

25th Annual
BIOSYMPIOSIUM
2016



James Madison University
Biology Department

Thursday, April 14 - Friday, April 15, 2016

The students and faculty in the Biology Department gratefully acknowledge support for their research from:

- ❖ Jean D. Acton Scholarship
- ❖ Betty Jo Loving Butler '58 Endowment for Undergraduate Research Scholarship
- ❖ Farrell Summer Research Scholarship
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C Research that is part of CGEMS (Center for Genome and Metagenome Studies)

★ Digital posters (mostly in room 2009, but some in hallway)

* Research that was supported by summer funding gift

★ Digital posters (mostly in room 2009)

Schedule: Thursday April 14th

SESSION 1	12:00-2:00pm	POSTERS	2nd Fl. Foyer
P1	Kristianna Bowles, Amanda Crandall, Jessie Doyle, Rhiannon English, Megan Moore, Joseph Noel, Cole Roberts, Nathan Robinson, Katherine Stanley, Erin Thady, Dr. Bruce Wiggins	Effects of Agricultural Restoration Practices on Stream Health in the Shenandoah Valley, Virginia	
P2	Annamarie Meinsen, Christophe Langouet, Dr. Stephen Turner, Isac Lee, Dr. Winston Timp, Dr. Ray Enke	Integrating Transcriptome & DNA Methylome Datasets Obtained from the Developing Chicken Retina	
P3	Brie Hayden, Dr. Patrice Ludwig	The Use of Drones in Ecological Research	
P4	Victoria Callahan, Dr. Marta Bechtel	Pro-Inflammatory Effect of Dengue Virus NS-1 and Envelope Proteins in Cultured Human Articular Chondrocytes	
P5	Madison Azzara, Alex Shafer, Dr. David McLeod	★ HOPping to it: engaging the community in amphibian and reptile education with the JMU Herpetology Outreach Program	
P6	Rachel Cisek, Dr. Patrice Ludwig	★ Species Diversity of Dung Beetles in Rockingham County, Virginia	
P7	Luke Bava, Megan Budnik, Emily Cooke, Michelle Lewis, Warner Lowry, Sarah Magee, Sabrina McCormack, Scott Melander, Madeline Quatannens, Nolan Scheible, Emmanuel Sempeles, Leigh Soderberg, Julio Soriagalvarro, Melanie Vasso, Kartik Viswanath, Brad Weidner, and Dr. Michael Renfro	Effect of synseed composition on emergence of endangered <i>Saintpaulia rupicola</i>	
P8 ^C	Courtney Stout, Nicholas Dunham, Dr. Chris Berndsen, Dr. Ray Enke	★ Investigating Epigenetic Regulation of CRX and NRL Binding to Regulatory Regions in the Vertebrate Retina	
P9	Shelby Snowden, Dr. Kerry Cresawn	★ Evaluation of a Science Outreach Program for all K-5: Madison Discovery	
P10	Mary Aland, Christina Gillespie, Maggie Shostak, and Dr. Katrina Gobetz	★ A study of burrowing behaviors of juvenile and adult <i>Rattus norvegicus</i> using morphometric analysis and digital burrow imaging	
P11*	Qiong Kang, Stephanie Thai, Jul Kim, Jake Braun, Corey Cleland	Dependence of the nociceptive withdrawal response of the tail on stimulus location and intensity	
P12	Shannon Palmer, Justin Rissmiller, Adam Geiger, Kristy Daniels, Michael Akers, Dr. Bisi Velayudhan	The Effect of Accelerated Feeding on Duodenal Morphology in Dairy Calves	
P13	Katherine Stanley, Dr. Conley McMullen	Floristic survey of the Smith Creek restoration area	
P14	Claire Gormley, Kristen Hoffman, Rana Ihsan, Dr. Tim Bloss	Characterization of cell-type specific responses to misfolded protein stress in <i>C. elegans</i>	
P15	Brianna Lee, Dr. Carol Hurney	No title	
P16	Nolan Scheible, Toma Matveeva, Nathan Ashley, Bejan Rasoul, Dr. Kimberly Slekar	Investigating the role of the B-NAC on stress response in baker's yeast	
P17	Ellen Jones, Emily Miller, Dr. Joseph Harsh	Unpacking Undergraduate Research Experiences Through the Use of Weekly Journal Data	

- P18 Michael Gay, Taylor Wright, Dr. Morgan Steffen
A systems biology approach to understanding ecologically threatened freshwater ecosystems in the Chesapeake Bay watershed: preliminary findings
- P19^C Shahzeb Khan, Dr. James Herrick
Isolation, Identification, and Genome Sequencing of *Aeromonas* Bacteria Native to Cooks Creek, a Stream in the Shenandoah Valley of Virginia
- P20^C J. Roberts-Torres, M. Partin, K. Libuit, J. Kurasz, and J. B. Herrick
Isolation and characterization of *Staphylococcus* spp. from manure contaminated streams in the Shenandoah Valley
- P21 Esraa Aldkhiel, Dr. Nathan Wright
Study of obscurin tandem Ig domain motion
- P22 Merwise Baray, Matt Kohler, Dr. Amanda Storm, Dr. Jon Monroe
Post-translational modification of b-amylase3 by S-nitrosoglutathione in *Arabidopsis*
- P23 Taylor Derby, Dr. Marta Bechtel
Characterizing methods of decellularization in the rabbit cornea model system for tissue engineering applications
- P24 Chris Dillingham, Dr. Mark Gabriele
Alignment of neurochemically defined modules in multimodal aspects of the mouse inferior colliculus

Schedule: Thursday April 14th

SESSION 2 1:00pm-4:30pm

ORAL PRESENTATIONS

Biosci 2007

- 1:00 T1. Thom Tears, Dr. Steve Baedke, Brian Beers, Dr. Thomas Benzing, Dr. Daniel Downey, Nate Wilke, Dr. Christine May
The Effects of Nitrogen Gas Saturation and Conductivity on the Mortality of Brook Trout (*Salvelinus fontinalis*) Eggs and Fry in Aquaculture and Deep Springs in South River, Waynesboro.
- 1:15 T2. Dorottya Boisen, Dr. Lihua Chen, Dr. Patrice Ludwig, Dr. Christine May
Using mark-recapture and artificial stream channel experiments to model burrowing patterns of freshwater mussel species in response to floods
- 1:30 T3. Jul Kim, June Kang, Stephanie J Thai, Jake A. Braun, Corey L. Cleland
The effect of stimulus location and initial posture modulation on the nociceptive tail withdrawal reflex in intact, un-anaesthetized rats
- 1:45 T4. Phoebe Cook, Rebecca Rasmussen, Edward Hsieh, Dr. Jonathan Brown, Dr. Idelle Cooper
Selection pressures on color dimorphism in the damselfly *Megalagrion calliphya*
- 2:00 *T5. Victoria Shuklis, Dr. Kristopher Kubow
Influence of fiber orientation on polarization and migration of fibroblast and fibrosarcoma cells
- 2:15 T6. Lane D. Gibbons, Dr. Conley K. McMullen
Using Morphometrics to Challenge Taxonomic Relationships in *Eleocharis tenuis* (Cyperaceae)
- 2:30 :::::::::: BREAK ::::::::::**
- 2:45 T7. Aubrey Siebels, Dr. Corey Cleland
Looming stimuli evoke a turning escape response mediated by cerci and vision in crickets
- 3:00 ^CT8. Nicholas Dunham, Annamarie Meinsen, Melika Rahmani, Dr. Raymond Enke
Epigenetic Characterization of Human Retina Cells
- 3:15 T9. Kevin Libuit, Curtis Kapsak, Dr. Jim Herrick
Next-Gen Sequencing of a Multi-Drug Resistance Plasmid
- 3:30 T10. Heather Maher, Dr. David McLeod
Using morphometrics to understand *Limnonectes kuhlii* complex
- 3:45 T11. Emily MacLeish, Dr. Joe Harsh
Exploratory Study of Graph Literacy on a Continuum of Expertise
- 4:00 T12. Catherine Torres, Dr. Amanda Storm, Dr. Jonathan Monroe
The Purification and Characterization of β -amylase6 in *Arabidopsis thaliana*
- 4:15 *T13. James Patterson, Dr. Grace Wyngaard
Genomes Size in Parasites: Reduced or Expanded Relative to Their Free-living

Schedule: Friday April 15th

SESSION 3 9:00-noon ORAL PRESENTATIONS BIOSCI 2007

- 9:00 T14. Alexandra Deal, Taelor Weaver, Dr. Terrie Rife
Modulation of nitric oxide synthase I transcription by tau and alpha-synuclein in Alzheimer's and Parkinson's Diseases
- 9:15 T15. Shannon Richard, Kara Rush, Dr. Rocky Parker
Searching for sex pheromones in Burmese pythons
- 9:30 * T16. Megan Hines, Sheikh Hossain, Dr. Jon Monroe, Dr. Amanda Storm
Searching for potential binding partners of *Arabidopsis* β -amylase2 using yeast 2-hybridization
- 9:45 T17. Melissa Gray, Dr. Adam Geiger, Dr. Kristy Daniels, Dr. R. Mike Akers, Dr. Bisi Velayudhan
Accelerated feeding in Dairy Calves Increased the Absorptive Surface Area in the Jejunum
- 10:00 T18. Katelyn Walters, Dr. Heather Griscom
Prioritizing eastern hemlock trees for secondary imidacloprid treatment in Shenandoah National Park
- 10:15 :::::::::: BREAK ::::::::::**
- 10:30 T19. Suzanne Allison, Benjamin Colligan, Dr. Idelle Cooper
Variation in female mating frequency and behavior of the Ebony jewelwing damselfly, *Calopteryx maculata*
- 10:45 T20. Haley Davis, Dr. Chris Lantz
Evaluation of interleukin-3 in blood-stage immunity against murine malaria *Plasmodium yoelii*
- 11:00 * T21. Shannon Fox, Dr. Susan Halsell
Reverse Genetic Screening of Innexin Gap Junction Proteins in *Drosophila* Neurons
- 11:15 ^C T22. Adrienne Janee Muetterties, Dr. Patrice Ludwig
Investigating The Effect Of Larval Diet Quality On Adult Body Size And Male Horn Morphology In The Beetle *Onthophagus taurus*
- 11:30 T23. Grant Rybnicky, Dr. Steve Cresawn
Bioinformatic Characterization of Cluster L Mycobacteriophages
- 11:45 T24. Brendon Perry, Dr. Chris Lantz
Role of interleukin-3 in an experimental model of mouse cerebral malaria caused by *Plasmodium berghei* ANKA

Keynote Presentation:

Dr. Ivor Knight, Sr. VP & CTO

Cannon U.S. Life Sciences, Inc.

From genomics to products: innovating genetic analysis
systems to improve human health

Bioscience 1007, 12:20-1:10

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

Schedule: Friday April 15th

SESSION 4	FRI 2:00-4:00	POSTERS	2nd Floor Foyer
P31	*Gregory Mansour, Melissa Encinias, Matt Riordan, Walker Webster, and Dean Cocking	Ambient detectable mercury within the invertebrate biota of “uncontaminated” terrestrial ecosystems in Rockingham Co., VA	
P32	*Melissa Encinias, Gregory Mansour, Matt Riordan, Walker Webster, and Dean Cocking	Ambient detectable mercury within the habitat of “uncontaminated” terrestrial forest ecosystems in Rockingham Co., VA.	
P33	Megan Budnik, Andrew Sharp, Dr. Heather Griscom	Experimental Trials with American Chestnut Hybrid: Seedlings in an Appalachian Cove Forest	
P34	Emilee Dize, Dr. Patrice Ludwig	The chemical decomposition of artificial and natural oyster shells	
P35	Melissa Kernstine, Kristen Grimshaw, Janee Muetterties, Rachel Cisek, Suzhen Zhang, Dr. Patrice Ludwig	Conservation action plan for the southern bog lemming	
P36	Anna Nordseth, Dr. Heather Griscom	Greenhouse trials of legume and timber shade trees on coffee	
P37	Brittany Culp, Abby Goszka, Chris Coggin, Dr. Heather Griscom	Searching for the ghost of the Appalachians: the American chestnut	
P38	Brittany Culp, Abby Goszka, Chris Coggin, Dr. Charles Ziegenfus	The role of banding stations in avian ecology and conservation	
P39	Christopher Coggin, Matthew Morrissey, Guy Stewart, Dr. Heather Griscom	A long-term experimental study with American chestnut hybrids in a 100 year old forest within the Ridge and Valley province of Virginia	
P40	Danielle Orlandi, Anna Labrozzi, Dr. Roshna Wunderlich	The Effect of Cage Size in Captivity on Physical Activity in <i>Lemur catta</i> and <i>Propithecus coquereli</i>	
P41	Benito Blanchfield, Kelly Burke, Elli Flora Samantha Hetrick, Kelcy Jackson, Lilly Nelson, Romie Powell, Alex Schmidt, Dr. Justin Brown	The Role of Brain Stem Neurotransmitters in the Thermoregulatory Response to Hypoxic Stress	
P42	Brittany Manning, Dr. Conley K. McMullen	Sampling, organizing, and digitizing the flora of the E.J. Carrier Arboretum	
P43	Abby Goszka, Ashley Warrington, Emily Thyroff, Dr. Heather Griscom	Where Does the Elusive American Ginseng Grow Best? Experimental Field Trials	
P44	Patricia Brown, Dr. Roshna Wunderlich	★ A Comparison of Plantar Pressure Data From Traditionally Unshod and Shod Children	
P45	Joshua Donohue, Sraavya Poliset, Dr. Ray Enke, Dr. Chris Lantz	★ Establishment of a mouse model to evaluate microvascular changes in the retina during malaria infection	
P46 ^C	Quinlin McCormick, Jocelyn Medrano, Dr. Elizabeth Doyle, Dr. Oliver Hyman, Dr. Raymond Enke	★ Integration of Geospatial Analysis into the JMU Biology Foundations Lab Curriculum	
P47	Elizabeth Rogers, Sybelle Djikeng, Suma Haji, Stephanie Masters, Monica Paneru, Yasmin Shahkarami, Dr. Kyle Seifert	The Antimicrobial Activity of Novel Amphiphiles	
P48	*Dakota Kobler, Katie Sipes, Dorottya Boisen, Dr. Christine May	Freshwater mussel detection: a research synthesis aimed at filling knowledge gaps to aid in conservation	

