

2019

28th Annual

BIOSYMPOSIUM





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James Madison University

Biology Department

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*Thursday, April 11 - Friday, April 12, 2019*

Cover image: *Arabidopsis*, by Isabelle Houston (colored pencil, 2018)

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\* Student authors whose research has been supported by

one of these gifts are noted with an asterisk.

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

\* Research that was supported by summer funding gifts

**g** Graduate student research

**Schedule: Thursday April 11th**

**SESSION 1 11:00am-1:00pm POSTERS (P) and Electronic Posters (E)**

**2nd Fl. Foyer (see monitors in 2009 for E)**

E1 Haley Powers, Emma Nelson, Dr. David McLeod

**A review of the diction describing superficial skin structures observed on Anura species**

E2 Brooke Patterson, David Thalman, Dr. David McLeod

***Plethodon cinereus* Presence at Nighttime vs. Daytime and Activity Levels in Optimal Weather Conditions**

E3Victoria Mendoza, Mitchell Green, Dr. Bryan Cage, Dr. Roshna Wunderlich

**Using Long-Range Wide Area Networks to Study Lemur Habitat in Madagascar.**

P01\* Z. Logan Holley, Katherine M. Bland, Zachary O. Casey, Christopher J. Handwerk, Brian D. Swinehart, Santosh Dasari, Eden Widener, Dr. George S. Vidal

**Cross-regional gradient of mouse cortical supragranular pyramidal neurons is regulated by integrin beta 3**

P02 cancelled poster

P03\* Kevin Reifenberg, Dr. Christine May

**Community Composition of Salamanders in Appalachian Streams**

P04 Zoe Bergman, Chris Coggin, Katelyn Harless, Dr. Heather Griscom

**Phenology, Pollination, and Seed Dispersal Syndromes in Reforested Dry Tropical Ecosystems**

P05 Rachel Boyce, Sarah Coleman, Julie Cumins, Joseph DeTrane, Dr. Joseph Harsh

**Investigating the longitudinal effects of an introductory biology course-based undergraduate research experience on students later in their academic career**

P06**g** Morgan Hussey, Christopher Will, Dr. Heather Griscom

**Avian species assemblages within *Bursera simaruba* trees in Panama**

P07\* Elisha Burton, Michael Pamonag, Abigail Hinson, Dr. Kristopher Kubow

**Influence of fiber orientation and fiber movement on cell polarization and migration**

P08 William Smith, William Meara, Kavanaugh-Faye Bushnell, Gianna Mangone, Dr. Justin W Brown

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

P09 Chantel Pence, Amber Lin, Zach Minor, Leykie Green, Dr. Cass

**DNA barcoding of marine macroalgae: identification of seaweed species sold for human consumption**

P10 Saidah Lerman, Katie Doherty, Dr. Terrie Rife

**Developing a better understanding of tau’s isoforms and DNA binding abilities using Western Blots and Electrophoretic Mobility Shift Assays**

P11\* Aya Andos, Ani Clem, Lexy Foor, Catherine Shola, Dr. Janet Daniel

**Investigating Phenotypic Differences Between the STP1 k/o and WT *Arabidopsis thaliana* in Response to Various Environmental Stresses​**

P12 Nathaniel Lucas, Callum Morton, Cortland Burke. Hope Kircher, Patrick Kilkenny, Klebert Feitosa, Dr. Roshna Wunderlich

**Measuring Intrinsic Foot Muscle Strength and Activation Using Novel Methodology and EMG Measurements**

P13 Adrian Brazell, Dr. Corey Cleland

**Contribution of extrinsic tail muscles to the tail nociceptive withdrawal response through reconstruction based on muscle primitives: Role of non-linearities**

P14 Katherine Kourmadas, Jocelyn Mackey, Mason Lee, Dr. Amanda Cass

**DNA barcoding commercially sold medicinal leeches: potential evidence of prior human blood meals**

P15 cancelled poster

P16 Emily M. Anglemyer, Kinsey L. Miller, Christine E. Robson

**Understanding epimorphic and morphallaxis regeneration in *Notophthalmus viridescens* can lead to biomedical engineering advancement in adult human cardiac regeneration**

P17 Katie Griffin, Olivia Jackson, Brian Willis, Dr. David McLeod

**Determining Invasive Potential of common pond slider *Trachemys scripta elegans* in Harrisonburg, Virginia**

P18\* Hayden Casassa, Dr. Jonathan Monroe

**Redox Regulation of BAM1 in *Arabidopsis thaliana***

P19**g** Melissa Encinias, Jack Doss, Dr. Idelle Cooper, Dr. Heather Griscom

**An Evaluation of Reforestation Pathways on Insect Richness in the Tropical Dry Forests of Panama**

P20**C** Abby Stapleton, Dr. Ray Enke

**Characterizing epigenetic demethylation of conserved cis-regulatory elements in the developing chicken retina**

P21 Laura Ferguson, Dr. Chris Rose

**Creating a developmental atlas for the American Toad (Anaxyrus americanus)**

P22**C** Destin Witmer, Dr. Ray Enke, Dr. Wendy Stapleton

**Sequence Analysis of Chronic Wasting Disease-associated SNPs in White Tailed Deer Native to Frederick and Shenandoah Counties**

P23 Desiree Edemba, Dr. Morgan Steffen, Dr. Rocky Parker, Dr. Louie Wurch

**Sexual variation in the skin microbiome of garter snakes**

P24-29**C** Dr. James Herrick, Dominique Lockwood, and the students of Bio 346

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

**Schedule: Thursday April 11th**

**SESSION 2 1:00-4:00pm ORAL PRESENTATIONS Biosci 2007**

1:00 Introduction by Dr. Marcus C. Davis, Associate Dean: *Integration of Teaching and Scholarship*, College of Science and Mathematics

1:15 T1.**g**\* Maddie Berg, Dr. Christine May

**Urban Stream Restoration: An Evaluation of Conveyance and Material Processing Channels**

1:30 T2. Zoe Bergman, Dr. Heather Griscom

**Response of Restoration Chestnut Seedlings to Forest Management Strategies**

1:45**gC** T3. Noah Greenman, Dr. James Herrick

**Assessing the Prevalence of Antibiotic Resistant *Salmonella enterica* in Stream Sediment and Poultry Litter from the Shenandoah Valley**

2:00 T4.**g**\* Tyler Kovacs, Dr. Heather Griscom

**Herpetological assemblages in reforested tropical dry forests of the Azuero Peninsula, Panama**

**2:15** : : : : : : : : **BREAK** : : : : : : : :

2:30 T5. **g** Hannah Eisemann, Dr. Christine May

**Assessing Brook Trout (*Salvelinus fontinalis*) Populations Above and Below Waterfalls in Virginia**

2:45 T6.Alexa Hoke, Kelsey Angell, Malia Gardner, Guadalupe Reynoso, Morgan Smith, Dr. Louie Wurch, Dr. Silvia Newell, Dr. Morgan Steffen

**The *Microcystis* microbiome: Bacterial interactions in the *Microcystis* phycosphere**

3:00 T7.**g**\* Melissa Encinias, Dr. Idelle Cooper

**Divergence of male mating preferences in sympatric *Calopteryx aequabilis* and C*. maculata* populations**

3:15 T8.**Cg** Rachael M. St. Jacques, Dr. Steven G. Cresawn

**Anti-CRISPR vs. CRISPR: The evolutionary arms race between microorganisms**

3:30 T9. Jeremiah PC Stinson, Isabel D Lamb-Echegaray, Dr. Mark L Gabriele

**Alignment of ephrin-B3 with extramodular zones in the lateral cortex of the inferior colliculus**

3:45 T10.**g**\* Chris Coggin, Dr. Heather Griscom

**The long-term effect of different reforestation strategies on forest composition on Block Island, Rhode Island**

**Schedule: Friday April 12th**

**SESSION 3 8:55am-noon ORAL PRESENTATIONS BIOSCI 2007**

8:55 Introduction

9:00 T11. Shannon Richard, Sanjiv Jayamohan, Paige Carrington, Dr. M. Rockwell Parker

**Behavioral Investigation of Chemical Communication in Argentine Tegus**

9:15 T12.\* Hanna Yu, Elizabeth Terry, Dr. Kyle Seifert

**Spacer length of novel cationic bipyrimidine amphiphiles dictates efficacy of antimicrobial activity**

9:30 T13.\* Rachel Barborek, Kendyl Combs, Matthew Knick, Althea Neighbors, Nico Nettemeyer, Ayshah Obaid, Heather Tolvay, Maddie Ward, Dr. Susan Halsell

**Detecting the Cold: Do Innexins Function in Cold Nociception?**

9:45\* T14. Erin K. Kavusak, Isabel D. Lamb-Echegaray, Dr. Mark L. Gabriele

**Early Targeting of lateral cortex of the inferior colliculus modular fields by descending somatosensory cortical projections**

10:00 T15.\* Z. Logan Holley, Katherine M. Bland, Zachary O. Casey, Christopher J. Handwerk, Dr. George Vidal

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

10:15 T16.\* Shelby Pedigo, Dr. Oliver Hyman, Dr. Pradeep V. Menon, Dr. Bisi Velayudhan

**Investigating the effect of Sodium benzoate on immune cells and microbial population in the small intestine of mice**

**10:30** : : : : : : : : **BREAK** : : : : : : : :

10:45 T17.**g** Bailie Lavan, Dr. Patrice Ludwig

**Examining the effect of interstitial space on Eastern oysters (*Crassostrea virginica*)**

11:00 T18. Baodan Collins, Madison DeVost, Parker Moore, Hadeel Elhaj, Dr. Tracy Deem, Dr. Chris Lantz

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

11:15 T19. Monica Gerber, Dr. Tim Bloss

**Analyzing the Effect of Apoptotic Mutations on the State of the Nascent Polypeptide-Associated Complex in *Ceanorhabditis elegans***

11:30 T20. Shane Chambers, Dr. Marquis Walker

**Characterization of Trpm1 function in mammalian iris constriction**

11:45 T21.\* Michael Pamonag, Elijah Burton, Abigail Hinson, Dr. Kristopher Kubow

**Influence of fiber orientation and fiber movement on cell polarization and migration**

**Keynote Presentation: *Bioscience 1007, Fri. 12:20-1:10pm***

Nick Pullen

University of Northern Colorado

**Taking control of inflammation: characterizing and fine-tuning mechanisms suppressing the immune system**

Dysfunction of inflammatory processes underlies a diverse array of pathologies such as allergy and asthma, large traumatic wounds, autoimmunity, and high-grade cancer. In these states we observe either the development of chronic immunosuppression or the inability to appropriately respond to classic immunosuppressive signals. My lab focuses on characterizing the molecular circuitry causing immune cells to become bad actors, and why some people are more prone to these problems than others. While the activities of lymphoid cells in immunity are critical, we find that the re-programming of mast cells, macrophages, and immature myeloid cells is a major driver in the development of immunosuppressive states. Specifically, we will discuss molecular mechanisms explaining such re-programming, the emerging topic of trained immunity (a.k.a. “innate memory”), and adjunctive therapies for taking back control of the myeloid lineage, such as exercise, and the use of natural product small molecules (e.g., lactones and alkaloids). We’ll also take a quick look at how I got here since my last Biosymposium talk 15-years ago as an undergraduate!

1:10-2:00 LUNCH RECEPTION FOR PRESENTERS - Second floor foyer

**Schedule: Friday April 12th**

**SESSION 4 2:00-4:00pm POSTERS (P) and Electronic Posters (EP)**

**2nd Fl. Foyer (see 2007 monitors for E)**

E4 Anna Golden, Kevin Dannaher, Maggie Delaney, Harrison Giknavorian, Cal Morton, Dr. Patrice Ludwig  
**Technology and songbirds: A new approach to look at impacts of urbanization**

E5 Sarah McKay, Dr. Bisi Velayudhan

**Understanding the Effects of Sodium Benzoate on Behavior in Mice**

P30\* Katherine M. Bland, Zachary O. Casey, Adam Aharon, Dr. Chia-Chien Chen, Irene Song, Andrew Lopuch, Dr. Yi Zuo, Dr. George S. Vidal

**Dendritic Spine Abnormalities Within Layer V Cerebral Cortical Neurons of a Heterozygous *Fmr1* Mouse Model**

P31 Lucas Manweiler, Cameron Baker, Andrew Douglas, Rhett Elliott, Haley Grove, Nicole McCroddan, Kathryn Motley, Andrea Navarro, Brittany Sweet, Dr. Bruce Wiggins

**Evaluating Stream Restoration Effectiveness by Using Benthic Macroinvertebrates as Proxy**

P32 Claire Ravenburg, Dr. Jonathan Monroe, Dr. Christopher Berndsen

**Investigating a putative dual-function β-amylase gene in rice**

P33**g** Ruth Bowers-Sword, Dr. Joshua Linder, Dr. Roshna Wunderlich

**Assessing hunting pressures and the population status of the Critically Endangered Preuss’s red colobus, *Piliocolobus preussi,* in Cross River National Park, Nigeria**

P34 Sabrina Circolo, Brandon Duda, Patrick Kilkenny, Dr. Roshna Wunderlich

**The influence of foot pad thickness and foot strike mechanics on plantar pressure distribution during walking**

P35 Benjamin Knick, Kayley Campbell, Madison Riahin, Olivia Hahn, Dr. Amanda Cass

**Barcoding milk: Identification of goat diet from trace plant DNA**

P36**C** Penelope-Marie B. Clanor, Calvin Chenault, Dr. Ray Enke

**Analyzing Cell-specific Patterns of DNA Methylation in Human Retinal Neurons**

P37 Christine Verdream, Brett Otsby, Dr. Christine May

**Habitat Utilization and Impact of Flooding on James spinymussel (*Parvaspina collina*) Populations in Virginia Streams**

P38 Rana Ihsan, Dr. Timothy Bloss

**Characterization of the role of the nascent polypeptide-associated complex during misfolded protein stress in *C. elegans***

P39\* Alexa Cornwell, Valerie Shvygin, Dr. Terrie Rife

**Role of tau protein in transcriptional regulation of nitric oxide synthase I**

P40 Paulina Bauer, Brian Anderson, Dr. Terrie Rife

**Characterizing the potential of big tau in DNA protection with CRISPR-Cas9 knockouts**

P41 Taylor Bryan, Dr. Anthony Tongen, Dr. Gabriel Niculescu, Dr. Bryan Cage, Dr. Roshna Wunderlich

**The influence of enclosure size and type on energy expenditure and locomotor behavior in captive *Lemur catta***

P42 Isabelle Houston, Dr. Jonathan Monroe

**Characterizing the role of 𝛃-Amylase 3 in cold stress recovery in *Arabidopsis thaliana***

P43**C** Emma Eisemann, Selena Hise, Liam Godbold, Dr. James Herrick

**Plasmids conferring resistance to late-generation clinical antibiotics captured from poultry litter and stream sediments in the Shenandoah Valley**

P44 Jeremy Rice, Shane Chambers, Dr. Marquis Walker

**Trpm1 Localization and Expression in Mouse Iris**

P45 Sydney Wicks, Logan Lee, Jane Choi, Jason Lee, Dr. Amanda Cass

**Can DNA barcoding reveal the geographic origin of honey?**

P46 Jennifer C. To, Morgan L. Hussey, Dr. Dana L. Moseley

**Determining the repertoire size within the songs of the gray catbird (*Dumetella carolinensis)***

P47**g** Cooper Brett, Dr. Mark Gabriele

**Microglial and CX3CL1 Patterning with Respect to the Developing Modular-Extramodular Framework in the Lateral Cortex of the Inferior Colliculus**

P48 Peyton Coady, Anna Fracasso, Reef Buckhalter, Jessica Cornell, Dr. Marta Bechtel, Dr. Kristopher E. Kubow

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

P49 Brady Simpson, Maria Ruggeri, Dr. Corey Cleland

**Dependence of the Nociceptive Withdrawal Response on Stimulus Location in the Intact, Unanesthetized Rat**

P50 Annie Hunger, Dr. Corey Cleland

**Identification of muscles that contribute to the tail nociceptive withdrawal response through selective tendon transection**

