Cover art by Melissa Encinias '17
The students and faculty in the Biology Department gratefully acknowledge support for their research from:

- Jean D. Acton Scholarship
- Betty Jo Loving Butler '58 Endowment for Undergraduate Research Scholarship
- Farrell Summer Research Scholarships
- Elizabeth McConnell Bliss Endowment for Undergraduate Research Scholarship
- Trelawny endowment
- Jeffrey E. Tickle '90 Family Endowment Scholarship
- Taliaferro Scholarship
- Farrell Scholarship
- Chappelear Scholarships
- Summer Research Scholarship (Anonymous Donor)

* Student authors whose research has been supported by one of these gifts are noted with an asterisk.

Research that is part of CGEMS (Center for Genome and Metagenome Studies)

Research that was supported by summer funding gifts

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*Barcoding the Amphibian Biodiversity of Brunei*

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Z. Logan Holley, Zachary O. Casey, Katherine M. Bland, Christopher J. Handwerk, Dr. George S. Vidal  
*Investigating the Role of Integrin Beta 3 in Dendritic Arborization in the Developing Cerebral Cortex*

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*Investigating cell-autonomous dendritic spine defects in a mouse model of Fragile X Syndrome*

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**P4**  
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*The Role of Brain Stem 5HT1A and GABA-A Receptors in the Thermoregulatory Response to Hypoxic Stress*

**P5**  
Rachel Barboreck, Kendyl Combs, Matthew Knick, William Meara, Dr. Susan Halsell  
*Identifying the molecular components of cold noiception in Drosophila melanogaster*

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*Antibacterial Properties of Novel Amphiphiles: Exploring Structure-Activity Relationships*

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*Antimicrobial Activity, Biofilm Disruption Capabilities, and Synergistic Interactions of Novel Amphiphiles* (same as P58 on Friday)

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*Microbial community structure during a Microcystis bloom in Lake Erie*
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P15  Maria Sokoloff, Olivia Mitran, Dr. Patrice Ludwig
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P16  Jared Martin, Lexi Eastburn, Toma Matveeva, Dr. Kimberly Sklar
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1:00  T1.  Jillian Breault, Lauren Pope, Dr. Chris Berndsen, Dr. Jon Monroe
An acidic domain in Arabidopsis β-amylase2 is required for K+ regulation

1:15  T2.  *Althea J. Neighbors, Sarah McGrath, Dr. Oliver Hyman, Dr. David McLeod
Novel hybrid survey technique: a clear alternative to traditional polyvinyl chloride pipe refugia

1:30  T3.  Holly Rucker, Dr. Rocky Parker
Decrypting female mimicry in red-sided garter snakes

1:45  T4.  Miguel Padilla, Matthew Harris, Dr. Patrice Ludwig
A novel technique for locating the nests of peregrine falcons using UAVs

2:00  T5.  *Sarah McGrath, Dr. David McLeod, Dr. Morgan Steffen, Dr. Reid Harris, Dr. Carly Muletz
Exploring the microbiome: diversity of the microbial community of three foam nesting frogs, Genus: Polypedates, across a developmental gradient

2:15  T6.  *Matthew Harris, Dr. Heather Griscom, Dr. Patrice Ludwig
Potential benefits of restored riparian zones in an agricultural matrix for bat communities

2:30  BREAK

2:45  T7.  C Charles Holmes II, Dr. James B. Herrick
joint talks
Whole-genome epidemiology of environmental Salmonella: monitoring potential threats to public health.

T8.  C Sophie K. Jurgensen, Dr. James B. Herrick
A CURE for Salmonella: Engaging Students in Pathogen Microbiology and Bioinformatics

Drone Application for Black Bear Conservation

3:30  T10.  G Matt Elder, Dr. Patrice Ludwig
An examination of the effects of magnesium enriched substrates on larval and juvenile eastern oysters

3:45  T11.  Taylor Hutchinson, Rana Ihsan, Dr. Timothy Bloss
Characterization of Misfolded Protein Stress Inducers in the Different Cell Types of C. elegans

4:00  *T12.  Kendyl Combs, Rachel Barborek, Matthew Knick, William Meara, Dr. Susan Halsell
Identifying the molecular components of cold nociception in Drosophila melanogaster

4:15  T13.  Shaw Camphire, Madeline Henwood, Dr. Terrie Rife
Characterizing Tau in the Nucleus

4:30  T14.  Augustus Snyder, Dr. Kerry Cresawn
Biosemiotics as an argument for the recontextualization of biological discoveries to attain a more satisfactory understanding of life: A critical analysis of the philosophy and biosemiotic model of Marcello Barbieri

4:45  T15.  Cecilia Rogers, Dr. Heather Griscom
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**Solanum conocarpum in Light of Climate Change**
5:00 T16. Isabel Lamb-Echegaray, Dr. Mark Gabriele

**Targeting of Central Nucleus Projections to Extramodular Zones of the Lateral Cortex of the Inferior Colliculus in Developing Mouse**

5:15 T17. * Jenny Russell, Dr. Tracy Deem, and Dr. Chris Lantz

**Assessment of Faithful Interleukin-3 Production by Transgenic Fluorescent Reporter Mice**

5:30 T18. Emily Murray, Dr. Heather Griscom

**The effect of soil type, liming, and commercial inoculum on American Ginseng (Panax quiquefolius)**

5:45 T19. Stephanie Sharpes, Elizabeth Rogers, Reafa Hossain, Elizabeth Terry, Smita Bajain, Julie Bjerring, Jessica Carolino, Rebecca Harkness, Melanie Kusakavitch, Ethan Smolley, Peyton Thompson, Angelica Tonder, Robert Walker, Dr. Kevin Caran, Dr. Kyle Seifert

**Antimicrobial Activity, Biofilm Disruption Capabilities, and Synergistic Interactions of Novel Amphiphiles**
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<td>T20. Searching for Potential Binding Partners of Arabidopsis β-amylase Using Yeast 2-Hybridization</td>
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<td>T25. Muscle synergies formed in the Sprague Dawley rat’s tail in response to nociceptive stimuli</td>
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<td>T29. Bitter taste behavior in the red-sided garter snake</td>
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<td>11:45</td>
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<td>T30. Contributions of Aδ and C Fiber Nociceptors to the Nociceptive Withdrawal Response in Intact Unanesthetized Rats</td>
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Disturbance, succession, and forest carbon sequestration: Confronting ecological theory with experiments and observations

Forests, as natural sinks of atmospheric carbon dioxide, play a prominent role in climate regulation and are primary sources of food, fiber, and fuel. As forests grow older and when they are disturbed, their capacity to sequester carbon and produce biomass is long-theorized to decrease, but only recently have ecologists tested these assumptions using experiments, observations, and new research tools. Empirical evaluation of these theoretical assumptions is timely, as large areas of forestland in North America will soon exceed the century mark in age and as these aging forests are increasingly disturbed by disturbance from pests, extreme weather, and age-related mortality. In temperate deciduous forests, where more moderate severity disturbances killing only a fraction of trees now prevail, there is little evidence from experiments or long-term observations for a marked decline in carbon sequestration or production. Rather, an increase in ecosystem physical and biological complexity under these disturbance regimes may counterintuitively drive – to a point – increases in the efficient use of growth-limiting resources, maintaining carbon sequestration in these forests well past the century mark (Figure 1). Conservation of aging and old-growth deciduous forests may therefore, counter to theory, sustain the land carbon sink and mitigate greenhouse gas emissions, while providing other goods and services afforded by these biologically and structurally complex ecosystems.

Figure 1. Moderate severity disturbance may sustain net ecosystem production (NEP), a key measure of ecosystem carbon sequestration, at higher-than-expected rates in aging forests by introducing physical and biological complexity as leaf area recovers, which in turn may result in the redistribution of growth-limiting resources and enhance resource-use efficiency. Canopies made more complex and physiologically efficient through periodic moderate disturbance may sustain NEP later into ecosystem development (from Curtis and Gough, New Phytologist, in review).
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The effect of noxious stimulation of the nociceptive tail and foot withdrawal response of unrestrained rats
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It’s now in their DNA: The Effect of the DNA Barcoding Research Experience on Introductory Students’ Program and Career Intentions
Rachel Boyce, Sarah Coleman, Julia Cumins, John Nguyen, Jonathan Popham, Beth Terry, Dr. Joseph Harsh

Assessing the effectiveness and impact of a large-scale two-semester course based undergraduate research experience focused on DNA-Barcoding for introductory biology students
Baodan Collins, Shelby Saroka, Dr. Tracy Deem, Dr. Chris Lantz

Assessment of Interleukin-3 production by Transgenic Fluorescent Reporter Mice Infected with the Nematode Nippostrongylus brasiliensis
Danielle Orlandi, Mark McGowan, Dr. Anthony Tongen, Dr. Rosha Wunderlich

Effect of Enclosure Type on Locomotion and Spatial Use in Captive Sifakas (Propithecus coquereli)
Lucas Manweiler, Danielle Orlandi, Dr. Anthony Tongen, Dr. Rosha Wunderlich

Using tri-axial accelerometry to quantify locomotor behavior in Propithecus coquereli and Lemur catta
Kinsey Miller, Sachin Sundar, Dr. Patrice Ludwig

Using unmanned aerial vehicles to identify invasive plants
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Geospatial analysis of Eastern Oyster habitat in the Chesapeake Bay
Madison Frongello, Bismah Khan, Dr. Marquis Walker

Characterizing the pathophysiology of Drosophila retinal degeneration mutant, rdgI
Alexa Cornwell, Katie Doherty, Elizabeth Staskal, Paulina Bauer, Saidah Lerman, Dr. Terrie Rife

Understanding the Impact of Tau Proteins in Alzheimer’s via CRISPR/Cas9
Stephanie Sharpes, Elizabeth Rogers, Reafa Hossain, Elizabeth Terry, Smita Bajain, Julie Bjerring, Jessica Carolino, Rebecca Harkness, Melanie Kusakavitch, Ethan Smolley, Peyton Thompson, Angelica Tonder, Robert Walker, Dr. Kevin Caran, Dr. Kyle Seifert

Antimicrobial Activity, Biofilm Disruption Capabilities, and Synergistic Interactions of Novel Amphiphiles (same as P12 on Thursday)
Kristen Grimshaw, Laura Yates, Kevin Lin, Sally Todd, Catie Willett, Kaleb Fasil, Dr. Amy Johnson

Grassland Bird Nest Identification Using Unmanned Aerial Vehicles
Rachel Prendergast, Dr. Grace Wyngaard

Freeze cracking: a histological method for preparing parasitic copepod tissues for genome size measurement
Kyle Cicalese, Dr. Tim Bloss

The State of the Translation Chaperone ICD-1 During Misfolded-Protein-Induced Apoptosis in Caenorhabditis elegans
Katherine M. Bland, Zachary O. Casey, Z. Logan Holley, Christopher J. Handwerk, Dr. George S. Vidal

Detecting dendritic spine pruning in cerebral cortex and a neuronal role for integrin beta 3
Katherine M. Bland, Zachary O. Casey, Z. Logan Holley, Christopher J. Handwerk, Dr. George S. Vidal
**ORAL PRESENTATIONS**

**T1**  Jillian Breault, Lauren Pope, Dr. Chris Berndsen, Dr. Jon Monroe

**An acidic domain in Arabidopsis β-amylase2 is required for K⁺ regulation**

*Arabidopsis thaliana* has nine β-amylase (BAM) genes that encode proteins that do a variety of functions related to starch metabolism. In chloroplasts, BAMs are primarily responsible for degrading starch into maltose at night, which the plant then uses for energy. Recently, our lab found that BAM2 is only active with the addition of KCl with optimal activity at 80 mM KCl. Further, BAM2 functions as a tetramer and displays sigmoidal kinetics due to a secondary binding site that is responsible for activating the enzyme when bound to starch. Using sequence alignments of BAM2 orthologs, our lab found a small N-terminal domain that contains a high percentage of glutamic and aspartic acids upstream from a four amino acid peptide (ERDF), which is only conserved in BAM2. Hypothesizing that this domain could interact with the positively charged cation from the salt, we created two mutant enzymes, one lacking the acidic domain (NDel1), and one lacking both the acidic domain and the ERDF peptide (NDel2). When the activity of each enzyme was compared to the wild-type, NDel1 displayed higher activity and NDel2 displayed lower activity. Interestingly, both of these mutants lacked the requirement for K⁺ in comparison to the wild-type enzyme, indicating that the acidic domain might be of importance to the salt dependency of BAM2.

**T2**  Althea J. Neighbors, Sarah McGrath, Dr. Oliver Hyman, Dr. David McLeod

**Novel hylid survey technique: a clear alternative to traditional polyvinyl chloride pipe refugia**

Amphibians are an important part of the ecosystem and are an excellent indicator of environmental health. In order to accurately determine amphibian population size and dynamics it is necessary to conduct population surveys. However, it can be difficult to get a clear sense of population composition without effective survey methods. For surveys of tree frog populations, the standard method is to use polyvinyl chloride (PVC) pipe artificial refugia. These refugia create space for frogs to hide in during the day, however, surveying can be difficult and typically requires forceful removal of the animal from the device. Therefore, we designed a novel style of PVC pipe refugia to make surveying easier for the surveyor and less disruptive to the frog. We have compared the novel refugia design to the traditional type of refugia at a site in east-central Virginia. The novel tubes consist of clear acrylic tubing inside of opaque PVC pipe. The frog does not need to be removed to identify species or collect morphometric data. This reduces the chance of disease transmission between organisms and induced distress. We checked the tubes for presence and absence of frogs once per week for 13 weeks to determine if the novel refugia is a viable survey technique. We observed 24 frogs of two different species (*Hyla versicolor* and *Pseudacris crucifer*) in both types of tube from May 2017 – October 2017. Initial results suggest frogs are equally as likely to inhabit the novel device as the traditional. We suggest the novel tubes are a superior field device for tree frog surveys and that they have tremendous potential as a tool for outreach and education, including citizen science. This is an exciting outcome we hope to continue to develop in the future.

**T3**  Holly Rucker, Dr. Rocky Parker

**Decrypting female mimicry in red-sided garter snakes**

Female sexual mimicry, the expression of female sexual signals by males, is a reproductive tactic that occurs in a wide range of species. Chemical cues, such as pheromones, are utilized by many species as sexual signals driving mate choice. There is only one example of chemical female mimicry in vertebrates: the red-sided garter...
snake, *Thamnophis sirtalis parietalis*. Female mimics in this species are males that produce female sex pheromones and are courted by other males. These female mimics have undetectable estradiol levels but elevated testosterone compared to normal males. Conversely, estradiol is necessary for females to produce the sex pheromone. Central to this is the link between estradiol and testosterone: testosterone is metabolized to estradiol via the enzyme aromatase. Female garter snake mimics are hypothesized to have higher expression of aromatase in their skin which would create estradiol locally to stimulate female pheromone production. Our project is the first empirical test of this hypothesis. Female mimics (n=20), males (n=20), and females (n=20) received injections of an aromatase inhibitor, fadrozole (FAD), or control injections (saline; SHAM) three times a week for three months. Skin lipids were extracted and fractionated from the shed skins of these snakes, and blood samples were collected to determine circulating hormone concentrations. We hypothesize that FAD treatment will prevent the production of female pheromone in the mimics and females, and if so will demonstrate that aromatase action is the key to female mimicry in garter snakes.

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T4  
Miguel Padilla, Matthew Harris, Dr. Patrice Ludwig  
**A novel technique for locating the nests of peregrine falcons using UAVs**

Advances in unmanned aerial vehicle (UAV) technology have allowed for numerous new technologies to develop including new methodologies for wildlife surveys. As part of an interdisciplinary team at James Madison University we are working to develop drones and survey protocols for the identification of peregrine falcon (*Falco peregrinus*) nesting sites in the mountains of Southwest Virginia. Eastern peregrine falcon populations have rebounded thanks to reintroduction efforts after the total extirpation of this population due to the effects of DDT. As peregrine falcons continue to move into their historic mountain habitat, it is imperative that biologists, state and federal agencies, and other land managers continue to identify breeding pairs and nest sites for the species. Current methodologies for locating nesting sites are inefficient and costly. By utilizing a novel approach which implements drone technology, we aim to provide biologists and land managers with a more efficient tool for locating nesting sites while reducing the potential for harm to the peregrine falcons and minimizing loss of equipment.

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T5  
Sarah McGrath, Dr. David McLeod, Dr. Morgan Steffen, Dr. Reid Harris, Dr. Carly Muletz  
**Exploring the microbiome: diversity of the microbial community of three foam nesting frogs, Genus: Polypedates, across a developmental gradient**

Characterization of microbial biodiversity, including that of the amphibian skin-associated microbiome, is a burgeoning frontier of research recently made accessible through advances in sequencing technology. The interaction between microbe and host has been shown to have profound influences on host health across a wide range of macroscopic organisms. Amphibians are currently one of the fastest disappearing vertebrate groups on the planet, due in part to skin-associated diseases caused by pathogenic microbes. Therefore, it is particularly important to characterize the amphibian skin-associated microbiome and to delineate the host-microbe relationships that may influence host health. In determining the microbial community of amphibian skin, it is important to consider how microbial communities are established. One of the fundamental questions related to the microbiome of amphibians and other organisms is: To what extent are skin microbes being passed down from parent to offspring (vertical transmission) or obtained from the environment? This study will focus on characterizing the cutaneous microbial diversity of three species of Southeast Asian tree frogs (Family: Rhacophoridae) that reproduce via the specialized breeding strategy of building a foam nest. Microbes associated with reproducing adults, foam nests (a reproductive specialization), tadpoles, and the surrounding environment will be compared. Delineating these ecological relationships (between host, microbe, and environment) is important because it adds a missing
piece to our knowledge of the natural world and can broadly inform conservation
efforts for amphibians worldwide.