- P49 Kendyl Combs, Will O'Connor, Osna Samady, Ryan Samuel, Rebekah Tenney, Dr. Susan Halsell
Identifying the molecular components of cold nociception with *Drosophila melanogaster*
- P50 No poster 50.
- P51 Giavanna Verdi, Kimberly Seamon, Chris Chrzan, Leanna Carter, Jason Lee, Julio Soriagalvarro, Miriam Kabore, Dr. Corey Cleland
Rat hind limb nociceptive withdrawal response to heat and mechanical stimuli depends on position of initial paw but not stimulus location
- P52 Ariel Childs, Aubrey Siebels, Kate Reiman, Dr. Corey Cleland
Determinants and mechanisms of the escape response to looming stimuli in crickets, *Acheta domesticus*
- P53 Jiangda Ou, Dr. Corey Cleland
Escape response of Madagascar cockroaches (*Gromphadorhina portentosa*) to looming and localized heat stimuli
- P54 Romie Powell, Benito Blanchfield, Kelly Burke, Elli Flora Samantha Hetrick, Kelcy Jackson, Lilly Nelson,, Alex Schmidt, Dr. Justin Brown
Exploration of the Role of Ambient Temperature in the Recovery From Major Surgical Stress
- P55 Kristianna Bowles, Amanda Crandall, Jessie Doyle, Rhiannon English, Megan Moore, Joseph Noel, Cole Roberts, Nathan Robinson, Katherine Stanley, Erin Thady, Dr. Bruce Wiggins
A comparative stream water quality survey of a Smith Creek restoration using benthic macroinvertebrates
- P56 *Stanley Peyton, Zackary Zayakosky, David Taves, Dr. Pradeep Vasudevan, Dr. Alice Besterman, Dr. Michael Pace, Dr. Joanna Mott
Isolation and enumeration of *Vibrio vulnificus* and *Vibrio parahaemolyticus* from coastal Virginia
- P57 Dustin Phillips, Daniel Breysse, Kimber Mapili, Elizabeth Dunlap, Dr. Janet Daniel
Investigating the Response of the STP1 k/o and WT *Arabidopsis thaliana* in Response to Various Environmental Stresses
- P58 Jillian Breault, Dr. Amanda Storm, Dr. Christopher Berndsen, Dr. Jonathan Monroe
see printed program for title
- P59 Sheikh Hossain, Megan Hines, Dr. Amanda Storm, Dr. Jonathan Monroe
Searching for Potential Binding Partners of *Arabidopsis* Beta-amylase 9 Using Yeast 2-Hybridization
- P60 Milos Lesevic, Grace Bauer, Dr. Terrie Rife
Examining Peroxisome Proliferator-activated Receptor Gamma Coactivator 1-Alpha (PGC1-a) Gene Transcription in Neurodegenerative Disease
- P61 Samantha Webster, Dr. Patrice Ludwig
Initial measurements of barnacle survivorship on alternative substrates
- P62 Madeline Henwood, Shaw Camphire, Sophie McGinnies, Dr. Terrie Rife
The effect of alpha-synuclein on gene expression in human cell lines SK-N-MC and HeLa
- P63 Ryan Hilton, Dr. David McLeod
Quantification of Tubercle Patterns As a Means To Decipher the *Limnonectes* Complex
- P64 Joshua Gerard Mata, Grace Dimond, Sarah Miller, Dr. David McLeod
★ Curation of a natural history collection: Completed, current, and future projects in the JMU Natural History Collection
- P65 Frank May, Jenna Salter, Dr. Katrina Gobetz
★ Examples of the Trelawny research experience: potential reservoirs for pathogenic bacteria and revolutionary ecological study of box turtles
- P66 Joshua Gerard Mata, Phoebe Cook, Dr. Idelle Cooper
★ Color variation within the Beautiful Hawaiian damselfly, *Megalagrion calliphya*
- P67 Noah Greenman, Kaitlyn Staples, Dr. David McLeod
★ Bad to the Bone: Frogs with Fangs and Claws

Abstracts

ORAL PRESENTATIONS

T1

Thom Tears, Dr. Steve Baedke, Brian Beers, Dr. Thomas Benzing, Dr. Daniel Downey, Nate Wilke, Dr. Christine May

The Effects of Nitrogen Gas Saturation and Conductivity on the Mortality of Brook Trout (*Salvelinus fontinalis*) Eggs and Fry in Aquaculture and Deep Springs in South River, Waynesboro.

The restoration of brook trout in Virginia's streams is of significant importance and aquaculture may play a major role in establishing brook trout fisheries. Research was performed to evaluate the potential for hatching brook trout at the Montebello Fish Culture Station (MFCS) as well as in deep springs along the South River in Waynesboro. Brook trout eggs were hatched at each site to test whether nitrogen gas saturation affected mortality. "Eyed" brook trout eggs were tested for 31 days at the three springs in South River with eggs also hatched in ponds 1-6 at MFCS to determine whether as nitrogen gas saturation decreased due to aeration from water falling from pond to pond, the mortality would decrease as well. The results indicated that although the South River springs have optimal temperature, hardness and alkalinity for the hatching of brook trout eggs, the nitrogen gas saturation was detrimental to egg hatch (average mortality of 30.5%, average nitrogen saturation 108.8%). The lowest mortality was found to be in the MFCS downstream ponds 3-6 (average mortality 5.5%) where average nitrogen gas saturation is 103.1%. Upstream MFCS ponds 1 and 2 had mortality of 20.6% and 11.1% with nitrogen levels of 105.5% and 104.9% respectively. For all treatments, there was a positive linear regression between nitrogen gas saturation and conductivity with mortality (adjusted R² = 0.62, p<0.001). South River deep springs and MFCS may be more effective in hatching of brook trout eggs if the water could be degassed to remove nitrogen gas saturation. This research demonstrates how aquaculture is an important tool for answering questions important to managing fisheries.

T2

Dorottya Boisen, Dr. Lihua Chen, Dr. Patrice Ludwig, Dr. Christine May

Using mark-recapture and artificial stream channel experiments to model burrowing patterns of freshwater mussel species in response to floods

Freshwater mussels are keystone species in their ecosystems, yet over 70% of freshwater mussel species are endangered. Freshwater mussel research is often limited by the difficulty in finding the rare and cryptic organisms. The endangered James Spiny mussel (*Pleurobema collina*) now has only a few populations existing in headwater streams of the James River. This study looks at the burrowing patterns of James Spiny mussels and other freshwater mussels in the field and after floods simulated in experimental stream channels. In the summer of 2014, a mark-recapture study was initiated using Passive Integrated Transponder (PIT) tags at Swift Run in Earlysville, VA. Mussels were recaptured approximately every month and their substrate, location along an x,y coordinate system, and whether they are surfaced or burrowed was recorded. More tagged mussels were seen on the surface after higher flows, and the odds of visually detecting a mussel increased by 5.4% with a 1cm increase in water depth. To study the pattern of surfacing in response to floods, artificial stream channels at James Madison University ran simulated floods on a common co-occurring species (*Villosa constricta*) also present at the field site. Preliminary experimental results indicate an overall decrease in the amount of mussels surfaced immediately after a flood followed by a rebound. Within two days, the number of mussels surfaced had come near to, if not reached, pre-flood counts. There was no difference in the number of mussels surfaced during the day and night. An understanding of mussels' burrowing behavior in response to floods may help researchers time their population surveys so that they are more accurate.

T3

Jul Kim, June Kang, Stephanie J. Thai, Jake A. Braun, Dr. Corey L. Cleland

The effect of stimulus location and initial posture modulation on the nociceptive tail withdrawal reflex in intact, un-anesthetized rats

The nociceptive withdrawal reflex (NWR) is a protective reflex that allows mammals to avoid noxious (potential or actual tissue damage and often painful) stimuli by withdrawing the affected part of the body away from the stimulus (Andersen, 2007). Early studies revealed the presence of the NWR in spinalized animals (Cleland and Bauer, 2002; Schouenborg et al., 1994; Kim et al., 2007) but the NWR is altered in spinally intact animals, suggesting that supraspinal pathways may influence the NWR (Cleland and Bauer, 2002). Also, the NWR can be modulated by stimulus location or initial posture of the limb in spinalized and decerebrated animals (Schouenborg and Kalliomaki, 1990; Levinsson et al., 1999; Baxendale and Ferrell 1981). The purpose of this study was to determine whether the NWR adapts to changes in stimulus locations and initial tail postures in intact and unanesthetized rats. Animals were stimulated at several different rostral-caudal locations and tail postures was either straight, curved, and/or rotated. Regardless of stimulus location and initial tail posture, two different types of movements were observed: a rotational movement around the base of the tail and a local bend near the stimulus site. Direction of the tail base rotation reversed as the initial tail posture became more curved/rotated while the magnitude of the local bend decreased. This study provides evidence that the NWR of the tail in intact and unanesthetized animals depends on stimulus location and initial tail posture.

T4

Phoebe Cook, Rebecca Rasmussen, Edward Hsieh, Dr. Jonathan Brown, Dr. Idelle Cooper

Selection pressures on color dimorphism in the damselfly *Megalagrion calliphya*

Sexual dimorphism is commonly assumed to be caused by sexual selection. The Hawaiian damselfly *Megalagrion calliphya* is an excellent system in which to study the causes of dimorphism because it has a dimorphism in color within females as well as between males and females. Males are always red, while females are either red (andromorphic) or green (gynomorphic). Populations vary in the frequency of these female morphs, from monomorphic green through dimorphic to monomorphic red. We tested the hypothesis that female coloration is under sexual selection due to male sexual harassment, which we expect to be greater in populations with high male frequencies. We also tested two possible forms of sexual selection on female morph. If andromorphs are male mimics, we expect that they will be harassed less than gynomorphs, but if frequency-dependent sexual selection is driving the dimorphism, we expect that the more common morph in a population, whichever it is, will receive more harassment. We measured sex and morph frequencies and performed behavioral trials in five populations on Hawaii Island. We did not find a relationship between male frequency and harassment, and we did not see either predicted pattern of sexual selection. There were no significant differences between harassment rates of andromorphs, gynomorphs, and males. These results do not support either the male mimicry or frequency-dependent sexual selection explanations for color dimorphism. However, the morph frequencies do follow an elevational cline, suggesting that this dimorphism may be a result of ecological rather than sexual selection. Previous research in this lab suggests a mechanism of ecological selection which could lead to both sexual and female-limited dimorphism in this species, and deserves further study.

T5

Victoria Shuklis, Dr. Kristopher Kubow

Influence of fiber orientation on polarization and migration of fibroblast and fibrosarcoma cells

Cell migration in development, wound healing, and numerous pathologies is guided by numerous external cues, in particular the physical properties of the surrounding extracellular matrix (ECM). For example, in cancer cell invasion, cells orient themselves to ECM fibers and manipulate the fibers to migrate; however how the ECM influences migration is not well understood. Although migration has been studied extensively with flat surfaces (e.g. glass), much less is known about fibrous environments, which are more analogous to in vivo tissue. Studies of cells on flat surfaces have shown that microtubule organization and actin-myosin activity are critical factors in determining cell polarity. Here, we asked whether ECM fiber

alignment could establish cell polarity by providing environmental orientation cues in the absence of intrinsic cues. We performed experiments with both mouse fibroblast (NIH 3T3) and human fibrosarcoma (HT-1080) cells. Both cell types were fluorescently labeled and seeded onto synthetic aligned fibers in the presence of inhibitors of microtubule cytoskeleton polymerization (nocodazole) and/or myosin II ATPase activity (blebbistatin). Time-lapse videos and still images were taken to measure migration and polarization. Even though both inhibitors altered cell morphology, cells were still able to polarize and extend oriented protrusions. This indicates that environmental factors influence cell orientation and migration even in the absence of intrinsic factors necessary for migration. We are currently developing a system to study how cells manipulate collagen fibers while migrating into three-dimensional ECMs as a general model for tissue invasion. Small collagen ECMs are seeded with NIH-3T3 cells and polymerized overnight, and then larger acellular collagen ECMs are cast over the smaller ones. We hypothesize that NIH-3T3 cells will manipulate the fibers to create a pathway for invading into the larger ECMs prior to invasion. Preliminary results show cellular protrusions extending into the larger ECMs prior to invasion between 24 and 48 hours after casting the larger gels. In the near future, we plan to use ECMs with fluorescently labeled collagen to determine how cells manipulate the fibers.