P51**C** Dominique Lockwood, Dr. Louie Wurch

**Microbial Community Structure During a *Microcystis* Bloom in Lake Tai: Cultured Versus Uncultured Representatives**

P52 Harrison Giknavorian, Dr. Grace Wyngaard

**Genome size of parasitic copepod *Lepeophtheirus salmonis* embryos**

P53\* Elizabeth Terry, Hanna Yu, Tyler Miller, Dr. Kevin Caran, Dr. Kyle Seifert

**Spacer length of novel cationic bipyrimidine amphiphiles dictates efficacy of antimicrobial activity**

P54**g** Tyler Kovacs, Kevin Reifenberg, Dr. Heather Griscom

**Avian communities of the tropical dry forests of the Azuero Peninsula, Panama: a comparative study of reforestation type**

P55\* Kaitlyn Harless, Dr. Patrice Ludwig

**Decomposition of Cattle Dung by Aphodius pseudolividus in Virginia is Density Independent**

P56 Jodi Cheung, Dr. Christopher Rose

**How thyroid hormones and their inhibitors affect bone development in the frog *Xenopus laevis*.**

P57**C** Scott Schumacker, Dr. Ray Enke

**Analysis of Cell-Type Restricted Transcriptional Networks in Human Photoreceptor Neurons**

P58 Quinn Adams, Alexander Barrett, Jasmine Benbei, Kelsey Broadwell, Rachel Dion, Valeria Erazo, Ashley Farnan, Malia Gardner, Lauren Johnson, Nicole Landry, Tess Leftwich, Frank May, Maz Maza, Rebecca Moiera, Bahar Osman, Kyle Rubino, Greg Shero, Kristen Snow, Beth Terry, Ryan Zoldork, Dr. Louie Wurch

**Aquatic Microbiology: An upper level CURE where students conduct research on the effects of bacterioplankton on toxic cyanobacteria**

P59 Shad Abdullah, Dr. Michael Renfroe

**Decrease in Antioxidant Concentration in Herbs over Time**

P60 Emily Williams, Dr. David McLeod and Dr. Louise Temple

**Culture Dependent Analysis of Microbiome Bacterial Growth in *Polypedates leucomystax***

P61 Daniel Bradford, Densel Dagdagan, Keegan Lowman, Lexa Treml, Jennifer To, Arcangelo Arecchi, Dr. Patrice Ludwig

**Usage of drones for counting flowers necessary for pollination**

P62 Yusuf Aboutabl, Dr. Chris Rose

**Investigating the cellular basis of hormone induced-shape changes in *Xenopus* lower jaw cartilage**

P63 Francis Gebhard, Dr. David McLeod

**A comparison of the effectiveness of two gecko diets**

P64 Monica Chiodo, Dr. Marquis Walker

**Site-directed gene editing in *Drosophila* using Crispr/CAS9**

P65 Michelle Bair, Shema Mohebi, Bailey Gotchel, Zeru Tadesse, Dr. Patrice Ludwig

**Biology in technology**

P66**C** Jennifer Anderson, Louisa Esteban, Dr. James Herrick

**Whole genome assembly and annotation of *Salmonella enterica* isolated from stream sediments and poultry litter in the Shenandoah Valley**

**Abstracts ORAL PRESENTATIONS**

T01**g**\* Maddie Berg, Dr. Christine May

**Urban Stream Restoration: An Evaluation of Conveyance and Material Processing Channels**

Due to the recent interest in stream restoration to help the Chesapeake Bay, this study was undertaken to evaluate the in-stream effectiveness of two restoration practices: conveyance channels and material processing channels. Ten streams, five of each restoration practice, were evaluated in terms of organic retention and macroinvertebrates. The upper and lower reaches of each stream were sampled with transects to measure organic retention percent cover and sampled with two methods for macroinvertebrates. Despite each site being evaluated only once during the summer of 2018, which was the highest rainfall on record in Maryland, trends were still apparent. Material processing channels had significantly higher organic retention compared to conveyance, as they had a larger average hydraulic radius and a greater presence of woody debris. Focusing on macroinvertebrate sampling methods, traditional kick-net sampling compared to novel habitube sampling collected similar species richness. Abundance varied greatly, though habitubes collected higher average abundance compared to traditional sampling. Results from this study suggest that urban stream restoration practices can impact organic retention within streams as well as the ability to provide the best habitat for in-stream biota. When designing streams to reduce downstream impacts, material processing channels should be considered as they retain organic matter and work to provide habitat potential. Due to similar species richness collections across all reaches, habitubes have the potential to be a valid future sampling technique. This, or a similar study, should be continued over multiple years through different seasons to see if the trends persist or get stronger as the site ages.

T02 Zoe Bergman, Dr. Heather Griscom

**Response of Restoration Chestnut Seedlings to Forest Management Strategies**

The American Chestnut (*Castanea dentata*) was once a dominant canopy species in Eastern forests of the United States. A pathogenic fungus *(Cryphonectria parasitica)* decimated this tree species to functional extinction over sixty years ago. Our research attempts to identify forest management strategies for increasing the success of hybrid chestnuts (Restoration Chestnuts 1.0) plantings in forested ecosystems. We manipulated factors that may facilitate seedling survival and growth in an Appalachian cove forested ecosystem in West Virginia. We created canopy gaps of different sizes (40% vs 60% canopy openness) to manipulate light with the prediction that seedlings would perform best in large gaps (~60% canopy openness). Within these gaps, we added landscape fabric on every other row to decrease vegetative competition. We placed 12” tree shelters around half of the seedlings planted within the gaps to protect them from rodent predation. After four years, seedlings had significantly greater diameter and survival (68.5%) in small gaps (p < 0.001). In comparison, only 47% of seedlings survived in large gaps across all treatments. Tree shelters and landscape fabric had no significant effect on planted seedlings in small gaps. However, in large gaps, landscape fabric had a positive effect on seedling height (p< 0.05). In conclusion, we recommend planting chestnut seedlings in small gaps without landscape fabric or tree shelters. Chestnuts compete best under these conditions in an Appalachian cove ecosystem.

T03**gC** Noah Greenman, Dr. James Herrick

**Assessing the Prevalence of Antibiotic Resistant *Salmonella enterica* in Stream Sediment and Poultry Litter from the Shenandoah Valley**

*Salmonella enterica* is one of the leading causes of gastroenteric disease in the US, afflicting over an estimated 1 million people each year. The continued emergence of multidrug resistant forms of *S. enterica* has caused concern since the only option for treating systemic infections are with antibiotics. While the impact of antibiotic exposure has been explored in clinical settings, the significance of environmental dissemination of antibiotic resistance genes (ARGs) has not been as well studied. We hypothesized that potentially clinically-relevant *S. enterica* can be found in stream sediment and poultry litter, many with the capacity to be resistant to one or more antibiotics. Streams near a variety of agricultural outfits including farms and poultry processing plants, as well as poultry litter from poultry houses, were sampled by members of the Herrick lab and 88 *S. enterica* were isolated from these sources. The entire genomes of these isolates were sequenced and assembled using either short read or a combination of short and long read DNA sequence technologies. *In silico* serotyping methods identified numerous clinically significant *S. enterica* such as *S.* Typhimurium and *S.* Infantis. *In silico* ARG identifiers found 32 isolates possessing resistance genes, with 26 of those isolates possessing 2 or more different classes of ARGs. Some ARGs within these *Salmonella* were predicted to be present on mobile genetic elements such as plasmids. Future studies will include determining if these *S. enterica* have an established niche in these environmental habitats or if they’re being reintroduced into the environment from common sources and exploring what plasmids exist in these environments that *S. enterica* could acquire.

T04\* Tyler Kovacs, Dr. Heather Griscom

**Herpetological assemblages in reforested tropical dry forests of the Azuero Peninsula, Panama**

Tropical dry forests are considered one of the most endangered tropical ecosystems making reforestation increasingly necessary to restore Panama’s unique ecoregion. The isolated dry ecoregion surrounding the Bay of Parita in Panama has a long history of deforestation and cattle grazing. Successful reforestation of this land is important to restore ecosystem health and biodiversity. In Panama, reforestation ranges from monocultures of exotic teak (*Tectona grandis*) to passive regeneration. Faunal recovery within these reforestation systems may vary due to different habitat characteristics. In this study, amphibian and reptile communities were compared in two types of reforestation systems and protected riparian forests in the dry ecoregion of the Azuero Peninsula, Panama. A 13-year-old secondary forest and a 13-year-old teak plantation were assessed, each containing a forested riparian area. Old secondary forests (80+ years) and an active cattle pasture were used as reference sites to represent low and high disturbance habitats. The 13-year-old secondary forest had higher site richness along with a more complex community composition compared to the 13-year-old teak plantation. Results indicate the importance of protected forested riparian areas, which had significantly more abundant herpetological communities at each site (p < 0.05). These riparian forests may serve as sources for species that are recolonizing reforested areas. Additionally, analyses of habitat characteristics indicated increasing tree diversity promotes a higher abundance of herpetofauna at reforestation sites. Along with the preservation of forested riparian areas, we suggest reforestation practices that increase tree diversity, even if timber production is the main goal.

T05 Hannah Eisemann, Dr. Christine May

**Assessing Brook Trout (*Salvelinus fontinalis*) Populations Above and Below Waterfalls in Virginia**

This study investigates brook trout occurrence above waterfalls in Virginia and compares brook trout populations found above to those found below them to determine if the landscapes waterfalls create above them support populations of trout that are good targets for conservation. One-hundred meter reaches above and below seven waterfalls in Virginia’s George Washington and Jefferson National Forest were sampled for brook trout via 3-pass, block-netted, backpack electrofishing depletions. All brook trout were counted, weighed, and measured for fork length. The response variables are differences in 1) percent dominance, 2) population size, 3) biomass, and 4) length-weight index (Fulton’s Condition Factor) between brook trout above and below waterfalls. Brook trout dominance (100 vs. 36.9%) is greater above than below waterfalls, but not significantly (p = 0.1003). We found abundance (26 vs.12 individuals per 100m) and overall biomass (885.3 vs 284.6 grams per 100m) of brook trout populations above waterfalls to be significantly greater than their below waterfall counterparts (p = 0.078 for both). We also found brook trout above waterfalls to have a higher condition factor (1.086g/cm3 vs 1.0636g/cm3) than those below waterfalls (p = 0.031). Lastly, we found populations above waterfalls where their occurrence was previously unknown. Despite being isolated, brook trout populations above waterfalls were just as if not more robust than those below and may be excellent targets for conservation.

T06 Alexa Hoke, Kelsey Angell, Malia Gardner, Guadalupe Reynoso, Morgan Smith, Dr. Louie Wurch, Dr. Silvia Newell, Dr. Morgan Steffen

**The *Microcystis* microbiome: Bacterial interactions in the *Microcystis* phycosphere**

Cyanobacterial harmful algal blooms (cHABs) can be detrimental to the environment and local economies by limiting access to potable water and impacting fishing industries. *Microcystis* is a freshwater cHAB organism with worldwide significance that is expected to increase in occurrence and biomass as global temperatures rise. While most research on *Microcystis* focuses on the abiotic factors that influence bloom formation, less is known about the specific role of bacteria in supporting *Microcystis* blooms. To help further understand the impact of microbial interactions on *Microcystis*, bacteria were isolated from a *Microcystis* bloom in the western basin of Lake Erie in August of 2017. *Acidovorax*, *Deinococcus*, *Paenibacillus*, *Exiguobacterium*, and *Enterobacter* spp were isolated and chosen for whole genome sequencing with the PacBio platform. Genome sizes range from 3.1Mb to 5.7Mb and are assembled in single chromosomes (*Acidovorax*) or large contigs. Three of the isolates can utilize environmentally relevant nitrogen sources such as urea and may play an important role in supporting *Microcystis* growth during periods of N-limitation. The production of other compounds by bacteria in the phycosphere could ultimately aid in the growth of *Microcystis*. To test whether these organisms are growth-promoting, they were also grown in co-culture with axenic *Microcystis* to determine their impact on the growth and cell physiology of the *Microcystis* cells.

T07**g**\* Melissa Encinias, Dr. Idelle Cooper

**Divergence of male mating preferences in sympatric *Calopteryx aequabilis* and C*. maculata* populations**

An ongoing evolutionary question is how co-occurring species maintain reproductive barriers when they are morphologically, behaviorally, and ecologically similar. Without geographic isolation, mate choice often forms these barriers through species recognition of males by females. However, because females typically have a greater reproductive investment, variation between females and male choice is commonly overlooked. In *Calopteryx* damselflies, wing pigmentation is sexually dimorphic and females appear to prefer dark-winged males. When the geographic distributions and female preferences of related species overlap, there is potential for misdirected mating. However, in sympatric populations of *C aequabilis*and *C. maculata*, hybridization is not common. Female wings also dramatically differ when these species co-occur. Due to the divergence of female wings in sympatric populations, we hypothesize that this character is under selection for species recognition by males. We conducted mate choice experiments in which we altered female wings by switching them between populations or species. We then measured male mating behavior of both species. Our results supported our hypothesis, as sympatric *C. aequabilis* males had significantly different wing preferences than allopatric *C. aequabilis* and sympatric *C. maculata*males. This finding suggests that male mating preferences diverged in sympatric populations and potentially evolved as a reproductive barrier to reduce misdirected mating of two closely related species.

T08**gC** Rachael M. St. Jacques, Dr. Steven G. Cresawn

**Anti-CRISPR vs. CRISPR: The evolutionary arms race between microorganisms**

CRISPR-Cas arrays are a defense mechanism employed by bacteria against bacteriophages. Anti-CRISPR proteins are produced by bacteriophages to stop the bacterial host’s CRISPR-Cas complex from interrupting the phage life cycle.

SEA-PHAGES is a bacteriophage research network of 120 colleges and is known at James Madison University as Viral Discovery. JMU uses *Streptomyces griseus* ATCC10137 as a host organism for bacteriophage screening. In this study we report the sequencing and analysis of this strain. To determine if the *S. griseus* ATCC10137 encodes CRISPR-Cas arrays, next generation sequencing and bioinformatic analyses were performed.

The MiniSeq and MinION were used to obtain whole genome sequence data from *S. griseus* ATCC 10137. A hybrid genome assembly using both sets of reads was generated using Unicycler, resulting in an assembly that was 8,576,363 bp long. CRISPRfinder was used to identify CRISPR-Cas arrays in the *S. griseus* genome. Prokka and RAST were used to predict genes in the *S. griseus* genome, but they produced substantially different outputs. We developed the genome browser Prokkrastinator to merge the two annotation methods. To search for anti-CRISPR genes in the genome of bacteriophage Wipeout, protein models were generated using Yasara. Of 259 Wipeout genes, 37 % were modeled successfully, including various phage structural proteins. The remaining 63 % of the Wipeout gene products could not be modeled, including 13 gene products in the same size range as other anti-CRISPR proteins (50-150 amino acids long). These 13 gene products should be further studied to determine if they are anti-CRISPR proteins.

T09 Jeremiah PC Stinson, Isabel D Lamb-Echegaray, Dr. Mark L Gabriele

**Alignment of ephrin-B3 with extramodular zones in the lateral cortex of the inferior colliculus**

The lateral cortex of the inferior colliculus (LCIC) is a multimodal center which receives major inputs of somatosensory and auditory origin. The LCIC exhibits characteristics in keeping with a discrete neural map, whereby somatosensory modular compartments are surrounded by extramodular auditory zones. Eph-ephrin guidance mechanisms have been implicated in instructing similar arrangements in other central structures, including the striatum and olfactory bulb. Previous studies in our lab have shown patchy EphA4 and ephrin-B2 expression during the early postnatal period that overlaps developing GAD-positive modules and is complementary to calretinin-defined extramodular zones. The present experiments examine another member of the Eph-ephrin signaling family, ephrin-B3, and correlate its early postnatal expression with developing LCIC compartments. Fluorescent immunocytochemical approaches were used in a developmental series of GAD67-GFP mice (P0-P12). This knock-in line specifically labels GABAergic neurons, facilitating easy visualization of developing LCIC modules. Ephrin-B3 expression was strong at birth and throughout the first postnatal week. Ephrin-B3 labeling was most concentrated in mid-rostrocaudal LCIC regions, exhibiting a pattern that was complementary to GAD-positive modules. Furthermore, ephrin-B3 patterning aligned with that of the extramodular marker, calretinin. By P12, once a clear modular-extramodular framework is readily apparent, ephrin-B3 expression appears downregulated. The present study reveals that ephrin-B3 is present during the critical period of the establishment of LCIC modular-extramodular zones. Its extramodular expression appears to complement that of previously described modular EphA4 and ephrin-B2 patterns. Taken together, these findings suggest a potential role for Eph-ephrin signaling in segregating developing multimodal LCIC compartments and their respective connections.