T6 Matthew Harris, Dr. Heather Griscom, Dr. Patrice Ludwig

Potential benefits of restored riparian zones in an agricultural matrix for bat
communities

Bat conservation must occur in multiple habitats beyond national parks and protected
forests if the ecosystem services bats provide are to be protected. This project
contributes to our understanding of the efficacy of current conservation practices in
mitigating bat habitat loss within agricultural settings. Current research suggests that
restored riparian forests within an agricultural matrix may provide bat species with
improved feeding opportunities and act as covered corridors between habitats.
Acoustic detectors were used to determine if CREP riparian zones (compared to
control sites with denuded riparian areas) promoted increased bat diversity within the
Shenandoah Valley of Virginia. The abundance of prey and physical structure at each site
was quantified to ascertain what aspects of these buffers were found to be most
influential on bat activity. Sites enrolled in the CREP program were found to have
greater levels of activity from bats within the medium guild phonic guild and a trend of
increased bat activity was observed as tree count increased, especially within the
medium phonic guild. These findings indicate that the number of trees present within a
sampling area had a significant impact on the number of bat calls recorded and support
current conservation measures in place within agricultural matrices. Our findings help
inform stakeholders and government agencies as to the value of riparian forests
established through the Conservation Reserve Enhancement Program (CREP) for
promoting bats.

T7 Charles Holmes II, Dr. James B. Herrick

Whole-genome epidemiology of environmental Salmonella: monitoring potential
threats to public health

Approximately 9.4 million cases of foodborne illness occur annually in the United
States, with Salmonella infections estimated to comprise about 1 million of these cases.
Environmental reservoirs of Salmonella -- particularly those related to agricultural
practices -- may contribute greatly to the dissemination of these potential human
pathogens, though such reservoirs are not well characterized. Furthermore, the use of
antibiotics in animal agriculture has potentially expanded the circulation of
antimicrobial resistance (AMR) genes in the environment. Surveillance of
environmental Salmonella is a critical step in monitoring the distribution of this
pathogen and can be accomplished through whole-genome sequencing of isolates.
Stream sediment from seven sites and chicken litter from five poultry houses in the
Shenandoah Valley were sampled between October 2016 and January 2018. Modified
FDA Bacteriological Analytical Manual methods of pre-enrichment, enrichment, and
isolation were used to isolate 42 putative Salmonella. Thirty-seven were isolated from
stream sediments and five from litter from a commercial chicken house. Putative
Salmonella were confirmed by polymerase chain reaction amplification of the
Salmonella-specific invA gene. Isolate genomes were sequenced by the Virginia
Department of Consolidated Laboratory Services or the FDA via Illumina whole-
genome shotgun sequencing. AMR profiles, including minimum inhibitory
concentrations, were determined using NARMS Sensititre MIC assays as well as
surveyed in silico using KmerResistance 2.2, indicating at least 10 isolates with
resistance to clinically or agriculturally relevant antibiotics. Combining genomic and
more traditional microbiological approaches can provide a more complete
understanding of the potential threat posed by environmental Salmonella.

T8 Sophie K. Jurgensen, Dr. James B. Herrick
A CURE for Salmonella: Engaging Students in Pathogen Microbiology and Bioinformatics

Advances in Next Generation Sequencing (NGS) technology have generated a vast amount of publicly available genomic data, creating a need for students with training in computational analysis. This laboratory lesson is a course-based undergraduate research experience (CURE) focusing on environmental Salmonella, a common foodborne pathogen that is of great interest to public health laboratories but is relatively less virulent than other such pathogens. As discovery is a central tenant of CUREs, students isolate Salmonella enterica and related strains from stream sediment, poultry litter, or other sources in the first half of the lesson (Module 1). They also carry out phenotypic detection of antimicrobial resistance and large plasmids. The genomes of these isolates may be sequenced by the FDA or public health laboratories (ours were sequenced by the Virginia Department of Consolidated Laboratory Services at no charge). The second half of the lesson (Module 2) concerns the bioinformatic analysis of this sequence data. Students use easily-accessible, primarily web-based tools such as GalaxyTrakr and Enterobase to assemble their genomes and investigate areas of interest including serotyping, identification of virulence genes and genomic islands, and evidence of plasmids. After completion of this course, students should be able to demonstrate skills in the isolation and identification of Salmonella from natural sources, as well as computational skills necessary for computational analysis of microbial genomic data, particularly of members of the Enterobacteriaceae. While this course consists of two modules, one focusing on laboratory skills and the other bioinformatics, either could be used as a standalone module.

Destiny Foley, Claire Naylor, Jonathan Popham, John Nguyen, Dr. Patrice Ludwig

Drone Application for Black Bear Conservation

As part of the 4VA sponsored Unmanned Systems for Biology course in the JMU X-Labs, Virginia Department of Game and Inland Fisheries is sponsoring students to address pertinent problems in the Shenandoah Valley regarding black bears. Among the two projects being presented are (1) Improvement of bear den location and (2) A new approach to aversive conditioning of bears. Locating bear dens involves outdated technology that is difficult and dangerous for the user. Team Collared Bears aims to innovate current methods, with support of VDGIF, via employment of drone technology: Overhead flight for location of bear dens, and thereby suitable mothers for bear cubs in VDGIF’s possession. Current practice for farmers, on observing bears inflicting crop damage, is to shoot on sight. As such, VDGIF has also tasked Team Nuisance Bears to implement drone technology to reframe nuisance bear management and reduce crop damage. Among these projects exists a common goal: Maximizing the safety of, and minimizing the encounters between, humans and black bears. By the application of drone technology, students in the Unmanned Systems course address these problem areas for biologists while emphasizing cost reduction, safety for humans and study species, and conservation.

Matt Elder, Dr. Patrice Ludwig

An examination of the effects of magnesium enriched substrates on larval and juvenile eastern oysters

The eastern oyster has lost over 95% of its historic population in the Chesapeake Bay since the late 1800’s. Overharvest, disease, and pollution have all contributed to remove adult oysters whose shells are the preferred attachment sites for larvae. Artificial substrates such as concrete have been employed to mitigate this loss of attachment substrate and help stimulate population recovery, but more could be done to aid restoration as concrete could be easily mixed with micronutrients to potentially improve the larval recruitment and health of attached oysters. Magnesium is one micronutrient that has been shown to benefit other bivalves but its potential effects on oyster health are unexamined. Artificial shell treatments were created from normal concrete and concrete enriched with magnesium carbonate. Treatments of natural shell, normal concrete, and magnesium enriched concrete shells (n = 120 each) were
left in the field for 4 months to determine if magnesium substrates attracted more oysters, altered growth of attached oysters, or exhibited lower oyster mortality than normal concrete or natural shells. Preliminary Kruskal-Wallis post hoc results indicate that oysters attached to magnesium substrates did not display significant differences in growth (p values > 0.05) or mortality (p values > 0.05) compared to either natural shell or concrete oysters. Natural shell oysters did exhibit significantly lower mortality and significantly higher growth rates than normal concrete, leaving magnesium substrates as a middle ground between the two. Future studies are needed to determine any other possible benefits magnesium may confer, or if other micronutrients could be incorporated into concrete and benefit attaching oysters.

**T11** Taylor Hutchinson, Rana Ihsan, Dr. Timothy Bloss

**Characterization of Misfolded Protein Stress Inducers in the Different Cell Types of *C. elegans***

Various stressors can cause proteins to misfold and aggregate, often leading to cell damage and even cell death. To manage this stress, the cell employs mechanisms that mitigate misfolded protein levels, including the presence of chaperone proteins that help other proteins fold properly. The nascent polypeptide-associated complex (NAC) is an α/β heterodimeric chaperone that assists in the folding and localization of nascent polypeptides to the Endoplasmic Reticulum (ER) during translation. Depletion of the NAC in *C. elegans* results in numerous cell-specific phenotypes, including a strong induction of the ER-specific unfolded protein response (UPR), which can either save the cell or initiate cell death by apoptosis. To better understand the nature of the stress induced in the ER when the NAC is depleted, we are comparing phenotypes seen in NAC-depleted *C. elegans* to those observed in worms treated with ER stressors with known mechanisms of action, i.e. thapsigargin and tunicamycin. We are observing stress effects in fluorescently marked hypodermal cells, specifically the viability and number of hypodermal cells in embryos. We will perform similar analyses in neurons to determine cell-specific responses to NAC depletion. Misregulation of the NAC has been associated with numerous diseases; a better understanding of the NAC’s role in protein stress management may help us understand why.

**T12** Kendyl Combs, Rachel Barborek, Matthew Knick, William Meara, Dr. Susan Halsell

**Identifying the molecular components of cold nociception in *Drosophila melanogaster***

Nociception refers to an organism’s perception and reaction to potentially damaging noxious stimuli. While this response is essential, humans suffer from chronic pain in which the pain signals abnormally persist months after trauma, injury or infection. This study aims to better understand the molecular mechanisms of pain by researching the potential role of eight individual *Drosophila* Innexin gap junction proteins in cold nociception. Similar to mammalian Connexins, some of these proteins are hypothesized to be involved in the electrical synapsis between neurons. The expression level of each protein is knocked-down by cell specific expression of innexin RNAi constructs in the class III da sensory neurons that mediate nociception. Wild type third instar *Drosophila* larvae exhibit a characteristic “cringe” response when exposed to noxious cold. Knocked-down larvae are assayed, their behavior is videotaped and analyzed to quantify statistically significant changes in the cold response. By comparing the proportion of cringers between the knocked down, experimental larvae and the wild type, we can infer if the knocked-down protein participates in the cold nociceptive signaling pathway. Controls utilizing Oregon-R wild type larvae and larvae in which tetanus toxin is expressed specifically in da neurons will be described. All eight *Drosophila* Innexins have been tested using two different RNAi constructs for each, except for the ogre innexin. To date, twelve of the fifteen constructs have been tested, and eight have shown significant change in cringing compared to wild type controls (Two-Tailed Homoscedastic TTest, p<0.1). Additional Innexins will be tested and a pan-da neuron driver will also be used to drive RNAi expression.
Characterizing Tau in the Nucleus
A hallmark of Alzheimer’s Disease (AD) is the aggregation of hyperphosphorylated tau protein into neurofibrillary tangles. Tau has six major isoforms which localize to both the cytoplasm and the nucleus; however, its nuclear role and isoform presence has not been fully defined. Tau has recently been shown to bind to purine-pyrimidine (R/Y) repeats in DNA and stabilize them into Z-DNA. Furthermore, evidence from our lab suggests that the binding of tau to R/Y repeats causes transcriptional changes of the NOS1 gene. Based on studies of mouse tau isoforms and our lab’s previous work, we hypothesized that the 4R tau and 3R tau would be found in equal ratios in the nucleus of normal human neuronal cells, and that tau would bind to the NOS1 R/Y polymorphism. To test these hypotheses, western blotting of collected nuclear proteins from human neuroblastoma cells (SK-N-MC) were completed to examine which tau isoforms were found in the nucleus. Additionally, the conditions for electrophoretic mobility shift assays (EMSAs) were worked out to better understand tau’s ability to bind R/Y repeats. The western blots showed that 3R tau was predominate in SK-N-MC cells, and that the distribution of tau isoforms was similar in the nucleus and cytoplasm. Our EMSAs showed that a nuclear protein is able to bind the NOS1 R/Y repeat, but we have not identified this protein. Future experiments will use western blotting to characterize nuclear tau in other cell lines and continue improving our EMSAs to identify the NOS1 R/Y repeat binding protein.

Biosemiotics as an argument for the recontextualization of biological discoveries to attain a more satisfactory understanding of life: A critical analysis of the philosophy and biosemiotic model of Marcello Barbieri
The primary purpose of this project was to investigate and explain the philosophical approach of biosemiotics to understanding living systems in contrast to the current scientific paradigm. Secondary goals were to evaluate the potential merits and relevance of this approach to biology and to introduce such a topic for discussion to biologists in a formal academic setting. My method consisted of critical textual analysis supplemented by analogy and biological examples where appropriate. In general, contemporary biosemiotics argues for a teleologic recontextualization of biological discoveries in practice and education. This is accomplished in a sophisticated fashion through the application and modification of the semiotic theory of Charles Peirce to biology. While such a philosophical proposal is not scientifically falsifiable, it is one of significant concern to current and future scientific practice. In particular, the biosemiotic model of Marcello Barbieri may prove to be more satisfactory than the popular Peirce-Sebeok model and boasts scientifically falsifiable foundations. However, it is thus currently based on theory rather than fact.

Investigating the Ecology of a Rare Species on St. John USVI: Reintroducing Solanum concarponum in Light of Climate Change
Approximately two thirds of St. John is National Park territory. However, the land has been threatened with tourism and development, greatly impacting island biodiversity. One species that may become extinct due to this degradation is Solanum concarponum. S. concarponum is a rare shrub, endemic to the dry tropical forests of St. John, USVI. This plant is a species of conservation concern and is one of very few native and endemic plants on this island. Very little is known about the ecology and reproduction of S. concarponum. Most plants are found on the southern half of the island. Recently it has been noted that the greatest recognized threat to it is a lack of natural reproduction, possibly due to suboptimal habitat conditions. This study investigated the ecology of S. concarponum in order to construct a habitat model and determine potential causes for failed reproduction. The location of populations had a significant impact on plant growth and reproduction. Plant basal diameter and reproduction were significantly
different between sites. Soil samples taken showed suboptimal soil conditions, but similarities between all sites, with the most similar being Reef Bay and Nanny Point. Foliar chemical analyses showed no presence of antitherbivory cyanogenic glycosides. The population at Nanny Point was determined to be the healthiest, however, in light of climate change it contained the highest level of hurricane damage. Due to the similarities in plant health and soil contents, Reef Bay will be the optimal reintroduction site as that population had virtually zero hurricane damage. Learning more about the ecology and biology of S. conocarpum is crucial to improving conservation strategies. Restoring this rare plant would help with preservation of the St. John National Park lands, providing a stronger argument to preserve the island. Species restoration is integral to saving St. John from further degradation in the midst of the sixth global mass extinction.

T16 Isabel Lamb-Echegaray, Dr. Mark Gabriele

Targeting of Central Nucleus Projections to Extramodular Zones of the Lateral Cortex of the Inferior Colliculus in Developing Mouse

The multimodal lateral cortex of the inferior colliculus (LCIC) exhibits a modular-extramodular micro-organization that is evident early in development. In addition to a set of neurochemical markers that reliably highlight its modular-extramodular organization, mature projection patterns in a variety of adult species suggest that major LCIC afferents also recognize and adhere to such a framework. This patch-matrix-like arrangement appears to segregate distinct afferent streams, with somatosensory inputs targeting LCIC modules and auditory inputs surrounding extramodular zones. Currently lacking is a detailed understanding of the development and shaping of multimodal LCIC afferents with respect to its modular-extramodular framework. The present study examines the ontogeny of one auditory input to the LCIC, that arising from the central nucleus of the inferior colliculus (CNIC), with respect to the neurochemical framework; and suggests an early specificity of patterned inputs to the LCIC that exhibit discrete modular-extramodular mapping characteristics. Projection adherence to the LCIC extramodular framework became increasingly clear over the early postnatal period, and readily apparent by hearing onset. Double-labeling studies confirm that bilateral projections from CNIC to LCIC occupy extramodular domains that surround LCIC glutamic acid decarboxylase (GAD)-positive layer 2 modules by hearing onset. Biocytin labeled axons in living slice preparations avoid LCIC modules, terminating heavily in calretinin (CR)-positive extramodular zones. Determining how this emerging spatial arrangement of multimodal LCIC input arrays may align with respect to each other, as well as how each interface with, and are potentially influenced by similarly configured Eph-ephrin guidance patterns is discussed.

T17 Jenny Russell, Dr. Tracy Deem, and Dr. Chris Lantz

Assessment of Faithful Interleukin-3 Production by Transgenic Fluorescent Reporter Mice

Interleukin-3 (IL-3) is an immunoregulatory cytokine secreted by CD4+ T cells and other immune cells. Although our laboratory has shown that IL-3 influences immunity in a number of infectious diseases such as malaria, we do not yet know the identity of IL-3-producing cells or the kinetics of IL-3 production during the course of these infections. To begin addressing these questions, we used novel transgenic mice that contain an endogenous fluorescent reporter gene (ZsGreen) for IL-3 expressing cells. In these reporter mice, transcription of the IL-3 gene results in the production of separate IL-3 and fluorescent ZsGreen protein products. To determine if cells from these mice are expressing ZsGreen and IL-3 as expected, we cultured spleen cells from wild-type and transgenic mice under conditions that promote the development of various types of CD4+ T cells. These cultures were then activated and examined for ZsGreen and IL-3 protein production. Examination of ZsGreen expression by flow cytometry indicated that T cells are the primary CD4+ T cell subset that produces IL-3 in vitro. Interestingly, we found that transgenic mice produce significantly less IL-3
protein than wild-type mice as measured by ELISA. However, transgenic mice do produce significant amounts of biologically functional IL-3 in vivo since we saw no difference in IL-3-dependent increases in blood basophils following infection of both genotypes of mice with the nematode *Nippostrongylus brasiliensis*. These results suggest that IL-3 reporter mice represent a valuable tool for examining IL-3 production in IL-3-dependent disease processes such as malaria.