T6 Lane D. Gibbons, Dr. Conley K. McMullen
Using Morphometrics to Challenge Taxonomic Relationships in *Eleocharis tenuis* (Cyperaceae)

North America contains a large portion of the most problematic and least resolved taxonomic relationships known in the genus *Eleocharis* (Cyperaceae). Of noteworthy significance are persisting taxonomic uncertainties involving plants referable to the *Eleocharis tenuis* species complex (subg. *Eleocharis*, sect. *Eleocharis*, ser. *Eleocharis*, subser. *Truncatae* Svenson). Consisting of six species, as currently circumscribed, three members of this complex (*E. compressa* Sullivant, *E. elliptica* Kunth, and *E. tenuis* (Willdenow) Schultes) exhibit broad geographic distributions, and consist of entities intermediate to currently recognized species. Confusion between taxonomic entities stems primarily from the variable vegetative structures, and diminutive morphological characters available for comparison and analysis within the genus. A morphometric reexamination of *E. tenuis*, inclusive of cytological and micro-morphological factors, offers insights to the current taxonomic status of subspecific entities associated with the species.

T7 Aubrey Siebels, Dr. Corey Cleland
Looming stimuli evoke a turning escape response mediated by cerci and vision in crickets

Animals respond to aversive stimuli with withdrawal or escape responses. Wind, which might normally be produced by an approaching predator, evokes an escape response in crickets that is mediated by cercal sensory receptors. Similarly, limited studies have shown that crickets also escape from looming stimuli. However, it is unclear whether crickets utilize the same or a different strategy and sensory mechanisms for looming stimuli. The goal of our research was to determine the strategy and sensory modalities used by crickets (*Acheta domesticus*) to escape from looming stimuli. Looming stimuli were created by projecting a 3" black polyurethane ball (1 m/s; 45 degrees to vertical), against a white background, toward the cricket. The direction of "attack" was varied in 45-degree increments around the cricket. The resulting response was captured with high speed video (650 fps, 2336x1728) and the location and orientation of the cricket over time was tracked in software. Looming stimuli consistently evoked a turn followed by walking or occasionally jumping. Our results (n=24) showed that turning response angle depended significantly ($p < 10^{-6}$, Pearson) on stimulus direction, such that crickets turned directly (slope= 1.14 deg/deg linear regression) away from the stimuli. There are four sensory organs - eyes, cerci, antennae, and filiform hairs over the body - that the cricket could use to sense looming stimuli. To identify the contribution of each modality to the escape response, we designed a series of lesion experiments to determine if each modality was necessary or sufficient for an escape response. Ablating eyes, cerci, or antennae tested necessity; ablating all modalities but eyes, cerci, or antennae tested sufficiency. While neither antennae nor filiform hairs support the escape, preliminary findings (n=32) suggested that

cerci are overall sufficient and necessary to evoke an escape response, yet may not be necessary when anteriorly approached by looming stimuli. Overall vision was neither sufficient nor necessary; however, vision may contribute when looming stimuli approached anteriorly. Looming stimuli, similar to wind stimuli, evoked an escape response that used a turning-walk strategy mediated largely but not exclusively by cercal sensory receptors.

T8 Nicholas Dunham, Annamarie Meinsen, Melika Rahmani, Dr. Raymond Enke
Epigenetic Characterization of Human Retina Cells

DNA methylation is an epigenetic modifier that modulates gene expression in plant and vertebrate genomes. The aim of this study is to characterize the role of DNA methylation in the human retina, particularly within rod and cone photoreceptor retinal neurons. Previous studies investigating DNA methylation in murine retinal cells and retina-derived human retinoblastoma immortalized cell culture lines demonstrate an inverse relationship between DNA methylation and transcriptional activity. Here, we used gene-specific bisulfite pyrosequencing analysis to measure DNA methylation in the genomes of human ocular cells in an effort to characterize the role of this important epigenetic modifier. These results can be summarized as follows: 1) human ocular tissues demonstrate tissue-specific patterns of DNA methylation on retina specific genes. These patterns demonstrate an inverse relationship with mRNA gene expression. 2) Within the human retina, cell type-specific patterns of DNA methylation are also observed between rod and cone photoreceptor neurons. These cell-specific patterns of DNA methylation demonstrate a more complex relationship with mRNA gene expression. 3) Putative CRX binding sites in rod and cone photoreceptors demonstrate differential methylation. Collectively these results demonstrate a previously undescribed role for DNA methylation in regulating gene expression in adult human retinal neurons and suggest insights into the specific mechanism of regulation.

T9 Kevin Libuit, Curtis Kapsak, Dr. Jim Herrick
Next-Gen Sequencing of a Multi-Drug Resistance Plasmid

Plasmids in agriculturally-impacted bodies of water may play a significant role in the dissemination of antibiotic resistance. Previously, Erika Gehr, as part of her M.S. thesis work in our laboratory, captured environmental plasmids without cultivation of host bacteria from stream sediment into *Escherichia coli*. Individual plasmids were capable of conferring resistance to a surprising array of antibiotics including aminoglycosides and extended-spectrum β -lactams. In this study, we developed a method to sequence multi-drug resistance plasmids using both Oxford Nanopore MinION and Ion Torrent PGM sequencers. Plasmid pEG1-1 was sequenced on both platforms and a hybrid assembly utilizing data from both sequencing platforms generated a single 73,320 bp contig that was annotated using automated and manual techniques. Analysis of the genome revealed pEG1-1 to be an IncP-1 β plasmid with two mobile genetic elements – a *atn21*-related transposon and an *in104* complex integron – both of which carry multiple antibiotic resistance genes. These findings suggest that plasmids in stream sediment are prone to the incorporation of mobile genetic elements that introduce a broad range of antibiotic resistance genes into their genome. This could cause serious risk to human health since IncP-1 β plasmids are capable of transferring into nearly all Gram-negative bacteria, including fecal pathogens that can be introduced to stream sediment.

T10 Heather Maher, Dr. David McLeod
Using morphometrics to understand *Limnectes kuhlii* complex

Recent studies have demonstrated that we have underestimated the biodiversity in South East Asia and elsewhere. As “common” species are more closely examined, especially those with broad geographic distributions, complexes of multiple species that have been hidden because of their morphological similarity are being elucidated. *Limnectes kuhlii*, a complex of fanged stream-dwelling frogs, exemplifies one of these complexes. Long considered to be a single species, this complex has been shown to comprise more than twenty species. This study explores the utility of morphometric analyses in species delimitation within the *L. kuhlii* complex. By resolving species boundaries true diversity can be understood and be used to increase conservation efforts.

T11 Emily MacLeish, Dr. Joe Harsh

Exploratory Study of Graph Literacy on a Continuum of Expertise

Recent national reform documents in college biology regularly identify the importance of developing students' competencies in graph literacy skills given the importance of communicating complex scientific information visually. However, despite this emphasis, and the ubiquity of graphs in our daily lives, prior research has revealed an array of difficulties that students and scientists have in making sense of and using graph data. As few studies have attempted to examine how discipline-based graph drawing skills develop for postsecondary learners, this research compared the cognitive and metacognitive strategies of individuals along a continuum of expertise in biology visually represent data. For this, an instrument was designed and validated based on graphing literature and expert feedback to test if differences exist in how individuals transform graph data and if those differences are a function of scientific expertise. Graph drawing and cognitive interview (i.e. think aloud) data were captured from 35 individuals of varying biology backgrounds, including: 13 non-biology majors, 9 non-senior biology majors, 7 senior biology majors and graduate students, and 6 biology faculty. Scoring rubrics were used to evaluate participant performance in their decision making (drawings and think-aloud rationale) in data display. While the results indicated no statistical differences between groups in total graph drawing performance, variation in graph design elements (e.g., graph type) were identified as a function of expertise. Significant differences were found between expertise groups in the cognitive and metacognitive strategies discussed in the think-aloud data (e.g., why a graph was drawn in such a manner). These findings begin to highlight differences between experts and novices, as well as the lack of alignment in what one may visually depict and actual understanding of graphing practices, which may be used to inform instruction to increase graph literacy. Additionally, the instrument designed for this study has high face validity, but future work will be needed to establish reliability as it is intended the measure will be made available to faculty interested in assessing their students' data display skills.

T12 Catherine Torres, Dr. Amanda Storm, Dr. Jonathan Monroe

The Purification and Characterization of β -amylase6 in *Arabidopsis thaliana*

Experimental evidence indicates that the family of β -amylase (BAM) proteins is largely responsible for the hydrolysis of starch in land plants. In *Arabidopsis thaliana* there are nine BAM genes, six of which are targeted to the chloroplast, but only four of those are presumed to be catalytically active: BAM1, -2, -3, and -6. Currently, little is known about the expression, characterization, or function of BAM6. Our study of starch accumulation in *Arabidopsis* indicates that BAM6 may be playing a role in older plants, although it has a minimal role in young plants. To further investigate the function of BAM6 we over-expressed the BAM6 protein by ligating the mature protein coding sequence in fusion with a His-tag into pETDuet-1, an *E. coli* expression vector and purified the protein by affinity chromatography. Using the purified BAM6 protein, β -amylase activity assays were conducted to begin to characterize BAM6. The effects of pH and temperature on BAM6 activity revealed maximum activity at pH 7.5 and 39 °C, which more closely resembles the profile of BAM1, an enzyme that is known to function primarily during the day. These findings indicate that BAM6 may also contribute to starch metabolism mostly during the day.

T13 James Patterson, Dr. Grace Wyngaard

Genomes Size in Parasites: Reduced or Expanded Relative to Their Free-living Ancestors?

The general thinking is that genome sizes of parasites are typically smaller than genome sizes of free-living animals. I hypothesize that parasitic copepods (Arthropoda: Crustacea) may contradict this paradigm. Three aspects of biology differ between parasitic and marine copepods: morphological structure, behavior, and the immune system. Numerous measurements of genome size exist for several orders of free-living copepods; but only one measurement exists for a parasitic copepod. Furthermore, this parasite is unrelated to those free-living forms that have been measured. While parasites often lose structures, they also modify or gain new structures, evolve new host-seeking behavior, and respond to host

defenses. I am comparing genome sizes in marine copepods that are either free-living or parasitize invertebrates and vertebrates. Nuclei were quantitatively stained with Schiff reagent in order to measure genome size. A combined system composed of the densitometric Bioquant software and microscope was used to quantify DNA based the amount of light that passes through a nucleus. I am focusing on the predominantly free-living Cyclopoida, and their derived parasitic forms. These free-living forms typically have small to very small genome sizes (0.5 - 2 pg DNA per nucleus). We are currently obtaining parasitic copepods for measurement of their genomes. This will be the first study of genome size in parasitic copepods.

T14 Alexandra Deal, Taelor Weaver, Dr. Terrie Rife

Modulation of nitric oxide synthase I transcription by tau and alpha-synuclein in Alzheimer's and Parkinson's Diseases.

Alzheimer's Disease (AD) and Parkinson's Disease (PD) are both progressive neurodegenerative disorders, which affect millions of Americans and for which there are no cures. AD can significantly impair the ability to think, remember, communicate, and carry out daily activities, while PD can significantly impair motor functions, balance, coordination, and the ability to speak. Both diseases are characterized by intracellular neurofibrillary tangles, composed of the tau protein in AD and the alpha-synuclein protein in PD. Both tau and alpha-synuclein can localize to the nucleus; however, their nuclear roles have not been fully elucidated. Both proteins have been shown to bind and stabilize alternative DNA structures, which form most readily at purine-pyrimidine repeats. One such repeat is found in the promoter of the Nitric Oxide Synthase I (NOS1) gene, which is misregulated in both AD and PD. The NOS1 repeat is polymorphic and has the sequence TGn(TA)TGm where n and m can vary from individual to individual. Genotyping shows that shorter dinucleotide polymorphisms are associated with Alzheimer's and Parkinson's Diseases, and that promoters with shorter repeats have decreased transcriptional expression compared to promoters with larger repeats. Because tau and alpha-synuclein can bind repeats such as these, we hypothesized that tau and alpha-synuclein may be modulating NOS1 expression through the TGn(TA)TGn repeat. Human neuroblastoma cells (Sk-N-Mc) and human cervical cancer cells (HeLa) with varying levels of tau and alpha-synuclein were used to test this hypothesis. Reporter genes directed by NOS1 1F promoter regions with and without the repeat regions were transfected into cells. Promoters with the TG repeat directed two-fold increases in expression, while promoters without the TG repeat caused no change in expression. These findings suggest that tau and alpha-synuclein modulate NOS1 expression through interaction with a dinucleotide polymorphism associated with disease development. Preliminary data also suggest that tau and alpha-synuclein can affect the longer repeats differently than shorter repeats.