T10**g**\* Chris Coggin, Dr. Heather Griscom

**The long-term effect of different reforestation strategies on forest composition on Block Island, Rhode Island**

Understanding patterns of forest succession can help advise management plans within New England nature preserves. This study took place on Block Island, 13 miles off the coast of Rhode Island. The island has greater than 200+ years of farming practices. After 1960, conservation groups began reforesting the island using different strategies, such as activing planting with native and exotic tree species, mowing, and preventing further development. In 2018, woody vegetation was inventoried along transects within four reforested sites. Sites were characterized as the following: actively planted with exotic and native tree species and mowed (AP-M), actively planted with exotic and native species with no mowing (AP-NM), passively managed (no planting or mowing) (NP-NM), and never deforested (F). Trees (>5 cm dbh) were measured and identified within 10m of four 20m transects at each site. Saplings or shrubs (< 5cm dbh, > 1 m in height) were counted and identified within 5m of each transect. Tree seedlings (10 cm to 1 m in height) were counted and identified within 1m of each transect. Soil samples were taken every 20m along each transect. Reforestation strategy had a significant effect on adult tree basal area and diversity (p-value < 0.001). AP-NM had a significantly greater basal area (38.06 m2/ha) compared to “NP-NM” (13.14 m2/ha). The greatest diversity of tree species was also found at “AP-NM” (H’=0.759) while the lowest diversity was at “AP-M”, which was represented by one species *(Prunus serotina*)(H’ = 0). Overall, seedlings were rarely encountered, but the greatest number of seedlings (660 individuals per ha) was found at “NP-NM”, most of which were shadbush (*Amelanchier canadensis*). In conclusion, “AP-NM” significantly increased the diversity and basal area but had no effect on seedling recruitment in the understory. This is most likely due to the overpopulation of deer on the island.

T11 Shannon Richard, Sanjiv Jayamohan, Paige Carrington, Dr. M. Rockwell Parker

**Behavioral Investigation of Chemical Communication in Argentine Tegus**

Locating mates is essential for reproduction, and most reptile species use chemical signals to do so. In numerous lizards, the role of chemicals for mate identification been studied. Reptiles also have a great capacity as invasive species, especially in Florida, and pheromones may be a potential control technique. The Argentine black and white tegu (*Salvator merianae)* is an invasive species in the Florida Everglades impacting native fauna. We aimed to determine if male Argentine tegus can recognize and follow conspecific scents and to describe behaviors associated with trailing using a Y-maze. Males did not follow female or male scent as their first choice but passed through the female scented arm more often when both male and female scent was present. Some quantifiable behaviors were exhibited and one increased in frequency when female scent was present. Additional tests are required to determine if pheromone traps could be an effective technique for controlling this species in the Everglades.

T12\* Hanna Yu, Elizabeth Terry, Dr. Kyle Seifert

**Spacer length of novel cationic bipyrimidine amphiphiles dictates efficacy of antimicrobial activity**

Antibiotics play a critical role in efficiently treating various bacterial diseases that commonly affect humans. However, over-administration of drugs and varying adaptive mechanisms of bacterial pathogens contribute to the increase in antibiotic resistance. The rising prevalence of drug resistant pathogens on medical equipment increase patients’ susceptibility to acquiring nosocomial infections that are difficult to treat. Amphiphilic compounds, containing a hydrophilic head and hydrophobic tail, have shown to express antimicrobial properties. By better understanding their ability to disrupt bacterial membranes, we hope to contribute to the development of effective antimicrobial agents to limit pathogen transmission. The synthesized novel cationic amphiphiles contain two bipyrimidine groups, each with a hydrocarbon tail and separated by a carbon linker of varying lengths (6-14). The focus of our study is to find the optimal carbon linker length that most effectively disrupts prokaryotic cellular membrane. We aimed to achieve maximum bacterial disruption at the lowest amphiphilic dilution concentration. The bipyrimidine amphiphiles with varying carbon linker lengths were diluted (500uM - 1uM) and tested against *P. aeruginosa, E. coli, S. aureus, E. faecalis, S. agalactiae,* and *K. pneumoniae* through minimum inhibitory concentration (MIC) assays. The results indicate that amphiphiles with 12 or 14 carbon spacers were the most effective at inhibiting bacterial growth. There were no obvious differences between the MICs of Gram positive and Gram negative bacteria. The data suggest that antibacterial ability of amphiphiles increases with the length of the carbon spacer between bipyrimidine groups. Improved understanding of structure dependence and antimicrobial activity mechanism in amphiphilic compounds is the first step to developing practical applications for improving sanitation and decreasing transmission of nosocomial drug-resistant infections.

T13\* Rachel Barborek, Kendyl Combs, Matthew Knick, Althea Neighbors, Nico Nettemeyer, Ayshah Obaid, Heather Tolvay, Maddie Ward, Dr. Susan Halsell

**Detecting the Cold: Do Innexins Function in Cold Nociception?**

Nociception is the perception of and response to harmful stimuli. Nociception is essential for minimizing tissue damage, but aberrant nociceptive pathways can result in chronic pain. Chronic pain in the U.S. is commonly managed with wide-acting opioids, and precisely defining the components of nociceptive pathways could uncover novel targets for pain therapies. We hypothesize that the vitally quick process of nociception would utilize electrical synapses because they transmit signals between neurons more quickly than chemical synapses do. This study, therefore, aims to uncover the potential role of the eight Drosophila melanogaster gap junction proteins, the Innexins, in cold nociception. Wild type Drosophila larvae exhibit a characteristic full-body contraction or cringe, in response to noxious cold. The expression level of each Innexin is knocked down in the peripheral dendritic arborization (da) neurons that mediate cold nociception via the Drosophila GAL4/UAS RNAi system. Knocked-down larvae are subjected to a cold behavioral assay, and their behavior is videotaped and analyzed to quantify the “percent cringe” value in order to identify the number of “cringers” for statistical analysis. By comparing the proportion of cringers between the knock-down larvae and the wild type, the involvement of the knocked-down Innexin in the cold nociceptive pathway can be inferred. A da neuron-specific tetanus toxin negative control will be described. All eight Drosophila Innexins have been tested with at least one RNAi construct expressed in class III da neurons. Thirteen of the fourteen total RNAi constructs resulted in significantly fewer cringers (Fisher Two-Tailed Exact Test, p<0.01).

T14\* Erin K. Kavusak, Isabel D. Lamb-Echegaray, Dr. Mark L. Gabriele

**Early Targeting of lateral cortex of the inferior colliculus modular fields by descending somatosensory cortical projections**

The lateral cortex of the inferior colliculus (LCIC) receives various multimodal inputs including those of somatosensory and auditory origin. During the postnatal period, the modular-extramodular LCIC arrangement emerges and can be visualized with a variety of neurochemical stains. Among these, glutamic acid decarboxylase (GAD) is a reliable marker of modular zones, while calretinin (CR) highlights surrounding extramodular domains. In the adult mouse, somatosensory inputs specifically target LCIC modules. The current study focuses on the development and shaping of descending corticocollicular projections that arise in the ipsilateral somatosensory cortex and target developing LCIC modules. Biocytin placements in somatosensory cortex labeled descending corticocollicular projections that reliably targeted the developing LCIC. Axonal terminal arborizations were robust ipsilaterally, ending in a series of patches along LCIC layer 2 that overlapped GAD-positive modules. Such projection patterns were evident during the early postnatal period, with discrete terminal distributions that aligned precisely with the developing neurochemical modularity. This early projection specificity became increasingly distinct with age, with highly refined adult-like modular terminal fields readily apparent by postnatal day 12. The present study provides evidence that descending somatosensory inputs exhibit an early projection alignment with developing LCIC modular zones. Ongoing studies aim to determine the developmental mechanisms that influence the segregation of multimodal LCIC afferent-efferent streams into its modular-extramodular framework.

T15\* Z. Logan Holley, Katherine M. Bland, Zachary O. Casey, Christopher J. Handwerk, Dr. George Vidal

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

Integrin subunits have been implicated in axonal and dendritic outgrowth. In particular, a strong positive association has been found between mutations in integrin beta 3 (*Itgb3*) and autism spectrum disorder, but little is known about neuronal *Itgb3* function in vivo. Many forms of autism spectrum disorder are thought to arise from dysfunctional dendritic arborization and synaptic pruning. Global knockout of *Itgb3* in mice leads to autistic-like behaviors. *Itgb3***-/-** mice also have reduced callosal volume, a key neuroanatomical correlate of autism. Here, we test the hypothesis that *Itgb3* is required for normal dendritic arborization in layer II/III pyramidal neurons of mouse neocortex. This was achieved by causing *Itgb3* loss of function through Cre-lox-mediated excision of *Itgb3* in a subset of layer II/III cortical neurons. Layer II/III cortical neurons were targeted for excision via in utero electroporation of GFP/Cre DNA constructs to the ventricular zone of developing telencephalon of mice in which exon 1 of *Itgb3* is flanked by loxP sites. Laminar positioning, regional targeting, and dendritic arborization of targeted neurons in juvenile mice (P23) were analyzed. Male and female mice were used for the study and analysis was blind to genotype. Results point to aberrant basal dendritic arborization of mutant neurons, when compared to C57BL6/J controls. Thus, integrin beta 3 appears to regulate basal dendritic arborization of layer II/III pyramidal neurons in the developing neocortex.

T16\* Shelby Pedigo, Dr. Oliver Hyman, Dr. Pradeep V. Menon, Dr. Bisi Velayudhan

**Investigating the effect of Sodium benzoate on immune cells and microbial population in the small intestine of mice**

Dietary ingredients can influence the mucosal surface morphology and mucosal immunity of the gastrointestinal tract. Additional health concerns and behavioral changes have been attributed to the consumption of foods containing preservatives and additives. Sodium benzoate (**SB**) is a commonly used bacteriostatic food and beverage preservative. This study investigates the effects of SB on mucosal health in the gastrointestinal tract. The extent of lymphocytic infiltration in the villi and granular density of Paneth cells can be used as evaluators of mucosal immunity. Adult C57BL/6 mice were randomly assigned to two groups (n=14). The control group and SB treated group received standard rodent chow. The SB treated group received 1% SB treated water. Food and water were available to all animals *ad libitum* for the experimental period of 30 days. Animals were monitored for body weight and food/water intake. Ileal samples for histological evaluation and caecal contents for microbial analyses were collected. Paneth cell granular density and lymphocytic infiltration into the lamina propria were evaluated by double blind scoring system on a scale from 1-4.  Culture and PCR analysis was performed on target species of gut bacteria. Statistical significance was declared at p<0.05. There was reduction in lymphocyte infiltration in response to SB suggesting possible alteration in mucosal immunity of the gut. Sodium benzoate increased the food intake and changed the gut microbial population compared to the controls. In conclusion, SB consumption may influence gut microbial population and mucosal immunity in murine species.

T17**g** Bailie Lavan, Dr. Patrice Ludwig

**Examining the effect of interstitial space on Eastern oysters (*Crassostrea virginica*)**

Eastern oyster populations, *Crassostrea virginica*, in the Chesapeake Bay have been historically decimated by overharvest, pollution, and disease. It has been well documented that current population numbers total less than 1% of their historic population and thus we know that the loss of natural shell reefs is imminent. While many restoration efforts are being focused on the structural shape and building material type of artificial reefs, very little, if any, research is being conducted on the effect of differing quantities of interstitial space on oyster recruitment and survival. Previous studies have concluded predictions stating the importance of interstitial space on predator-prey relationships occurring within oyster reefs; however, no practical method has been developed for quantifying this space. In this study, interstitial space has been defined as the following: As the structural complexity of an object increases, the object’s interstitial space increases, while the physical volume of the space decreases. Quantifying interstitial space will allow us to capitalize on recruitment, and thus survival, of oysters by mitigating the effects of predation. This method would allow for an increase in oyster reef populations and therefore an increase in oyster harvest and economic revenue, while additionally filling the knowledge gaps in quantifying interstitial space that exist across biomes. The goal of this research is to examine the effect of interstitial space on Eastern oyster recruitment and survival.

T18 Baodan Collins, Madison DeVost, Parker Moore, Hadeel Elhaj, Dr. Tracy Deem, Dr. Chris Lantz

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

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 generated CRISPR knockin mice that contain an endogenous fluorescent reporter gene (ZsGreen) for IL-3 expressing cells. To determine if these mice are accurately marking cells with the capacity to secrete IL‑3, we examined ZsGreen production by *ex vivo* developed and activated CD4 T cells as well as from CD4 T cells isolated from *Nippostrongylus brasiliensis* (*Nb*)-infected mice. Results indicate that *ex vivo* activated CD4 TH0, TH1, and TH2 but not TH17 cells from reporter mice express ZsGreen and secrete IL-3 protein. Likewise, primary and secondary infection of reporter mice with Nb induced small increases in the number of ZsGreen positive CD4 T cells present in mesenteric lymph nodes and lung. 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.

T19 Monica Gerber, Dr. Tim Bloss

**Analyzing the Effect of Apoptotic Mutations on the State of the Nascent Polypeptide-Associated Complex in *Ceanorhabditis elegans***

Cells experiencing misfolded protein stress can become debilitated and die, contributing to the onset of disease. The nascent polypeptide-associated complex (NAC) is a heterodimeric translational chaperone that protects against misfolded protein stress by mediating proper protein folding and localization during translation. Depletion of this complex results in misfolded protein accumulation in the endoplasmic reticulum (ER). To determine the importance of the NAC to proteostasis, we have previously artificially depleted the complex in *C.elegans* and observed numerous dose-dependent effects, including apoptosis of neuronal cells and changes in gene expression of hypodermal cells. In addition to characterizing cell-specific responses to misfolded protein stress triggered by NAC depletion, we are also investigating the state of the NAC in cells undergoing misfolded protein stress faced *in vivo*. Preliminary studies indicate that the beta subunit of the NAC is cleaved in worms undergoing chemically and heat induced misfolded protein stress at a functionally conserved caspase cleavage site, and we are determining if this cleavage is dependent on the core elements of the *C. elegans* apoptotic pathway. By understanding the cell-specific responses to misfolded protein stress induced by NAC depletion in combination with the fate of the NAC in the face of chemically induced stress, we hope to elucidate the role of this highly conserved complex in proteostasis and biologically relevant cell survival.

T20 Shane Chambers, Dr. Marquis Walker

**Characterization of Trpm1 function in mammalian iris constriction**

In mammals, the retina is the photosensitive tissue responsible for the initial capture of light and transduction of light-induced signals to the brain. These visual signals help drive image and non-image forming behaviors. Pupillary light reflex (PLR) is an involuntary non-image forming visual behavior which involves the constriction of the iris muscle tissue in response to ambient light intensity. A subset of photosensitive retinal ganglion cells provides the principal pathway for all light input to the olivary pretectal nucleus which directs the neuronal input driving iris constriction. Recently, transient receptor potential melastanin 1 (Trpm1) knockout mice have shown to have a severe defect in PLR, but it remains unclear how Trpm1 contributes to this behavior. We hypothesize that Trpm1 is necessary for PLR response and has novel activity in iridial cells to regulate constriction. We demonstrate that the reduced PLR in Trpm1-/-  mice is due to a functional loss of the Trpm1 channel in the iris. Using RT-PCR and immunohistochemistry, we demonstrate Trpm1 expression and localization in the iris, respectively. To further test the requirement of Trpm1 in pupil constriction we measured light responses in enucleated eyes of control and Trpm1 knockout mice. Tests in enucleated eyes show light-driven constriction independent of CNS input and a decrease in the response in eyes of Trpm1-/- mice. Pharmacological trials further demonstrate that Trpm1 expression in the eye is required for normal PLR.  Our results indicate that Trpm1 has a novel and necessary role in iridial cells and is required for light-driven constriction.