T18 Emily Murray, Dr. Heather Griscom
The effect of soil type, liming, and commercial inoculum on American Ginseng (*Panax quiquefolius*)

American ginseng (*Panax quiquefolius*) is a perennial herb that is threatened or endangered throughout most of its range, due to overharvesting for its medicinal properties and high profit. American ginseng is now protected in both the United States and Canada, limiting, and regulating harvest of the plant. Restrictions have led to the cultivation of the plant. This greenhouse study examines how soil type (2 levels), liming (2 levels), inoculation (2 levels), autoclaving (control 2-levels) affect plant growth. Two distinct soil types were collected from the field. Stratified American ginseng seeds were planted in cone-tainers in a regulated greenhouse system in a factorial design, with fifteen cone-tainers for each treatment combination. At 7 months seedlings were measured for root length, stem length, leaflet width, above-ground biomass, and percent inoculation. Root lengths were significantly greater in treatments with lime and inoculation (mean = 117.2 p-value<0.001) compared with plants without lime and inoculation (mean=72.9). Stem lengths were significantly greater in treatments with lime and inoculation (mean=59, p-value<0.001) when compared with plants that were not (mean=52). In addition to lime and inoculation, soil type had an effect on stem length (p-value<0.001). Liming and inoculation combined had a greater effect in poorer soils on both root length and stem length. This indicates that liming and inoculation can help the plant allocate nutrients to the roots and the stem, even in nutrient poor soil. *P. quiquefolius* intentionally inoculated with commercial mycorrhizal fungi could yield larger crops.

T19 Stephanie Sharpes, Elizabeth Rogers, Reafa Hossain, Elizabeth Terry, Smita Bajain, Julie Bjerring, Jessica Carolino, Rebecca Harkness, Melanie Kusakavitch, Ethan Smolley, Peyton Thompson, Angelica Tonder, Robert Walker, Dr. Kevin Caran, Dr. Kyle Seilert
Antimicrobial Activity, Biofilm Disruption Capabilities, and Synergistic Interactions of Novel Amphiphiles

The increased prevalence of antimicrobial resistant bacteria requires development of new control strategies. Preventative measures such as development of disinfectants and antiseptics with faster killing and antibiotic capabilities would help limit the spread of resistance and reduce the incidence of hospital acquired infection. Several series of novel amphiphiles, including three bis-cationic, four tris-cationic and three tetra-cationic double tailed amphiphile series, as well as one hepta-cationic, triple tailed amphiphile series were synthesized and tested for antimicrobial properties. These amphiphiles were previously tested for MIC value against several Gram-positive and negative bacterial species. This work expanded on the antimicrobial capabilities of these amphiphiles by determining time to kill a population of cells, biofilm disruption activity, and synergistic interactions with other compounds. Bis-cationic amphiphiles were the fastest at killing *S. aureus*, as 10X 12.12 killed within 1 minute. Oxacillin, a Gram-positive acting antibiotic, had synergistic interactions with novel amphiphiles against *E. coli*, with FIC’s ranging from 0.5 to 0.19. The highest biofilm disruption activity disrupted 90% of *P. aeruginosa* preformed biofilms. Synergistic combinations of these amphiphiles with oxacillin and other compounds could prove useful in overcoming bacteria antimicrobial resistant mechanisms. These results contribute to the development of cationic amphiphiles with increased biofilm disruption activity and faster kill time, ultimately better disinfectants and antiseptics that will better reduce the spread of antibiotic resistant pathogens especially in a hospital setting.
T20 Sheikh Rubana Hossain, Dr. Amanda Storm, Dr. Jon Monroe

Searching for Potential Binding Partners of Arabidopsis β-amylase9 Using Yeast 2-Hybridization

In plants, starch is a major carbon and energy storage compound. Starch is made as a product of photosynthesis while plants are in light and is degraded at night. Our lab is interested in the cellular mechanism of starch degradation in plants and for our studies we use Arabidopsis thaliana as a model. β-amylases are primarily responsible for the hydrolysis of starch in plants and a total of nine β-amylases genes are encoded in Arabidopsis thaliana. These nine genes are identified as BAM1-9. BAM9 is located in the chloroplast where starch is located and is present in all flowering plants but it is not catalytically active. It was published that BAM9 was very strongly expressed in the transition between nighttime and daytime. BAM9 may have an altered activity as a regulatory protein. Since regulatory proteins function by interacting with other proteins, we used the yeast two-hybrid system to attempt to identify interacting protein(s). As a first step, yeast cells were transformed with a BAM9 bait plasmid. Next, a cDNA library screen was performed where yeast cells with the bait is transformed with a library that encodes for potentially interacting proteins. The expression of reporter genes was observed. False positives were then eliminated by a series of control experiments. Lastly, sequencing and bioinformatics analysis was used to identify the potentially interacting proteins(s). AMY3 was identified four times in the bioinformatics analysis and a conserved coil region of AMY3 was identified in with each of the prey plasmids. Obtaining more comprehensive information about protein-to-protein interactions will aid our understanding of BAM9’s activity.

T21 Jonathan Studio, Dr. Christine May

Competition and Predation: Interactions between American eels (Anguilla rostrata) and brook trout (Salvelinus fontinalis) in Virginia mountain streams

American eel (Anguilla rostrata) and brook trout (Salvelinus fontinalis) populations are declining over their native range due to anthropogenic alterations to their habitat, such as fragmentation. Recent dam removals have increased eel populations inland; therefore, increasing their co-occurrence with brook trout. The purpose of this study was to consider the impact that restoring eel migration has on brook trout populations through two of the most influential ecological interactions, competition and predation. The study was conducted at Crabtree Falls in Nelson County, Virginia, which acts as a natural barrier to eels migrating upstream. The falls were an ideal sampling location because the control site (above, only trout) and the treatment site (below, trout and eels) were on the same stream to limit confounding variables. Eel and trout diets (n = 30 and 120, respectively) were sampled via gastric lavage (stomach pumping) three separate times between May and August 2017, and coincided with sampling of their potential prey items (invertebrates). Mean Schoener’s diet overlap was found to be biologically significant (73%), which indicates competition; however, brook trout most preferred prey item (terrestrial invertebrates) did not change in the presence of eels, which indicates limited competition. Further, zero predation by eels on brook trout young-of-the-year was observed. It appears that restoring eel migration is not adversely affecting brook trout populations, and may even be beneficial as increased resilience of their ecosystem results from less fragmentation.

T22 Francesca Circosta, Dr. Corey Cleland

Effects of molting on movement patterns in Chromatopelma cyanopubescens (Green Bottle Blue tarantulas)

Molting is the process in which an organism sheds its skin, exoskeleton, fur, feathers, or wool. In arthropods, molting arises at least in part from neurohormone release. Previous studies have explored the behavioral changes associated with molting in vertebrates, however, less is known about behavioral changes that occur in invertebrates. The specific aim of this project was to determine whether Chromatopelma cyanopubescens, or Green Bottle Blue tarantulas, experience
significant changes in their patterns of movement due to molting. Since many arthropods decrease their activity over development, there are two possible effects of molting during development. One hypothesis is that tarantulas will gradually decrease movement. An alternative hypothesis is that overall movement could decrease abruptly following a molt. A webcam (8 fps) recorded tarantulas’ (n = 4) movement on an LED light panel. Tarantulas received a 15-minute acclimation period and were then recorded for two hours. This protocol was repeated approximately every other day for roughly 20 days before molting and 20 days after. Raw video was then processed and tracked using ProAnalyst and analyzed in Matlab, Excel, and Sigmplot. Results suggest that the spiders’ overall movement gradually – not abruptly at molt - decreased over development. In contrast, qualitatively spiders traveled more irregularly immediately after molting. Further, tarantulas turned less frequently after molting. Both of these changes were abrupt and not persistent. Control tarantulas not undergoing molting did not show similar changes. Taken together, our results support both hypotheses - overall movement was not affected by molting but alterations in patterning of movement were correlated with molting. Whether the two changes arising from molting represent evolutionarily valuable processes or "side effects" of molting remains to be determined.

T23  Sean Gay, Cooper Brett, Dr. Mark Gabriele
Alignment of Eph-ephrin Guidance Patterns with Modular-Extramodular Framework in the Lateral Cortex of the Inferior Colliculus
In the multimodal lateral cortex of the inferior colliculus (LCIC) there are two neurochemically and connectionally distinct compartments, termed modular and extramodular zones. Modular fields span LCIC layer 2 and are recipients of somatosensory afferents, while encompassing extramodular domains receive auditory inputs. Recently in developing mouse we identified several markers (among them glutamic acid decarboxylase, GAD) that consistently label the same modular set, as well as a reliable extramodular marker, calretinin, (CR). Previous reports from our lab also show strikingly similar modular-extramodular patterns for certain Eph-ephrin guidance members in the nascent LCIC. Here we confirm early complementary GAD/CR-positive LCIC compartments, and characterize the registry of EphA4 and ephrin-B2 expression patterns with respect to its developing modular-extramodular framework. Immunocytochemical approaches in GAD67-GFP knock-in mice reveal patchy EphA4 and ephrin-B2 domains that precisely align with GAD-positive LCIC modules, and are complementary to CR-defined extramodular zones. Such patterning was detectable neonatally and further sharpened with age, yielding discrete compartments prior to hearing onset. Despite similar global patterns matching GAD-defined modules, EphA4 immunolabeling was largely fibrous in nature, while ephrin-B2 expression appeared more cellular. A dense plexus of EphA4-positive fibers was consistently observed within modular confines, encasing the identified GABAergic cell population. These results suggest an early compartmentalization of the LCIC that is likely instructed in part through Eph-ephrin guidance mechanisms. The overlap of developing LCIC neurochemical and guidance signatures is discussed in the context of its seemingly segregated multimodal input-output streams.

T24 Justin Nguyen, Dr. Corey Cleland
Reconstruction of the tail nociceptive withdrawal response from combinations of movement primitives associated with individual muscles in the rat
In response to noxious stimuli, animals withdraw the affected body part using the nociceptive withdrawal response (NWR). The rat tail, which contains many hyperredundant muscular degrees of freedom (DOF), presents a substantial computational challenge which the CNS simplifies through muscle synergies. The specific aim of our study is to reconstruct the behavioral NWR through combinations of movement primitives arising from the contraction of individual muscles. Adult Sprague-Dawley male rats were loosely restrained in an acrylic tube and 18 evenly spaced marks were made on the dorsal surface of the tail in the distal region. Heat stimuli were delivered
to the lateral surface of the tail adjacent to the marks with a laser diode (980nm) and
the NWR was recorded using high-speed video (650 fps). Subsequently, the same rat
was anesthetized with pentobarbital (60 mg/kg i.p) and a 2 cm incision was made on
the dorsal-lateral surface of the proximal tail. Individual tendons arising from pelvic
muscles (n=20-40) were identified and pulled rostrally to create tail, “movement
primitives”, and recorded by video. Computationally, the behavioral movements were
reconstructed by combining movement primitives to identify possible patterns of
muscle activity that could possibly coordinate the NWR. Motor primitives were
diverse, creating movements that resulted in local bends distributed over the distal
portion of the tail. In contrast, the NWR from heat stimuli resulted in complex
movements of the tail, suggesting that multiple motor primitives contribute to the
overall tail NWR. Ongoing studies should distinguish between alternate muscle
strategies underlying the tail NWR.

T25 Hasti Izadpanah, Dr.Corey Cleland
Muscle synergies formed in the Sprague Dawley rat’s tail in response to
nociceptive stimuli
Noxious stimuli can evoke the nociceptive withdrawal response (NWR), which
protects the affected part of the body from injury. The rat tail, because of the large
number of joint and muscle degrees of freedom, may present a computational
challenge to the central nervous system. Previous studies have revealed that synergies
act to reduce the number of degrees of freedom. The long-term specific aim of this
project is to test the hypothesis that during the NWR muscle synergies controlling rat’s
tail reduce the muscular degrees of freedom by recording the electromyograms (EMGs) from intrinsic tail muscles during heat evoked NWRs. Adult, male Sprague
Dawley rats were anesthetized [isoflurane]. The tail was marked in thirteen equally
spaced locations on dorsal surface of the tail. To record EMG, 15 stainless-steel wires
(0.002", Teflon insulated, 7 strands, de-insulated for 2 mm) were inserted
subcutaneously with 25-gauge, 5/8” needles. 14 wires were inserted at seven adjacent
marks for recording. Heat stimuli (980 nm infrared laser diode) were delivered at the
11 marked locations to evoke a NWR that was captured by high speed video (650 fps).
EMG was conventionally amplified and filtered. Robust single and multi-unit EMG
recording were obtained. EMG was highly modulated by behavior, typically tonically
active at rest and increased significantly during tail movement; in some instances EMG
became quiescent. These results demonstrate that intrinsic tail muscles may
contribute to the NWR and raise the experimentally addressable question whether
synergies of intrinsic tail muscles contribute to control of the tail NWR.

T26 Bejan A. Rasoul, Jeremy A. Bravo, Dr. Raymond Enke
Characterizing Epigenetic Regulation in the Chicken Retina
The retina, the sensory neuronal tissue within the eye, is composed of three layers of
neuronal cells connected by two synaptic layers lining the inside of the anterior
portion of the eye. Multipotent retinal precursor cells are genetically homogeneous
and differentiate into mature retinal neurons due to differential gene expression,
which has been correlated with epigenetic modifications such as DNA methylation.
DNA methylation of upstream regulatory elements is associated with transcriptional
silencing of gene expression. Years of research in retinal development has identified
the numerous genes expressed during the main steps of retinal development, however,
it is unclear how epigenetic modifications such as DNA methylation influence the
expression of the photoreceptor genes. In an attempt to characterize the role of DNA
methylation in regulating developmental-specific patterns of gene expression in the
retina, this project correlates chicken (Gallus gallus) whole-genome bisulfite
sequencing (WGBS) data with RNA-seq data to identify a novel set of epigenetically-
regulated genes involved in retinal development. Further gene specific analyses
indicate an inverse relationship between methylation and expression in several retinal
genes (PRPH2, FSCN2, LRIT1) while other genes (ARR3, PDE6B, PDE6C, GNAT1) do
not show the same relationship. Additional analysis of the DMRs accompanying the DEGs can answer questions about the mechanisms by which DNA methylation is influencing gene expression and the role of DNA methylation in producing functional retinal cells from retinal pluripotent cells. This knowledge can give insights into how to generate retinal neurons to better treat retinal degenerative diseases.

**T27** Courtney H. Neumeyer, Dr. Christopher S. Rose

**Lung Morphogenesis in Three Species of Amphibians**

Amphibians are an essential model for understanding the evolution of air breathing organs in vertebrates. Most generally, they occupy an intermediate phylogenetic position between fish and tetrapods and their uniquely biphasic life style allows them to occupy aquatic and terrestrial habitats at different stages of life. Because their larvae are primarily aquatic, amphibians begin life using multiple organs for gas exchange, which means that they are unique among tetrapods in being able to delay the onset of lung use and lung development to different postembryonic stages. It also means that amphibians develop their lungs while they are using them, which opens up the possibility that their rate of lung development is controlled in part by their breathing behavior. Here lung morphogenesis is described for *Lithobates sylvaticus*, *Anaxyrus americanus*, and *Ambystoma maculatum*. In addition, the onset and frequency of breathing was described for these same three species. Lungs were first present early in development for *L. sylvaticus* and midway through larval development for *A. americanus* and *A. maculatum*. Lung morphogenesis generally occurred by the appearance of lungs, the expansion of lung lumen, the appearance of folds, the extension of folds into septa, and then septa connecting to form a septa network. Not all of these stages of lung development occurred in all three species. *Ambystoma maculatum* were never seen with septa or a septa network.