T15 Shannon Richard, Kara Rush, Dr. Rocky Parker

Searching for sex pheromones in Burmese pythons

The Burmese python is an invasive predator in the Florida Everglades that is causing a decrease in the abundance of native species in this biodiverse region of the U.S. Snakes employ pheromones, a type of chemical cue, to locate and select mates. Burmese pythons may also use these sex-specific cues to maintain their reproductive ecology in the Florida Everglades. Specific behaviors were identified in this species from video recordings of male pythons in a Y-maze using chemical cues extracted from male and female Burmese python skin sheds. When pursuing a chemical trail, male pythons exhibited head raises, pauses, turning, and head shakes. We noticed that some behaviors varied depending on the gender origin of the chemical cues presented, such as males displayed significantly higher rates of tongue flicking behavior, a form of chemical sampling, when encountering a female scent. Our results indicate that conspecific pheromones affect male trailing behavior. In future experiments, we will determine if these behaviors are seasonally-dependent.

T16 Megan Hines, Sheikh Hossain, Dr. Jon Monroe, Dr. Amanda Storm

Searching for potential binding partners of *Arabidopsis* β -amylase2 using yeast 2-hybridization

BAM2 is a chloroplast-targeted member of the β -amylase gene family that currently has an unknown function in starch hydrolysis. Previous research indicated that BAM2 did not have significant catalytic activity, but, because the gene is highly conserved and there is a starch-excess phenotype in older plants lacking BAM2, it was hypothesized that BAM2 may instead have a regulatory function. Many regulatory proteins function by interacting with other proteins, so we wanted to test for potential protein binding partners for BAM2 using the yeast two-hybrid system. A plasmid containing the BAM2 gene from *Arabidopsis thaliana* was co-transformed into strain Y190 yeast (*Saccharomyces cerevisiae*) along with a second plasmid from library of plasmids containing cDNA of mRNA isolated from mature *Arabidopsis* leaves and roots. If BAM2 interacts with any of the proteins encoded within the cDNA library, transcription in that co-transformed yeast is activated for certain reporter genes whose expression is monitored by growth on selective media and a colorimetric assay. We observed 23 colonies with expression of both reporter genes from the first cDNA library screen and 55 colonies from a second screen. Plasmids containing cDNA were extracted from these colonies and are being tested further for false positives. The cDNA insert in plasmids from 45 potential positive results were sequenced and analyzed to provide information about the validity of interaction with BAM2. Meaningful positive results may reveal the function of BAM2 in the process of starch hydrolysis and may identify previously unknown proteins involved in starch metabolism.

T17 Melissa Gray, Dr. Adam Geiger, Dr. Kristy Daniels, Dr. R. Mike Akers, Dr. Bisi Velayudhan
Accelerated feeding in Dairy Calves Increased the Absorptive Surface Area in the Jejunum

Small intestinal morphology is known to play a major role in nutrient absorption, and therefore affects the growth performance in different species. We hypothesized that feeding a high protein high fat diet at an accelerated rate would increase the small intestinal absorptive area and consequently improve nutrient absorption in dairy calves. Pre-weaned dairy heifers were randomly distributed to either the control group (n=6; fed standard milk replacer 450g/day) or the accelerated group (n=5; fed high fat, high protein milk replacer 1.2kg/day) for 8 weeks. Samples of jejunum were collected and processed for histological measurements of villus height and width, crypt depth, submucosa, muscularis externa, and total wall thickness using image analysis software. As expected, the accelerated group gained more body weight than the control group (40.08 vs. 10.51 kg; $p < 0.001$). There was an increase in villus height (606.2 vs. 430.2 μm), villus width (126.5 vs. 103.9 μm), and crypt depth (507.0 vs. 374.8 μm) in the accelerated group compared to the control group ($p < 0.001$). Although the submucosal thickness was decreased in the accelerated group (58.4 vs. 104.6 μm ; $p < 0.001$), the total wall thickness was greater in the accelerated group than the control (1511.9 vs. 1328.6 μm ; $p < 0.05$). There was no significant difference in muscularis externa thickness between treatment groups. Moreover, there was no significant difference in the villus height to crypt depth ratio indicating an efficient turnover of crypt cells into absorptive epithelium. Overall, our data suggest that increased food intake changes the small intestinal surface morphology to allow for maximum nutrient absorption.

Key words: accelerated feeding, jejunal morphology, dairy calves

T18 Katelyn Walters, Dr. Heather Griscom
Prioritizing eastern hemlock trees for secondary imidacloprid treatment in Shenandoah National Park

Shenandoah National Park (SNP) contains over 20,000 eastern hemlocks (*Tsuga canadensis*); a foundation species in the southern Appalachian Mountains. Hemlock is shade-tolerant and retains a dense needle canopy year-round, creating a unique microclimate providing habitat for many species. The decline in eastern hemlock from hemlock woolly adelgid (*Adelges tsugae*) infestation has negative implications for the overall function of forest ecosystems. We quantified the effect of slope aspect and time since imidacloprid insecticide treatment on crown health change and diameter growth of eastern hemlock in SNP. We compared data from hemlock trees located on southeastern (SE) and northwestern (NW) aspects at sites that were either treated two, five or eight years ago. Trees at control sites received no treatment. Change in crown health was significantly affected by aspect and time since treatment

($p < 0.001$) but change in diameter growth rate was not affected by either variable. Crown health decreased in trees treated eight years ago on both aspects and increased in trees treated two years ago with a significantly greater increase on NW aspects. The NW aspect sites have 2919 adult hemlocks whereas, the SE aspects have 1283. This current data along with historical distribution data suggests that hemlocks are more successful on NW aspects in the park. This may explain why hemlocks are recovering more quickly on the NW aspects after treatment. A concerning observational finding was the lack of cones on either aspect, despite evidence of treatment effectiveness. The few trees with cones were located in areas receiving more sunlight, suggesting stress from infestation is reducing reproductive ability. Aspect may have a role in treatment effectiveness initially, but within five years, hemlock trees will exhibit similar health decline. Furthermore, treatment may result in short-term hemlock recovery and survival, but not reduce adelgid stress long enough to allow for reproduction.

T19 Suzanne Allison, Benjamin Colligan, Dr. Idelle Cooper

Variation in female mating frequency and behavior of the Ebony jewelwing damselfly, *Calopteryx maculata*

Traditionally, the study of sexual selection has focused on the evolution of elaborate male traits and how they enhance the ability to out-compete other males directly (access to females) and indirectly (access to desirable territories or resources). Female trait studies have focused most on evolved preferences for male traits. While we know much about how sexual selection acts on males, there is a deficit of equivalent study on females. In insects, including damselflies, male size and pigmentation are positively correlated with fat reserves and immune abilities, and therefore with male competitive ability. Here, we show that phenotypic variation that has been well-documented in males of the Ebony jewelwing damselfly, *Calopteryx maculata*, is also present in females of the species. We measured female mating success and behavior of *C. maculata* at Smith Creek in Rockingham County, Virginia. Males were marked with multiple colors of fluorescent powder that was transferred to females when mating. Uniquely-numbered females were digitally scanned and repeatedly observed throughout the summer. We determined the extent of variation in female mating frequency, body morphometrics, and wing pigmentation. The study of trait variation within females, and thus the opportunity for selection to act on those traits, is essential in understanding how evolution on females may have contributed to sex differences, and may change the way we think about the role of females in sexual selection.

T20 Haley Davis, Dr. Chris Lantz

Evaluation of interleukin-3 in blood-stage immunity against murine malaria *Plasmodium yoelii*

Malaria is a mosquito-borne infection caused by the parasitic protozoan *Plasmodium*. This disease infects over 200 million people and causes nearly 600,000 deaths per year. Our laboratory previously examined malaria infection caused by *Plasmodium berghei* NK65, a lethal rodent strain that induces symptoms similar to those observed in humans. The results of this previous study indicated that the hematopoietic growth factor and immunoregulatory cytokine interleukin-3 (IL-3) suppressed protective immunity against infection with *P. berghei* NK65. However, the extent to which IL-3 contributes to host defense against blood-stage malaria infection caused by other *Plasmodium* species remains to be determined. We investigated the influence of IL-3 in infection by using IL-3-deficient or "knockout" (KO) and wildtype (WT) mice infected with either nonlethal *P. yoelii* 17XNL or lethal *P. yoelii* YM parasites. Survival, parasitemia, increases in spleen size, and anemia were measured to monitor the course of infection. Surprisingly, we found that IL-3 did not significantly influence the clinical course of infection with these two parasite strains, indicating that IL-3's influence on disease progression is likely species-specific.

T21 Shannon Fox, Dr. Susan Halsell

Reverse Genetic Screening of Innexin Gap Junction Proteins in *Drosophila* Neurons

The reflexive response and perception of pain (nociception) is an evolutionary conserved process in animals. Pain can be a major health concern and current treatments often prove

insufficient, especially in regards to chronic pain. Greater understanding of the molecular processes underlying pain sensation could lead to new and more effective treatments. The aim of this study is to investigate the molecular mechanisms of cold nociception in *Drosophila melanogaster*. A specific subset of peripheral sensory neurons (Class III dendritic arborization (da) neurons), are implicated in *Drosophila* larvae's response to noxious cold. Previous literature has associated a family of gap junction protein, termed innexins, to be responsible for various roles in the mediation of the central nervous system and the giant fiber system in *Drosophila*. It is unknown if the innexin family plays a role in the Peripheral Nervous System (PNS). This study focused on innexin family members as potential mediators of noxious cold-evoked sensory behavior, due to their association with the central nervous system. A cold behavioral assay was used to investigate the role of two innexin family members. The analyses revealed that shaking-B (Innexin 8) is required for nociceptors to react properly to a cold stimulus. Ogre (Innexin 1) was revealed to have the inverse effect, in which *Drosophila* larvae responded more strongly to a cold stimulus. These studies indicated that innexins do in fact play some sort of role in the peripheral nervous system and in cold nociception.

T22 Adrienne Janee Muetterties, Dr. Patrice Ludwig
Investigating The Effect Of Larval Diet Quality On Adult Body Size And Male Horn Morphology In The Beetle *Onthophagus taurus*

The aim of this experiment is to test the extent to which two resources, commonly used by the sexually dimorphic burrowing dung beetle *Onthophagus taurus*, differ in their effects on adult body size and male horn development. This experiment is based on those done by Moczek (1998) and Hunt and Simmons (2004). Pairs of beetles were placed in breeding tubes with thawed dung, and the brood balls were collected and weighed. With the use of digital imaging and ImageJ, horn length and thorax width were measured for each emerging offspring. Statistical analyses (Mann-Whitney-Wilcoxon, regression, and Chi Square) tested the following hypotheses: there is a difference in the number and mass of brood balls that produce live offspring; there is a difference in the thorax size and horn length of resulting male offspring based on resource quality. Results showed a significant difference between brood ball mass and the type of dung, and additionally a significant difference between the brood ball mass and the sex of the resulting offspring. The Chi Square test revealed that frequencies for emerging offspring were significantly different between the two treatments. Finally, regression analysis showed no significant correlation between brood ball mass and thorax width and horn length. The results of this work implicate that the form in which the resource is available may affect parental energy investment in offspring, which may in turn affect the sex of the offspring.

T23 Grant Rybnicky, Dr. Steve Cresawn
Bioinformatic Characterization of Cluster L Mycobacteriophages

Bacteriophages, viruses that infect bacteria, are the most abundant biological entities in the biosphere, collectively representing a vast reservoir of novel genetic information. Mycobacterium smegmatis phages are the most robustly isolated class of phages, including 6899 members, 1132 of which have been sequenced. All members are categorized into clusters and subclusters as determined by dot plot analyses and pairwise nucleotide alignments. Although cluster assignments are useful for determining basic genomic relationships between phages, the method does little to describe the functional relationships of genes amongst members of the same cluster. Prior studies have taken a comparative genomics approach to characterize clusters J, K, M, O and others. Cluster L has not previously been analyzed and represents a unique set of viral genomes. Notable features of cluster L include one genome with a large internal deletion, two closely related genomes with over 99% identity, and a large number of sequence repeats that are of unknown function. By expanding characterization methods beyond dot plot and pairwise nucleotide alignment, mycobacteriophage clusters can represent a more introspective organizational system. Further bioinformatic analysis will also inform the creation of hypotheses that will be tested using targeted mutation. Results from this study have implications in mycobacterial genetics, as phages serve as a window into host genetics.

Brendon Perry, Dr. Chris Lantz

Role of interleukin-3 in an experimental model of mouse cerebral malaria caused by *Plasmodium berghei* ANKA

Malaria is a life-threatening mosquito-borne disease caused by parasites of the genus *Plasmodium*, with about 200 million new cases reported each year. In rodent models of malaria, a variety of immune proteins called cytokines have been shown to either promote or suppress protective immunity. While the cytokine interleukin 3 (IL-3) clearly promotes host defense against some intestinal nematode parasites, few studies have reported a similar function for IL 3 in the pathophysiology of malaria. In this study, we investigated the role of IL-3 in a mouse model of cerebral malaria caused by *Plasmodium berghei* ANKA. We infected wild-type (WT) and IL-3 deficient (IL-3 KO) mice with *P. berghei* ANKA and characterized parameters indicative of a protective host response to infection. We found that male IL-3 KO mice generally survived longer than corresponding WT mice, although no difference between blood parasitemia or hematocrit levels was observed between the two genotypes. In addition, male IL-3 KO mice had an increased splenomegaly, and at day 6 p.i. showed less vascular damage in the brain than did corresponding infected WT mice. These findings suggest that IL-3 plays a role in suppressing protective immunity in a mouse model of cerebral malaria.