T21\* Michael Pamonag, Elijah Burton, Abigail Hinson, Dr. Kristopher Kubow

**Influence of fiber orientation and fiber movement on cell polarization and migration**

Directed cell migration plays a critical role in numerous physiological processes, such as cancer cell metastasis and tissue regeneration, and is guided by numerous factors including the physical structure of the extracellular matrix (ECM). Indeed cells have long been observed to follow anisotropic substrate features such as blood vessels and aligned fibers. However, migrating cells can also align ECM fibers, suggesting a positive feedback system in which cells simultaneously follow and align fibers, making migration persistence self-reinforcing. This phenomenon has typically been studied in the context of large cell masses and large-scale ECM deformations. Here we investigate whether the same positive feedback system is able to influence individual cell directionality, polarity, and migration. To observe this phenomenon, HT-1080 cells were formed into spheroids to stimulate directional migration and seeded into a methacrylated collagen type I matrix that was photocrosslinked or non-photocrosslinked. Our contraction assays suggested that photocrosslinking decreases cell-mediated fiber rearrangement. Cells in the crosslinked matrix showed decreased migration persistence, suggesting that cells’ ability to align fibers affects migration persistence. A similar effect was observed when spheroids were seeded on top of the matrices. Additionally, spheroids were embedded on rigid PCL scaffolding to determine if cell migration can be affected solely by fiber orientation. Scaffolds with unaligned PCL fibers showed significantly less directional persistence, suggesting that fiber orientation affects cell migration. These findings have implications for the control of cell invasion, tumor metastasis, and other complications regarding cell growth and migratory tendencies.

**Abstracts POSTERS**

E1 Haley Powers, Emma Nelson, Dr. David McLeod

**A review of the diction describing superficial skin structures observed on Anura species**

Skin is one of the most obvious features of any organism.  Skin plays a vital role in an organism’s defense mechanisms, communication, and interactions with its environment.  This is especially true for amphibians such as frogs (Order: Anura) and though this organ has been well studied with respect to its structure and function, much remains unknown. Many different terms are used to describe the various bumps and protrusions on anuran skin. Currently, there is no widely accepted standard definition for many of these terms.  Definitions of terms vary by author and study, some terms are used synonymously, while others are applied to very different structures. This creates ambiguity and confusion and may even confound results of past and future research efforts.  The objective of this study is to review the available literature that uses, defines or discusses the various structures found on the skin of anurans in order to formulate clear and specific definitions for them. This will include terms such as tubercles, warts, verrucae, spines, spicules, and cones. Based on a synthesis of this literature we provide recommendations for standardization of terms in an effort to improve the clarity of communication within the field.

E2 Brooke Patterson, David Thalman, Dr. David McLeod

***Plethodon cinereus* Presence at Nighttime vs. Daytime and Activity Levels in Optimal Weather Conditions**

*Plethodon cinereus* (Eastern Red-backed Salamander) is a common and widely distributed species in North America. Previous research found that *P. cinereus* is more active at night in order to avoid desiccation (Gergits and Jaeger 1990). This study addresses two aspects of the ecology of *P. cinereus*. Our first hypothesis is on the activity level of *P. cinereus* during diurnal cycles, which we expect to see more salamanders under cover objects during the day than we do in the leaf litter at night. Our second hypothesis is that we expect to see an increase in activity level when the temperature is above 10 degrees Celsius and with rain occurring within 24 hours of search time. For both these hypotheses we collected air and soil temperatures as well as soil moisture to determine how these factors may correlate with *P. cinereus* activity levels. Data will be collected in a 50 square meter transect in the Edith J. Carrier Arboretum during the months of January to April, 2019. For the daytime surveys, the salamanders presence is recorded by looking under rocks and logs, recording their stage of life (adult or juvenile) and whether or not a stripe is present. The nighttime surveys only consist of observations of salamanders activity on top of the leaf litter. Surveys are not conducted when temperatures are below freezing in order not to expose the salamanders skin to harsh weather conditions.

E3Victoria Mendoza, Mitchell Green, Dr. Bryan Cage, Dr. Roshna Wunderlich

**Using Long-Range Wide Area Networks to Study Lemur Habitat in Madagascar.**

All lemurs are endemic to the island of Madagascar and most are listed as endangered at some level. Madagascar is one of the world’s biodiversity hotspots with 101 endemic species and substantial habitat loss due to human activities. An understanding of the interactions between lemurs and their environment will help researchers manage protected areas, but this requires detailed quantitative data on both lemur behavior and environmental factors. The objective of this study is to employ long-range wide area networks (LoRaWAN) technologies to collect environmental data (surface temperature of trees, atmospheric temperature and pressure, humidity, and ambient light) throughout 80 Ha of the Beza Mahafaly reserve. We aim to automate the transmission of copious amounts of data in near real-time and with limited human interaction. While Wi-Fi (I EEE 801.11.x) is the preferred technology for network connectivity of remote sensory devices composing the Internet of Things (IOT), high energy expenditure and the need for reliable Wi-Fi is prohibitive in remote locations such as Beza Mahafaly, so LoRaWAN are more suitable. Sensory nodes can transmit small data packets over several kilometers and can run continuously for months to years on battery power. Data in this study will be collected by distributed nodes consisting of connected sensors. Data packets will be sent via long range radio modules to LoRaWAN gateway routers (LoRa Gateways). Such information when overlaid with lemur movements and activity may provide a better understanding of habitat use and insights to their overall survival.

E4 Anna Golden, Kevin Dannaher, Maggie Delaney, Harrison Giknavorian, Cal Morton, Dr. Patrice Ludwig  
**Technology and songbirds: A new approach to look at impacts of urbanization**

Although large cities and urban areas have continued to grow since the industrial revolution, little research has been done on the impact these areas have on the surrounding environment and wildlife. Previously undisturbed natural habitats are being destroyed and replaced with sidewalks and skyscrapers which may disturb various types of native wildlife, especially birds. Because of this, we are attempting to determine how urbanization has impacted the growth rate and feeding habits of songbirds by calculating the growth of songbird chicks. To do this, we are building birdhouses with a battery powered arduino and a load cell at the bottom to measure mass. The change in mass can be measured over time and the growth rate of the chicks will be determined. The birdhouses are being built using the Eastern Bluebird, *Sialia sialis,* as the model songbird since there is a significant number in the Harrisonburg/Rockingham area. The birdhouses will be placed in both rural and urban environments to compare the differences in the growth rates in hopes that it will aide biologists in determining the effects of urbanization. Using this integrated technology will also allow researchers to have a cost effective and streamlined way to collect important data on a number of different native birds.

E5 Sarah McKay, Dr. Bisi Velayudhan

**Understanding the Effects of Sodium Benzoate on Behavior in Mice**

Sodium Benzoate (SB) is a common food preservative found in an assortment of soft drinks and acidic foods. Previous studies have reported ADHD-like behaviors in children consuming carbonated beverages. The current study focuses on the effects of SB on anxiety and depression-like behavior using a mouse model. Adult C57BL/6 and BALB/c mice were randomly assigned to the control or SB-treated group. Both groups received standard rodent chow and water *ab litum* for 30 days. The treatment group received water containing 1% SB. The extent of mobility and grooming behavior were assessed in the home cage and in the open field before and after the treatment period. A forced swim test was also performed to assess depression-like behavior. SB treated animals showed increased grooming behavior in the home cage and decreased movement in the open field. There was no difference in the latency period during the forced swim test between the two groups. Further research would be necessary to definitively determine the effects of SB consumption on depression-like behavior in mice. Our data suggests that consumption of SB for a prolonged period may impact anxiety-like behavior in mice.

P01\* Z. Logan Holley, Katherine M. Bland, Zachary O. Casey, Christopher J. Handwerk, Brian D. Swinehart, Santosh Dasari, Eden Widener, Dr. George S. Vidal

**Cross-regional gradient of mouse cortical supragranular pyramidal neurons is regulated by integrin beta 3**

A strong positive association has been found between mutations in integrin beta 3 (Itgb3) and autism spectrum disorder, and global knockout of Itgb3 in mice leads to autistic-like behaviors.  However, little is known about the role of Itgb3 on neuronal structure and function in vivo. Here, we test the hypothesis that Itgb3 is required for normal dendritic arborization in layer II/III pyramidal neurons throughout mouse neocortex. This was achieved by causing Itgb3 loss of function through Cre-lox-mediated excision of Itgb3 in a subset of layer II/III cortical neurons. Layer II/III cortical neurons were targeted for excision via in utero electroporation of GFP/Cre DNA constructs to the ventricular zone of developing telencephalon of mice. Previous work in the lab established that dendritic morphology of mouse supragranular excitatory pyramidal neurons across much of the tangential plane of the cerebral cortex is partly shaped by a developmental gradient spanning several functional regions. Results point to the loss of this tangential, cross-regional morphological gradient across mutant Itgb3 neurons, when compared to controls. Thus, integrin beta 3 appears to regulate the systematic organization of basal dendritic arbors in layer II/III pyramidal neurons throughout developing neocortex.

P02 poster cancelled

P03\* Kevin Reifenberg, Dr. Christine May

**Community Composition of Salamanders in Appalachian Streams**

Salamanders can serve as an important bioindicators of water quality because they require clean, non-acidic water. This is of main concern because many Appalachian streams in the past century have been catastrophically affected by acid rain and coincidentally also support the highest diversity of salamanders in the world. In addition, salamanders are often a food source for native brook trout (*Salvelinus fontinalis*) which could influence the overall community composition of stream salamanders. The main goal of this study was to analyze the community composition of stream salamanders in response to varying brook trout densities and stream morphologies above and below waterfalls. Designated sections of streams both above and below waterfalls were established prior to sampling. Each sampling event took place after dark through June and July. Headlamps were used to look for salamanders both within the stream and one meter along each side. There was no significant correlation between percent slope, basin size, brook trout density, and rock type on salamander abundance or diversity. Future studies should include more study sites throughout Appalachia and diet analysis of brook trout to determine if they have a major impact on stream salamander density and diversity.

P04 Zoe Bergman, Chris Coggin, Katelyn Harless, Dr. Heather Griscom

**Phenology, Pollination, and Seed Dispersal Syndromes in Reforested Dry Tropical Ecosystems**

Dry tropical forests are one of the most endangered ecosystems. Pollination and seed dispersal syndromes are strong drivers of forest recovery. Animal pollination dominates tropical forests while animal seed dispersal can represent 50% of tree species in dry tropical forests. In dry tropical forests, a pronounced dry season can result in harsh conditions for both plants and animals. Many animals hibernate or migrate to wetter areas. However, the dry season is also a time of abundant flowers and fruit, both of which are important resources for animal pollinators and seed dispersers. Diversity and abundance of flowers and fruit in the dry season may vary within dry tropical forests of different successional ages and management regimes. In Panama, most of the original extent of dry tropical forest is gone. Remnants, serving as sources for propagules, animal pollinators and seed dispersers, persist in more remote locations. Over the last 30 years, reforestation has become a popular strategy to reclaim degraded pastureland. Common reforestation strategies include planting teak in monocultures, planting native timber species or relying on natural regeneration. However, little is known about the effect these different strategies have on biodiversity. During the dry season (March 2019), surveys will be conducted in three reforestation types (all 15 years old) as well as within old secondary forest. All flora (canopy and understory) will be identified and recorded as having flowers, fruit, or both. Four random transects will be set up in each of the four forest types. Any visitations by insect or bird pollinators will also be recorded. The prediction is that 15 year secondary forests will have the greatest number of species and individuals in flower and fruit while teak plantations will have the least. This is predicted to be positively correlated with bird and insect richness (quantified in two parallel studies).

P05 Rachel Boyce, Sarah Coleman, Julie Cumins, Joseph DeTrane, Dr. Joseph Harsh

**Investigating the longitudinal effects of an introductory biology course-based undergraduate research experience on students later in their academic career**

In line with national calls to engage all students in authentic research practices in preparation for the challenges of the 21st century, the JMU Biology Department redesigned its introductory majors labs as a two-semester research experience focusing on DNA Barcoding. Implemented in the fall of 2016, students (n>3,300 to date) in the BIO 140 and 150 labs learn research-related skills and concepts from the fields of ecology, molecular biology, and bioinformatics through cataloging local biodiversity and student-generated research projects. As earlier research has documented a range of conferred cognitive, affective, and behavioral outcomes self-identified by students upon completion of these research courses, the purpose of this study is to assess how the BIO 140/150 lab experience affects students as they continue in their undergraduate program. Using a quantitative and qualitative survey design, data were collected from 149 students that, on average, had completed the course two to three semesters earlier. Students were surveyed about the continued contributions of the 140/150 labs to their research-related competencies, science affect, and lifelong learning skills as well as their perceptions of the lab courses. Students most commonly identified that the 140/150 labs enhanced their abilities in scientific writing, laboratory techniques, collaboration, and how to cope with scientific challenges/failure – which they saw to benefit them in their later coursework. Student feedback also highlighted design features such as research independence, group collaboration, the sequential nature of the labs, and semester-long projects as being important to the learning process. Study results provide evidence to the intermediate effects of the 140/150 labs in supporting students’ developmental trajectory.

P06**g** Morgan Hussey, Christopher Will, Dr. Heather Griscom

**Avian species assemblages within *Bursera simaruba* trees in Panama**

Tropical dry forests are highly threatened ecosystems. Unlike tropical rainforests, dry forests are easily burned and cleared to be used for farming and livestock. Those remaining are a mosaic of land cover types including old growth forest, secondary forest, riparian forest fragments, pastures, and plantations. In these fragmented habitats, frugivorous bird species act as seed dispersers for fruiting trees and enhance forest regeneration in previously cultivated pastures. Here, we aim to quantify bird species richness and abundance at a 15-year-old secondary forest fragment on the Azuero peninsula of Panama (Cocoloche) in two *B. simaruba* trees. In addition, we classified species into habitat and foraging guilds using existing guild data. We collected data on the abundance of different bird species foraging on *B. simaruba* trees from sunrise to 9:00 AM in five 30-minute periods. A total of 33 species were observed within a 20 ft radius of the *B. simaruba* trees, 17 of which directly foraged on the trees’ fruits. The omnivorous and insectivorous guilds had the highest number of species represented, and open habitat species were significantly more numerous than closed habitat species. Our study demonstrates that fruiting tree species such as *B. simaruba* are important food sources for various foraging guilds and predominately forest/forest edge species. Fruiting tree species may be used to enhance regeneration and create suitable foraging areas for various bird species.

P07\* Elisha Burton, Michael Pamonag, Abigail Hinson, Dr. Kristopher Kubow

**Influence of fiber orientation and fiber movement on cell polarization and migration**

Directed cell migration plays a critical role in numerous physiological processes, such as cancer cell metastasis and tissue regeneration, and is guided by numerous factors including the physical structure of the extracellular matrix (ECM). Indeed cells have long been observed to follow anisotropic substrate features such as blood vessels and aligned fibers. However, migrating cells can also align ECM fibers, suggesting a positive feedback system in which cells simultaneously follow and align fibers, making migration persistence self-reinforcing. This phenomenon has typically been studied in the context of large cell masses and large-scale ECM deformations. Here we investigate whether the same positive feedback system is able to influence individual cell directionality, polarity, and migration. To observe this phenomenon, HT-1080 cells were formed into spheroids to stimulate directional migration and seeded into a methacrylated collagen type I matrix that was photocrosslinked or non-photocrosslinked. Our contraction assays suggested that photocrosslinking decreases cell-mediated fiber rearrangement. Cells in the crosslinked matrix showed decreased migration persistence, suggesting that cells’ ability to align fibers affects migration persistence. A similar effect was observed when spheroids were seeded on top of the matrices. Additionally, spheroids were embedded on rigid PCL scaffolding to determine if cell migration can be affected solely by fiber orientation. Scaffolds with unaligned PCL fibers showed significantly less directional persistence, suggesting that fiber orientation affects cell migration. These findings have implications for the control of cell invasion, tumor metastasis, and other complications regarding cell growth and migratory tendencies.

P08 William Smith, William Meara, Kavanaugh-Faye Bushnell, Gianna Mangone, Dr. Justin W Brown

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

P09 Chantel Pence, Amber Lin, Zach Minor, Leykie Green, Dr. Cass

**DNA barcoding of marine macroalgae: identification of seaweed species sold for human consumption**

In the United States, seaweed consumption is growing in popularity, making assessment of the health risks associated with its consumption an increasing concern for Americans. Some marine macroalgae (seaweed) species accumulate heavy metals and other minerals, posing a potential hazard for human consumption; but since edible seaweeds are often dried or otherwise processed, they can be difficult to identify based on morphology alone. DNA barcoding allows identification of species based on short species-specific DNA sequences, or barcodes. We asked whether DNA barcoding could identify the seaweeds present in edible products. Using a new DNA extraction protocol designed to manage the high polysaccharide concentration found in seaweeds, and degenerate primers designed to amplify DNA from two of the three seaweed phyla, we successfully extracted and amplified DNA from four seaweed samples. However, only three samples were successfully sequenced. All three samples were identified as species of brown algae; two samples were identified as *Undaria pinnatifida* (wakame), and one sample was identified as *Saccharina japonica* (kombu). Both of these species have the potential to bioaccumulate harmful substances. Our results demonstrate that our extraction protocol and primers can successfully isolate and amplify DNA from brown algae samples and that DNA barcoding is a potentially useful technique for identifying potentially hazardous seaweed species based on their genetic code.