**T28** Madison Thomas, Victoria Gaudin, Dr. Corey Cleland

**Escape Behavior of the Grammostola rosea Tarantula and Phidippus regius Jumping Spider in Response to Heat Stimuli**

Insects often respond to aversive stimuli such as wind, looming, and heat by escaping in a direction opposite the stimulus. Spiders, because they have eight legs, have potentially a greater repertoire of escape responses. However, there are few published studies on the escape response of spiders, especially regarding the effects of stimulus location or direction. The specific aim of this project was to determine the relationship between the stimulus location and direction of response in *Phidippus regius* (Regal jumping spider) and juvenile *Grammostola rosea* (Chilean Rose tarantula) for heat stimuli delivered to the tarsi of each leg. Chilean rose tarantulas were chosen because they are docile and readily obtained while jumping spiders have complex predatory strategies. To evoke an escape response, the tarsi of each of the spiders’ 8 legs was stimulated in random order at 5 minute intervals with an infrared laser (980 nm). The resulting escape response was captured with high-speed video (300 fps). Following the experiment, movement was tracked (Proanalyst), allowing quantification of the animals’ location and orientation over time. Jumping spiders (n=9) and tarantulas (n=5) displayed similar responses in which they withdraw the stimulated leg and then translated their body directly away from the stimulus. In contrast to responses of crickets and cockroaches to aversive stimuli, the spiders only minimally turned. The translation direction depended significantly on the location of stimulated tarsi, suggesting that the stimulus location on the body is used to program the escape. These results demonstrate that tarantulas and spiders have a well-organized response to aversive stimuli.

**T29** Julia Kaiser, Dr. Rocky Parker

**Bitter taste behavior in the red-sided garter snake**

In vertebrates, the sense of taste is important for indicating whether something is safe to eat. Specifically, bitterness is a taste modality typically associated with unsafe or bad food. Predators, including snakes, are especially reliant on their ability to taste...
bitterness since they are often obligate carnivores and have subsequently lost multiple
taste genes enabling diverse taste modalities (e.g., sweet). Because snakes are an
evolutionarily ancient group of vertebrates and all species are obligate carnivores, it
has been hypothesized that snakes may lack the ability to sense multiple modalities of
taste, including bitter. We therefore tested male red-sided garter snakes (n=10) with
natural feeding stimuli (earthworm extract) applied to a lure to obtain baseline data.
We recorded latency to attack and rates of tongue-flicking, the latter being a proxy
used in snakes and lizards for quantifying chemosensory interest in stimuli. After the
baseline trials, the same males were then tested in two bitter taste exposure trials
where the earthworm extract was mixed with a compound known to be bitter to most
vertebrates: quinine HCl (QHCl). First, the earthworm extract was mixed with a
solution (0.1M) of QHCl; the second trial used QHCl powder applied directly to the
earthworm extract-coated bait. There was no significant behavioral change when the
snakes were introduced to the bitter compound in liquid form, however, there was
evidence of hesitation and a decrease in a metric (tongue-flick attack score) when
presented with the powdered compound. This indicates that the snakes may only be
able to sense the bitterness if it is in a high enough concentration and/or in a non-
aqueous form. To further explore this possibility, more trials will be conducted. These
new trials will utilize both forms of the compound and help accumulate more data.
Eventually, the trials may be conducted with live bait instead of earthworm extract.

Kristin Sammons, Zuby Okafor, Dr. Corey Cleland

Contributions of Aδ and C Fiber Nociceptors to the Nociceptive Withdrawal
Response in Intact Unanesthetized Rats

The nociceptive withdrawal response (NWR), characterized by rapid withdrawal of
stimulated body parts, can be evoked by stimulation of two classes of nociceptors: Aδ
and C-fiber. Previous studies revealed conflicting results concerning the factors that
determine the direction and magnitude of the NWR. Some showed that the direction of
the NWR depends upon stimulus location. In contrast, other studies from our
laboratory showed that the direction of the NWR does not depend on stimulus location
but rather depends on posture. However, it is likely that the heat stimuli delivered in
our studies stimulated a mixture of C-fiber and Aδ nociceptors. The effect of C-fibers
may have obscured the effect of Aδ nociceptors because their receptive field size
differs. C-fibers have large receptive fields, sometimes encompassing the whole paw of
the rat, while Aδ nociceptors have smaller receptive fields. Consequently, we
hypothesized that stimulus location would affect the Aδ but not the C-fiber evoked
NWR. Our overall specific aim was to preferentially stimulate C-fiber, Aδ, or a mixture
of the two nociceptors to determine their relative contributions to the NWR. Sprague-
Dawley rats (n=23, n=799 trials) were placed on a mesh or glass surface, and the
plantar aspect of the hind left foot was stimulated in five locations with brief electrical
(200μs), heat pulse (100ms), or varying intensity heat stimuli, that are known to
preferentially stimulate Aδ nociceptors, C-fibers, or a mixture of the two. Upon
stimulation, the rat rapidly withdrew and then replaced its paw on the surface. The
initial and final positions of the foot were recorded using a camcorder placed
underneath the surface. The difference between the initial and final positions
represented the NWR response vector. Consistent with previous studies, for electrical,
heat pulse, and varying heat stimulation, we found no dependence of stimulus location
on the direction and magnitude of the NWR in rostral-caudal and lateral-medial axes
(p>0.24, ANCOVA) or on the change in foot angle from initial to final positions
(p>0.05), even though only Aδ nociceptors were stimulated. However, the direction
and magnitude could be explained in part by the initial position of foot prior to
movement (average r²=0.19, p<0.001, correlation); for example, when the foot was
initially rostral the movement was caudal and when initially caudal the movement
was rostral, thus avoiding disruption of the rat’s balance. Our results falsify the
hypothesis that Aδ-evoked NWRs vary with stimulus location and suggest that over evolution the
NWR has traded off optimal withdrawal movement direction for maintaining postural
stability.
EP1  Paige Baedke, Dr. Rocky Parker
Circannual and sexual variation in skin lipid production of invasive tegu lizards from Florida
The Argentine black and white tegu (Salvator merianae) is an invasive species in the United States, specifically in southern Florida which has a climate that approximates the species’ natural habitat. S. merianae, like all reptiles, not only sheds its skin multiple times a year, but also produces lipid compounds that we hypothesize have sexual communication function. Lizards and snakes have complex chemosensory anatomy and physiology that allows them to detect these compounds for use in recognition, communicating mate quality, and trailing prey. To date, there has been little investigation into the chemical ecology of tegu lizards, especially in their invasive range, and how skin lipid components and concentrations vary between the sexes and seasons. By examining the shedding frequency and the amount of lipid per gram of shed produced by male and female S. merianae over time, we have concluded that there are sexually dimorphic and circannual changes that occur in this species. Both sexes produce more skin lipid during the spring and summer months, with males producing more skin lipids than females during every season. Males also shed more frequently than females, which may be indicative of using skin sheds as markers for male location during mating. Future experiments will be conducted using Y-mazes and the extracted skin lipids to solidify that they are used in chemical signaling and trailing between sexes.

EP2  Jadelin McLeod, Toma Matveeva, Dr. David S. McLeod
Barcoding the Amphibian Biodiversity of Brunei
Amphibians play an important role in ecosystems around the world, but are rapidly disappearing from their native distributions. This study documents amphibian biodiversity in Brunei Darussalam (Borneo), a global biodiversity hotspot, with a focus on tadpoles (the larval life stage of frogs). DNA barcoding (mitochondrial CO1 and 16S genes) was used to determine species identification and match tadpoles to adult specimens. Results from a 2016 survey yielded a total of 29 species of amphibians based on adult and larval samples. Two species were detected only through the collection of tadpoles. These results demonstrate the importance of specimen collection in amphibian surveys and the utility of tadpoles as a means of capturing this rapidly disappearing aspect of global biodiversity.

EP 3  Daniel Yaquib, Angelia Sprys, Elena Younossi, Madison Hodge, Julia Wease, David Weisenbeck, Dr. David McLeod
Mark-recapture of turtles on James Madison University's East Campus
Trachemys scripta elegans, the Red-eared Slider, is native to the Midwestern United States of America, but occurs in Virginia as an invasive species. In this study, the populations of T. s. elegans and the native Painted Turtle (Chrysemys picta) were analyzed. Mark recapture was used to estimate population sizes in various locations around the James Madison University campus. Traps were placed in the two retention ponds on JMU’s East Campus and the pond in the Edith J. Carrier Arboretum. The carapace length and weight of the collected specimen were recorded and analyzed in order to try to search for disparities in the dimensions of each species. Turtles were found in the retention ponds, but were in low numbers initially due to the unpredictable cold weather in the area.

EP 4  Matthew Graziano, Claire Naylor, Jack Doss, Selena Moats, Anna Golden
Biodiversity survey and herpetofauna inventory of the Edith J. Carrier Arboretum
Biodiversity surveys are often used to provide pertinent data for specific locales. The survey being conducted here will be used to inventory the herpetofauna present in the Edith J. Carrier Arboretum. This survey uses coverboards, visual encounter surveys, turtle traps, drift fences, and anuran call surveys to obtain a comprehensive picture of the herpetofauna present in the Edith J. Carrier Arboretum at James Madison University. We present the results of the first year of this study which will serve as a foundation for subsequent surveys and a long-term study of the herpetofaunal community at this site. Providing the arboretum with amphibian and reptile diversity data will facilitate management decisions at the arboretum, as well as raising awareness for conservation of local biodiversity. The results of the survey will also be used to develop a public education and outreach program that will accurately represent the biodiversity of the area.

P1
Z. Logan Holley, Zachary O. Casey, Katherine M. Bland, Christopher J. Handwerk, Dr. George S. Vidal

Investigating the Role of Integrin Beta 3 in Dendritic Arborization in the Developing Cerebral Cortex

Many neurological diseases, such as autism spectrum disorder, Alzheimer’s, and epilepsy, are thought to be associated with disorders of the synapse. Autism spectrum disorder (ASD) is characterized by repetitive behaviors, deficits in communication, and overall impaired social interaction. ASD is accompanied by an excess of synapses formed by excitatory neurons within the cerebral cortex. Many forms of ASD are believed to be caused by dysfunctional dendritic arborization and synaptic pruning. Integrins are cell adhesion molecules that are required for normal structural plasticity of dendrites and synapses, as well as for construction of cortical circuits within the brain. In population studies, there have been positive associations between integrin beta 3 (Igfb3) mutations and ASD. As ASD is thought to be due to dysfunctional dendritic arborization and synaptic pruning, and integrins have been implicated in this process, it is necessary to further examine the role Igfb3 specifically plays within neuroanatomical development. We hypothesize that integrin beta 3 coordinates growth and arborization of excitatory neuronal dendrites of the cerebral cortex. In order to test this hypothesis, cell-specific loss of function of integrin beta 3 will be analyzed within excitatory (layer II/III pyramidal) neurons of the cerebral cortex. Here, we explore initial findings and approaches. Causing the loss of function of Igfb3 within neurons will allow for the comprehension of what neurological mechanisms are dysfunctional due to the absence of Igfb3 within neurons. This study will therefore enhance our understanding of normal brain function, and may also inform novel treatments for diseases of the cerebral cortex.

P2
Zachary O. Casey, Katherine M. Bland, Adam Aharon, Dr. Chia-Chien Chen, Dr. Yi Zuo, Dr. George S. Vidal

Investigating cell-autonomous dendritic spine defects in a mouse model of Fragile X Syndrome

Fragile X syndrome is the most common form of intellectual disability that arises from the dysfunction of a single gene: Fmr1. A strong neuroanatomical correlate of Fragile X Syndrome is elevated dendritic spine density on cortical pyramidal neurons. To investigate possible cell-autonomous roles for Fmr1 in this phenotype, we are investigating dendritic spine density on cortical pyramidal neurons of Fmr1 mosaic mice. The genotype and dendritic spine density of each neuron is assessed through immunohistochemistry and confocal microscopy. We expect that Fmr1 KO neurons in mosaic cortex will develop a higher density of apical dendritic spines in layer V compared to controls, which would recapitulate the elevated spine density found in Fmr1 global KO mice. We also expect that Fmr1 WT neurons in mosaic brains will have a normal density of apical dendritic spines when compared to WT controls. If our hypotheses are validated, results would suggest that Fmr1 regulates dendritic spine
density in a cell-autonomous manner and uncover a key mechanism for Fragile X Syndrome etiology.

P3 *  Kevin Reifenberg, Jon Studio, Dr. Christine May

**Freshwater Invertebrate Population Response to the Presence of Predatory Fish**

Macroinvertebrates play a pivotal role in freshwater ecosystems by influencing nutrient cycles, breaking down organic matter, directly affecting primary producers, and serving as a major food source for numerous fish species. The goal of this study was to examine if macroinvertebrate density and diversity were affected by the number of predatory fish species present. As dams are removed along the east coast, American eels (*Anguilla rostrata*) are able to migrate further inland. Crabtree Falls in Nelson County, Virginia represents the westward boundary for the American eel in the Tye River, and also contains high numbers of Brook trout (*Salvelinus fontinalis*). The falls are an ideal sampling location because the two treatments of interest are incorporated and confounding variables are limited. Brook trout are the only fish species present above the falls, but below the falls trout and eels co-occur. Designated reaches above and below the falls were divided up into three distinct pool/riffle sequences. Benthic invertebrate sampling was conducted using a D-frame kick net for three minute timed samples, each broken up proportional to the habitat available. Drifting invertebrates were collected overnight after placing drift nets across a narrow section of the stream. Three collection events occurred, both above and below the falls, from May-July, 2017. Comparisons will be made between density and diversity of invertebrates above and below the falls for each sample date. Comparisons will also be made between invertebrate availability and prey selection by assessing diet samples of trout and eels. This data may be used to gain insight regarding the effects of migratory species on upstream food webs post dam removal and on the effect of multiple predators.

P4 *  Samantha Hetrick, Lilly Nelson, Alex Schmidt, Dr. Justin Brown

**The Role of Brain Stem 5HT1A and GABA-A Receptors in the Thermoregulatory Response to Hypoxic Stress**

Sudden Infant Death Syndrome (SIDS) is a leading cause of infant mortality (1). Alterations in brainstem development of Serotonin (5HT) and GABA are linked to its cause (2). The sympathetic premotor neurons located in the Nucleus of the Raphe Pallidus (NRP) in the brainstem have both 5HT1A and GABA-A receptor subtypes that mediate protective cardiovascular responses to environmental stress (3). It is hypothesized that alteration in these receptors at the NRP will also modify protective thermoregulatory responses to hypoxic stress such as hypothermia. Using aseptic techniques, male & female Sprague-Dawley rats (225-325g) were instrumented with radiotelemetry probes to non-invasively measure core temperature (Tc). Using a stereotaxic device, a steel cannula was inserted into the brainstem which allowed microinjection at the NRP. After recovery (1 week), rats were housed in a thermal gradient which allowed them to select their ambient temperature (STA) and thereby facilitated behavioral thermoregulation. Once acclimated to the gradient, 30mM of either a 5HT1A agonist (8OH-DPAT or “DPAT”), antagonist (WAY100635), a GABA-A agonist (Muscimol), antagonist (Bicuculline) or ACSF (control vehicle) was then microinjected into the NRP immediately before exposure to either 6% O2 (hypoxia) or 21% O2 (normoxia) for 60 min. In the normoxic group, the typical short term hyperthermic response to handling was abolished in rats injected with Muscimol but persisted in all other groups. Rats exposed to 6% O2 stress (hypoxia) demonstrated a typical hypothermic response. In the control group (ACSF) the Tc drop was ~2.0˚C. When the 5HT1A receptor was activated by DPAT, this protective hypothermic response was exacerbated (~3.0˚C decrease). Similar responses resulted from injection of the 5HT1A antagonist (WAY). Modulation of the GABA-A receptor however had no effect versus control. There were mild decreases in STAs of ACSF injected rats (4.3˚C) which was exacerbated in DPAT injected rats (8˚C). Rats injected with WAY
seemed to reverse this trend initially with an increase in STa (3˚C) which quickly faded. Importantly, the STa responses to hypoxic stress helped facilitate Tc changes suggesting coordination between behavioral and autonomic thermoregulatory mechanisms which facilitated the protective hypothermic response. Previous data confirmed that GABA-A and 5HT1A receptors in the NRP help mediate cardiovascular responses to stress. Although there was a sympatholytic effect from Muscimol injection in the normoxic group, the GABA-A receptors do not seem to facilitate thermoregulatory responses to hypoxic stress. This suggests that hypoxic stress is such a salient stimulus that it over rides the sympatholytic effect of GABA – A receptor activation or does so via alternative pathways. Hypoxic stress may instead mediate its hypothermic responses via the 5HT1A receptor. When that receptor is activated by DPAT there is an exacerbation of the hypothermic response to hypoxia. The behavioral thermoregulatory responses also facilitate the hypothermia in this group. The results from blockade of the 5HT1A receptor with WAY are confounded by the short half-life of this receptor antagonist. Alterations in 5HT neuronal development in the brain stem may cause inadequate behavioral (STa decrease) and autonomic (Tc decrease) thermoregulatory responses to hypoxic stress. Understanding how dysfunction in brainstem 5HT leads to impairment in these protective responses to stress is essential in the diagnosis, and eventual prevention, of SIDS.