Abstracts

POSTERS

P1 Kristianna Bowles, Amanda Crandall, Jessie Doyle, Rhiannon English, Megan Moore, Joseph Noel, Cole Roberts, Nathan Robinson, Katherine Stanley, Erin Thady, Dr. Bruce Wiggins

Effects of Agricultural Restoration Practices on Stream Health in the Shenandoah Valley, Virginia

The Shenandoah Valley encompasses some of the highest agricultural producing regions in Virginia, many of which are large contributors of nutrients and sediment. The Conservation Reserve Enhancement Program (CREP) assists landowners in the installation of riparian restoration projects in which cattle are fenced out or a riparian buffer is planted. We examined the temporal effects of riparian restoration and the impact of upstream land use on water quality for eleven farms participating in the CREP program for various times (from 1 to 14 years). We hypothesized that the length of time that the CREP program has been established would have a positive effect on the water quality of a stream. Water quality was quantified by measuring benthic macroinvertebrate assemblages using the Hilsenhoff Biotic Index (HBI), Virginia Stream Condition Index (VA-SCI), Shannon Diversity Index, and total abundance. GIS analysis was also employed to calculate upstream land use and stream channel characteristics: land use, canopy cover, slope, impervious surface, relief, road density, and watershed area were assessed for the watersheds and 100-meter stream buffers at each sampling site. Single variable and multiple linear regressions were performed separately within the watershed and buffer zones. While no single variable showed a significant relationship, the time since restoration and the percentage of upstream forested land use predicted HBI values, both in the watershed ($p = 0.003$, $R^2 = 0.712$) and in the buffer zone ($p < 0.002$, $R^2 = 0.748$). VA-SCI was predicted by time since restoration and upstream impervious surface in the buffer zone only ($p = 0.001$, $R^2 = 0.777$). These data show that CREP efforts are having a positive effect on water quality, although upstream land use is also an important factor.

P2 Annamarie Meinsen, Christophe Langouet, Dr. Stephen Turner, Isac Lee, Dr. Winston Timp, Dr. Ray Enke

Integrating Transcriptome & DNA Methylome Datasets Obtained from the Developing Chicken Retina

Development of the vertebrate retina requires complex temporal orchestration of transcriptional activation and repression. The chicken embryo is a classic model system for studying the developing retina. During chick development, embryonic day 8 (E8) retinas are

packed with multipotent neuronal precursors on the cusp of differentiation into all retinal cell types. By E18 the retina is nearly fully mature with all major retinal cell types differentiated and expressing cell type-specific genes. The epigenetic modification DNA methylation modifies the functionality of the genome, in part by regulating mRNA gene expression at certain loci. However, genome-wide patterns of DNA methylation in the chicken retina are currently unexplored. In this study we used Illumina Next-Generation RNA-sequencing (RNA-Seq) as well as Whole Genome Bisulfite Sequencing (WGBS) to characterize both the mRNA transcriptome and the DNA methylome of E8 and E18 chicken retina. Current analyses are aimed at integrating these two large datasets to further understand how retina-specific patterns of DNA methylation contribute to transcriptional regulation in rod and cone photoreceptors.

P3 Brie Hayden, Dr. Patrice Ludwig
The Use of Drones in Ecological Research

The use of unmanned aerial vehicles, more commonly referred to as UAVs or drones, is becoming increasingly popular in ecological research because of their versatile use in data capture. Drones are a beneficial tool not only economically and for safety, but also for obtaining data that scientists may not have been able to access otherwise, due to their small size and the ability to plan a flight mission without human error. Last fall I was part of the JMU Drones project and worked with six other undergraduates from other disciplines to explore drone use in ecology. Our different backgrounds helped us to work in a unique way, learning unfamiliar concepts from one another and working as a single unit to accomplish a goal. Acting similar to a case-study, we focused on using a drone to help save the James spiny mussel, a cryptic endangered mussel endemic to the James River watershed. Our research led us to detailing a study using a drone to create maps through aerial photography. Using Agisoft and GIS software, aerial photographs can be georeferenced and mosaicked to create a map of the stream site. Overlaying maps show changes in the stream course, change in sediment deposits after weather disturbance, and have the potential in helping create predictive models used for changes in similar typology streams. This semester, I have continued researching the use of drones in ecology, with a particular focus on oyster reef restoration in the Chesapeake Bay. I am exploring the different ways both aerial and underwater drones can be used and what types of data they can capture.

P4 Victoria Callahan, Dr. Marta Bechtel
Pro-Inflammatory Effect of Dengue Virus NS-1 and Envelope Proteins in Cultured Human Articular Chondrocytes

Dengue Virus (DENV) is part of the Flaviviridae family of viruses, along with Chikungunya Virus and Zika Virus. DENV is endemic to more than 100 sub-tropical or tropical countries in the world. Infection with any single DENV serotype causes Dengue Fever (DF) as well as severe arthralgia. Arthralgia has been associated with pro-inflammatory cytokine expression in articular cartilage tissue. To better understand the effects of Dengue virus in severe arthralgia, we profiled the expression patterns for select pro-inflammatory cytokines in cultured normal human articular chondrocytes (NHACs) treated with either DENV surface envelope protein (sE) or the DENV non-structural protein-1 (NS-1). Experiments were performed over a six-hour timecourse to evaluate early gene expression patterns. Analysis of gene expression was completed using quantitative Real-time PCR.

P5 Madison Azzara, Alex Shafer, Dr. David McLeod
HOPping to it: engaging the community in amphibian and reptile education with the JMU Herpetology Outreach Program

Herpetology is the study of amphibian and reptile evolution, diversity, and natural history. Globally, more than 20% of reptiles and 30% of amphibians are currently facing extinction due to habitat loss and degradation, climate change, disease, invasive species, and over collecting. The JMU Herpetology Outreach Program (JMU HOP) exists to communicate the importance of amphibians and reptiles, challenge misinformation, promote curiosity and engage citizens in biodiversity conservation. JMU HOP collaborates with teachers and their classroom to develop experiential learning programs using Virginia State Standards to understand the ecological

significance of amphibians and reptiles. JMU HOP empowers students as informal science educators, provides real experiences with live amphibians and reptiles for K-12 students, and engage participants in learning about the conservation needs of these animals. Future goals for this project include developing a quantitative assessment to measure the success of the program, provide volunteer opportunities for JMU students interested in scientific education and conservation, and develop a sustainable curriculum for future use by the JMU Biology students and faculty.

P6 Rachel Cisek, Dr. Patrice Ludwig

Species Diversity of Dung Beetles in Rockingham County, Virginia

The aim of this experiment is to determine the species diversity of dung beetles in Rockingham county, Virginia. Beetles were collected in early August, September, and October. Eight tins were put outside and each hour a tin was taken away to determine the rate in which the beetles entered and exited the dung pat. The beetles genus and species was identified using a dissecting microscope. The degree of diversity was determined using a Simpson's index of diversity and Simpson's reciprocal index of diversity to test the following hypothesis: there is a pattern in the succession of dung beetles in Rockingham county, Virginia. Preliminary results showed that there was the greatest index of diversity in October, followed by August, then September. The hourly results showed a slight correlation exhibiting the highest diversity in hours 4 and 5 for August, hours 7 and 8 for September, and hours 5 and 7 for October. The initial results implicate that the time of the year has an effect on the species diversity of dung beetles more so than the time of day within each month.

P7

Luke Bava, Megan Budnik, Emily Cooke, Michelle Lewis, Warner Lowry, Sarah Magee, Sabrina McCormack, Scott Melander, Madeline Quatannens, Nolan Scheible, Emmanuel Sempeles, Leigh Soderberg, Julio Soriagalvarro, Melanie Vasso, Kartik Viswanath, Brad Weidner, and Dr. Michael Renfroe

Effect of synseed composition on emergence of endangered *Saintpaulia rupicola*

Saintpaulia rupicola is a critically-endangered species native to Kenya. There is a need to develop alternative, efficient propagation methods. Synthetic seed technology (synseeds) has emerged as a promising method of rapid propagation that may increase the population of this endangered species. Alginate synseeds were prepared by axenically encapsulating shoot primordia. Synseeds included only alginate, or alginate with supplements of sucrose and/or inorganic nutrients. Synseeds composed of alginate only had significantly greater emergence than other types of synseeds. There were no statistically significant differences among the synseeds with supplements. Synseeds containing inorganic nutrients and sucrose as supplements had the greatest mortality. Results demonstrate that synseed technology may be a useful technique for the propagation of an endangered plant species.

P8

Courtney Stout, Nicholas Dunham, Dr. Chris Berndsen, Dr. Ray Enke

Investigating Epigenetic Regulation of CRX and NRL Binding to Regulatory Regions in the Vertebrate Retina

The vertebrate retina is a neuronal tissue of the eye containing rod and cone photoreceptors that make vision possible. Highly regulated gene expression controls differentiation in the developing retina. DNA methylation is an epigenetic modification inversely correlated with gene expression in vertebrates and plants. Currently in our lab, the relationship between DNA methylation and the ability of two retina-specific transcription factors to bind in the genome is being studied. These transcription factors known as cone-rod homeobox (CRX) and neural leucine zipper (NRL) have been shown to act synergistically to control photoreceptor expression. Preliminary data has supported the hypothesis that DNA methylation is critical for modulating cell-specific binding of CRX and NRL to target recognition sites. Full length coding sequences and DNA binding domain sequences of the human CRX and NRL proteins were cloned into expression vectors, were transformed into competent *E. coli* cells, and transformants were selected for induction of protein expression. Post-induction time course experiments indicated successful expression in each culture except cells transformed with an NRL full-length construct. Batch cultures of successfully expressed proteins will be affinity

purified for further biochemical analysis including gel shift assays to determine the ability of CRX to bind to unmethylated and methylated oligonucleotides in vitro as well as x-ray crystallography structural analysis. Collectively, these studies will contribute to a better understanding of how epigenetic modifications influence the development, homeostasis and pathology of retinal neurons.

P9 Shelby Snowden, Dr. Kerry Cresawn

Evaluation of a Science Outreach Program for all K-5: Madison Discovery

Research has shown that elementary school is a critical time to peak children's interest in science (Maltese and Tai, 2010, Tai et al., 2006). However, many science enrichment activities are not available to students of low socioeconomic status, English Language Learners, racial minorities, and students with disabilities (Weiss et al., 2003, Wilson and Chizeck, 2000). In addition, science outreach by higher education and STEM professionals often consists of activities that are beyond the cognitive level of most students (Wilson and Chizeck, 2000). These activities impress students with higher-level "sophisticated" science, but do not create lasting interest in science or facilitate deeper understanding of scientific concepts. These activities can also be unattractive for elementary school teachers who do not have the resources to carry out these expensive and complex lessons and who are already rushed to cover material required by the Virginia Standards of Learning (SOLs). Therefore, we are assessing a unique outreach model that consists of hands-on activities based on VA SOLs and focused on life science concepts with which K-5 students struggle the most. We visit inclusive classrooms in order to make science enrichment experiences accessible to all students. We will use drawings to assess student understanding before and after the lessons, because drawings reveal more about student thinking than a question-based assessment (Anderson et al., 2014, Holliday, Harrison, and McLeod, 2009). We hope to use our results to evaluate the outreach program and possibly re-design it to be more effective, as well as to encourage other higher education science departments to implement this type of educational outreach program in their local community.

P10 Mary Aland, Christina Gillespie, Maggie Shostak, Dr. Katrina Gobetz

A study of burrowing behaviors of juvenile and adult *Rattus norvegicus* using morphometric analysis and digital burrow imaging

This study represents a multidimensional approach to explore the burrowing behavior of *Rattus norvegicus* (Norway rat). Burrowing behavior of juvenile mammals is poorly known because nursing offspring are assumed to have little or no role in burrow system creation and maintenance. Animals such as rats make large colonial tunnel systems, which may be maintained by juvenile rats while adults forage above ground and defend the colony from predators. We hypothesize that juvenile rats burrow with greater efficiency than older rats, due to their different body proportions and metabolic rate. In this study, *R. norvegicus* pups were measured and weighed each day from date of birth to determine statistically significant morphometric trends in body parameters that might affect digging ability. Pups showed digging ability between 21-24 days old, and were filmed for comparison of their burrowing movements during ontogeny. In addition, digital scans were made of burrows made by juvenile and adult rats to quantitatively compare morphology. Ultimately, these different data sources will be combined to assess whether juveniles can make significant contributions to community burrow ecosystems.