P10 Saidah Lerman, Katie Doherty, Dr. Terrie Rife

**Developing a better understanding of tau’s isoforms and DNA binding abilities using Western Blots and Electrophoretic Mobility Shift Assays**

Aggregation of tau protein in the form of neurofibrillary tangles in neurons is a hallmark of many neurodegenerative diseases such as Alzheimer’s Disease, and other tauopathies. A leading cause for neurodegeneration is DNA damage, which tau is known to protect against. However, little is known about how tau protects against DNA damage, nor how tau binds with DNA. Tau has 7 major isoforms, and four domains, the N-terminal, microtubule binding domain, the C-terminal domain, and the proline rich domain. The N-terminal, proline rich domain, and the microtubule binding domain all can bind to DNA and tau seems to bind best to DNA with purine/pyrimidine repeats. We hope to determine which domains, and isoforms, are most likely to be found in the nucleus and which have the strongest binding affinity with DNA using cell fractionation, western blots and electrophoretic mobility shift assays (EMSA’s). We are finding, through cell fractionation and western blots that all tau proteins are found in the nucleus, but in chromatin there is a slight predominance for the 3R1N isoform, over the others, suggesting 3R1N tau binds better to DNA. To more closely examine tau’s ability to bind to DNA we are using the EMSA technique to confirm which isoforms of tau bind most strongly to DNA. We will also determine if the length of TG repeat affects tau DNA binding. Overall, this study will help us better understand how tau interacts with DNA so that we can determine how tau’s misregulation during neurodegenerative disease affects the cell.

P11\* Aya Andos, Ani Clem, Lexy Foor, Catherine Shola, Dr. Janet Daniel

**Investigating Phenotypic Differences Between the STP1 k/o and WT *Arabidopsis thaliana* in Response to Various Environmental Stresses​**

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. Previous work in the lab show that STP-1k/o seedlings grown on agar plates containing 50-100mM NaCl have increased root length, stalk length, and more leaves at 4 weeks.  These results suggest that STP1 k/o influences plant osmoregulation. Over the last year, we have been characterizing the halotropic response of WT and STP-1 k/o plants by plating seeds on 0mM/200mM split plates to determine genotype specific response to salt exposure. In addition to characterizing the halotropic response and root length, we are also measuring the angle of displacement from gravitropic response. Because the hypersaline environment decreases plant growth, we have decreased the salinity to 0mM/200mM split plates to allow roots to grow long enough to observe phenotypic differences. We are also developing methods to increase the harvest of  roots, shoots and leaf tissue for tissue-specific gene expression studies. This includes hydroponic tank sets that generate more material for measurement. These studies will enable us to better understand the role of STP-1 in the plant. We also plan to extend these studies to compare the gene expression patterns of both genotypes in high saline environments.

P12 Nathaniel Lucas, Callum Morton, Cortland Burke. Hope Kircher, Patrick Kilkenny, Klebert Feitosa, Dr. Roshna Wunderlich

**Measuring Intrinsic Foot Muscle Strength and Activation Using Novel Methodology and EMG Measurements**

Intrinsic foot muscles (IFM) play a critical role in arch support and balance. IFM atrophy has been observed in diabetic patients and may be associated with neuropathic ulceration. Nevertheless, a quantitative measure of strength and function of many IFMs remains elusive. Currently measures of IFM strength and function have characterized a limited number of the IFMs and only measure strength and function during flexion despite general acceptance that the action of many intrinsic foot muscles is abduction or adduction. We designed and assessed a novel instrument for measuring strength in abduction using capacitive force sensors. We compared electromyographic (EMG) data in six IFM during the novel test and two traditional tests of toe flexion, a static plantar pressure and paper grip tests. We found a strong relationship between knee angle (45, 90, 180) and static peak plantar pressure, suggesting the ability to isolate intrinsic from extrinsic foot muscles. There was a strong relationship between force produced by the first and second toes during our novel test and abductor hallucis and first dorsal interosseous EMG, respectively. However there was no relationship between force sensor data and EMG of the abductor digiti minimi or any force data with extensor or flexor digitorum brevis. We determined that it is possible to isolate IFM function in certain positions and that surface EMG electrodes can be used gather IFM activity. Ultimately, the goal of our project is to develop strengthening techniques to improve function, prevent injury, and enhance performance of the intrinsic foot muscles.

P13 Adrian Brazell, Dr. Corey Cleland

**Contribution of extrinsic tail muscles to the tail nociceptive withdrawal response through reconstruction based on muscle primitives: Role of non-linearities**

In the past, our laboratory has focused on identifying muscular synergies involved the nociceptive withdrawal response (NWR) in the rat tail. One approach was to record individual movement primitives associated with individual muscles and summing them to recreate the movement seen in the NWR. However, in these experiments we assumed linearity when adding up the movement primitives. Our specific aim for this study was to see to what extent movement primitives add linearly or non-linearly. In deeply anesthetized rats, we will first pulled two tendons acting on the tail individually and recorded the resulting tail movements for each using a conventional webcam positioned overhead. Next, we pulled these same tendons simultaneously and again recorded the resulting tail movements. Finally, we mathematically added up the movements from individual muscle pulls and compared them to the simultaneous pull to determine if the addition is linear. Our preliminary analysis suggests that as the magnitude of tail movement progresses, the contribution of each tendon to the movement is smaller when compared to when they were recorded separately. We can therefore conclude that addition of movement primitives is non-linear.

P14 Katherine Kourmadas, Jocelyn Mackey, Mason Lee, Dr. Amanda Cass

**DNA barcoding commercially sold medicinal leeches: potential evidence of prior human blood meals**

Medicinal leeches have long been utilized in medical practice dating back to ancient Egypt. While the anticoagulant properties of leech saliva makes them excellent for resolving blood clots, there are risks associated with their use, including infection, damage to healthy tissue, and transmission of pathogens from previous blood meals.  We used DNA barcoding to determine whether the species of leech sold by an online vendor is safe for use in medicinal leeching, as well as whether we could identify traces of previous vertebrate blood consumed by each leech. We conducted PCR with four different primer sets on DNA extracts from two leech individuals, and successfully amplified both invertebrate and vertebrate DNA.  Through sequencing the invertebrate sequence, we determined the species of leech to be *Hirudo verbana,* a species that is commonly used in medicinal leeching.  After sequencing the vertebrate DNA sample, we were surprised to find that it sequenced as human DNA. While these results may reflect contamination during the DNA extraction or amplification process, if these leeches have been feeding on humans previously, there is a high potential risk of pathogen transfer through blood.  This study brings into question the safety of online medicinal leech vendors and indicates that further investigation is needed to distinguish between harmless in-lab contamination with human DNA, and potentially hazardous cross-contamination of human blood and pathogens through medicinal leech use.

P15 poster cancelled

P16 Emily M. Anglemyer, Kinsey L. Miller, Christine E. Robson

**Understanding epimorphic and morphallaxis regeneration in *Notophthalmus viridescens* can lead to biomedical engineering advancement in adult human cardiac regeneration**

Unique to most vertebrates, certain animals such as the zebrafish and the newt, have the ability to regenerate tissues in the limbs, jaw, retina and even heart. Many mammals, including humans, are able to partially heal cardiac damage by creating scar tissue, but this does not ensure full functionality and often leads to heart failure if not treated by a doctor. Embryology research shows prior to birth, all vertebrates possess complete generative and regenerative abilities of all tissues but it is unknown why this feature disappears post-birth and in adulthood. Newts retain this by being able to regress specialized cells back into a simpler state, such as regressing them to stem cells, allowing those cells to redevelop into specialized cells and replace damage. Multiple signaling pathways found to maintain development and signal transmission have been studied to better understand the mechanism, including hedgehog, NOTCH, FGF and WNT. The gene for Sonic Hedgehog (SHH) has been found to be universal, but possibly dormant across the animal kingdom suggesting medicinal potential as science continues to advance. The current review will focus on the pathways related to newt limb and heart regeneration, specifically sonic hedgehog, to create a concise source on the mechanism to aid future cardiac research projects.

P17 Katie Griffin, Olivia Jackson, Brian Willis, Dr. David McLeod

**Determining Invasive Potential of common pond slider *Trachemys scripta elegans* in Harrisonburg, Virginia**

The introduction of invasive species into native communities can have extensive detrimental effects on species richness and population stability, particularly to organisms competing for an overlapping niche. The invasive pond turtle, *Trachemys scripta elegans*, has been displacing native pond turtles across the United States as they have been unintentionally introduced into local wetlands by pet owners (Somma et. al., 2018). Our survey explores population dynamics of turtle species present on James Madison University’s campus and in Harrisonburg, Virginia. Native species include *Chrysemys picta picta* (Eastern painted turtle), *Chelydra serpentina* (Snapping turtle); and introduced *T.s. elegans* (Red-eared slider), *Trachemys scripta scripta* (Yellow-bellied slider) and *Mauremys sinensis* (Chinese stripe-necked turtle). Possible application of these data includes evaluation of the invasive potential of *T.s. elegans*. These data are will determine if action needs to be taken to preserve native populations within the community. Data collection was conducted using hoop net trapping and visual observation surveys. Individual information was collected on carapace length, weight, age, and sex. Environmental conditions such as air and water temperature, water pH and local weather at time of capture were also recorded. The goal of these surveys is to build a robust dataset which can be used to conduct a demographic analysis of local turtles on an annual basis.

P18\* Hayden Casassa, Dr. Jonathan Monroe

**Redox Regulation of BAM1 in *Arabidopsis thaliana***

β-Amylases (BAMs), are found in plants, algae, and some bacteria, where they catalyze the hydrolysis of the α-1,4-glycosidic bonds of starch to form maltose. One of the nine BAMs in *Arabidopsis thaliana*, BAM1, is plastid localized, and is expressed in guard cells and mesophyll cells. It was shown using BAM1 purified in *E. coli* that the enzyme’s activity is redox regulated, being inactive when an internal disulfide bond is formed. The enzyme is reduced by thioredoxin such that when Cys-32 and Cys-470 are reduced the enzyme is active *in vitro*. However, upon knockout of Cys-470, the enzyme still shows signs of redox regulation suggesting that an alternative cysteine plays a role not previously discovered. Many chloroplast proteins are known to be active during the day and are regulated by light-induced reduction of disulfide bonds. In a study of starch metabolism in guard cells, BAM1 was shown to only break down starch during the day, consistent with redox regulation. To understand if redox regulation occurs in vivo is challenging because there are five catalytically active BAM’s in Arabidopsis. In order to investigate the redox regulation of the native protein, a quadruple knockout of every catalytically active BAM except BAM1 was generated. However, upon assay of native BAM1 from leaf extract, it was determined that the protein was active at night and was not oxidizable as predicted. These experiments pose questions as to why native BAM1 isn’t oxidizable along with which cysteine plays a role in the redox sensitivity.

P19**g** Melissa Encinias, Jack Doss, Dr. Idelle Cooper, Dr. Heather Griscom

**An Evaluation of Reforestation Pathways on Insect Richness in the Tropical Dry Forests of Panama**

Tropical dry forests are one of the most threatened ecosystems on the planet, and conservation is dependent on reforestation. Insects play important ecological roles in tropical dry forests and can act as valuable bioindicators of reforestation success. On the Azuero Peninsula in Panama, reforestation practices have been increasing over the last 30 years. To evaluate the effect of different reforestation strategies, we compared insect richness between three 15-year-old forests (an exotic-teak plantation, a native-species plantation, and a 15-year-old secondary forest) as well as within a mature-secondary forest. During a week period in the middle of the dry season, we sampled using nets at four transects in each forest type. Here we discuss insect richness in relation to forest type, canopy tree diversity, and herbaceous cover. We also discuss the abundance of pollinator species relative to flower abundance and the species relatedness between reforested site and the mature-secondary forest. Data from this study will be added to the PREDICTS database to assist collaborative effort to understand how terrestrial species respond to human pressures.

P20 Abby Stapleton, Dr. Ray Enke

**Characterizing epigenetic demethylation of conserved cis-regulatory elements in the developing chicken retina**

DNA hydroxymethylation is an epigenetic modifier signaling the process of active demethylation and transcriptional activation of target loci. Current DNA sequencing methods do not distinguish between methylated and hydroxymethylated DNA and are therefore of limited use for conducting epigenetic analysis of target genes. Here we employ a modified methyl sensitive restriction endonuclease assay followed by qPCR that will distinguish unmodified, methylated and hydroxymethylated cytosine bases to accurately characterize epigenetically modified target loci in the developing chicken retina. qPCR primers were designed to amplify regulatory regions surrounding six retina-specific genes previously identified as being involved in retinal development in chicken tissue to test experimental method.

P21 Laura Ferguson, Dr. Chris Rose

**Creating a developmental atlas for the American Toad (Anaxyrus americanus)**

A photographic record of the external and internal development of animals presents a valuable resource for comparative studies of how developmental processes and anatomies change in evolution. Developmental staging systems are already available for vertebrate model organisms including mouse/rat, chick, Xenopus and other frogs, axolotl salamanders, and zebrafish. However, making developmental atlases that record changes in internal and external anatomy throughout the body and throughout life was largely abandoned in the early 1900s. We are producing one for the American toad because this species is readily available and representative of a large, morphologically conservative family distributed throughout the world. Some toads also have distinctive developmental features including late onsets of ossification and lung use. We have produced developmental series of photographs of external anatomy, skeletally stained whole mounts, and specimens sectioned in transverse, sagittal and frontal planes; whole mounts were stained red for bone and blue for cartilage; embryonic and early tadpole stage slides were stained with hematoxylin and eosin; later ones were with a quadruple connective tissue stain. Our study confirms that ossification and lung inflation occur in late tadpole and early metamorphic stages in *A. americanus*.

P22**C** Destin Witmer, Dr. Ray Enke, Dr. Wendy Stapleton

**Sequence Analysis of Chronic Wasting Disease-associated SNPs in White Tailed Deer Native to Frederick and Shenandoah Counties**

With the recent identification of Chronic Wasting Disease (CWD) in Frederick and Shenandoah Counties, an understanding of the factors impacting disease spread is necessary to inform an effective response and containment. DNA sequences from local white tailed deer were analyzed for nine single nucleotide polymorphisms (SNPs) in the prion gene PRNP. Of these, five have shown significant association with CWD in midwestern deer populations, indicating an impact on susceptibility. These initial results have prompted our investigation of the five SNPs in deer populations navtive to Frederick and Shenandoah Counties. DNA sequencing and bioinformatics analysis will provide further insign in understanding the potential molecular factors impacting CWD spread in Virginia.

P23 Desiree Edemba, Dr. Morgan Steffen, Dr. Rocky Parker, Dr. Louie Wurch

**Sexual variation in the skin microbiome of garter snakes**

The reptilian microbiomes are not well understood and there are a limited number of examples of reptilian microbiomes. The model organism used for this study was the red-sided garter snake (Thamnophis sirtalis parietalis), whom are a species where males choose their mates based on the pheromones produced in the female’s skin. The goal of this experiment is to characterize the skin microbiome of the garter snake and its potential sexual dimorphisms, by both characterizes the skin microbiome of the red-sided garter snake and then comparing the skin microbiome between hosts of different sex. The microbial community was assessed using 16S amplicon sequencing.

P24-29**C** Dr. James Herrick, Dominique Lockwood, and the students of Bio 346

***Bacterial Discovery*, a CURE 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 uses 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’ (Course-Based Undergraduate Research Experience) in which students engage in authentic, potentially publishable research. The course was developed last Spring (2018) as the subject of an honors thesis by Sophie Jurgensen, a former student in the biology department. The 24 students in the course this semester sampled local stream sediments and poultry litter, enriched, isolated, identified, and characterized their isolates using standard microbiological techniques, the Enterotube multitest, PCR of the *invA* invasion gene, and antibiotic resistance phenotyping. The whole genomes of seven *Salmonella enterica*, one *E. coli*, and one *Klebsiella* isolates were sequenced and the students are carrying out bioinformatics analyses of these raw sequences. Six posters on their preliminary results are presented here.