Rachel Barboreck, Kendyl Combs, Matthew Knick, William Meara, Dr. Susan Halsell
Identifying the molecular components of cold nociception in Drosophila melanogaster
Nociception refers to an organism’s perception and reaction to potentially damaging noxious stimuli. While this response is essential, humans suffer from chronic pain in which the pain signals abnormally persist months after trauma, injury or infection. This study aims to better understand the molecular mechanisms of pain by researching the potential role of eight individual Drosophila Innexin gap junction proteins in cold nociception. Similar to mammalian Connexins, some of these proteins are hypothesized to be involved in the electrical synapsis between neurons. The expression level of each protein is knocked-down by cell specific expression of innexin RNAi constructs in the class III da sensory neurons that mediate nociception. Wild type third instar Drosophila larvae exhibit a characteristic “cringe” response when exposed to noxious cold. Knocked-down larvae are assayed, their behavior is videotaped and analyzed to quantify statistically significant changes in the cold response. By comparing the proportion of cringers between the knocked down, experimental larvae and the wild type, we can infer if the knocked-down protein participates in the cold nociceptive signaling pathway. Controls utilizing Oregon-R wild type larvae and larvae in which tetanus toxin is expressed specifically in da neurons will be described.

All eight Drosophila Innexins have been tested using two different RNAi constructs for each, except for the ogre innexin. To date, twelve of the fifteen constructs have been tested, and eight have shown significant change in cringing compared to wild type controls (Two-Tailed Homoscedastic TTest, p>0.1). Additional Innexins will be tested and a pan-da neuron driver will also be used to drive RNAi expression.

Gabriela Constancia, Dr. Marquis Walker
Site-directed gene editing in Drosophila using Crispr/CAS9
Retinal degenerative diseases (RDDs) are a growing health problem of great clinical interest, especially within our expanding aging population. RDDs are defined as disorders that cause photoreceptor cell death in the retina, which ultimately leads to a loss of vision or blindness. These diseases include Age-related macular degeneration, retinitis pigmentosa, diabetic retinopathy, and many other neurodegenerative diseases. Our lab uses Drosophila as a genetic model to study gene expression and function in the retina. In recent years the bacterial Crispr/Cas9 system has been modified to direct site-specific gene editing in many animal models including the fly. We used transgenic flies that expresses Cas9 enzyme in germ line cells to generate a
site-directed mutation in the rhodopsin (Rh1) gene. To generate these mutants we modified the Crispr/Cas9 procedure to enhance and simplify the transformation of embryos. We replaced the standard microinjection procedure with an electroporation method to transform embryos. This change allowed us to transform many embryos with our guide RNA vector in a single step in contrast to injecting each embryo individually. This modification in the transformation step can significantly reduce the time and materials needed to generate site-directed mutations in *Drosophila*.

**Development of a cell culture system to study the effects of physical confinement and spatial arrangement on the maintenance of chondrocyte phenotype**

Articular cartilage, a frictionless connective tissue in articulating joints, mitigates the mechanical stresses of movement on the body. Over time, however, stress can lead to chronic cartilage degradation in which chondrocytes lose their normal, lacunae-enclosed phenotype and adopt an inflamed, fibroblast-like phenotype. Stimulating chondrocytes to repair cartilage tissue while maintaining their phenotype may prevent this chronic condition. Unfortunately, little is known about how chondrocytes produce cartilage and how chondrocyte phenotype is maintained, in part because chondrocytes alter their phenotype in standard, two-dimensional culture and are difficult to study in 3D matrices.

Our goal is to develop a system to study chondrocyte phenotype in a 3D environment that is easy to image and has controllable parameters. Ultimately, we want to study how altering chondrocyte confinement (simulating lacunae) and the molecular composition of their environment affects their phenotype. We have developed tools to stamp “microwells” (wells fitting one or several cells) into different gel materials. These wells allow us to modify cell confinement and shape, and the stiffness and molecular composition of the environment. Microwell stamps were produced using photolithography and molded in silicone (PDMS). These stamps were then used to generate microwells of varying shapes and sizes in a thin layer of PDMS. The microwells were functionalized with the extracellular matrix protein fibronectin to induce the chondrocytes to inhabit the microwells. Experiments are currently being conducted to analyze how long chondrocytes remain viable within the microwells and to determine the preference of microwell size among the chondrocytes. Future projects will use the data obtained from the viability and size preference experiments to create a new quartz photomask that will produce microwells that are optimized for the chondrocytes. Additional projects will include producing wells in physiologically relevant materials such as collagen I (simulating wound healing) and functionalizing PDMS wells with other extracellular matrix proteins such as collagen II (simulating lacunae). These models will be used to study how the microenvironment affects chondrocyte phenotype.

**Purcell Park Tree Inventory**

Trees provide a myriad of benefits to a community and its citizens, both economically and recreationally. Currently, invasive insects and diseases have taken a toll on specific tree populations throughout the United States. As these invasive pressures spread to new areas, especially urban areas already facing anthropogenic pressures, the impact can provide unique challenges in terms of management. The aim of our project was to assist the city of Harrisonburg, VA in facing these challenges by conducting a tree inventory of Purcell Park, an area of recreational and environmental importance to our community. First, we created a baseline assessment for the tree distribution (species and size) throughout Purcell Park. Then we focused on the Ash tree population, a community currently being decimated by the invasive Emerald Ash Borer beetle. This beetle is affecting the park’s Ash trees, which make up 20% of the overall tree community. A treatment is available, but only lasts for a limited time.
period and may be cost prohibitive. These assessment results will help influence management decisions to determine the best course of action in terms of park management and resource allotment for the betterment of the park and the Harrisonburg community.

Sanjiv Jayamohan, Dr. Rocky Parker

**Male Burmese python behavior in a Y-maze**
The Burmese python is a large predatory species that is an invasive species in the Florida Everglades. The Burmese python reproduces at a rapid rate, consuming many native mammals and birds posing a significant competition risk to native reptiles in the Everglades. For example, raccoon, bobcat, and fox populations have been over predated to near local extinction in South Florida, and this has been attributed directly to the increasing python population. The purpose of our study is to determine and analyze the different types of behaviors exhibited by male pythons in the presence of conspecific chemical trails in a Y maze. When analyzing these videos, I have been looking for specific and unique behaviors the male pythons show in this experimental apparatus. Examples of these behaviors include reassessing, a behavior where the python will stop all forward moment and flick its tongue usually in response to a stimulus, and head raises, a behavior in which the python raises its head to the top of the maze and is associated with evaluating a chemical trail. Additionally, several behaviors may be linked to facilitate chemical trailing. For example, head raises occur before or immediately after reassessments. We are attempting to help contribute to the removal of the pythons in the Everglades by studying their behavior which in turn can reveal important aspects of the Burmese python chemical ecology.

Joy Zhang, Dr. Terrie Rife

**Using Dual Luminescence-Based Reporter Gene Assay: Luciferase and beta-Galactosidase to explore the functions of tau protein**
Alzheimer’s Disease (AD) is defined neurofibrillary tangles made up of hyper-phosphorylated tau protein. Although these proteins are synonymous with having the diseases, the cellular role of these proteins is not entirely understood. Current literature has noted that tau is found in the nucleus and functions to bind DNA. It is hypothesized that the tau proteins may assume the function of transcription factors. Reporter gene assays can be used to better understand the role of tau in gene expression. These assays use synthesized promoters to determine where tau may bind and function. The synthesized promoters direct firefly luciferase expression. In these assays a second viral promoter which directs expression of beta-galactosidase (β-gal) must be used as a normalization control. The Dual-Light Reporter Gene Assay System (Applied Biosystems) allows for the measurement of both luciferase and beta-galactosidase activities on a machine called the H1 Synergy. My research has involved setting up this assay system for our laboratory so that it can be used to further explore the function of tau in the lab.

Reafa Hossain, Stephanie Sharpe, David Duncan, Elizabeth Terry, Fadak Alali, Emily Anderson, Smita Bajain, Julie Bjerring, Jessica Carolina, Rebecca Harkness, Melanie Kusakavitch, Emily Lewis, Ethan Smolley, Peyton Thompson, Angelica Tonder, Robert Walker, Dr. Kevin Caran, Dr. Kyle Seifert

**Antibacterial Properties of Novel Amphiphiles: Exploring Structure-Activity Relationships**
The increased cases of antibiotic resistance have large implication in hospital settings where infections by antibiotic resistant bacteria are harder to treat resulting in longer stays at the hospital. To address this matter, many research groups are searching for an alternative to antibiotics. One option is the development of amphiphiles, some of which have antibacterial properties. Amphiphiles contain a hydrophilic, polar head group, and a hydrophobic, nonpolar tail, which may intercalate into the cell membrane, resulting in cell lysis. Understanding the impact of amphiphile geometry on antibacterial activity allows for the synthesis of potential novel antimicrobial
Novel bipyridine amphiphiles were synthesized and evaluated for antibacterial properties against seven bacterial strains. Amphiphiles contained two pyridinium headgroups attached by a carbon chain of varying linker lengths. A 12-carbon tail was also attached to each pyridinium head. A linker length of 12 carbons had optimum antibacterial activity against each strain. Amphiphiles with longer and shorter linker lengths were less effective. The research and development of novel compounds can be used to reduce spread of nosocomial infections and decrease negative impacts of antibiotic resistance.

**Antimicrobial Activity, Biofilm Disruption Capabilities, and Synergistic Interactions of Novel Amphiphiles**

The increased prevalence of antimicrobial resistant bacteria requires development of new control strategies. Preventative measures such as development of disinfectants and antiseptics with faster killing and antibiofilm capabilities would help limit the spread of resistance and reduce the incidence of hospital acquired infection. Several series of novel amphiphiles, including three bis-cationic, four tris-cationic and three tetra-cationic double tailed amphiphile series, as well as one hexa-cationic, triple tailed amphiphile series were synthesized and tested for antimicrobial properties. These amphiphiles were previously tested for MIC value against several Gram-positive and negative bacterial species. This work expanded on the antimicrobial capabilities of these amphiphiles by determining time to kill a population of cells, biofilm disruption activity, and synergistic interactions with other compounds. Bis-cationic amphiphiles were the fastest at killing *S. aureus* in as low as 1 minute. Oxacinil, a Gram-positive acting antibiotic combined with amphiphiles against *E. coli*, had synergy, with FIC's ranging from 0.5 to 0.19. The highest biofilm disruption activity disrupted 90% of *P. aeruginosa* preformed biofilms. Synergistic combinations of these amphiphiles with oxacinil and other compounds could prove useful in overcoming bacteria antimicrobial resistant mechanisms. These results contribute to the development of cationic amphiphiles with increased biofilm disruption activity and faster kill time, ultimately better disinfectants and antiseptics that will better reduce the spread of antibiotic resistant pathogens especially in a hospital setting.

**Microbial community structure during a Microcystis bloom in Lake Erie**

It has been well recognized that cyanobacteria and co-occurring bacterioplankton can be intimately associated. However, the exact nature of the association is far less understood. For example, the potential impact that these bacterioplankton have in supporting blooms of cyanobacteria remains a critical area of research. To better understand these impacts, we identified and characterized over 100 different bacterial isolates from four stations in the Western Basin of Lake Erie from an August 2017 *Microcystis* bloom. A subset of these isolates will be used in a series of co-culture experiments assessing the nature of the interactions between the cyanobacteria and specific bacterial partners.

**The WASP: An unmanned system to solve the high costs of managing reintroduced populations.**

As a collaborative project team working in JMU’s Unmanned Systems for Biology course, Team Dart is developing a prototype to solve a common issue limiting the scale and success of reintroduction efforts for large endangered mammals. Managing reintroduced populations of the scimitar-horned oryx and other similar “extinct-in-the-wild” animals is both costly and dangerous – requiring frequent use of helicopters
to track and chase down fleeing individuals in need of medical care or GPS tagging/collaring. The Smithsonian Conservation Biology Institute (SCBI) is partnering with us to obtain a solution; one which addresses cost, danger to the researchers involved, and stress induced in the animals. To this end, we are testing a lightweight fixed-wing drone which can safely impact the oryx and deliver an appropriate dose of tranquilizer. If successful, this prototype could make large scale conservation efforts more cost effective for many species.

P15  Maria Sokoloff, Olivia Mitrano, Dr. Patrice Ludwig

Surveying Elk Population in Southwest Virginia Using Unmanned Aerial Vehicles

The Elk/Deer Team is working on a collaborative project between the Virginia Department of Game and Inland Fisheries and JMU’s X Labs to develop an unmanned aerial vehicle system to help track elk populations in southwest Virginia. The VDGIF has implemented an elk restoration program in Buchanan, Dickenson, and Wise counties since 2011 to bring back elk herds extirpated in the 20th century. To appropriately respond to herd stressors and maintain an accurate estimate of the reintroduced population, costly and dangerous helicopter surveys are conducted annually over mountainous terrain. The Elk/Deer Team is proposing a safer, affordable, and more efficient alternative by designing a drone system that will survey transects with a thermal and video camera to identify elk under canopy cover. The proposed drone would fly roughly 10m above the tree line along a transect at a randomized location, and footage can then be reviewed by researchers to determine a specific individual count. The future potential of this project could help establish a new precedent in wildlife surveying as well as ensure the survival of Virginia’s only elk herds to benefit both our ecosystem and local economies.

P16  Jared Martin, Lexi Eastburn, Toma Matveeva, Dr. Kimberly Slekar

Generation of NAC Gene Deletions and their Effects on Stress Response in Baker’s Yeast

Our lab aims to better characterize and understand the role of the Nascent Polypeptide Associated Complex (NAC) using Saccharomyces cerevisiae (baker’s yeast) as a model organism. The NAC is a ribosome associated protein complex with an alpha and beta subunit, thought to serve as a chaperone for newly synthesized proteins. Deletion of either NAC subunit causes embryonic lethality in most organisms including conventional model organisms. However, baker’s yeast is shown to survive deletion of the NAC encoding genes with no significant detrimental phenotypes being reported. S. cerevisiae’s survival with these mutations enables study of the NAC under different stress conditions to improve our understanding of its role in stress response. We have generated deletion mutations in genes encoding both the alpha and beta NAC subunits in baker’s yeast utilizing plasmid cassette methods. Disruption of the NAC in yeast appears to have observable consequences for cellular response to stress, including impacts on lifespan, response to oxidative stress, and sensitivity to heat shock. Further investigation of the yeast NAC mutants will enable us to better understand the role of chaperone proteins in stress response, which has implications for the study of neurodegenerative disease.

P17  Christopher Coggin, Dr. Heather Griscom

The effect of management practices on forest succession after agricultural abandonment on Block Island, Rhode Island

Understanding patterns of forest succession on oceanic islands will help advise management plans within New England nature preserves. This study will take place on Block Island, 13 miles off the coast of Rhode Island. The island has an intensive history of farming practices, which were abandoned in the 1960’s. Since agricultural abandonment, conservation groups with different land management strategies purchased these areas. These management practices include mowing shrubland, planting native and exotic tree species, and protecting natural regeneration from
human disturbance. Currently, there is no data on the effect of these active and passive management practices on forest succession. Woody vegetation will be inventoried along random transects within four sites that are approximately 60 years in age. The four sites are characterized as the following: site 1 was planted with exotic and native tree species and mowed after abandonment; site 2 was planted with exotic and native species but not mowed after abandonment; site 3 was not planted or mowed after abandonment, and site 4 was never converted to agriculture. All trees greater than 5 cm dbh will be measured (dbh) and identified within 10 meters of each transect. All saplings or shrubs (< 5cm dbh, > 1 m in height) will be counted and identified within 5 meters of the transect. Tree seedlings (10 cm to 1 m in height) will be counted and identified within 1 meter of the transect. Soil samples will be taken every 20 meters along the transects to identify the soil series according to the USGS geologic survey. Tree species diversity is predicted to be greatest where native and exotic trees were initially planted and where shrubland has been suppressed with mowing.

P18 Tyler Kovacs, Dr. Heather Griscom

Herpetological assemblages along riparian habitats of the Azuero Peninsula, Panama: An assessment of restoration success

Tropical dry forests are one of the most endangered tropical ecosystems on earth. In Panama, this ecosystem has been almost completely eliminated due to a long history of deforestation for agriculture, timber extraction, and cattle grazing. This land is becoming increasingly abandoned due to changes in socio-economic factors and declining productivity. Reforestation of this land is becoming increasingly important to restore this ecosystem’s health and biodiversity. Reforestation has been increasing within the past 20 years, however most are exotic tree plantations, which may not support native floral and faunal communities. Biodiversity of species that are susceptible to environmental change, like amphibian and reptiles, serve as bioindicators of a healthy ecosystem. Herpetological assemblages will be examined at four different locations to determine if reforestation sites support the recovery of herpetological communities. Two of these sites represent the extreme ends of the disturbance spectrum. The most disturbed site is an active cattle pasture, and the least disturbed site is comprised of an 80+ year old secondary forest. Two additional study sites represent reforested land that has been protected from cattle and fire for 15 years. One is an exotic teak plantation (monoculture) and the other was allowed to regenerate. Habitat and vegetation characteristics will be investigated to determine which factors support the recovery of these communities. The results will identify the amphibian and reptile species present and relative abundances within these communities to be able to compare restoration success. This will help guide future reforestation projects of tropical dry forest ecosystems.

