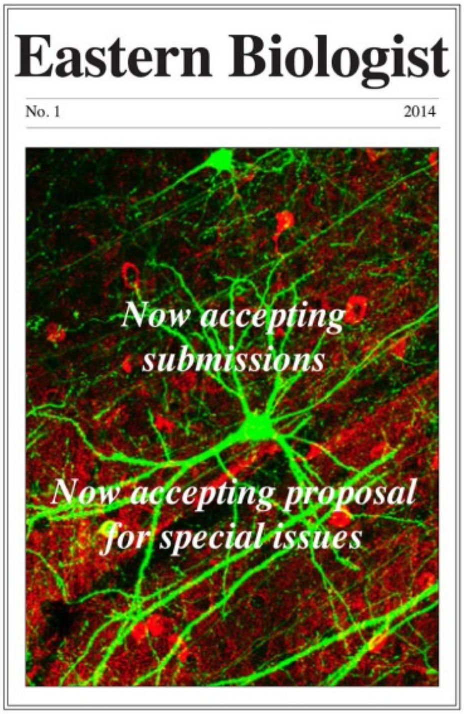

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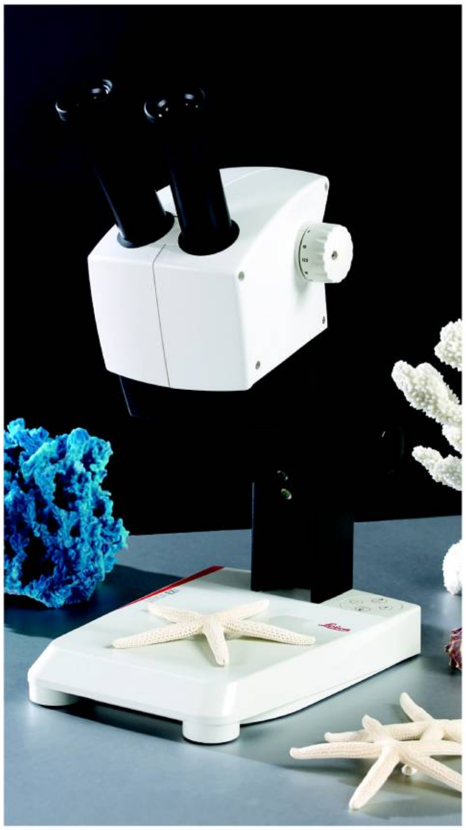

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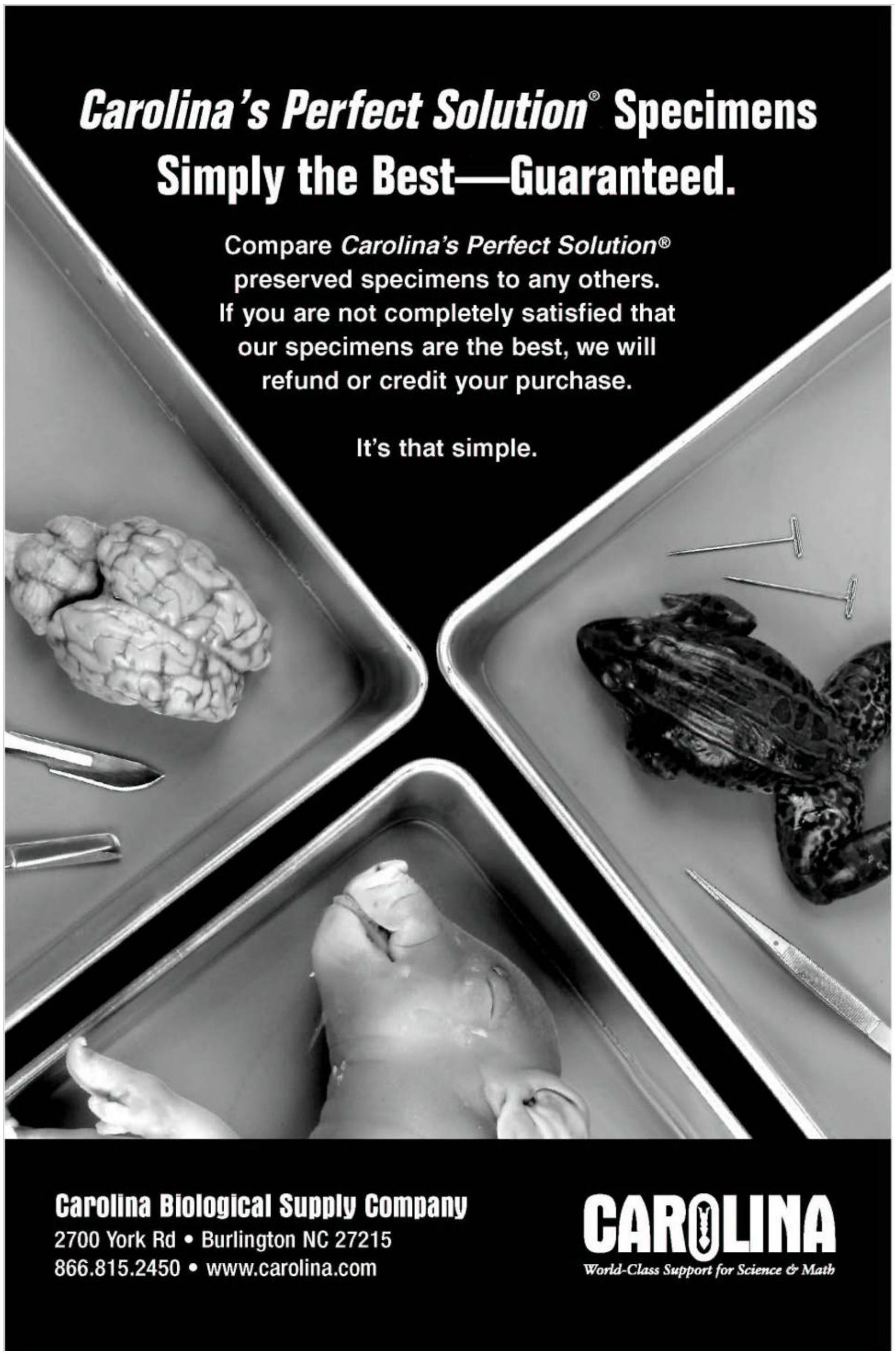
NashVitality