P30\* Katherine M. Bland, Zachary O. Casey, Adam Aharon, Dr. Chia-Chien Chen, Irene Song, Andrew Lopuch, Dr. Yi Zuo, Dr. George S. Vidal

**Dendritic Spine Abnormalities Within Layer V Cerebral Cortical Neurons of a Heterozygous *Fmr1* Mouse Model**

Fragile X Syndrome is considered to be the most common form of intellectual disability caused by mutations in a single gene: *Fmr1*. Fragile X Syndrome patients have abnormal cortical dendritic spine sizes, shapes, and densities. Fragile X Syndrome is an X-linked chromosomal disorder, meaning that females normally carry two copies of the *Fmr1* allele while males only carry one. Here, we hypothesize that female heterozygous mice for *Fmr1* exhibit a mosaic of FMRP-positive and FMRP-negative cells across layer V excitatory pyramidal neurons in the cerebral cortex. We also hypothesize the dendritic spine density will be increased within neurons lacking FMRP. To test these hypotheses, we employed an immunohistochemical approach on heterozygous *Fmr1* mice expressing GFP in a subset of layer V pyramidal neurons. This approach identified neurons expressing or lacking FMRP. Dendritic spines of FMRP- positive and FMRP-negative neurons were analyzed within layer V of the primary visual, auditory, and somatosensory regions of the cerebral cortex. Current results suggest that cell-specific FMRP expression is necessary for normal dendritic spine development within layer V of the cerebral cortex.

P31 Lucas Manweiler, Cameron Baker, Andrew Douglas, Rhett Elliott, Haley Grove, Nicole McCroddan, Kathryn Motley, Andrea Navarro, Brittany Sweet, Dr. Bruce Wiggins

**Evaluating Stream Restoration Effectiveness by Using Benthic Macroinvertebrates as Proxy**

The Conservation Reserve Enhancement Program (CREP) aims to maintain environmental integrity in agricultural areas of Virginia, such as the Shenandoah Valley, by incentivizing land owners to block off streams from livestock and replant riparian buffers. These programs have become very popular, but there has been little research into the effectiveness of their restoring ecosystem health. With this discrepancy in mind, our research evaluated the effectiveness of riparian buffer programs by studying the factors of time elapsed since restoration and stream health based on the Virginia Stream Condition Index (VSCI). We hypothesized that that the length of time the buffer has been in place has an effect on the VSCI score of a stream and predicted that streams with older buffers will have higher VSCI scores. The health of the streams was evaluated by collecting benthic macroinvertebrates in a one meter2 net and identifying invertebrates to family, based off the VSCI. Streams were then plotted in GIS to evaluate each stream’s watershed area, and to determine time since restoration implementation, land cover types, and road and stream density inside the restoration sites’ watersheds. A 100-meter buffer was determined for the streams as well, and single variable and multiple variable linear regression analyses were performed within watershed areas and buffer zones. Regression analysis showed that time since restoration implementation and higher amounts of forested land cover up-stream led to higher VSCI scores inside stream buffers and within stream watersheds. These data showed that restoration programs do have a positive effect on the health of a stream, but that land-use upstream of the restoration project has an effect as well.

P32 Claire Ravenburg, Dr. Jonathan Monroe, Dr. Christopher Berndsen

**Investigating a putative dual-function β-amylase gene in rice**

In most plants, starch provides the carbon and energy necessary to sustain metabolism at night when photosynthesis is inactive. One class of enzymes involved in plant starch metabolism is the β-amylase (BAM) family. In *Arabidopsis thaliana*, there are nine structurally and functionally diverse members of the BAM family. This work will focus on two members: BAM2, which is localized in the chloroplast and is catalytically active and BAM7, which functions as a nuclear transcription factor. Sequence alignments revealed that BAM7 is very closely related to BAM2 and is hypothesized to have evolved by the fusion of a BZR1-like domain with BAM2. Moreover, our analysis of various angiosperm genomes revealed that some plants, including rice, may contain a single gene predicted to encode both BAM2 and BAM7. We will use rice to test our hypothesis that some flowering plants contain a single gene with two transcriptional start sites allowing one gene to encode two functionally diverse proteins. We plan to compare the structures and activity of the long and short forms of rice BAM7 to that of Arabidopsis BAM2 and BAM7. We will begin by designing cDNA clones to be synthesized by GenScript so that we can express, purify, and analyze both forms of rice BAM7. Overall, this project seeks to better understand the evolution of and role of BAM2 and BAM7 in plant starch metabolism. This knowledge will not only help us characterize the BAM family, but also contribute to our understanding of how genes evolve.

P33**g** Ruth Bowers-Sword, Dr. Joshua Linder, Dr. Roshna Wunderlich

**Assessing hunting pressures and the population status of the Critically Endangered Preuss’s red colobus, *Piliocolobus preussi,* in Cross River National Park, Nigeria**

Red colobus monkeys are the most endangered group of primates in Africa with all 19 forms threatened with extinction. The Critically Endangered Preuss’s red colobus (*Piliocolobus preussi*) is endemic to the forests of southeastern Nigeria and western Cameroon. Across its limited range, hunting and habitat loss are the greatest threats to the long-term outlook of Preuss’s red colobus. While most of the research on this species has been conducted in Cameroon, the conservation status of the Nigerian population remains poorly understood. Political unrest and violence has created a major obstacle to conservation efforts in Cameroon, making the Nigerian population within the contiguous CRNP forest extremely important. The goals of this research are to (1) determine the population status of Preuss’s red colobus in Cross River National Park (CRNP), Nigeria and (2) identify the spatiotemporal patterns of gun hunting in CNRP. I will conduct forest reconnaissance surveys in CRNP to collect data on the geographic distribution, abundance, and population structure of Preuss’s red colobus. I will deploy passive acoustic monitoring sensors to record the sounds of gunshots to quantify the geographic and temporal patterns of gun hunting in Preuss’s red colobus habitat areas. The project will be the first to focus on the population status of Preuss’s red colobus in CRNP and will introduce to park managers a novel, cost efficient tool – passive acoustic monitoring - to improve law enforcement monitoring and evaluation. This research will improve our understanding of the conservation status of Preuss’s red colobus, assess a novel application of acoustic technology for conservation, and contribute to anti-poaching management strategies within CRNP.

P34 Sabrina Circolo, Brandon Duda, Patrick Kilkenny, Dr. Roshna Wunderlich

**The influence of foot pad thickness and foot strike mechanics on plantar pressure distribution during walking**

Habitually unshod individuals have lower, more evenly distributed plantar pressures than individuals who habitually wear shoes, yet it is unclear whether this represents an anatomical or biomechanical difference. Adipose tissue in the foot can decrease plantar pressure by dissipating energy, attenuating shock, and dispersing force over the plantar surface, while foot strike angles have been shown to influence the peak force and rate of loading at touchdown. We examined the relationships among foot pad thickness, foot and leg kinematics at touchdown, and plantar pressure distribution beneath the heel and first metatarsal head in order to assess the extent to which soft tissue properties and foot strike dynamics contribute to plantar pressure distribution during walking. We used ultrasound to measure heel and first metatarsal pad thickness. Subjects walked across an EMED plantar pressure mat while being videotaped from lateral view (240 fps). We regressed peak plantar pressure, maximum force and pressure-time integral under the heel and first metatarsal against foot pad thickness, and touchdown angles of the leg, foot, and ankle. Preliminary results indicate that there is no significant relationship between foot pad thickness or kinematics at touchdown and plantar pressure distribution, possibly due to a small subject pool or time of data collection. Our findings suggest that other factors may contribute to the lower pressures observed in unshod populations than soft tissue properties or foot strike dynamics. Future studies could examine the effects of foot morphology on plantar pressure distribution and foot pad thickness in both shod and unshod populations.

P35 Benjamin Knick, Kayley Campbell, Madison Riahin, Olivia Hahn, Dr. Amanda Cass

**Barcoding milk: Identification of goat diet from trace plant DNA**

Animal products make up a large part of many consumer diets. Consequently, farmers strive to provide diets that meet the animals’ nutritional requirements so said animals can maximize production. Our study aims to help agricultural researchers by providing a basis to analyze the plant species composition of a goat’s diet. We asked if plant DNA could be extracted and identified from goat milk using DNA barcoding, and whether the extracted DNA could make distinctions between a goat fed on two different diets. A total of four milk samples were collected; two while the goat was on a grain-based diet and two after the goat had been on a forage diet for 24 hours.Using a modification of published milk DNA extraction protocols, we successfully extracted plant DNA from each milk sample. The DNA extracts were then PCR amplified and sequenced for identification. Three of the four samples sequenced successfully, and were all identified as members of the *Festuca*-*Lolium* grass complex, grasses commonly found in animal feeds and pastures. Due to lack of sequence divergence between species, we were unable to identify our samples to the species level. We were also not able to detect the shift from a grain to forage diet. However, these findings support the success of our milk extraction protocol, and though we could not distinguish between the two diets, they expand the potential of diet tracing in goats and other agricultural mammals.

P36 Penelope-Marie B. Clanor, Calvin Chenault, Dr. Ray Enke

**Analyzing Cell-specific Patterns of DNA Methylation in Human Retinal Neurons**

DNA methylation is an epigenetic mechanism responsible for regulating gene expression by the process of an addition of a methyl group to a cytosine nucleotide. In retinal cells, DNA methylation has been identified having a disproportionate relationship with gene expression, specifically in rod and cone photoreceptor-specific genes. Cone-rod homeobox (CRX) is a critical transcription factor in gene regulation for photoreceptor differentiation and maturation. CRX functions by binding to cis-regulatory elements and promotes histone acetylation to ultimately initiate transcription. Although CRX characterization and inverse correlation between gene expression and DNA methylation are known, the specific mechanism linking DNA methylation and expression of photoreceptor genes is lacking. By performing gene-specific bisulfite pyrosequencing on retinal tissue DNA, patterns of DNA methylation found in the peripheral retina, macula, and cornea, may provide insight into the role of DNA methylation in CRX binding.

P37 Christine Verdream, Brett Otsby, Dr. Christine May

**Habitat Utilization and Impact of Flooding on James spinymussel (*Parvaspina collina*) Populations in Virginia Streams**

Considering the ecosystem services that mussels provide and their high percentage of threatened species, specifically over half the freshwater mussels in Virginia, one avenue for future research could prioritize upstream mussels in downstream conservation plans. This project will provide information that could be applied to recovery plans for mussels in the James River watershed. In addition, the results will help bridge the gap between studies in freshwater and coastal systems through informing the release of propagated mussels to high survival habitats. Thus, increasing nutrient retention before reaching coastal systems. The objectives of the proposed research are: determine the relationship between flood disturbance and mussel population dynamics (abundance and variation through time) by compare a stream with flood disturbance to a dammed stream without flooding to determine if flooding and identify habitat preferences for *Parvaspina collina*. Analysis will use a four-year mark-recapture data set for sites in the James River watershed. Including a comparison of immigration and emigration between flooding events. Habitat preferences will be determined between two streams through a comparison and analysis of substrate, base-flow, water depth and velocity, and distance to the stream bank in areas where mussels have persisted. Our observations suggest that many mussels are temporarily occupying unstable habitats, understanding where mussels are most likely to survive and reproduce is crucial to identifying potential habitat and determining where propagated mussels should be released. Understanding the effect flooding has on *P. collina* populations can be vital in restoring the diminishing population and other endangered mussels in flood prone streams. Restoring populations will have positive ramifications for the filtration capacity of the populations of mussels in upland waters, benefiting nutrient retention downstream.

P38 Rana Ihsan, Dr. Timothy Bloss

**Characterization of the role of the nascent polypeptide-associated complex during misfolded protein stress in *C. elegans***

Cells experiencing misfolded protein stress can become debilitated and die, contributing to the onset of disease. The nascent polypeptide-associated complex (NAC) is a heterodimeric translational chaperone that protects against misfolded protein stress by mediating proper protein folding and localization during translation, and depletion of this complex results in misfolded protein accumulation in the endoplasmic reticulum (ER). To determine the importance of the NAC to proteostasis, we have previously depleted the complex in *C.elegans* and observed numerous dose-dependent effects, including those specific to neurons. High levels of NAC depletion result in neuronal apoptosis correlated with embryonic lethality, while sub-lethal depletion generates worms with multiple neuronal defects including mislocalization of cells, changes in neuronal-specific protein expression and malformed axons and dendrites. Our current work shows effects of NAC depletion on hypodermal cells that mirror neuronal defects in some, but not all, ways. Unlike neurons, hypodermal cells are not observed to undergo apoptosis in embryos strongly depleted of the NAC, but, as with neurons, hypodermal-specific protein expression decreases in NAC-depleted embryos, indicating a change in the gene-expression patterns of these cells. Consistent with this interpretation are embryonic enclosure defects observed in NAC-depleted cells indicative of malfunctioning hypodermal seam cells. In addition to characterizing cell-specific responses to misfolded protein stress triggered by NAC depletion, we are also investigating the state of the NAC in cells undergoing chemically induced misfolded protein stress. Preliminary studies indicate that the beta subunit of the NAC is cleaved in worms undergoing chemically induced misfolded protein stress at a functionally conserved caspase cleavage site, and we are determining if this cleavage is dependent on the core elements of the *C. elegans* apoptotic pathway. By understanding the cell-specific responses to misfolded protein stress induced by NAC depletion in combination with the fate of the NAC in the face of chemically induced stress, we hope to elucidate the role of this highly conserved complex in proteostasis and cell survival.

P39\* Alexa Cornwell, Valerie Shvygin, Dr. Terrie Rife

**Role of tau protein in transcriptional regulation of nitric oxide synthase I**

The neuronal protein tau has been heavily investigated in the context of neurodegenerative disease, through studying tau’s role in microtubular stabilization. Recently tau has been identified as binding to DNA and regulating gene transcription. Five different alternatively spliced isoforms (1N3R, 1N4R, 2N3R, 2N4R, and 0N3R) of tau are found in adult neurons. It is still unknown which part of tau binds DNA; however, isoforms with 1N inserts are found most often associated with chromatin and isoforms with the 3R insert are more likely to be increased within diseased neuronal tissue. To determine which specific region of tau is involved in DNA binding and transcriptional regulation, we are making knockouts specifically targeting exons 10 (4R isoforms) and 2 (1N isoforms). Once made we will utilize transcriptional reporter gene assays to quantify the effect of these knockouts on transcription from the nitric oxide synthase I promoter known to be transcriptionally regulated by tau. The sensitivity of this assay allows for careful quantification of small-scale changes in transcription at the cellular level as well as the degree of promoter strength present. Developing a better understanding of which tau isoforms help regulate transcription will help us better understand how changes in tau expression during disease affect transcription.

P40 Paulina Bauer, Brian Anderson, Dr. Terrie Rife

**Characterizing the potential of big tau in DNA protection with CRISPR-Cas9 knockouts**

Tau proteins are microtubule associated proteins (MAP) that might be essential for the stability of neuronal cells in the brain. In the Alzheimer’s (AD) brain, tau becomes hyperphosphorylated and loses its affinity for microtubules, aggregating into neurofibrillary tangles. Tau might play a role in the protection of neuronal genomic DNA from oxidative stress, which further suggests that tau might be related to the DNA and RNA oxidative damage that is observed in the AD brain. Peripheral nervous system (PNS) neurons contain an isoform of tau called, “big tau” that is not found in the neurons of the CNS. PNS neurons have been suggested to be more prone to DNA damage, thus we suggest that big tau may increase DNA protection. SK-N-MC cells are human cultured neuroblastoma cells that make a good model to study the role of big tau, as they contain all isoforms of tau and can be made susceptible to double strand breaks. To study the function of the big tau in protection against double strand breaks, CRISPR-gRNAs were designed to induce total and big tau knockouts in SK-N-MC cells. CRISPR gRNAs that are effective for making total and big tau knockouts were identified using Surveyor assays and Western Blots. Once stable knockout lines are established with effective gRNAs, comet assays will be used to quantitate DNA strand breaks present after stress. It is expected that total and big tau knockouts will have more strand breaks following stress than cells containing all of the tau isoforms.