P19 Jonathan Popham, Dr. Joseph Harsh

Sustainability with a Side of Kimchi: The JMU Fueled Project

Reform calls in higher education place an emphasis on engaging learners in student-driven inquiry through real-world problems. At JMU, the Fueled course provides students an opportunity to connect with university and community stakeholders as they undertake sustainability, health, and education-focused projects linked to a locally-sourced campus food truck. To assess the effectiveness and impact of this innovative course, quantitative and qualitative retrospective survey data were collected from student participants (n=22) in Spring 2017. Results identify a range of conferred cognitive (e.g., project design, troubleshooting, conceptual understanding), affective (i.e. confidence), and behavioral (e.g., increased interest in community engagement) outcomes for students. In support of these outcomes, students identified being able to develop a plan to solve problems, understanding the practical knowledge related to their projects (e.g., dealing with “red tape”), and feeling they were more involved with the JMU and Harrisonburg community. These early findings support the positive contributions of the Fueled course on student learning and personal growth.
and helps validate the role of courses such as this at JMU in preparing students for future careers and the challenges of the 21st century.

**P20 Luke Crosmun, Sawyer Kearns, Maddie Smith, Christopher Thrasher, and Dr. Michael Renfroe**

**Effects of Storage Conditions on Saintpaulia rupicola Propagation by Synseeds**

*Saintpaulia rupicola* is a critically endangered species of African violet that is native to Kenya. Loss of habitat and low rates of sexual reproduction in the wild threaten the survival of this species. This species has the potential for commercial development, as with *Saintpaulia ionantha* which is a valuable horticultural species. Therefore, means of rapid and efficient asexual propagation are needed. Leaves of *Saintpaulia rupicola* were isolated, surface-sterilized, sectioned, and placed on a caulogenetic medium with a high cytokinin to auxin ratio to induce adventitious shoot formation. Small shoot tips (approx. 5 mm or less) were isolated from caulogenetic cultures of *Saintpaulia rupicola* and were encapsulated in 2% alginate synseeds. Synseeds were stored for 0, 3 and 6 days in cryovials that contained either water, 1% sucrose or half-strength Hoagland and Arnon nutrient solutions. After the appropriate storage times, synseeds were planted on half-strength Murashige and Skoog basal medium. Synseeds were evaluated for survival, shoot emergence and shoot elongation. This research demonstrates the potential for mass propagation and shipping of propagules for germplasm conservation and commercial development.

**P21 C Emily Williams, Dr. David McLeod, Dr. Louis Temple, Sarah McGrath**

**Culture dependent analysis of Microbiome bacterial growth in Polypedates leucomystax and Polypedates otilophus**

The purpose of this project is to provide an analysis of what bacterial components make up the micro biome of two frogs species native to Borneo. This was achieved through the process of culturing micro biome samples collected during the course of the 2017 study abroad trip to Brunei led by Dr. McLeod. Following the culturing of samples, bacterial colonies were distinguished by morphology and were isolated using isolation steak techniques. DNA was extracted using the DNeasy kit before undergoing PCR and gel electrophoresis to confirm DNA results. These results are to be sent off for sequencing once DNA for each sample is collected.

**P22 C Aaron Moyer, Abby Stapleton, Dr. Wendy Stapleton, Dr. Ray Enke**

**Use of MSRE-PCR for the study of methylation status in the developing chicken retina**

Epigenetic modifications to the genome of chicken embryos determine if retina-specific, cornea-specific, and RPE-specific genes are transcribed during embryonic development. Differential methylation is a commonly used modification to control gene expression and can be observed in certain regulatory regions. Methylation is time and gene specific and, therefore, the comparison of the methylation status of particular genes in the retina and cornea can identify potential proteins involved in retinogenesis. We have designed primers and describe a method that will be used to employ MSRE-PCR to further elucidate proteins involved in the development of the chicken retina.

**P23 C Victor Pou, Destin Witmer, Dr. Wendy Stapleton, Dr. Ray Enke**

**Non-coincident results of phenotypic and molecular identifications of environmental isolates**

As more advanced scientific technologies are developed, existing technologies are often rendered obsolete. However, it is important to evaluate newer technologies against more traditional methods. Polymerase Chain Reaction (PCR) and 16s rDNA gene sequencing has emerged as an effective and efficient method of identifying bacteria. We endeavored to compare its accuracy against traditional phenotypic
methods. Environmental samples were collected from common areas at Eastern Mennonite School and tested using biochemical tests as well as 16s rDNA sequencing. In five of the six strains tested, results for phenotypic and molecular tests were divergent. Attempts at identifying bacteria solely using biochemical testing were unsuccessful, and, for some strains, the gene sequencing results did not yield a conclusive single strain match. Previous reports have shown the high levels of divergence between the phenotypic and molecular identifications. Therefore, the study supports that it remains most effective to combine traditional phenotypic methods with 16s rDNA sequencing for reliable identification of bacterial environmental isolates.

P24 C Gwen Wagner, Dr. Wendy Stapleton, Dr. Ray Enke

**Synthetic peptides as an alternative to traditional antibiotics in treatment of infectious diseases**

Antimicrobial peptides (AMPs) have been explored as a viable alternative to traditional antibiotics with the reported advantage of having a decreased likelihood of resistance selection. We tested the efficacy of antimicrobial peptides of varying origins as an antibiotic agent against environmental isolates and determined the level of resistance. Bacterial resistance to peptides was tested using both the agar diffusion method and peptide infused media. Few environmental isolates presented susceptibility throughout testings. Barcoding was used to identify some of the environmental isolates. A promising trend in the data was that isolates obtained from human skin or environmental structures with high levels of human contact had a higher likelihood of being susceptible.

P25 C Raechel Davis, William Maza, Dr. James Herrick

**Whole-Genome Sequencing of Staphylococcus sciuri Isolated from a Shenandoah Valley Waterway**

The genus *Staphylococcus* is comprised of 41 known species and many strains are often associated with antibiotic-resistant infections. Most of the research surrounding *Staphylococcus* involves medical and agricultural settings due to its known colonization of mammalian skin and mucous membranes. The environmental presence of *Staphylococcus* is often overlooked, especially in freshwaters. Intensive farming within the Shenandoah Valley of Virginia results in contaminated runoff leading to the presence of *Staphylococcus* within these waterways. Eleven strains were detected in sediment samples collected from Muddy Creek, a stream located in Hinton, Virginia. These strains, including *Staphylococcus sciuri* (isolate PS-5), were isolated by the Herrick lab using Mannitol Salt Agar (MSA). Our goal was then to construct and evaluate a draft assembly of the PS-5 genome using sequence data from both the MiniSeq (Illumina, incorporation) and Minlon (Oxford Nanopore Technologies). The MiniSeq provided short read data while the Minlon provided long read data, creating a hybrid assembly that consists of a single contig representative of the entire *S. sciuri* genome as well as a smaller plasmoidal contig. Bioinformatic tools such as Geneious, Galaxy and GalaxyTrakr were then used to further analyze the assembly. Genomic evaluation of *Staphylococcus sciuri* directly reinforced antibiotic resistant phenotypes, as shown by Kirby-Bauer tests, of methicillin and oxacillin resistance conferred by the *meca* gene. Further genomic analysis also revealed additional drug resistances such as tetracycline resistance. The discovery of the antibiotic resistance genes within the *Staphylococcus sciuri* genome is particularly important because *S. sciuri* is one of the most primitive *Staphylococcus* species; thus giving possible insight into the developing virulence of other *Staphylococcus* species, such as *Staphylococcus aureus*.

P26 C Alexis Schneider, Sophie Jurgensen, Charles Holmes, James Herrick

**Using Short Read DNA Sequence Data to Generate Draft Genome Assemblies and to Serotype Strains of Salmonella enterica Isolated from Stream Sediment**
Salmonella enterica is responsible for 1.2 million incidences of disease and 450 deaths annually in the U.S. There are approximately 2500 different serotypes, a classification of Salmonella based on cell surface antigens, of S. enterica. It is important to know the distribution of S. enterica serotypes for epidemiological tracking during outbreaks. However, little is known of their occurrence and distribution in environmental and agricultural settings. Thirty-nine strains of S. enterica were isolated from stream sediment and poultry litter by members of the Herrick lab from October 2016 through January 2018 and were sequenced by the Virginia Department of Consolidated Laboratory Services. Raw reads of seven of these isolates were filtered using Trimmomatic to eliminate poor quality reads. Both trimmed and untrimmed reads were assembled using SPAdes on GalaxyTrakr, a web-based platform for the analysis of genomic data for foodborne pathogens. The quality of the sequence assemblies was determined by running QUAST on each sequence and comparing it to a set of standards established by the CDC. The serotype of each sample was determined using Seqsero_v2 in GalaxyTrakr. Three of the isolates serotypes were found to be Cerro, three were Braenderup, one was Anatum, and one was Montevideo. Assembling and serotyping the genomes of these isolates is important because it gives a better understanding of the S. enterica in this region and its possible impact on human health.

Bacterial Discovery, a New Course on the Isolation and Genomics of Environmental Salmonella and its Relatives in the Shenandoah Valley

Bacterial Discovery (BIO 346) is a new laboratory course within the Microbiology concentration. It integrates methods developed in the Herrick research laboratory to isolate and characterize novel environmental Salmonella and other members of the Enterobacteriaceae using laboratory and bioinformatics techniques. BIO 346 is a ‘CURE’, or ‘Course-Based Undergraduate Research Experience’, in which students engage in authentic, potentially publishable research. The course is being piloted this semester with Dr. Herrick as the instructor and Sophie Jurgensen serving as teaching assistant. It is also the subject of Ms. Jurgensen’s honors thesis. The seventeen students in the course sampled local stream sediments and poultry litter, enriched, isolated, and characterized their isolates using standard microbiological techniques, PCR, and antibiotic resistance phenotyping. Salmonella and E. coli isolates were sequenced by the Virginia state public health laboratory (DCLS) and the students are currently carrying out bioinformatics analyses of these raw sequences. Six posters on their preliminary results are presented here.

Implementation of a Device for Photochemically Controlled Tissue Engineering

A central goal of tissue engineering is growth of functional cellular assemblies in vitro to provide authentic models of cellular physiology and replacements for human tissue. This controlled growth of cellular assemblies requires automation of tissue culture processes that direct cellular behaviors in space and time. We are developing an approach to tissue engineering that uses photochemical generation of molecular signals to spatially and temporally control cell proliferation, differentiation, and migration. Toward that end, we are deploying and testing a device to automate delivery of engineered chemical factors to mammalian cells and spatially patterned illumination to activate the factors. The device is designed to maintain stable culture temperature, deliver, at timed intervals, growth media of different compositions to the culture, illuminate the culture for programmable intervals through transparent windows in a custom-built culture chamber, and enable real-time microscopic visualization of the culture to monitor growth and behavior of the cells. These functions will be coordinated with custom software. We have assembled the fluid delivery system, using a peristaltic pump to move media from reservoir bottles to the culture chamber. We have incorporated thermocouples into the culture environment and used them to monitor the temperature of the system. The output temperature measurement will be used to thermostatically regulate resistive heaters to maintain
the appropriate temperature for cell culture. We have also implemented a microscope, integrated with the system to allow visualization of cells on the culture stage. As we implement the full system, we are initially using H1299 human lung tumor cells as a test culture. We aim to be able to maintain a continuous culture of these cells in the automated device.

P34 Jack Doss, Claire Naylor, Matthew Harris

**Preliminary Comparisons of Flying Insects at Restored and Denuded Riparian Zones within the Shenandoah Valley**

Biodiversity among insect populations varies with land use. This project aims to compare the abundance and diversity of flying insects between two different types of land use areas. Insects were collected from May 21 to August 20 using malaise style insect traps on six different sites. Three pairs of sites were selected consisting of a riparian buffer planted through the Conservation Reserve Enhancement Program (CREP) and a traditional cattle pasture which acted as a control site. Sites were paired based on the size and general health of the streams within them and the surrounding landscapes of these sites. While data is still being collected and analyzed, preliminary abundance and diversity of flying insects has been quantified. Increases in abundance and diversity of flying insect populations can attract more and varied types of predators, such as bats, increasing the overall biodiversity of the area.

P35 Orquidea Aleagha, Christina Modolo, Nicole Hoguet, Dr. Christopher Rose

*Xenopus laevis* tadpole unique tail function and development over time

*Xenopus laevis* tadpoles are filter feeders, which means that they feed by hovering in the water column and pumping water through their mouth and gill chamber. This requires that they use their lungs throughout tadpole development, and this makes their bodies positively buoyant. We observed that the tails of *Xenopus* tadpoles are often dorsally curved which may be to create neutral buoyancy for remaining in the water column. A dorsally curving tail is rare in fish as vertical flexibility of the axial skeleton does not evolve until primitive mammals. We also observed that *Xenopus* tadpole tails grow to become whip-like in both shape and the lateral undulations of its movement. This study uses morphometrics, developmental morphology and video recording to look at the ontogeny of tail shape, tail anatomy and tail movement in both vertical and lateral directions. This study also aims to do comparative studies of tail development and shape to determine whether the whip-like shape and behavior of *Xenopus* tails and their ability is curve dorsally is unique to *Xenopus*, or specific to filter feeding forms.

P36 Bethany Esser, Shelby Pedigo, Kathryn Mahach, Dr. Bisi Velayudhan

**Investigating the effect of sodium benzoate in Paneth Cell granular density in Crypt Units of the Small Intestinal Tract**

Various health concerns and behavioral changes have been reported recently which are attributed to consumption of foods containing preservatives and additives. Sodium benzoate (SB) is a commonly used food preservative in acidic foods to prevent microbial growth. Our study investigates the effects of SB on the gut mucosal immunity by assessing the Paneth cell granular intensity. Adult C57BL/6 mice were randomly assigned to two groups (n=9 per group). The treatment group received standard rodent chow and drinking water mixed with 1% SB. Control group received normal food and water. All animals received food and water ad libitum for the duration of 4 weeks and they were monitored for weight, activity, and food/drink intake. Animals were euthanized and samples were collected for histopathological analysis. Ileum samples were fixed with formaldehyde and tissues were processed for hematoxylin and eosin (H&E) staining. Paneth cell granular intensity was graded on a scale from 1-4 by a double blinded analysis. There was significant reduction in Paneth cell score in the SB treated group compared to the control (p<0.05) indicating a decrease in the secretion of antimicrobial peptides from Paneth cells. Our data suggests that SB intake can possibly affect the mucosal immunity of the gut.
Characterization of isolates with contradictory phenotypic tests from turkeys infected with *Bordetellosis*

*Bordetellosis* is a disease in turkeys commonly caused by the Gram negative bacterium, *Bordetella avium*. The closely related species, *B. hinzii*, is known to colonize turkeys but was not thought to cause disease. However, over the past few years, *B. hinzii* was also isolated from turkeys diagnosed with *Bordetellosis*. The presumed identification of isolates was done through standard identification tests, including hemagglutination, *B. avium* specific PCR, 16s rDNA PCR, carbohydrate utilization tests, and sequencing of a few strains. Recently, identification tests have yielded contradictory results using the standard tests. These tests have, in the past, clearly differentiated between *B. avium* and *B. hinzii*. Out of ~150 isolates, 10 yielded contradictory results. We are investigating these ambiguous strains to determine whether they are *B. avium* or *B. hinzii* that have small differences that affect the typical genotypes and phenotypes or whether they represent a novel species or strain. It has also never been determined if *B. avium* and *B. hinzii* are present together in turkeys diagnosed with *Bordetellosis*. To test this, whole samples were obtained and tested through replicate plating on Citrate and MacConkey media. From these findings, we know that *Bordetella* species infecting turkeys and causing disease are evolving, and further testing is ongoing to reveal what is causing the apparent genotype and phenotype. In spite of antibiotics and vaccines, *Bordetellosis* continues to cause financial losses in the poultry industry, so our work with detailed analysis of these isolates could be useful information in dealing with the problems.

**Age-Related Macular Degeneration (AMD): genotypic study of the retinal disease and its associated genes with common and rare variants**

Age-related macular degeneration (AMD) is a progressive ocular disease that affects the central retina, serving as a predominant cause in blindness for elder populations and industrialized countries. AMD is detrimental to retinal pigment epithelial (RPE) cells and photoreceptors, inducing central vision loss and legal blindness. Gaining further knowledge of rare variants may support the relationship of causal genes within the genetic loci and AMD diagnosis. Following DNA extractions of 15 donor human eyes diagnosed with and without AMD, polymerase chain reactions (PCR) and restriction enzyme digestions are being completed to denote genetic variation and correlation in patients. The following variants are being studied as a result of high genetic priority with genes CFH, CFI, TIMP3, and SCLC16A8: rs10922109, rs10033900, rs429358, rs5754227, rs8135665, and rs72802342. Although few genome-wide studies have been completed to highlight the effects of rare and common variants within AMD populations, further research must be completed as risks for developing the disease has increased over the past decade. Lack of effective therapy on the market has yielded deeper and critical insight to AMD-associated genes.

**Comparing clinical and molecular diagnosis of age-related macular degeneration (AMD) in post-mortem human donor eyes**

In the United States, age-related macular degeneration (AMD) is the leading cause of vision loss, particularly among the aging population. It is estimated that by the year 2050, the number of people with AMD is expected to be around 5.4 million, the majority of who will go undiagnosed. Research is currently being conducted to learn more about the disease but due to the complexity of AMD, there are limited diagnostic and therapeutic treatment plans. RNA-sequencing (RNA-seq) technology allows researchers to view and analyze the transcriptomes of different individuals. With the use of RNA-seq transcriptome analysis, we analyzed the mRNA from post mortem retinal tissue of individuals who are diagnosed with AMD during their lifetime as well
as those who are not. Our preliminary results show that due to complexity of the disease, diagnosing AMD at the clinical and phenotypic level is challenging. We are currently analyzing differentially expressed genes (DEGs) from our tissue samples and comparing the data with other AMD gene expression literature in an attempt to use molecular markers to diagnose AMD in tandem with clinical phenotypes.