P11 Qiong Kang, Stephanie Thai, Jul Kim, Jake Braun, Dr. Corey Cleland

Dependence of the nociceptive withdrawal response of the tail on stimulus location and intensity

The nociceptive withdrawal response (NWR) allows mammals to avoid harmful stimuli that could cause tissue damage. The NWR has been studied across diverse groups of animals revealing that stimulus location can influence the spatial organization of the NWR. However, previous studies in non-human animals have been conducted largely under either light anesthesia or following decerebration. The aim of this study is to determine in intact, unanesthetized rats how the nociceptive withdrawal response to localized heat stimuli depends on rostral-caudal stimulus location and stimulus intensity. Adult intact,

unanaesthetized Sprague-Dawley rats were placed inside an acrylic tube with their tail protruding straight from the rear of the tube. Thirteen circular dots were marked dorsally along the length the tail with a black marker. Localized (1mm diameter) heat stimuli were delivered continuously until withdrawal with a laser diode (980nm) to the lateral surface of the tail at the caudal 12 levels. The resulting NWR of the tail was recorded using high speed video (650 fps) positioned directly overhead. Latency was used a proxy for stimulus intensity and varied between 0.5 and 15 s. The 13 dots were tracked automatically in software to obtain the location of each of the dots in the rostral/caudal – lateral/medial plane over time. The resulting movement stayed largely within the horizontal plane. The movement of the tail was quantified in terms of tail base rotation and local bend along the length of the tail. Preliminary results revealed that rotation of the tail at its base and local bend at various levels along the tail were the primary features of the withdrawal response. The level of the local bend typically progressed caudal through the movement. The rotation of the base of tail depended non-linearly with stimulus level; magnitude increased as the stimulus moved caudal from the base but then decreased as the stimulus level approached the caudal end of tail and actually reversed in direction for stimuli delivered to the last two levels. These results suggest that movement associated with nociceptive withdrawal of the tail is both complex and depends on stimulus location.

P12 Shannon Palmer, Justin Rissmiller, Adam Geiger, Kristy Daniels, Michael Akers, Dr. Bisi Velayudhan

The Effect of Accelerated Feeding on Duodenal Morphology in Dairy Calves

Deviations in the nutrient composition of diet are known to alter small intestinal morphology. The aim of this study was to determine the effect of accelerated feeding with a high fat, high protein milk replacer on the duodenal morphology in dairy calves. Dairy heifers within the first week of age were randomly fed either a standard milk replacer at the rate of 450g powder per day (control, n=12), or a high protein high fat milk replacer at the rate of 1.2kg powder per day (accelerated, n=10) for 8 wks, and then euthanized for sample collection. Duodenal samples were processed for routine histological evaluations. Quantitative measurements of villus height, crypt depth, villus width, thickness of submucosa, and muscularis externa were determined using ImageJ software. The accelerated group showed an increase in villus height (average 246.87 ± 66.7 vs 288.09 ± 52.9 μm , $P < 0.0001$) and crypt depth (average 257.4 ± 77 vs 306.7 ± 106.7 μm , $P < 0.001$) compared with the control group. However, there was no difference in villus height to crypt depth ratio, submucosal thickness, or the width of the muscularis externa ($P > 0.05$) between the treatments. Overall, our data show that the duodenal architecture of the calves was altered in response to accelerated feeding, but limited to the mucosal layer.

P13 Katherine Stanley, Dr. Conley McMullen

Floristic Survey of Smith Creek Restoration

This study was conducted to determine the location and taxonomy of plant biota that flourished after riparian buffer restoration of Smith Creek was implemented, in 2006. To assess the growth and taxa within the restoration area, specimens were properly collected, mounted, and identified. Various collectors working on this project took GPS coordinates with various devices. These results were mapped using ArcGIS in order to look at the biodiversity as well as a visual projection of growth around the creek. The majority of the GPS coordinates fell outside of the Restoration Area and across Rockingham County, Shenandoah County and one within Greene County. This study is inconclusive of the location of the 500 specimen collected from the restoration area due to the unsuspected sprawl of data points, however the identification and rank of endangered species has been confirmed and filed appropriately at the James Madison University Herbarium.

P14 Claire Gormley, Kristen Hoffman, Rana Ihsan, Dr. Tim Bloss

Characterization of cell-type specific responses to misfolded protein stress in *C. elegans*

Cells experiencing misfolded protein stress can become debilitated and die, contributing to the onset of disease. Different cell types display varying sensitivities to this stress, with neurons

being particularly susceptible to death. When a cell experiences misfolded protein stress in the endoplasmic reticulum (ER), the unfolded protein response (UPR) initiates cell-saving mechanisms that mitigate stress and, if the stress cannot be resolved, triggers cell death by apoptosis. The nascent polypeptide-associated complex (NAC) is a heterodimeric chaperone that assists in the proper folding and localization of nascent polypeptides during translation, and is also believed to help trigger the UPR when the ER experiences misfolded protein stress. The role of the NAC in relation to the UPR is not well understood, nor is it known if this role is different in different cell types; our goal is to characterize the relationship of the NAC with the UPR in different cell types in the model organism *C. elegans*. We are characterizing how neurons respond to misfolded protein stress in the absence of the NAC by depleting the NAC via RNA interference and quantifying the number of neurons observed in the ventral nerve cord. Generally, depletion of the NAC decreases the number of ventral nerve cord neurons while also leading to the mislocalization of the neurons that remain. In addition, we are characterizing the effects of depletion of the NAC in hypodermal cells, which are relatively more resistant to stress-induced death. Through these experiments, we hope to better understand how different cell types handle misfolded protein stress, and why some cell types are more likely to die in response to this stress while others live.

P15 Brianna Lee, Dr. Carol Hurney
No title

No abstract.

P16 Nolan Scheible, Toma Matveeva, Nathan Ashley, Bejan Rasoul, Dr. Kimberly Slekar
Investigating the role of the B-NAC on stress response in baker's yeast

Molecular chaperones are proteins that interact with other proteins to ensure their proper folding and cellular localization. The nascent polypeptide-associated complex (NAC) is a molecule with two subunits, alpha and beta, that is thought to be a protein chaperone that acts on newly emerging proteins at the ribosome. The NAC is also believed to play a role in the stress response in *Saccharomyces cerevisiae*. Here we report initial findings indicating that mutant yeast lacking the gene for the beta subunit of the NAC protein have longer life spans when compared to isogenic wild type yeast. After being grown to a non-replicative state the mutant yeast survived three times longer than the wild type yeast. This could indicate a role of the NAC in the stress response pathway that allows the yeast to remain viable. In order to confirm these results we are repeating lifespan experiments with a newly constructed NAC mutant to determine if this result is reproducible. We are also conducting experiments to determine whether the yeast NAC mutant has an altered response to oxidative stress and heat stress. These experiments are important because the NAC is a highly conserved protein complex and increased understanding of its function will expand our understanding of cellular stress response.

P17 Ellen Jones, Emily Miller, Dr. Joseph Harsh
Unpacking Undergraduate Research Experiences Through the Use of Weekly Journal Data

Undergraduate research experiences (UREs) are an increasingly sought after educational opportunity for the preparation of students for science careers. However, while prior literature has identified a variety of participant gains, most work to date is based on survey data collected at the end of a research program with limited attention directed towards the actual means (i.e. day-to-day in situ practices) by which UREs affect student learning. Using data collected as part of a large mixed-methods project investigating how UREs benefit students, this study will analyze weekly electronic journals (i.e. short surveys) in which participants provided information about the nature of their research activities, interactions with other members of the scientific community, perception of the weekly events, and general feelings toward their work. Over an 8-week period in the Summer of 2012 and the Spring of 2013 and a 9-week period in the Summer of 2013, and Fall of 2013, 183 students submitted 1078 weekly journal entries, with 85% of these students completing more than half of the weekly journals during that time. Quantitative and qualitative data analysis will be undertaken to identify trends in participant experiences and engagement at the individual and group

levels. By focusing on participants' weekly research practices, it is anticipated that the results of this novel study will provide a finer-grain resolution to the nature of these experiences that, in cooperation with other data forms (i.e. surveys and interviews), will help identify key URE features for the advancement of participant outcomes. The goal of this work is provide information to faculty and administrators that can be used to refine these experiences in support of student learning.

P18 Michael Gay, Taylor Wright, Dr. Morgan Steffen

A systems biology approach to understanding ecologically threatened freshwater ecosystems in the Chesapeake Bay watershed: preliminary findings

Toxic cyanobacterial harmful algal blooms (cHABs) have recognized and numerous deleterious effects on freshwater ecosystems. Conventional analysis of cHABs focuses on the toxin-producing organisms and largely disregards co-occurring microbes, despite recent evidence of their importance to bloom success. In comparison, systems biology presents the potential for a more comprehensive understanding of cHAB communities. Lake Shenandoah is a 36 acre impoundment that drains into the Shenandoah River. Lake Shenandoah has had chronic problems with excessive nutrient influx that results in algal blooms. The Shenandoah River is the largest tributary of the Potomac River. Despite the documentation of cHABs for over thirty years in the Potomac River, the ecological status of its most important tributary has never been comprehensively studied. Ecological genomics, traditional molecular biology, and environmental chemistry were used to track patterns in the microbial communities of Lake Shenandoah and the Shenandoah River from August to November of 2015. Samples were collected from Lake Shenandoah and two sites along the Shenandoah River. Duplicate metagenomes from the Shenandoah River have been constructed and will be analyzed for community structure, nutrient metabolism capabilities, and potential cyanotoxin production. In addition to metagenomic analysis, targeted genomics demonstrated the presence of potentially toxic cyanobacteria at Lake Shenandoah and both sites surveyed in the Shenandoah River. Trends in conductivity, temperature, depth, chlorophyll a, and nitrogen (NH₄⁺ and NO₃⁻) concentrations were determined through parallel water quality probing. These preliminary data provide initial insight into the microbial ecologies of Lake Shenandoah and the Shenandoah River.

P19 Shahzeb Khan, Kevin Libuit, Curtis Kapsak, and Dr. James Herrick

Isolation, Identification, and Genome Sequencing of *Aeromonas* Bacteria Native to Cooks Creek, a Stream in the Shenandoah Valley of Virginia

The genus *Aeromonas* is comprised of 16 known species. It is common to aquatic environments and certain species are opportunistic human pathogens acquired via open wounds or ingestion. The main purpose of this study was to isolate and characterize one or more strains of *Aeromonas* to be used as model native stream bacteria in plasmid capture studies. We are also interested in the virulence and antibiotic resistance genes and mobile genetic elements these may contain. Our study site was located on Cooks Creek, a stream near Harrisonburg, Virginia that passes through agricultural pastureland and a small town before joining with the North River. Both stream and water samples were collected in November, 2014. Water samples were directly plated, while sediment samples were plated after cells were released using 0.1% sodium pyrophosphate, onto ampicillin dextrin agar, which is selective for *Aeromonas*. Nine colonies, from the sediment sample plate, appeared yellow on the agar and were further plated onto trypticase soy agar. Of these, seven were found to be Gram negative, catalase positive, oxidase positive, and indole positive using standard microbiological tests. The complete 16S rRNA genes of these presumptive *Aeromonas* were amplified and sequenced. Six of the seven isolated were identified as members of the genus *Aeromonas* and isolate 3 was identified as *A. hydrophila*. The seventh isolate was identified as *Shewanella putrefaciens*. The full genomes of two of the *Aeromonas* isolates were sequenced on an Illumina MiSeq using paired-end sequencing and are in the process of being annotated. For future work, *Aeromonas* strains will be cured of their plasmids and, using an antibiotic gradient plate assay, rendered resistant to rifampicin in order to use them as recipients for exogenous antibiotic resistance plasmid capture.

J. Roberts-Torres, M. Partin, K. Libuit, J. Kurasz, Dr. J. B. Herrick

Isolation and characterization of *Staphylococcus* spp. from manure contaminated streams in the Shenandoah Valley

The genus *Aeromonas* is comprised of 16 known species. It is common to aquatic environments and certain species are opportunistic human pathogens acquired via open wounds or ingestion. The main purpose of this study was to isolate and characterize one or more strains of *Aeromonas* to be used as model native stream bacteria in plasmid capture studies. We are also interested in the virulence and antibiotic resistance genes and mobile genetic elements these may contain. Our study site was located on Cooks Creek, a stream near Harrisonburg, Virginia that passes through agricultural pastureland and a small town before joining with the North River. Both stream and water samples were collected in November, 2014. Water samples were directly plated, while sediment samples were plated after cells were released using 0.1% sodium pyrophosphate, onto ampicillin dextrin agar, which is selective for *Aeromonas*. Nine colonies, from the sediment sample plate, appeared yellow on the agar and were further plated onto trypticase soy agar. Of these, seven were found to be Gram negative, catalase positive, oxidase positive, and indole positive using standard microbiological tests. The complete 16S rRNA genes of these presumptive *Aeromonas* were amplified and sequenced. Six of the seven isolated were identified as members of the genus *Aeromonas* and isolate 3 was identified as *A. hydrophila*. The seventh isolate was identified as *Shewanella putrefaciens*. The full genomes of two of the *Aeromonas* isolates were sequenced on an Illumina MiSeq using paired-end sequencing and are in the process of being annotated. For future work, *Aeromonas* strains will be cured of their plasmids and, using an antibiotic gradient plate assay, rendered resistant to rifampicin in order to use them as recipients for exogenous antibiotic resistance plasmid capture.