P41 Taylor Bryan, Dr. Anthony Tongen, Dr. Gabriel Niculescu, Dr. Bryan Cage, Dr. Roshna Wunderlich

**The influence of enclosure size and type on energy expenditure and locomotor behavior in captive *Lemur catta***

Captive environments are beneficial for the rehabilitation and protection of endangered species, public education, and research, yet health issues such as obesity, diabetes, and cardiovascular disease have been associated with captive environments. Inactivity plays a well-known role in metabolic processes related to development of obesity. Cage size is positively related to activity in some primates, but previous studies in our laboratory have demonstrated that sifakas (*Propithecus coquereli*) in caged habitats (CGE) at the Duke Lemur Center move more than those in the natural habitat enclosures (NHE), possibly due to their density and habitual locomotor mode of leaping. To understand the extent to which this effect is species specific, we are examining the influence of cage design (CGE vs NHE) on *Lemur catta* locomotor energy expenditure and behavior. We will use inertial sensors to collect 3D acceleration and gyroscope data while simultaneously collecting behavioral data to identify how locomotor behaviors are represented as acceleration. The overall dynamic body acceleration (ODBA) will be calculated as a proxy for energy expenditure. Locomotor behavioral analysis data will be used to train a locomotor behavior detection program. Acceleration and behavioral data collected will be used to assess the manner in which animals use their habitat space. Ultimately, we will compare our results to data collected in the wild to assess how closely their behaviors resemble those in the wild and improve the simulation of NHE.

P42 Isabelle Houston, Dr. Jonathan Monroe

**Characterizing the role of 𝛃-Amylase 3 in cold stress recovery in *Arabidopsis thaliana***

Starch is a predominant energy reserve in plants that accumulates during the day to store the products of photosynthesis and is broken down at night to supply carbon and energy to sustain plant function in the absence of light or under abiotic stress. **𝛃**-Amylases, BAMs, comprise a protein family named for its catalytic members that hydrolyze starch into maltose. Of the nine BAMs in Arabidopsis, five are catalytically active, but BAM3 is the principle nocturnal starch-degrading enzyme in chloroplasts and is thought to play a role in cold stress. Cold stress leads to elevated BAM3 mRNA, however, we showed that BAM3 enzymatic activity decreases during cold stress suggesting the influence of an additional regulator that deactivates BAM3 to preserve starch reserves. Posttranslational modifications have been explored as a potential regulator. Cold stress is known to lead to nitric oxide (NO) signaling and nitrosoglutathione (GSNO) accumulation. BAM3 was found to be strongly inhibited by GSNO in vitro, but we do not know if this is what causes the reduction of BAM3 activity by cold stress in vivo. By utilizing a quadruple mutant plant, BAM3Q which lacks BAMs 1, 2, 5, and 6, BAM3 can be investigated in vivo without the masking effects of the other BAMs. By treating extracts of BAM3Q with reductant to reverse the effects of GSNO at different time points from the start of cold stress, BAM3’s GSNO sensitivity may be confirmed in vivo as well as determine a time frame for the effects of GSNO.

P43**C** Emma Eisemann, Selena Hise, Liam Godbold, Dr. James Herrick

**Plasmids conferring resistance to late-generation clinical antibiotics captured from poultry litter and stream sediments in the Shenandoah Valley**

Antibiotic-resistant bacteria in runoff from the farms may have a significant effect on the reservoirs of resistance genes in bacteria native to soils and streams. These genes, commonly carried on plasmids, can be transmitted by conjugation. Plasmids conferring resistance to tetracycline, a common agricultural antibiotic, were captured from environmental samples of poultry litter. This capture method requires no culturing of plasmid ‘donor’ cells and thus is potentially able to detect plasmids in uncultured bacteria. Plasmids conferring resistance to tetracycline were captured by releasing cells from sediments and conjugating with a rifampicin-resistant recipient *E. coli* cell culture. Six transconjugants were randomly selected and Stokes tests were used to determine susceptibility to nine additional antibiotics. Five transconjugants exhibited phenotypic resistance to piperacillin, a broad-spectrum antibiotic reserved for serious, hospital-acquired infections. Phenotypic resistance to streptomycin and piperacillin/tazobactam (a beta lactam/beta lactamase-inhibitor combination) were also observed. Three transconjugants were intermediately resistant to imipenem. This is of particular concern as resistance to this broad-spectrum antibiotic is rare. We intend to determine the Minimum Inhibitory Concentration of these antibiotics using a Sensititre 96-well test. Additionally, we are developing a method for sequencing multiple transconjugants from a single capture plate using the Oxford Nanopore MinION™ and a bioinformatic method to computationally separate and assemble multiple plasmids simultaneously. The Isolation of plasmids with resistance to late-generation clinical antibiotics from poultry litter is of concern, as it indicates that a reservoir of genes conferring transmissible resistance to these antibiotics may exist in bacteria native to these environments.

P44 Jeremy Rice, Shane Chambers, Dr. Marquis Walker

**Trpm1 Localization and Expression in Mouse Iris**

Pupillary light reflex (PLR) is an involuntary light response in the eye of all vertebrates where the muscular tissue of the iris constricts in response to ambient light intensity. Visual signaling that drives PLR is transmitted to the olivary pretectal nucleus by a subset of intrinsically photosensitive retinal ganglion cells (ipRGCs). These light signals are finally transmitted from the brain to iris sphincter muscle by ocular motor efferent fibers. Recently, it has been shown that isolated mammalian iris tissue can also directly respond to light. This intrinsic light-driven constriction is activated by the melanopsin photopigment. The terminal channel in this light-signaling cascade still remains unclear. Experimental tests from our laboratory strongly suggest that transient receptor potential melastanin 1 (Trpm1) is required in iridial cells for pupil constriction. We hypothesize that all light-dependent activity in the iris requires the Trpm1 channel.  We have used immunohistochemistry to localize signaling component expression. We hope to use these experiments as a foundation for identifying the expression of all signaling proteins in the iris.

P45 Sydney Wicks, Logan Lee, Jane Choi, Jason Lee, Dr. Amanda Cass

**Can DNA barcoding reveal the geographic origin of honey?**

In 2017, the United States produced 147.6 million pounds of honey, making honey a major source of agricultural revenue. Most honey is mass produced and distributed nationally, but locally produced honey can be a valuable contributor to the local economy. Studies have demonstrated that consumers will pay more for locally produced honey, leading honey producers to mislabel their products as locally produced to increase profitability. However, determining honey authenticity is difficult. Because honey is often mislabeled as local, the goal of our study was to use DNA barcoding to test whether the pollen suspended in samples of local honey was derived from wildflowers from the Rockingham/Harrisonburg area. We collected four samples of honey, three from local apiaries and one commercialized product from hives in Argentina, Canada, and the United States, and extracted the pollen from each sample. DNA extracts were then PCR amplified and sequenced. DNA sequences will be analyzed through the Blue Line of DNA Subway and identified to the lowest taxonomic level possible. We will then determine whether these taxa are found in the Rockingham/Harrisonburg area, thus supporting the local label. These results will allow consumers to make informed decisions regarding the authenticity of the food, specifically honey, they are purchasing.

P46 Jennifer C. To, Morgan L. Hussey, Dr. Dana L. Moseley

**Determining the repertoire size within the songs of the gray catbird (*Dumetella carolinensis)***

Songbirds use songs to attract mates, fend off other males, and to defend their territories. Most songbirds have small repertoires of fewer than five songs and are often learned from conspecifics in their environment. However, the main focal species of this study, the gray catbird (*Dumetella carolinensis*) possesses a large song repertoires that includes mimicry of other species’ songs. In this research, I investigated the repertoire size and composition of the gray catbird. Additionally, I aim to determine how often elements are repeated within and across bouts of song as well as their element-singing rate. For five individual catbirds from which we have the greatest number of recordings, I processed songs using sound analysis software called Raven. I identified the bouts and elements of the song to measure features such as bout length and number of elements in each bout. Using this information, I measured the average elements per bout as well as identified unique and repeating elements within and across bouts. Using the sound spectrograms of songs, I have catalogued the most common elements within individuals’ repertoires. In the future, we can investigate how often these elements are shared across birds’ repertoires and between urban and rural males.

P47**g** Cooper Brett, Dr. Mark Gabriele

**Microglial and CX3CL1 Patterning with Respect to the Developing Modular-Extramodular Framework in the Lateral Cortex of the Inferior Colliculus**

Microglial cells (MGCs) are versatile and implicated in shaping discrete neural maps in a variety of systems. MGCs respond to numerous cues in their microenvironment, among them the neuronally-expressed chemokine, CX3CL1 (fractalkine). The present study examines MGC and CX3CL1 patterns with regard to the emerging modular-extramodular framework within the lateral cortex of the inferior colliculus (LCIC). A host of modular markers, including glutamic acid decarboxylase (GAD), together with an extramodular marker, calretinin (CR), enable visualization of modular-extramodular domains in the nascent mouse LCIC. Major multimodal afferent and efferent systems of the LCIC appear to interface with its neurochemically-defined patch-matrix-like organization. Here we utilize iba-1 (a microglial marker) and CX3CL1 labeling to explore the involvement of MGCs and fractalkine signaling in establishing LCIC compartments. GAD-positive LCIC modules emerge shortly after birth and sharpen over the first two postnatal weeks. Iba-1 staining confirms MGCs are present in the LCIC and that their spatial organization and morphological appearance changes over peak periods of shaping. MGCs are present in the IC at birth, albeit sparse and with no clear distribution or pattern. By P8 and up to hearing onset, MGCs are more prevalent, with most residing at modular-extramodular borders. Labeling for CX3CL1 is strong at P12 and modular, in keeping with fractalkine signaling of resident MGCs. Ongoing studies utilizing transgenic lines with compromised fractalkine signaling aim to determine the precise role of MGCs in synaptic pruning events and the shaping of multimodal LCIC compartments.

P48 Peyton Coady, Anna Fracasso, Reef Buckhalter, Jessica Cornell, Dr. Marta Bechtel, Dr. Kristopher E. Kubow

**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 have been conducted to analyze how long chondrocytes remain viable within the microwells and to determine the preference of microwell size among the chondrocytes. The chondrocyte cells from these experiments were found to reside in microwells with a cross-sectional area of either one or two times the cell’s area of 300 microns and survived up to 7 days. These experiments have allowed us to create a new quartz photomask that produce microwells optimized for the chondrocytes. This optimized mask allows for maximization of stamps, desired stamp type, and number of wells. Future 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.

P49 Brady Simpson, Maria Ruggeri, Dr. Corey Cleland

**Dependence of the Nociceptive Withdrawal Response on Stimulus Location in the Intact, Unanesthetized Rat**

The nociceptive withdrawal response (NWR) is a critical movement characterized by the avoidance of noxious or otherwise unwanted stimuli. The response is mediated in mammals by withdrawal of the hind limb. Although the NWR has been studied in humans and spinalized animals, it is unclear whether there is a dependence on stimulus location in intact, unanesthetized, non-human animals. The specific aim of my research is to use high speed video of the intact, unanesthetized rat’s limb to determine if there is an effect of stimulus location on hind limb movement during the NWR evoked by heat stimuli. I hypothesize, based on previous work in this laboratory, that there may be only a limited dependence on stimulus location. The rat hind foot was stimulated in multiple locations on the plantar surface with a laser-based heat stimulus and the resulting NWR movement was recorded using high speed video to determine if the time course of joint angle (ankle, knee, hip) changes are influenced by stimulus location. Preliminary results show that there is only limited effect of stimulus location on the movement. More specifically, stimuli delivered to the toes resulted in initial upward movement of the front of the foot while stimuli to the heel resulting in initial upward movement of the back of the foot. However, stimuli delivered to both the front and back of lower leg resulted in the same flexion movement around the knee. Taken together, the NWR appears more complex than previously reported.

P50 Annie Hunger, Dr. Corey Cleland

**Identification of muscles that contribute to the tail nociceptive withdrawal response through selective tendon transection**

The nociceptive withdrawal response (NWR) is a protective movement in animals in response to noxious stimuli. It is unknown how extrinsic pelvic muscles contribute to the movement of the tail during the NWR in response to noxious stimuli. This research explores the contribution of extrinsic muscles regarding the overall flick of the rat’s tail. By performing a tendon lesion procedure, we are able to selectively knock out the contribution of muscles from one side of the tail, and measure the corresponding difference in movement compared to a control animal. In order to do this, under anesthesia we selectively cut bundles of tendons in the upper, dorsal portion of the tail. Following the lesion procedure and a one week recovery, we tested the rat by applying a small, noxious heat stimulus to both sides of the tail at various rostral-caudal levels and recorded the subsequent motion using high speed video. Preliminary findings showed that the rat, unexpectedly, moved its tail *toward* the stimulus instead of away from it in cases where the stimulus was applied to the same side of the tail as the tendon lesion was performed. These results suggest that movement arises from activation of muscles on *both* sides of the tail (co-contraction). Our novel approach should provide new insights into the control of the tail during the NWR.

P51**C** Dominique Lockwood, Dr. Louie Wurch

**Microbial Community Structure During a *Microcystis* Bloom in Lake Tai: Cultured Versus Uncultured Representatives**

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 (or antagonizing) toxic blooms of cyanobacteria remains a critical area of research. To better understand these impacts, we identified and characterized over 100 different bacterial isolates from an August 2018 *Microcystis* bloom from Lake Tai. A subset of these isolates is currently being used in a series of co-culture experiments assessing the nature of the interactions between the toxic cyanobacteria and specific bacterial partners. This information will provide a deeper understanding of the role bacterioplankton play in harmful cyanobacteria bloom dynamics as we work toward better protecting our freshwater resources.

P52 Harrison Giknavorian, Dr. Grace Wyngaard

**Genome size of parasitic copepod *Lepeophtheirus salmonis* embryos**

The life history and genetics of the salmon louse *Lepeophtheirus salmonis*, a parasitic copepod, is of interest because of the hundreds of millions of dollars in damage they inflict annually on salmon fisheries. There are no published estimates of genome size, but recently our lab has obtained estimates in both adult males and females. This discovery entailed developing new methods involving freeze-cracking of histological preparations. The males have larger genome sizes than females, due to having an additional chromosome. To support these estimates, we have measured genome size in embryos, which are carried in strings by the female. This difference in genome size between the sexes enables estimation of sex ratio at birth, data that is difficult to obtain in which adult males and females have the same chromosome number.One possible life history strategy is for adults to produce sex ratios biased by females. The egg strings presented new challenges in obtaining histological preparations suitable for genome size measurement due to the structure of the egg cases of embryos which are less penetrable to histological staining methods than free-living forms. We further modified standard protocols of free-living forms, incorporating freeze-cracking methods, to a refined protocol for parasitic egg cases. These new protocols and genomes size measurements will enable broader surveys of genome size in copepods, as well as a possible tool for addressing questions about sex ratio in natural populations.

P53\* Elizabeth Terry, Hanna Yu, Tyler Miller, Dr. Kevin Caran, Dr. Kyle Seifert

**Spacer length of novel cationic bipyrimidine amphiphiles dictates efficacy of antimicrobial activity**

Antibiotics play a critical role in efficiently treating various bacterial diseases that commonly affect humans. However, over-administration of drugs and varying adaptive mechanisms of bacterial pathogens contribute to the increase in antibiotic resistance. The rising prevalence of drug resistant pathogens on medical equipment increase patients’ susceptibility to acquiring nosocomial infections that are difficult to treat. Amphiphilic compounds, containing a hydrophilic head and hydrophobic tail, have shown to express antimicrobial properties. By better understanding their ability to disrupt bacterial membranes, we hope to contribute to the development of effective antimicrobial agents to limit pathogen transmission. The synthesized novel cationic amphiphiles contain two bipyrimidine groups, each with a hydrocarbon tail and separated by a carbon linker of varying lengths (6-14). The focus of our study is to find the optimal carbon linker length that most effectively disrupts prokaryotic cellular membrane. We aimed to achieve maximum bacterial disruption at the lowest amphiphilic dilution concentration. The bipyrimidine amphiphiles with varying carbon linker lengths were diluted (500uM - 1uM) and tested against *P. aeruginosa, E. coli, S. aureus, E. faecalis, S. agalactiae,* and *K. pneumoniae* through minimum inhibitory concentration (MIC) assays. The results indicate that amphiphiles with 12 or 14 carbon spacers were the most effective at inhibiting bacterial growth. There were no obvious differences between the MICs of Gram positive and Gram negative bacteria. The data suggest that antibacterial ability of amphiphiles increases with the length of the carbon spacer between bipyrimidine groups. Improved understanding of structure dependence and antimicrobial activity mechanism in amphiphilic compounds is the first step to developing practical applications for improving sanitation and decreasing transmission of nosocomial drug-resistant infections.