P40 Penelope-Marie B. Clanor, Dr. Ray Enke
**DNA Analysis of Patient and Family to Determine Mutation in hPAX6 Gene**
Bilateral optic nerve aplasia is a rare developmental anomaly that can be characterized by an absence of an optic nerve, midline brain defects, and cerebral, nervous system, and pituitary abnormalities. A family from the Rockingham County area has an affected daughter with optic nerve aplasia, and an unaffected mother, father, and daughter. Because the PAX6 gene codes for a transcription factor that turns on other genes for eye, brain, spinal cord, and pancreas development, with known clinical mutations at various exons, the family's genes are to be analyzed to find a possible mutation to explain the daughter's optic nerve aplasia. To extract DNA, hair from each family member was obtained and DNA was extracted using DNA alkaline lysis. Then, the DNA was amplified using Polymerase Chain Reaction, which can be sent for sequencing. Once the DNA is obtained, the sequence can be trimmed and analyzed using DNA Subway and ApE-A Plasmid Editor. A mutation in exon 7, exon 9, or exon 11, is expected in the affected daughter but not in the other unaffected family members because of the known clinical mutations. The DNA sequence can help determine the mode of inheritance of the mutation. If no mutation is found, then the other exons can be sequenced to search for a mutation to explain the cause of the optic nerve aplasia.

P41 Nathaniel Lucas, Callum Morton, Colin Haigh, Dr. Roshna Wunderlich, Dr. Klebert Feitosa
**Measuring Intrinsic Foot Muscle Strength and Activation Using Novel Methodology and Electromyography Measurements**
The intrinsic foot muscles (IFM), twenty muscles that originate and insert within the foot, can be susceptible to atrophy in conditions such as diabetic neuropathy. This can lead to foot deformities, plantar fasciitis, ulceration, and falls in affected populations. The IFM are involved in flexion, extension, abduction, and adduction of the toes. They support the longitudinal arch, assist in balance, and are active during walking, although the extent of their function is largely unknown. Traditional tests used to quantify IFM strength rely primarily on toe flexion measurements, but toe abduction/adduction are important actions of these muscles that currently cannot be measured. The goal of this study is to analyze IFM activation and strength during traditional tests and to create a novel force sensor test to measure abduction and adduction muscle strength. We measured IFM activation using surface electromyography (EMG) and strength using traditional tests (plantar pressure mat, balance, paper grip) and our new custom abduction/adduction force sensor test. Our preliminary data suggests that while some traditional tests activate and measure strength in muscles that exhibit a strong flexion component, our new sensor is more robust for measuring strength in the IFM that have a primarily abduction/adduction component. Ultimately we aim to develop a reliable mechanism to quantify IFM strength in all twenty muscles and develop techniques for strengthening these muscles that can enhance arch support, balance, and potentially athletic performance.

P42 Amanda Leonard, Brooke Thompson, Dr. Heather Griscom
**Panax quinquefolium: What environmental factors affect American ginseng growth?**
*Panax quinquefolium,* commonly known as American Ginseng, is a shade tolerant, herbaceous non-timber forest product found in the deciduous forests of the eastern United States. American ginseng's native range includes most of the eastern and central United States, however wild ginseng is becoming increasingly rare due to overharvesting, loss of habitat, poaching, and wildlife browsing. This study analyzed
experimental field trials to determine the optimal habitat for American ginseng growth. Soil type and aspects were used in a 3 x 2 factorial design. Therefore it was hypothesized that there would be significant differences in ginseng growth (height, leaf area, reproduction, survival) due to aspect and soil type. It was predicted that leaf area, height, berries, and survival of three-year-old plants would be significantly greater in limed loam soil on north-facing slopes. The soil used for the study was collected from three forest sites: cobbly, sandy loam, fertile loam, and fertile loam that was limed. In the fall of 2014, 49 seeds were distributed amongst seven subplots in raised beds at six different sites. All beds were placed in gaps with approximately 30% light. Ginseng plants were significantly taller in limed loam soils (p<0.001) on northern aspects (p=0.006). They also had greater leaf area on limed loam soils (p<0.001). Survival was not affected by either of these factors. An understanding of how habitat conditions affect ginseng’s growth will aid in ginseng reintroduction in national forests and private lands.

Zoe Bergman, Cassie Stark, Dr. Heather Griscom
Implications for Successful Reintroduction of the Restoration Chestnut 1.0 to Southern Appalachian Cove Forests

The American Chestnut (Castanea dentata) was once a dominant hardwood species on the east coast of the United States. In the last 100 years an invasive parasitic fungus known as blight (Cryphonectria parasitica) decimated the chestnut population. Although the scientific community is close to creating a blight resistant American Chestnut hybrid, the successful reintroduction of the chestnut depends on the ecological niche it occupies in the modern temperate forest. This study is an ongoing experiment involving Restoration Chestnut 1.0 saplings on eight plots in West Virginia. The data represents year three of an ongoing five-year study. The experiment had three variables; small (40% light) and large (60% light) gaps, landscape fabric (with and without), and application of 12” tree shelters (with and without). Gap size accounted for varying light level percentage, landscape allowed for competition variance, and tree shelters prevented girdling by rodents. On every plot 7’ deer fences were erected. It was predicted that chestnut seedlings would grow and survive significantly better in small gaps, with both landscape fabric and tree shelter treatment. Height and diameter were significantly greater in small gaps (p-value <0.03, p-value <0.001). Diameter was also significantly greater with landscape fabric (p-value <0.005). An interaction effect showed that chestnuts planted in large gaps performed just as well as in small gaps as long as there was landscape fabric. Survival was significantly greater in small gaps (78.5%) than in large (53.0%) (p-value <0.003). In conclusion, we recommend planting chestnuts in small gaps in southern Appalachian cove forests given greater growth and survival and less initial investment.

Rhiannon English, Breckin Walsh, Brian Anderson, Dr. Bruce Wiggins
A Comparative Stream Water Quality Survey of Smith Creek Restoration Using Benthic Macroinvertebrates

The Shenandoah Valley encompasses some of the highest agricultural producing regions in Virginia, many of which are large contributors to non-point source pollution. To help reduce this, the Conservation Reserve Enhancement Program (CREP) aids participating landowners in fencing out cattle and planting saplings to restore riparian buffers. The 2017 study was undertaken to determine how temporal factors impact the effectiveness of riparian buffer restoration by measuring overall water quality through macroinvertebrate biotic indices (HBI, VA-SCI, and Shannon Diversity). We hypothesized that greater lengths of implementation time will have a positive effect on the water quality of the streams. An increase in sensitive species is predicted, resulting in a lower HBI index, increase in VA-SCI, and increase in Shannon Diversity Index. An independent t-test was conducted to compare the metrics of Shannon, HBI, and VA-SCI. HBI was found to be significant in the restored compared to the upstream (3.8 and 4.418 respectively (p-value = 0.009)), but VA-SCI and Shannon were not different. A multi-year linear regression test was performed to determine the effect of time on all
variables. The predicted trends were in the appropriate directions, but not significant. Though no obvious trend was apparent in a multi-year regression, a paired t-test comparing the restored and upstream averages of the VA-SCI was found to be significantly improved (60.73 and 55.42 respectively (p-value= 0.031)).

P45  Aya Andos, Ana Clem, Lexy Foor, Catherine Shola, Dr. Janet Daniel
**Investigating Phenotypic Differences Between the STP-1 k/o and WT Arabidopsis thaliana in Response to Various Environmental Stressors**
Sugar transport protein-1 (STP-1) is an H+/monosaccharide co-transporter in model organism Arabidopsis thaliana. We are investigating this protein because its impacts on the growth and function of the plant are not well known. For a better understanding of how STP-1 contributes to this plant, we are growing wild type (WT) and STP-1 knock-out (k/o) plants on agar plates to measure their responses to different environmental stressors. To evaluate the salt resistance of these plants, the WT and STP-1 k/o seeds were plated on 0mM/300mM split plates, with seeds placed in a line at varying distances above the split on the 0mM NaCl concentration. Root length has shown, on average, a longer tendency in the STP-1 k/o than WT under exposure to higher NaCl conditions. In addition to root length variation, a qualitative halotropic response has been observed in both WT and STP-1 where roots may angle left to avoid the higher NaCl environment. Overall, our studies suggest that the STP-1 k/o plant may have an alternative phenotype of higher salt stress resistance. Our preliminary observations of halotropic responses may suggest an alternate approach to plating should be taken to account for gravity pulling the roots straight down into the higher salt concentration. To properly evaluate the halotropic response of WT and STP-1 roots, further experimentation will consider plating seeds on a slant to prevent the gravitropic response of the plants from serving as a confounding variable.

P46  Alexander Zeher, Dr. Corey Cleland
**Antennae pointing and the escape response in the cricket, Acheta domesticus**
The escape response varies across animals. In the cricket, Acheta domesticus, the escape response is mostly directed by cercal detection of incoming wind stimuli, though previous experiments showed that vision and other sensory modalities may play a role. It is known that the angle of incoming stimuli affects the angle and magnitude of the escape response. The escape response is often accompanied by the pointing of the antennae toward an incoming object. To date, little research has been done on antennae pointing and its relationship to escape in crickets. The goal of this research focuses on determining the primary sensory modality responsible for antennae pointing in Acheta domesticus. We hypothesize that the presence of antennae pointing in crickets will be most affected by vision rather than cercal detection. Looming stimuli were presented by a 3” black polyurethane projected toward the cricket from eight circumferential directions. The cricket was constrained in a cylinder and placed into a rotatable arena of white canvas and roof flashing. Escape responses were recorded using a high-speed camera (650fps). Video was manually tracked in software. Preliminary findings showed stimuli presented from the posterior end of the cricket often resulted in running or jumping with little movement of the antennae. Anterior stimuli resulted in a turn and run, with more frequent antennae pointing. We noticed that when antennae pointing occurred there was an attempt by the cricket to maintain the pointing throughout the escape response. Further results may identify the primary sensorimotor factors responsible for antennae pointing.

P47  Victoria Gaudin, Dr. Corey Cleland
**Escape responses from looming stimuli in Phidippus audax**
Animals use withdrawal and escape responses to retreat from threats. Looming stimuli, which represents the approach of a predator, evokes an escape response in jumping spiders that is mediated primarily by visual cues. The majority of studies have focused on the spider jumping in response to prey; only limited studies have explored
the escape response from a predator. The goal of our research was to determine the strategy used by jumping spiders, *Phidippus audax*, to escape from looming stimuli. Looming stimuli was created by using a controlled projection of a 3” black polyurethane ball, 1 m/s at a 45 degrees angle, against a white background, towards the spider, without actually hitting the spider. The direction of “attack” was varied in 45-degree increments, totaling in 8 angles, around the spider. The resulting response was captured with high speed video (300 fps) and automated software particle was used to quantify the location and orientation of the spider throughout the escape response. Looming stimuli consistently evoked a side-step, or turn followed by walking. Our results (n=9) showed that turning response angle depended significantly on stimulus direction. Preliminary findings (n=9 spiders) showed that the spiders uniformly escaped from the looming stimulus. In most (~80%) of the trials the spiders translated without turning and in ~20% of the trials both turned and translated. Typically, spiders showed multiple temporal components to their response. Surprising, 3 spiders jumped away from the looming stimulus, a response previously reported only associated with prey capture. These preliminary results suggest jumping spiders may use novel strategies to escape from looming stimuli.

**P48 Seerat Mavi, Mary Pegelow, Michael Wentzel, Dr. Corey Cleland**

**The effect of noxious stimulation of the nociceptive tail and foot withdrawal response of unrestrained rats**

The nociceptive withdrawal response (NWR) is a protective movement of a body part away from a noxious stimulus. Research in restrained rats, either in boxes or tubes, has shown that when the tail receives a heat stimulus, the rats move their tails away from the stimulus. However, no research has been conducted in rats to evaluate the movement of unrestrained rats when provided similar type of stimulus. The specific aim is to determine whether an unrestrained rat will move its body when provided a tail stimulus to its tail or feet. Rats were anesthetized to mark five points on the body with one at the urethra, another under the chin, a third between the shoulder blades, fourth at the hollow opening of the rib cage, and the last one between the rib cage and the urethra. There were 12 evenly spaced points marked on the ventral side of the tail, along with five points on the lateral surface which were used as the locations for tail stimulation. Each of the individual paws were marked with three points on the hind feet and one centralized point on the front paws. The animal was placed on a 3”x3” glass table with two LED lights and a standard camera (60 fps) placed underneath. A heat stimulus was randomly delivered to either one of the five points on the lateral side of the tail for tail stimulation or one of the centralized points on the paws using an infrared laser (980nm) with a 2 to 5 min interval before the next stimulus was delivered. A total of 60 trials were conducted for each stimulation type (tail or foot) with 30 trials taking place on a single day. Movements recorded using the video camera were analyzed and tracked in software. In addition to tail or foot withdrawal, we observed that concomitant body movement always occurred. The direction of body movement consisted of both forward translation and rotation away from the stimulus. The timing of body movement during tail stimulation, based on initial foot movement, lagged tail movement by only 167 ms [median], however, the timing was not dependent on the stimulus location (p=0.37). The initial foot movement did depend on tail stimulus location; when the base of the tail was stimulated, the back left foot moved first, but when the tip was stimulated the front right paw moved first. These results indicate that while the tail and foot movement occurs similarly to previous studies, body movement also plays an integral part in their nociceptive withdrawal responses.

**P49 Rachel Boyce, Sarah Coleman, Julia Cumins, Emily Miller, Thomas O’Neil, John Nguyen, Jonathan Popham, Dr. Joseph Harsh**

**It’s now in their DNA: The Effect of the DNA Barcoding Research Experience on Introductory Students’ Program and Career Intentions**
To help offset shortages in the science and technology workforce, national reform documents have called for all undergraduates to participate in an authentic research experience within their first two years of college. For this, course-based undergraduate research experiences (CUREs) have become an increasing popular feature of undergraduate science curriculum as they provide students a window to research practices and careers. While existing research has championed the positive impact of CUREs on STEM pursuits, few studies have examined large-scale and multi-semester CUREs for introductory science students. This ongoing study examines the effect of the new two-semester DNA Barcoding laboratory courses (140L/150L) at James Madison University on first-year biology students’ future intentions. Quantitative and qualitative post-survey data over three terms were analyzed to assess the influence of course participation on student interest in pursuing elective coursework and research opportunities, major, postgraduate plans, and how the lab courses influenced their plans. Early findings suggest that first-year students’ career aspirations remain largely unchanged over the DNA barcoding labs; however, participants regularly identified the experience sustained or clarified existing interests with a smaller subset indicating that course participation resulted in more substantial career changes. After taking the class, students described how the experience increased their understanding and interest in pursuing future research opportunities and elective coursework in the areas of ecology, bioinformatics, and molecular biology. These initial results provide insight to how the new DNA Barcoding CURE on students’ influence future intentions and supports calls for early research experiences.

Assessing the effectiveness and impact of a large-scale two-semester course based undergraduate research experience focused on DNA-Barcoding for introductory biology students

National calls in science, technology, engineering, and mathematics (STEM) education have emphasized the wide-scale engagement of all students in early research experiences in promotion of a workforce and citizenry to attend to the challenges of the 21st century (e.g., PCAST, 2012). Beginning in Fall 2016, the Department of Biology at James Madison University, a public Master’s grant institution, implemented a two-semester DNA-barcoding focused course-based research experience (CURE) for our large enrollment introductory biology labs. In the first semester, students learn techniques in molecular biology, ecology, and bioinformatics to document campus diversity. During the second semester, students develop and conduct independent research projects using their previously learned skills. To assess the efficacy and impact of the experience, this project analyzed survey data collected - using self-ratings and open-response questions - from students (n=1348, 69% female) near the beginning and end of each course. Overall, students reported shifts in their ability to practice science, affect (e.g., self-confidence), and interest in pursuing later STEM coursework/careers as a result of participation. These outcomes were attributed by students to the authentic nature of the experience marked by high project ownership, the iterative practice of scientific techniques, independence in the research space, collaboration, and the opportunity to learn from failure. Results from this study highlight the contributions of this innovative CURE to student development and will inform future refinements to maximize learning. More broadly this work may be of concern to faculty at other institutions interested in adopting a comparable experience for their students.