P21 Esraa Aldkhiel, Dr. Nathan Wright

Study of obscurin tandem Ig domain motion

The genus *Staphylococcus* is comprised of 41 known species; of these, eighteen are capable of colonizing humans. While *Staphylococcus* has consistently been studied in agriculture and hospital settings, its presence in freshwater environments has yet to be fully demonstrated. Studies on contamination of poultry and other meats by *Staphylococcus* led us to hypothesize that these bacteria may be introduced into stream waters and sediments via runoff from farms and agricultural industries. Previously, our lab isolated and screened eleven putative *Staphylococcus* colonies from water and sediment samples collected at Muddy Creek in Hinton, Virginia; this stream runs through various agricultural lands and adjacent to a poultry processing plant. Ten of the eleven isolates exhibited methicillin resistance, and all were coagulase-negative staphylococci. Water and sediment samples were more recently collected from the sediments of two additional streams within the Shenandoah Valley. Sequencing of the 16S rRNA genes revealed that ten of eleven were strains of *Staphylococcus sciuri*, *S. equorum*, and *S. lentus* (the sequence of the 11th was of low quality). The genomes of two of the methicillin-resistant isolates from Muddy Creek were sequenced on an Illumina MiSeq, are currently being assembled and annotated. The presence of methicillin-resistant staphylococci in freshwater environments raises concerns about human health, as they may be opportunistic pathogens or act as reservoirs of transmissible antibiotic resistance genes for other pathogenic bacteria.

P22 Merwise Baray, Matt Kohler, Dr. Amanda Storm, Dr. Jon Monroe

Post-translational modification of β -amylase3 by S-nitrosoglutathione in Arabidopsis.

Abiotic and biotic stress can cause the accumulation of starch in chloroplasts, presumably so plants can recover from stress using the stored starch as an energy source. A possible mechanism for starch accumulation could be lowered activity of starch degrading enzymes. Arabidopsis contains a family of nine known starch-degrading enzymes called β -amylases and out of the nine, β -amylase3 (BAM3) and β -amylase1 (BAM1) are the most active BAMs located in chloroplasts. We tested the activity of these enzymes in both extracts of plants treated with sodium nitroprusside (SNP) and as purified proteins treated with S-nitrosoglutathione (GSNO). During cold stress, nitric oxide (NO) accumulates in Arabidopsis and can possibly

post-translationally modify the BAMs. Arabidopsis plants were treated with SNP, which elevates NO levels, and plant expressing only BAM3 showed a decline in α -amylase activity while plants expressing only BAM1 were not significantly affected. In testing the pure proteins, we also witnessed this reduction of BAM3 activity but not BAM1 when treated with GSNO. GSNO is an NO reservoir that is capable of covalently modifying cysteine residues by attaching its glutathione or nitroso moiety to the sulfur on cysteine and also is found to be elevated during cold stress. GSNO treatment caused a dramatic reduction in BAM3 activity but not BAM1 indicating BAM3 post-translational modification as a possible mechanism for starch accumulation in Arabidopsis. In a search to find which particular cysteine residue(s) out of seven on BAM3 were being modified, mutants were made where single or multiple cysteine residues were mutated to see what effects the changes had on activity and sensitivity to GSNO. We found three specific cysteines that when substituted out in combination caused BAM3 insensitivity to GSNO. We also found that when these three cysteines were substituted into the corresponding positions in BAM1, it became sensitive to GSNO. Single and triple mutants of BAM1 and BAM3 were tested to see the effects of the mutations on enzyme activity.

P23 Taylor Derby, Dr. Marta Bechtel

Characterizing methods of decellularization in the rabbit cornea model system for tissue engineering applications

The ability of the cornea to heal and maintain transparency has paramount importance in preserving eyesight. Corneal blindness due to trauma or disease affects over 10 million individuals worldwide, and corneal transplants are currently the only treatment. Tissue engineering aims to resolve this crisis through development of a bioengineered cornea. One current strategy being investigated uses decellularized xenograft scaffold tissue, in which cells and proteins are stripped from cornea tissue scaffold of one species and then human cornea cells are embedded into the xenograft tissue. However, problems with xenograft tissue rejection have hampered progress with this approach. An alternative strategy employs an allogeneic graft, in which cells are stripped from a human donor cornea and the remaining scaffold is embedded with donor cells from the patient receiving the transplant. This allograft model system eliminates problems associated with xenograft transplants, and employs a naturally-derived tissue scaffold. The rabbit cornea is a model commonly employed for cornea tissue research. This study aims to characterize and compare two methods for rabbit cornea decellularization, NaCl, or SDS, and their impact on subsequent recellularization. To evaluate the relative success of each method, overall tissue appearance, including the maintenance of transparency, was recorded, and the success of cell attachment to the tissue surface was monitored during the recellularization process. Further investigation will include histological analysis of the cornea tissue obtained from each decellularization method, both before and after recellularization.

P24 Chris Dillingham, Dr. Mark Gabriele

Alignment of neurochemically defined modules in multimodal aspects of the mouse inferior colliculus

The inferior colliculus is situated in the mesencephalon and receives a complex pattern of ascending, descending, and intrinsic projections. While the layered, tonotopic arrangement of the central nucleus of the inferior colliculus (CNIC) is well-established, less is known about the organization of its neighboring lateral cortex (LCIC). A series of discontinuous neurochemical modules have been described for Layer 2 of the LCIC in a host of adult species (Chernock et al., 2004). These modules and their surrounding extramodular domains may serve as an anatomical substrate that interfaces with converging multimodal input arrays (Stebbins et al., 2014). The present study examined the emergence of this periodic modular network in developing mouse. In a series of early developmental C57BL/6J mice, immunocytochemical and histochemical stains were performed for glutamic acid decarboxylase (GAD), acetylcholinesterase (AChE), cytochrome oxidase (CO), and nicotinamide adenine dinucleotide phosphate-diaphorase (NADPH-d). Following fixation, brains were blocked in the coronal plane, cryoprotected, and sectioned at 50 μ m on a sliding freezing microtome. Brightfield images were captured using a Nikon C1si TE2000 microscope equipped with Nikon Elements software. LCIC modularity reconstructions were performed utilizing a MBF Biosciences

NeuroLucida system. Distinct LCIC Layer 2 GAD, AChE, CO, and NADPH-d modules were evident in the period preceding hearing onset and up to the latest developmental stage studied, postnatal day 20. This periodic patchy network of discontinuous modules was consistent for all markers, each spanning much of the rostrocaudal dimension of the nascent LCIC. Modular location and relative size in age-matched mice at comparable levels in the coronal plane appeared qualitatively similar for all markers. Serial reconstruction and alignment of different markers in adjacent sections suggest staining of the same set of LCIC modules. Extramodular zones, comprised of Layer 2 intermodular domains and neighboring aspects of Layers 1 and 3, were consistently negative. As multiple neurochemical stains reveal developing LCIC compartments, a logical next step will be assessing how these modules align with similar patchy expression of Eph-ephrin guidance molecules and multimodal modular/extramodular LCIC projection patterns.

****No posters numbered 24-30****

**P31 Gregory Mansour, Melissa Encinias, Matt Riordan, Walker Webster, and Dean Cocking
Ambient detectable mercury within the invertebrate biota of “uncontaminated”
terrestrial ecosystems in Rockingham Co., VA**

Forest ecosystems in the Shenandoah Valley of Virginia are not directly exposed to major sources of mercury (Hg) contamination. Therefore, Harrisonburg, located in Rockingham County in the Shenandoah Valley of Virginia, was thought to be a suitable control habitat for comparison of Hg concentrations with sites previously studied in Waynesboro, VA. As detailed in the companion presentation, these were not “zero concentrations;” low detectable Hg does occur under these background conditions. Three locations in Rockingham Co. were examined in 2014 with the focus being to characterize differences in Hg concentrations of multiple components of the invertebrate community. All samples were air dried, digested with nitric/sulfuric acid at 95-98°C, and then analyzed with a Perkin-Elmer FIMS spectrophotometer. Preliminary surveys during the summer of 2014 identified greater than 0.05 $\mu\text{gTHg}\cdot\text{gdw}^{-1}$ concentrations associated with a variety of beetles, hornets, small samples of centipedes and millipedes, thunder and peacock flies, and also pill and stink bugs. Japanese beetles, ants, spiders, wasps, bees and daddy-longlegs exceeded this baseline with some having 0.20 $\mu\text{gTHg}\cdot\text{gdw}^{-1}$ or greater content. However, common house flies, moths, butterflies yellow jackets did not contain Hg in these concentrations. Summer 2015 collections are in process with larger sample sizes to expand and refine this data base. It is anticipated that the tendency toward greater Hg content within higher trophic levels will continue to be demonstrated in the final analysis. It is thought that none of the concentrations attained at these sites are great enough to be considered a health hazard and no adverse effects on the biota were observed. Mercury is identified as merely associated with these organisms; this study does not confirm whether the association is superficial or internal.

**P32 Melissa Encinias, Gregory Mansour, Matt Riordan, Walker Webster, and Dean Cocking
Ambient detectable mercury within the habitat of “uncontaminated”terrestrial
forest ecosystems in Rockingham Co., VA.**

Industrial mercury contaminates the South River within Waynesboro, VA. Elevated terrestrial total mercury (THg) concentrations are documented in the South River Science Team studies. Floodplain soils downstream from the point source in Waynesboro range from 6 – 14 $\mu\text{gTHg}\cdot\text{g}^{-1}$ at several sites, and garden crop soils 20 km downstream contains as much as 40 $\mu\text{gTHg}\cdot\text{g}^{-1}$. Significant mercury contamination was not expected 50 km away in Rockingham County, and this was assumed to be a suitable control for a survey of airborne mercury deposition. In several studies, the JMU Mercury Research Laboratory used an inexpensive passive multi-site sampling method involving inverted plastic petri dishes containing Tangletrap® adhesive substrate to collect particulates, vapor, and other airborne THg. It turned out that Hg in detectable amount occurred both in Harrisonburg, making it a low level (rather than zero) control, and Waynesboro. Ultimately 85 locations in Harrisonburg and Rockingham Co. have been sampled for airborne deposition. Three sites with detectable THg were selected for more detailed analysis of airborne, soil, and duff concentrations. Detectable mercury presence in invertebrate biomass is quantified in the comparison poster. Preliminary

analysis in Summer 2014 found airborne THg deposition on the order of 0.4 – 0.7 $\mu\text{g}\cdot\text{m}^{-2}\cdot\text{mo}^{-1}$, with 0.04 $\mu\text{gTHg}\cdot\text{g}^{-1}$ in soil, and 0.02 $\mu\text{gTHg}\cdot\text{g}^{-1}$ in the duff. This is consistent with multiple control sites along the South River near Waynesboro. Concentrations around 0.01 $\mu\text{gTHg}\cdot\text{g}^{-1}$ occurred in a low mercury control plot on the floodplain at the Augusta Forestry Center in a 2006 study of garden crops. In our 1999 study of woody floodplain plants in Waynesboro, the control location upstream from the point source also contained 0.1 $\mu\text{gTHg}\cdot\text{g}^{-1}$, while in an 1986 study, the upstream control was 0.2 $\mu\text{gTHg}\cdot\text{g}^{-1}$. Therefore, detectable THg is present in the soils of Rockingham Co. habitats, but these background concentrations are significantly lower than contaminated floodplain soils.

P33 Megan Budnik, Andrew Sharp, Dr. Heather Griscom

Experimental Trials with American Chestnut Hybrid: Seedlings in an Appalachian Cove Forest

The American chestnut, *Castanea dentata*, was a foundation species in the eastern United States prior to a devastating fungal blight. After many years of functional extinction, The American Chestnut Foundation (TACF) has produced potentially blight-resistant hybrids ("Restoration Chestnuts 1.0"). We conducted an experimental study in an Appalachian cove system of West Virginia in which we created four small (40% light) and four large gaps (60% light) by cutting canopy trees and clearing all vegetation. In March 2014, we planted seeds, protected by aluminum flashing tubes, within the 8 fenced plots but seed predation was greater than 85% in 7 of the 8 plots. One year later, we planted 50 hybrid chestnut container seedlings within the same plots. Large gaps, due to their higher light levels, were predicted to have more intense competition with herbaceous species. In each plot, half the seedlings were planted within landscape fabric to quantify the effect of herbaceous competition. We randomly placed 12" tree shelters around half of the seedlings to quantify the effect of rodent girdling on growth and survival. After one growing season, chestnut survival across all plots was 91%. Seedlings in large gaps were significantly taller (mean = 48.99 cm) than those grown in small gaps (mean = 46.29 cm) ($p=0.035$). Landscape fabric and canisters had no effect on measured growth variables. We predict that in subsequent growing seasons, the overall height of chestnuts in large gaps will suffer due to more intense competition or physical crushing by *Rhus* spp. Continued monitoring is critical to understand how these trees will respond to different management treatments as they grow beyond the seedling stage.