ASB Membership Form

ASB membership includes discounts on annual meeting registration and on subscriptions to Southeastern Naturalist (SENA), the official journal of ASB.

To join or renew and pay by cash, check, or money order, complete contact information below, enclose cash, or check/money order payable to Association of Southeastern Biologists, & send by mail. **To pay by credit card**, complete contact information & credit card information, & send by reply e-mail, mail, or fax. If you would like further information or have questions, contact: **Edgar B. Lickey, ASB Interim Treasurer, Department of Biology, Bridgewater College, Bridgewater, VA 22812; (502) 828-5426; elickey@bridgewater.edu.**

Name:

Work E-mail:

Personal E-mail:
(At least one valid e-mail address is required.)

Work Address:

City: State: Zip Code:

Work Telephone: Fax:

Home Address:

City: State: Zip Code:

Cell Phone: Home Telephone:

Card Type: American Express_____ Discover_____ Visa_____ Master Card_____

Card Number:

Card CVV Number: __ __ __ __ (Three- or four-digit number on back of card.)

Card Expiration Date: __ __/__ __

Cardholder Name:
(Exactly as it appears on card.)

ASB ENRICHMENT FUND CONTRIBUTION AMOUNT: $_________________

ASB MEMBERSHIP
ASB MEMBERSHIP WITH SOUTHEASTERN NATURALIST SUBSCRIPTION

_____ Regular One-Year Membership -- $50
_____ *Regular One Year Membership with Southeastern Naturalist Subscription -- $70 (SAVE $30 with this option!)*

_____ Student One-Year Membership -- $20
_____ *Student One-Year Membership with Southeastern Naturalist Subscription -- $40 (SAVE $18 with this option!)*

_____ Emeritus One-Year Membership -- $20
(Any member who has been a member continuously for 10 or more years, & who has retired from professional duties, may request Emeritus status.)
_____ *Emeritus One-Year Membership with Southeastern Naturalist Subscription -- $40 (SAVE $20 with this option!)*

_____ Life Membership -- $500 (Life Membership is a one-time payment. All others are annual.)
(Southeastern Naturalist [SENA] does not offer a Life Subscription option. Life Members who wish to receive SENA must pay $32 per year for the SENA Subscription, an $18 per year discount.)

_____ Patron One-Year Membership -- $1000
_____ *Patron One-Year Membership with Southeastern Naturalist Subscription -- $1020 (SAVE $20 with this option!)*

_____ Life & Patron – New, $1500; Renewal, $1000
(Requires $500 initial, one-time Life Membership payment, plus $1000 each year Patron membership payment.)

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Patron Members

Associated Microscope, Inc., Elon, NC
Breedlove, Dennis and Associates, Inc., Winter Park, FL
Breedlove, Dennis & Young, Inc., Nashville, TN
Carolina Biological Supply Co., Burlington, NC
Marilyn Pendley, Marion, NC
Martin Microscope Company, Easley, SC
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