P54**g** Tyler Kovacs, Kevin Reifenberg, Dr. Heather Griscom

**Avian communities of the tropical dry forests of the Azuero Peninsula, Panama: a comparative study of reforestation type**

Panama possesses one of the most endangered tropical ecosystems on earth. Tropical dry forests have been historically cleared throughout Central America, leaving about 2% of forests intact. In Panama, this unique ecosystem has been nearly eliminated due to cattle ranching. Reforestation efforts of the tropical dry forests range from monoculture plantations to natural regeneration of secondary forests. Avian communities may be responding differently to these reforestation systems, which has implications for their future. In this study, avian communities were investigated within three reforestation systems in the tropical dry forests of Panama. During the dry season in March 2019, avian communities were compared within three 15 year old forests with different reforestation strategies (an exotic monoculture of *Tectona grandis*, a mixed species tree plantation, and a young secondary forest) as well as within a mature secondary forest. Point count surveys were conducted between 6 and 9 AM for one week along 4 randomly placed transects in each forest type. Data was collected on bird species richness, abundance and dietary guild to compare communities within each of the four forests. The young secondary forest had the highest diversity of birds. The mature secondary forest had low total bird diversity, however it had the most unique community compared to the other sites. This data will be added to the collaborative PREDICTS database project to increase our understanding of how biodiversity is responding to land-use changes around the globe.

P55\* Kaitlyn Harless, Dr. Patrice Ludwig

**Decomposition of Cattle Dung by Aphodius pseudolividus in Virginia is Density Independent**

Dung beetles are responsible for a multitude of ecosystem services including the decomposition of dung pats, which in turn enriches the soil with nutrients for local vegetation to utilize. There are three different types of dung beetles in North America; rollers, tunnelers, and dwellers. Research suggests a positive correlation between density of tunneler dung beetles and the rate of dung decomposition (Yamada, 2006). We built on this finding with an experiment to determine the effect dweller dung beetles have on the rate of decomposition of cattle dung. The density of a dweller species, Aphodius pseudolividus, was manipulated for this field experiment. The number of individuals per sample was determined by the natural density of A. pseudolividus, which was found to be 40 individuals per pat. A control treatment of dung that was not manipulated from the field was also used. The 0.5 kg frozen and thawed dung samples were placed according to a randomized plot design had either half, equal to, or double the natural density of A. pseudolividus. Replicates were destructively sampled on days 1, 2, 4, and 7 and the control destructively sampled on day 7. The wet and dry mass (g) and moisture (%) of the samples were measured. The dry mass of the dung was measured for all samples after collection, the dry mass was then used to determine the amount of decomposition that had occurred. Decomposition was defined as the difference between the control and experimental pats. It was expected that pats with a higher density of A. pseudolividus would also have the highest amount of decomposition. The data, however, showed no significant difference between treatments. This could mean that dweller species are not efficient decomposers or that the species used was too small in size to make a significant difference.

P56 Jodi Cheung, Dr. Christopher Rose

**How thyroid hormones and their inhibitors affect bone development in the frog *Xenopus laevis*.**

Unlike most vertebrates, amphibians acquire their bones gradually over sometimes prolonged periods of larval growth and metamorphic development. The appearance of bones and other postembryonic changes are known to be mediated by thyroid hormones (TH) and they are commonly studied by inducing them prematurely in premetamorphic stage tadpoles. To date, however, there has been no systematic attempt to work out the effects of TH type (T4 and T3), dose and larval stage on induced bone development in the lab animal most commonly used to study amphibian metamorphosis, the aquatic frog *Xenopus* *laevis*. We used specimens from a previous study on hormone-induced cartilage development in *Xenopus* (Rose and Cahill, 2018) to study how TH type (T4 and T3), dose and larval stage affect the order of bone appearance and degree of ossification that can be induced in tadpoles. The tadpoles had been treated at early, mid and late larval stages with T4 or T3 at doses that encompass the plasma concentrations measured in naturally developing *Xenopus* and commonly used to induce tissue responses in *Xenopus* in the literature (1, 5, 10 and 50 nM). Methimazole and iopanoic acid were additionally applied as thyroid inhibitors to isolate the effect of each hormone. We scored specimens from 12 experiments for the presence and extent of development of the first 13 bones to appear naturally. The results will be presented in 3D graphs that show the differences between TH-treated, controls and naturally developing animals as functions of stage and concentration.

P57**C** Scott Schumacker, Dr. Ray Enke

**Analysis of Cell-Type Restricted Transcriptional Networks in Human Photoreceptor Neurons**

The retina is a layered neuronal tissue lining the posterior portion of the eye that converts photons of light into visual images in the brain. Rod and cone photoreceptors are highly specialized light sensitive neurons that initiate this process of phototransduction. Though they are similar cell types, rods and cones have distinct functionalities, synaptic connections, and are affected by different blinding disease alleles. In order to characterize cell-type specific transcriptional networks in human photoreceptors, rod and cone-enriched samples were biopsied from the eyes of 13 post-mortem human donors. Total RNAs were extracted from retinal samples using a Qiagen AllPrep Mini Kit. High quality RNAs were prepared into cDNA libraries representing cellular mRNAs and sequenced using an Illumina NextSeq 500 sequencer. Sequencing reads were assessed, trimmed and visualized using FastQC, Trimmomatic, and MultiQC software respectively. High quality reads were then aligned to the human hg38 reference transcriptome using the high speed pseudoaligner Kallisto. The Sleuth RStudio package was used to quantify read alignments and calculate differentially expressed transcripts (DETs) between rod and cone-enriched sample groups. These analyses identified 10,875 DETs between sample groups with a FDR adjusted p-value ≤0.05. Of these DETs, 4,365 are transcribed at higher levels in rod-enriched retinal tissue while 6,519 demonstrate increased transcription in the cone-enriched retina. We are currently testing the hypothesis that differential patterns of DNA methylation contribute to cell-type restricted transcription in photoreceptor neurons. These data will contribute to a better understanding of epigenetic regulation of gene expression networks in the human retina.

P58 Quinn Adams, Alexander Barrett, Jasmine Benbei, Kelsey Broadwell, Rachel Dion, Valeria Erazo, Ashley Farnan, Malia Gardner, Lauren Johnson, Nicole Landry, Tess Leftwich, Frank May, Maz Maza, Rebecca Moiera, Bahar Osman, Kyle Rubino, Greg Shero, Kristen Snow, Beth Terry, Ryan Zoldork, Dr. Louie Wurch

**Aquatic Microbiology: An upper level CURE where students conduct research on the effects of bacterioplankton on toxic cyanobacteria**

Aquatic Microbiology is an upper level Course-embedded Undergraduate Research Experience (CURE). As part of an NSF grant, students in this class are conducting research into the impacts of bacterioplankton on toxic algae, specifically the toxic cyanobacteria *Microcystis*, which forms in freshwater and is found globally. Water samples from a bloom of *Microcystis* were collected in Summer of 2018 from Lake Tai, China. Students in Aquatic Microbiology took those water samples and cultured multiple different bacteria isolates. Students then characterized those isolates and identified them based upon their 16S rDNA gene. Finally, students conducted co-culture studies to examine the impacts those isolates had upon *Microcystis*.

P59 Shad Abdullah, Dr. Michael Renfroe

**Decrease in Antioxidant Concentration in Herbs over Time**

Dietary antioxidants play numerous important roles in human health. Culinary herbs and spices are important sources of dietary antioxidants, but those antioxidants can decrease in concentration over time. We extracted hydrophilic and lipophilic antioxidants from dried schizocarps of seven species from the plant family Apiaceae. Antioxidants were extracted at the time of purchase and after six months of room storage. Significant differences were present among the herbs at each time of extraction. All herbs also decreased significantly in their antioxidant concentration over six months when stored at room temperature. These findings may have implications for dietary recommendations and can inform consumers as to use and storage practices of common culinary dried herbs.

P60 Emily Williams, Dr. David McLeod and Dr. Louise Temple

**Culture Dependent Analysis of Microbiome Bacterial Growth in *Polypedates leucomystax***

Within each organism exists complex communities of bacteria and fungi, which collectively make up the microbiome. An organism’s microbiome provides many benefits, such as resistance to disease, adaption to the environment, and contributes to the health of the individual. However, the much about the microbiome remains unknown. This project focuses on analyzing the bacterial strains that make up the microbiome of the Southeast Asian foam-nest building frog *Polypedates leucomystax*. Specifically, I determine which bacterial strains can be specifically cultured in comparison to metagenomics data presented in previous studies. Field sampling of frogs and their microbiome was conducted in the Temburong District of Brunei on the island of Borneo. All field work was conducted at Kuala Belalong Field Studies Center. Bacterial strains were grown on R2A media and isolated to obtain pure bacterial cultures. Specimen identification was confirmed using the 16s rRNA gene sequence. DNA sequence results were compared to previously identified samples using the NCBI Basic Local Alignment Search Tool (BLAST) database as well as the RDP sequence match as a cross reference. The identity of the cultured bacteria are compared to results from previous studies, providing a comparison between culturable and non-culturable aspects of the microbiome.

P61 Daniel Bradford, Densel Dagdagan, Keegan Lowman, Lexa Treml, Jennifer To, Arcangelo Arecchi, Dr. Patrice Ludwig

**Usage of drones for counting flowers necessary for pollination**  
With environmental problems in the last three decades, there has been a sharp decrease in both pollinators and flora pollinated. A prime example is the bee species (*Anthophila*) and the flowers they pollinate. Despite being one of the most efficient pollinators, many factors have contributed to the drop in the bee population. Factors include pesticides and climate change, which resulted in a misalignment between flower blooming and natural bee activity. Although there has been a lot of support for the pollinator population, there has been little research on how successful it is on creating flowers that support these pollinators. This project aims to use a drone to digitally count patches of flowers at Blandy Experimental Farm. The intention is to cut down on time that would have otherwise been used to count manually. We flew a 3DR drone over transects of Blandy Experimental Farm to capture multispectral images with the onboard RedEdge camera. We will run these pictures through an algorithm in order to quantify the amount of flowers in a picture, based on the values integrated from five different spectral images. In the future, we can refine the algorithm to be able to differentiate individual flowers rather than patches, and potentially be able to identify the type of flower. On a larger scale, this use of conservation technology will able to more efficiently track trends in pollinator resources.

P62 Yusuf Aboutabl, Dr. Chris Rose

**Investigating the cellular basis of hormone induced-shape changes in *Xenopus* lower jaw cartilage**

Metamorphosis in amphibians results in drastic changes in the shape of the feeding skeleton as the organism transitions to suction feeding to biting and tongue protrusion. These changes are mediated by thyroid hormones and they are commonly studied by inducing them prematurely in premetamorphic stage tadpoles. However, previous research in our lab has shown that premature induction can produce abnormal shape changes depending on the stage, hormone type (T4 or T3) and hormone concentration used. We aim to understand how the shape changes induced in the lower jaw are produced at the level of changes in cell size, shape, arrangement and extracellular matrix secretion. Since these variables change with tadpole development, we also aim to understand how the starting cartilage histology affect the outcome of induced shape changes. We induce shape changes by immersing posthatching and early tadpole stage specimens of *Xenopus laevis* in 10 nM of either T4 or T3; methimazole and iopanoic acid were used as thyroid inhibitors to isolate the effect of each hormone. Animals were sampled a day or two before death was expected to occur in T3 treatments and fixed in 10 % formalin. They are being prepared as skeletally stained whole mounts to visualize shape changes and as histological slides to visualize cell size, shape, arrangement, and matrix secretion. Documenting induced morphological changes on a cellular level allows us to better understand how thyroid hormones induce morphological changes and how the cellular properties of cartilage might constrain the amount and kind of shape changes that evolve.

P63 Francis Gebhard, Dr. David McLeod

**A comparison of the effectiveness of two gecko diets**

The crested gecko, *Correlophus ciliatus,* is the most common captive maintained species of Diplodactylid gecko. This old-world gecko (New Caledonia)is primarily frugivorous, feeding on insects, fruit, and seeds in the wild. In captivity, however, they can be fed solely on commercially available meal replacement powders specifically formulated for Diplodactylids. Protein, fat, and calcium are three of the main nutritional components found in these diets, and proportions of these vary between products. To date, no published research has tested the effectiveness of these diets for *C. ciliatus.* The purpose of this study is to test the effectiveness of two dietary products on the growth rates of *C. ciliatus.* Pangea Fruit Mix™ Watermelon Mango Complete Gecko Diet (PFW) and Black Panther Zoological Original Complete Gecko Diet (BPZ), were selected because of the differences in nutrient content, BPZ having higher amounts of protein, fat, and calcium (BPZ, 2018) than PFW (Parks, 2018). Sibling pairs of captive bred geckos were raised on PFW and BPZ and monitored for changes in size and weight during an 18-month study. Using a one sample t-test, it was determined that hatchlings fed PFW diet grew at a significantly greater rate (p<.001) than those fed BPZ. This information can now be used by keepers of diplodactylid geckos so that they can provide a diet that promotes the best health and growth of these animals.

P64 Monica Chiodo, Dr. Marquis Walker

**Site-directed gene editing in *Drosophila* using Crispr/CAS9**

In recent years, the Crispr/Cas9 gene editing system has proven to be a powerful tool for generating site-specific mutations in the genome of many research animals. Our lab uses *Drosophila* as a genetic model to study gene expression and function in the retina. 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 express Cas9 enzyme in germ line cells to generate site-specific cleavage in the genome of offspring of treated flies. 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*. To measure the efficiency of genome editing, we have targeted the expression of an EGFP transgene. This system allows us to rapidly induce mutation and quantify the frequency of mutation in treated embryos.

P65 Michelle Bair, Shema Mohebi, Bailey Gotchel, Zeru Tadesse, Dr. Patrice Ludwig

**Biology in technology**

Our projects demonstrate the implications of biology and technology by working in interprofessional groups. Our team members are working together in a course for “Robots for humanity” during the spring semester of 2019. The class is comprised of biology, computer science, as well as engineering majors that have been working together throughout the semester to developing projects that will be presented at the innovation summit on April 26. In this presentation we will be using two projects that have been developed by two different groups. One project involves brain monitoring interface (BMI) technology for controlling precise position arm movements for the purpose of assisting cargo loaders; the aim to this developmental prosthetic is to prevent injury and fatigue for this labor intensive position. The other project is the process of creating a fully autonomous drone that would eventually be able to complete tasks such as delivering blood and other vital materials to the scene of an accident before emergency response vehicles arrive. The drone utilizes biological aspects by mimicking the ultrasonic waves of bats through an ultrasonic sensor in order to detect objects around it. With the use of interdisciplinary practice as well as the efforts to combine technology and biological concepts, we hope to have an impact on other developing projects as well as to help improve everyone's quality of life long term.

P66**C** Jennifer Anderson, Louisa Esteban, Dr. James Herrick

**Whole genome assembly and annotation of *Salmonella enterica* isolated from stream sediments and poultry litter in the Shenandoah Valley**

*Salmonella enterica* is comprised of over 2500 known serovars and is estimated to cause 1.2 million illnesses and 450 deaths annually in the United States. This study is an analysis of the whole genomes of 39 *Salmonella enterica* strains (representing 14 different serovars) isolated by the Herrick lab from local poultry litter and stream sediment. Raw sequencing reads were trimmed and filtered using Trimmomatic and assessed for quality using FastQC on GalaxyTrakr, a proprietary instance of the bioinformatics toolkit Galaxy. Genomes were assembled using SPAdes Genome Assembler and the assembly quality assessed using QUAST, also on GalaxyTrakr. Assembled output fasta files were then input to the BacWGSTdb Single Genome Analysis database. Outputs included identification of closely related isolates using both single nucleotide polymorphism (SNP) and core genome multilocus sequence typing (cgMLST) approaches, as well as annotation of antimicrobial resistance genes and virulence genes. The results will allow for a comprehensive analysis of the phylogenetic relationships between all 39 isolates as a collection, as well as the relationship between these isolates and strains isolated elsewhere. BacWGSTdb outputs include annotations on antimicrobial resistance and virulence genes as well as their contig position, which can be used in the future in directed studies of these genes specifically. These analyses will provide a platform for future studies to determine possible sources of these strains, as well as to assess their potential for horizontal gene transfer via plasmids.

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| Tolvay, Heather | | T13 | | | | | | | | |
| Tonger, Anthony | | P41 | | | | | | | | |
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| Walker, Marquis | | P44, P64, T20 | | | | | | |
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