Assessment of Interleukin-3 production by Transgenic Fluorescent Reporter Mice Infected with the Nematode Nippostrongylus brasiliensis

Interleukin-3 (IL-3) is a hematopoietic growth factor and immunoregulatory cytokine that is secreted by various immune cells in response to infection with certain pathogens. However, the in vivo cellular sources and the kinetics of IL-3 production
during infection is unknown. To address these questions, we used novel transgenic mice that contain an endogenous fluorescent reporter gene (ZsGreen) for IL-3 expressing cells. In these mice, transcription of the IL-3 gene results in the production of separate IL-3 and fluorescent ZsGreen protein products. To determine if the reporter mice are accurately marking cells with the capacity to secrete IL-3, we activated IL-3-producing T cells in vivo by injection of mice with anti-CD3 antibodies or by infection with the parasite Nippostrongylus brasiliensis (Nb). Spleen, lymph node, and/or lung cells were then harvested and the expression of ZsGreen by CD4 T cells assessed by flow cytometry. Results indicate that anti-CD3 antibody stimulation induces the production of ZsGreen by a small percentage of CD4 T cells. Likewise, primary infection of reporter mice with Nb induced small increases in the numbers of ZsGreen positive T cells, with higher percentages present following secondary Nb infection. These results suggest that the transgenic reporter mouse represents a reliable tool that can be used for future experiments to assess in vivo IL-3 production in various disease models.

Danielle Orlandi, Mark McGowan, Dr. Anthony Tongen, Dr. Roshna Wunderlich

**Effect of Enclosure Type on Locomotion and Spatial Use in Captive Sifakas (Propithecus coquereli)**

The assessment of physical activity in captive primates is important to health and husbandry decisions and to the interpretation of experimental studies. The purpose of this experiment was to assess differences in locomotor activity, energy expenditure, and spatial use during locomotion in sifakas in caged enclosures (CGEs) and natural habitat enclosures (NHEs) at the Duke Lemur Center (DLC). Using a datalogger inertial sensor attached to 7 sifakas, we collected three-dimensional acceleration and barometric pressure (related to height) for a total of 113 hours in CGEs (528.5-843.5 ft^2 x 10 ft), and 195 hours in NHEs (1.5-14 acres) at the DLC. We used continuous focal animal sampling to ground-truth the acceleration data. We compared the number of leaps, ODBA, activity and rest time, and barometric pressure between enclosure types. Sifakas in NHEs did not differ in uses of low, middle, and high spaces of their environment (p = 0.25, 0.28, and 0.37, respectively) but did leap less (p = 0.003), were less active (p = 0.02), rested more (p = 0.02), and exhibited lower ODBA (p = 0.007) than those in CGEs. Our results demonstrate that activity levels can be higher in an extensive CGE than in an NHE. Spatial usage in captive sifakas is likely influenced more by location of resources than cage size. We also demonstrate that inertial sensors provide a useful tool for quantifying locomotor behavior, spatial usage, and energy expenditure in captive primates. The assessment of activity in captive environments is essential to animal health, animal husbandry decisions, and the interpretation of experimental studies performed in these environments. We have presented a tool for assessing locomotor behavior, energy expenditure, and spatial use that can be used to quantify these aspects of physical activity in both captive and wild primates.

Lucas Manweiler, Danielle Orlandi, Dr. Anthony Tongen, Dr. Roshna Wunderlich

**Using tri-axial accelerometry to quantify locomotor behavior in Propithecus coquereli and Lemur catta**

The assessment of primate activity in captivity is important for physical health and husbandry decisions. The purpose of our research is to investigate activity and locomotor behavior of two lemur species, Propithecus coquereli and Lemur catta, in different captive environments. P. coquereli is a vertical clinger and leaper, while L. catta uses quadrupedal walking, running, and leaping. We collected tri-axial acceleration and behavioral data on 7 P. coquereli and 1 L. catta who used both caged enclosures (CGE) and natural habitat enclosures (NHE) at the Duke Lemur Center for a total of 113 hours in CGE and 195 hours in NHE for P. coquereli and 23 hours in CGE for L. catta. We quantified how well we could identify leaps and calculated leap counts and overall dynamic body acceleration in P. coquereli. We were able to identify leaps in P. coquereli with 92% accuracy and determined that they leaped less (p = 0.003) and were less active (p = 0.02) in the NHEs than in the CGEs. For L. catta we collected video data from
which we were able to synchronize behavior and accelerations. Our preliminary results suggest we can identify specific 3D acceleration patterns indicative of leaping, walking, and running in *L. catta*. Our results demonstrate the feasibility of using triaxial accelerometry on captive primates to assess the impact of cage setting on locomotor behavior and energy expenditure. These data can ultimately inform animal husbandry decisions that influence captive animal health and experimental analyses that seek to simulate natural behavior.

**P54** Kinsey Miller, Sachin Sundar, Dr. Patrice Ludwig

**Using unmanned aerial vehicles to identify invasive plants**

Invasive species can negatively impact the biodiversity of an ecosystem due to their lack of natural deterrents yet current tracking methods for invasive plants is hindered by extensive amounts of time, labor and cost. Team Invasive Plants, (composed of two biology students, two design majors and a physics major) has partnered with Blue Ridge Prisms as part of the Unmanned Systems for Biology course to work together on this issue. We are currently using multispectral imaging and analysis techniques to differentiate between native and invasive plants by drone. These aerial photos will be digitally stitched together to create a spectral data map that allows landowners to see where specific plant species are located on their property. Team Invasive Plant’s goal is to identify a consistent spectral signature for Tree of Heaven in order to identify the species using multispectral imaging. This would allow ecologists to take more efficient terrestrial surveys so that we can better control and eventually eliminate dangerous species.

**P55** Hannah Bradley, Dr. Patrice Ludwig

**Geospatial analysis of Eastern Oyster habitat in the Chesapeake Bay**

The number of *Crassostrea virginica* in the Chesapeake Bay is only 1% of historic levels, relative to a peak in landings in 1884 of 600,000 metric tons, despite being considered a resilient species. Causes of the decline include overharvesting, disease, and habitat loss, and the most essential key to recovering the population is coordinated habitat restoration. The first goal of this study was to determine the water quality parameters necessary for oyster population restoration and to locate where those conditions exist concurrently. To identify these areas that are suitable for restoration, a habitat analysis was performed using GIS data of water quality parameters in the bay consisting of temperature, salinity, dissolved oxygen, pH, and bathymetry. Data for the parameters were obtained from monitoring stations throughout the bay and were interpolated using inverse distance weighting to create continuous rasters of seasonal averages for each parameter. Rasters were then analyzed using geospatial processing to determine the areas that contain the most favorable conditions for oyster growth at both larval and adult life stages. The second goal of this study was to determine the potential changes to suitable oyster habitat area following water temperature increases of 2, 4, and 6 degrees potentially resulting from climate change conditions. Results showed a decrease in total area of suitable habitat for larvae when compared to adult habitat. Analysis of changes to the suitable habitat for both larval and adult oysters showed a decrease in the total area, correlating with increasing water temperature models.

**P56** Madison Frongello, Bismah Khan, Dr. Marquis Walker

**Characterizing the pathophysiology of Drosophila retinal degeneration mutant, rdgI**

The *Drosophila melanogaster* visual system is a well-established model for the study of light-dependent visual signaling. Our laboratory is interested in identifying novel factors that are essential in photoreceptor function and homeostasis. Here we are studying a *Drosophila* mutant called Retinal degeneration I (rdgI). The rdgI mutant line was first isolated in a large-scale mutagenesis screen to identify essential eye-specific genes. As the name indicates, these mutants display severe retinal degeneration in adult flies. Our work shows that rdgI adult flies have a severe
reduction in rhodopsin (Rh1) expression which precedes photoreceptor degeneration. Surprisingly, despite the loss of Rh1 expression in rdgI flies, the overall photoreceptor morphology still remains similar to the wild-type. In addition, the genetic locus of the rdgI mutation is unknown. To identify this site, we use deletion mapping and sequence analysis to determine the gene disrupted by the rdgI mutation. Through this study, we will identify the gene disrupted in rdgI mutant flies and uncover its essential role in rhodopsin expression and photoreceptor function.

Alexa Cornwell, Katie Doherty, Elizabeth Staskal, Paulina Bauer, Saidah Lerman, Dr. Terrie Rife

Understanding the Impact of Tau Proteins in Alzheimer’s via CRISPR/Cas9

Tau (tubulin associated units) proteins provide structural stability and flexibility to microtubules, a structural component of neurons that aids in cell division and axonal transport. In neurons of those with Alzheimer’s, it has been observed that tau proteins become hyperphosphorylated and aggregate into neurofibrillary tangles. Because neurofibrillary tangles are cytoplasmic, tau’s role has been studied extensively in the cytoplasm, however tau is also present in the nucleus. In the nucleus tau binds DNA and has been found to protect DNA from double strand break repair and tau protein also has been suggested to be a transcription factor. The protein is encoded by the microtubule associated protein tau (MAPT) gene. The gene is alternatively spliced and in neurons gives six major isoforms These are known as 0N3R, 0N4R, 1N3R, 1N4R, 2N3R, and 2N4R. Tau also has an additional non-neuronal isoform called Big Tau. The 1N4R form seems to predominate in the nucleus of mouse neurons. In our research we are using CRISPR/CAS9 technology to make various tau knockouts in human Sk-N-MC and SH-SY-5Y cells to better understand the role of tau and its isoforms in the nucleus. In this poster we show our progress toward making the CRISPR/CAS9 knockouts of tau. We will use the models to test several hypotheses including that the 4R and 2N containing tau isoforms may be able to bind DNA better than 3R and 1N tau isoforms respectively and that tau may be acting as a transcription factor to regulate the expression of genes with purine/pyrimidine repeats.

Stephanie Sharpes, Elizabeth Rogers, Refa Hossain, Elizabeth Terry, Smita Bajain, Julie Bjerring, Jessica Carolino, Rebecca Harkness, Melanie Kusakavitch, Ethan Smolley, Peyton Thompson, Angelica Tonder, Robert Walker, Dr. Kevin Caran, Dr. Kyle Seifert

Antimicrobial Activity, Biofilm Disruption Capabilities, and Synergistic Interactions of Novel Amphiphiles

The increased prevalence of antimicrobial resistant bacteria requires development of new control strategies. Preventative measures such as development of disinfectants and antiseptics with faster killing and antibiofilm capabilities would help limit the spread of resistance and reduce the incidence of hospital acquired infection. Several series of novel amphiphiles, including three bis-cationic, four tris-cationic and three tetra-cationic double tailed amphiphile series, as well as one hexa-cationic, triple tailed amphiphile series were synthesized and tested for antimicrobial properties. These amphiphiles were previously tested for MIC value against several Gram-positive and negative bacterial species. This work expanded on the antimicrobial capabilities of these amphiphiles by determining time to kill a population of cells, biofilm disruption activity, and synergistic interactions with other compounds. Bis-cationic amphiphiles were the fasted at killing S.aureus in as low as 1 minute. Oxacillin, a Gram-positive acting antibiotic combined with amphiphiles against E.coli, had synergy, with FIC’s ranging from 0.5 to 0.19. The highest biofilm disruption activity disrupted 90% of P. aeruginosa preformed biofilms. Synergistic combinations of these amphiphiles with oxacillin and other compounds could prove useful in overcoming bacteria antimicrobial resistant mechanisms. These results contribute to the development of cationic amphiphiles with increased biofilm disruption activity and faster kill time, ultimately better disinfectants and antiseptics that will better reduce the spread of antibiotic resistant pathogens especially in a hospital setting.
Grassland bird nest identification using unmanned aerial vehicles

Grassland bird populations have declined significantly within the past few decades due to injurious agricultural practices, namely mowing. Current methods to locate nests within fields chiefly involve resource-intensive walking surveys, which lead predators to nests via scent trails. Students enrolled in the 4VA sponsored Unmanned Systems for Biology course partnered with the Smithsonian Conservation Biology Institute to develop a manner through which grassland bird nests can be located efficiently and non-invasively. Team Grassland Birds deployed an unmanned aerial vehicle (UAV) outfitted with a GoPro and FLIR Vue Pro thermal camera to capture the heat signature of hard-warmers, intended to emulate eggs within a nest. Photogrammetry was employed to couple thermal and digital imagery, and nests geotagged within the final image. SCBI aims to perform ground-truthing of the data generated from this process, with the ultimate goal of providing land owners with best management practices regarding land use and conservation of grassland bird nests.

Freeze cracking: a histological method for preparing parasitic copepod tissues for genome size measurement

It is widely believed that an organism’s genome size is indicative of certain characteristics of that organism, such as body size and developmental rate. However, few studies have explored the relationship between genome size and lifestyle, such as parasitism. Copepods present an opportunity to explore these relationships because they have many free-living and parasitic members. Additionally, a survey of copepod genome size might inform us of their evolutionary transitions from free-living to parasitic lifestyles. Genome size in fungal and bacterial microparasitic species appears to be constrained to be small. We are asking if a similar constraint on genome size exists in parasitic copepods. During our investigation of the relationship between genome size and lifestyle, we encountered an unexpected problem with preparing tissues of copepod parasites that are suitable for genome size measurement. Unlike the free-living copepods whose nuclei disperse well and are amenable to microdensitometry analysis, nuclei of parasites clump together and adhere to the tough and thickened cuticle, preventing measurements of both background and individual nuclei to be obtained. To remedy this problem, we are modifying a freeze-cracking method that has been successful in removing the tough cuticle of other invertebrate parasites. The preliminary results of this method, as applied to copepods, will be discussed. If successful, this will enable the first publication quality estimates of genome sizes in parasitic copepods.

The state of the translation chaperone ICD-1 during misfolded-protein-induced apoptosis in Caenorhabditis elegans

The unfolded protein response (UPR) is a signal transduction cascade that mitigates misfolded protein stress in the endoplasmic reticulum (ER). Prolonged ER stress eventually leads to the initiation of apoptosis (programmed cell death) by the UPR to prevent damage to the organism. In vitro studies suggest that the beta subunit of the heterodimeric translational chaperone, nascent polypeptide complex, βNAC, contains putative caspase cleavage sites independent of the caspase CED-3. The purpose of this investigation was to determine the state of inhibitor of cell death-1 (ICD-1), the βNAC homolog in C. elegans, during apoptosis in vivo. Western blot analyses with wild type lysates and tunicamycin, thapsigargin, and ICD-1 RNAi stressed lysates were used to determine the state of ICD-1 in various cellular conditions. Initial results indicated that a polyclonal BTF-3 (human βNAC homolog) antibody had high affinity for a protein of similar molecular weight as ICD-1, suggesting antibody specificity. 72-hour ICD-1 RNAi time course trials were inconclusive, however, the findings from similar studies suggest a gradual depletion of ICD-1, further suggesting antibody specificity.
Tunicamycin and thapsigargin stressed populations indicated strong signaling of bands not present in wild type populations, suggesting stress-specific expression of apoptotic proteins. Because the BTF-3 antibody appears to be specific to ICD-1, it is suggested to incorporate additional stressors to understand the state of ICD-1 and the expression of stress-specific proteins in other stressed conditions. Follow-up experiments with CED-3 and CED-4 RNAi populations could allow for in vivo evidence of the CED-3-independent apoptotic pathway found in previous studies.

**P62** Katherine M. Bland, Zachary O. Casey, Z. Logan Holley, Christopher J. Handwerk, Dr. George S. Vidal

**Detecting dendritic spine pruning in cerebral cortex and a neuronal role for integrin beta 3**

Synaptic pruning in the cerebral cortex is a normal developmental process. Early in postnatal development, the cerebral cortex normally overproduces synapses, and then undergoes a period in which synapses are pruned away, leaving only synapses that are important for neural function. Dysregulation of synaptic pruning in excitatory neurons of the cerebral cortex may lead to neurological disorders such as intellectual disability and autism spectrum disorder, and is thought to be detectable by examining dendritic spine pruning. Integrin subunits have been implicated in axonal and dendritic outgrowth, as well as dendritic spine plasticity. In particular, a strong positive association has been found between mutations in integrin beta 3 (Itgb3) and intellectual disability, but little is known about neuronal Itgb3 function in vivo. To examine the role of Itgb3 in shaping cortical circuits early in life, here we use an approach that targets layer II/III cortical pyramidal neurons to either simply label them (controls) or to label them and cause Itgb3 loss of function (mutants). Results show that, when comparing neurons across the entire cerebral cortex, dendritic spine density on Itgb3 mutant neurons is unchanged compared to controls, and spine pruning is undetectable in both conditions. However, regional analysis reveals that dendritic spine pruning can be detected in controls. In summary, these results point to specific ages and regions in which dendritic spine pruning may be observed to investigate the role of Itgb3 in neurological disorders.

**P63** Savannah Stivers, Connor Marshall, Jonathan Jackson, Dr. Conley K. McMullen

**Herbarium studies of the Smith Creek restoration area**

This research project aims to provide updated documentation of specimens collected from the Smith Creek Restoration Area from 2007-2013. This inventory will reflect any changes in the taxonomic nomenclature of species previously identified, mounted, and housed in the Norlyn L. Bodkin Herbarium at JMU. A spreadsheet with description of GPS location, family name, species name, authority, and collection date was created to determine progress at Smith Creek following the implementation of the riparian buffer restoration in 2006. The spreadsheet contains 493 specimens comprising 269 different species within 173 genera and 60 families. GPS coordinates of each specimen have been added to a map in ArcGIS to provide a visual representation of the collections made at Smith Creek.
## BIOSYMPOSIUM 2018 - Author Index

Numbers refer to (T)alks, (P)osters, (E)lectronic (P)osters

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