P34 Emilee Dize, Dr. Patrice Ludwig

The chemical decomposition of artificial and natural oyster shells

The oyster of the Chesapeake Bay, *Crassostrea virginica*, had a disastrous population decline in the 1920s and 1950s. In the 1920s, the gradual effects of over harvesting amounted to a 2-3 million bushel per year decline of oyster harvests. In the 1950s, two major diseases depleted the remaining oyster population in the Bay. The current oyster population in the Bay stands less than 1% of historical quantity. Efforts to restore populations focused around using natural oyster shells as a base for new reefs but shells are becoming rare and therefore more expensive. Current work on alternative substrate for oyster reef restoration investigates the use of concrete made with limestone sand (from the Shenandoah Valley). Limestone sand provides additional calcium carbonate to benefit the growth of the oysters shells. My project investigates how the limestone concrete will affect the chemistry of the water around the reef as the substrate deteriorates. I used a Slake Durability Apparatus to tumble artificial concrete and natural oyster shells for two hours per trial. Calcium concentration and pH were measured every 30 minutes during the tumbling. The results showed no significant trend, therefore the results are inconclusive.

P35 Melissa Kernstine, Kristen Grimshaw, Janee Muetterties, Rachel Cisek, Suzhen Zhang, Dr. Patrice Ludwig

Conservation action plan for the southern bog lemming

The southern bog lemming, a rodent native to North America, is predominantly found in grassy vegetation, wetlands, and forests, with their range including southeastern Canada to northeastern parts of the United States. Two subspecies of this particular lemming, the Nebraska bog lemming and the Kansas bog lemming, are currently extinct (Fahey, 2011). With

the elimination of grasslands, increased roadways, and deforestation in and around lemming habitat, there is major concern for the same fate as their sister species to occur: local, and then eventually true, extinction. If these populations globally died out, the ecological dynamics of the ecosystems surrounding the lemming would lead to the disruption of food chains, and a potentially catastrophic domino effect could occur (World Wildlife Fund). A conservation action plan, that focuses on gathering data of the population sizes of the southern bog lemming for use for monitoring the species, would be crucial in order to maintain diversity and stability of these ecosystems. Using the R coding program, predictions and projections were made to analyze and determine which life stage was the most influential for these lemmings. The juvenile stage was found to be the most sensitive stage and also had the highest reproductive value of all of the stages. This then was the stage we ultimately wanted to focus on conserving. Utilizing a monitoring protocol, establishing protected wildlife refuges, as well as educating the general public about this lemming, would allow population sizes to not only increase, but also thrive in this ever-changing world.

P36 Anna Nordseth, Dr. Heather Griscom

Greenhouse trials of legume and timber shade trees on coffee

Coffee (*Coffea arabica*) is the second most traded commodity crop worldwide with cultivation covering 11 million ha in the tropics. Although coffee originated as an understory plant, its production has shifted to intensive, full sun plantations. In recent years, shade has been 'reintroduced' into coffee plantations through the implementation of agroforestry systems. Effects of shade on coffee vary greatly with local climate and also with the specific shade tree characteristics. Legume trees are the most widely used shade trees but timber species are being increasingly utilized because they can add to plantation profitability. This study seeks to compare the effects of legume and timber trees on coffee—specifically with regards to competition for soil nutrients. A single coffee seedling will be planted in a 2 gallon pot with a seedling of either a legume species, *Inga densiflora*, a timber tree, *Eucalyptus deglupta* or *Cordia alliodora*, or alone. Soil analysis determined that a Lodi silt loam would most closely resemble soils commonly found on suboptimal coffee sites, with similar levels of macro and micronutrients. Greenhouse conditions will mimic suboptimal coffee growing conditions with mean temperature of 26°C, 1,100 mm annual precipitation and a three-month dry season. Height, leaf area, and diameter of coffee and shade tree seedlings will be monitored throughout the first year of growth in a greenhouse environment. Soil nitrogen will also be measured. We anticipate that coffee seedlings will grow equally well with timber trees as with legume trees or alone. If timber species have no deleterious effects on coffee growth, they could be incorporated into coffee agroforestry systems in replacement of full sun systems. Additionally, utilization of timber shade trees would diversify farmers' incomes, protecting them against fluctuations that often accompany the coffee market.

P37 Brittany Culp, Abby Goszka, Chris Coggin, Dr. Heather Griscom

Searching for the ghost of the Appalachians: the American chestnut

An essential part of any species recovery plan is understanding how environmental factors affect survival and reproduction. Our species of interest, the American chestnut (*Castanea dentata*), was first infected with the chestnut blight (*Cryphonectria parasitica*) in 1904 and the entire species was pushed to the brink of extinction by 1940. This species' ability to re-sprout from existing root systems, enabled it to persist as an understory shrub. Our study aims to determine if the distribution of chestnut sprouts in Shenandoah National Park (SNP) is correlated with the environmental factors: soil texture, elevation, slope, aspect, pH. The American Chestnut Foundation (TACF) provided the coordinates and tree health data used in the study from their 2013 Appalachian Trail MEGA-transect Project. This is the first study to examine sprouting patterns within SNP using a large dataset. ArcGIS (Desktop10.3) and SPSS were used to analyze the significance of the impact certain environmental factors have on sprout distribution, blight presence, and reproductive indicators (presence of burs and/or flowers). Based upon the historic record and past studies we hypothesized each factor would have a significant effect on sprouting distribution and reproduction. Sprouts were predicted to be most abundant in environments with sandy soil, on mid to low slopes, at approximately 875m elevation, on southern to southwestern aspects, and pH of 4 to 5. pH ($R^2 = 0.891$), slope

($R^2 = 0.862$), and elevation ($R^2 = 0.397$) had a significant effect on sprouting distribution (p-value < 0.0001) while aspect ($R^2 = 0.029$, p-value = 0.687) and percent sand ($R^2 = 0.218$, p-value = 0.533) were found to not be significant. Statistical analysis showed sprouts are most abundant in locations with: 20-30% sand, slopes with 10-20% incline, 500-700m elevation, and a pH of 4.6-4.9. The results of this study could help direct future searches for American chestnut sprouts within SNP.

P38 Brittany Culp, Abby Goszka, Chris Coggin, Dr. Charles Ziegenfus
The role of banding stations in avian ecology and conservation

The integral role of banding stations is often overlooked in the grand scheme of avian ecology and conservation. Banding stations provide raw data to avian ecologists and biologists about an avian species on the community, population, individual levels. The aim of this study is to summarize the data collected during the Fall 2015 field season focusing on the Northern saw-whet owl (*Aegolius acadicus*), and to shed light on the value of having operational banding stations not only for ecologists but for students and the general public as well. This study centers around the Highland Retreat banding station in Northwest Rockingham County which has been operational since 2001. Although all field collection done by the authors was conducted at the Highland Banding Station, other banding stations in the area have contributed valuable species composition data regarding the northern saw-whet owls. Through the presentation of this data we hope that viewers can see the many roles banding stations play in data collection, population monitoring, educational outreach, building field experience, and directing the careers of undergraduates given the opportunity to participate.

P39 Christopher Coggin, Matthew Morrissey, Guy Stewart, Dr. Heather Griscom
A long-term experimental study with American chestnut hybrids in a 100 year old forest within the Ridge and Valley province of Virginia

This experimental field study investigated the effects of slope position and gap size on the survival and growth of pure American chestnuts (*Castanea dentata*), chestnut hybrids, and tulip poplar (*Liriodendron tulipifera*) in the Ridge and Valley province of Virginia. Twelve gaps were created on upper ridge positions with xeric soil and lower slope positions with mesic soil. In 2008, one year old seedlings were planted within large (60-75% light) and small gaps (30-45% light). A two meter tall nylon mesh fence (100 x 100 meters) surrounded all gaps to protect seedlings from deer browse. Survival, height, and diameter at root collar were quantified at the end of every growing season. Chestnut saplings had the greatest average RGR diameter data for large, mesic (LM) plots, but only had significant differences between the LM and large, xeric (LX) sites ($p = .04$). Interestingly, chestnut survival was higher within the plots located on upper slopes. This trend is due to higher predation by rodent girdling in the first several years on the lower slopes. Chestnut survival was significantly greater in the small xeric (SX) plots compared to the other treatments ($p < .001$). Tulip poplar had the greatest RGR diameter in LM plots, and the highest survival in SX plots, however chestnut survival was significantly greater than tulip poplar in these same plots. There was a large drop in survival compared to last year, when tulip poplar survival was higher than chestnut. This can be explained by an increase in intraspecific competition causing a heavy decline in tulip poplar survival (43%), thereby lessening interspecific competition with chestnuts.

P40 Danielle Orlandi, Anna Labrozzi, Dr. Roshna Wunderlich
The Effect of Cage Size in Captivity on Physical Activity in *Lemur catta* and *Propithecus coquereli*

Enrichment in zoos is important for physical and psychological health of animals. The purpose of this experiment is to assess whether caged and/or natural habitat enclosures at the Duke Lemur Center provide a level of physical activity similar to physical activity levels of lemurs in the wild. We will assess overall dynamic body acceleration (ODBA) as a proxy for energy expenditure in *Lemur catta* and *Propithecus coquereli* at the Duke Lemur Center in Durham, North Carolina. Two different enclosure types will be assessed: small indoor/outdoor cage enclosures and an enclosed forested natural habitat enclosure (NHE) available for free ranging. Activity dataloggers will be attached to the back of 4 animals of each species. The animals will

be released into the enclosure and monitored for the entire day. To ground truth our data, we will use focal animal sampling to collect basic locomotor and positional behavior data. Data will be compared to data from wild *Propithecus coquereli* and *Lemur Catta* from southwest Madagascar. We anticipate that these data will contribute to animal husbandry at zoos and other captive primate facilities by providing quantitative data on locomotor activity and energy expenditure in captive settings.

P41 Benito Blanchfield, Kelly Burke, Elli Flora Samantha Hetrick, Kelcy Jackson, Lilly Nelson, Romie Powell, Alex Schmidt, Dr. Justin Brown

The Role of Brain Stem Neurotransmitters in the Thermoregulatory Response to Hypoxic Stress

Sudden Infant Death Syndrome (SIDS) is a leading cause of infant mortality (1). Alterations in brainstem development of Serotonin (5HT) and GABA are linked to its cause (2). The sympathetic premotor neurons located in the Nucleus of the Raphe Pallidus (NRP) in the brainstem have both 5HT1A and GABA-A receptor subtypes that mediate protective cardiovascular responses to environmental stress (3). It is hypothesized that alteration in these receptors at the NRP will also impair protective thermoregulatory responses to hypoxic stress such as hypothermia. Using aseptic techniques, male Sprague-Dawley rats (225-325g) were instrumented with radiotelemetry probes to non-invasively measure core temperature (T_c). Using a stereotaxic device, a steel cannula was inserted into the brainstem which allowed microinjection at the NRP. After recovery (1 week), rats were housed in a thermal gradient which allowed them to select their ambient temperature (ST_a) and thereby facilitated behavioral thermoregulation. Once acclimated to the gradient and to handling, 30mM of either a 5HT1A agonist (8OH-DPAT or "DPAT"), antagonist (WAY100635), a GABA-A agonist (Muscimol), antagonist (Bicuculine) or ACSF (control vehicle) was then microinjected into the NRP immediately before exposure to 6% O₂ for 60 min. In rats injected with ACSF, T_c decreased by 1.8°C while the T_c of those injected with DPAT and WAY decreased by 3.8°C and 2.8°C respectively. Those injected with Muscimol and Bicuculine exhibited similar hypothermic responses to control in that the T_c dropped by 2.0°C and 1.9°C respectively. There were mild decreases in ST_a of control group rats (4.3°C) which was exacerbated in DPAT injected rats (8°C). Importantly, the ST_a responses to hypoxic stress helped facilitate T_c changes suggesting coordination between behavioral and autonomic thermoregulatory mechanisms which facilitated the protective hypothermic response. Rats injected with WAY seemed to reverse this trend initially with an increase in ST_a (3°C) which quickly faded. Muscimol and Bicuculine seemed to have minimal effect on ST_a responses. These preliminary data suggest that GABA-A receptors have minimal role in the thermoregulatory response to hypoxic stress. However, activation of the inhibitory 5HT1A receptor exacerbates the hypothermic response to hypoxic stress and may facilitate this protective response. Alterations in 5HT neuronal development may cause inadequate behavioral (ST_a decrease) and autonomic (T_c decrease) heat loss responses to hypoxic stress and may be a significant factor in the etiology of SIDS.

P42 Brittany Manning, Dr. Conley K. McMullen

Sampling, organizing, and digitizing the flora of the E.J. Carrier Arboretum

This research project intends to create a digital database, complete with images, of the vascular plants both native and cultivated that inhabit the E.J. Carrier Arboretum. The specimens collected and mounted over the past three decades have updated to reflect any changes in nomenclature and organized into a digital database. In the future, the specimens will be photographed as well. The data will eventually be in the form of a map of the arboretum with specimens' images and descriptions linked to the location of their collections. Professors, students, and the general public can then use the database as a reference for identification and study of vascular plants in the arboretum as well as in the greater Rockingham area.

P43 Abby Goszka, Ashley Warrington, Emily Thyroff, Dr. Heather Griscom

Where Does the Elusive American Ginseng Grow Best? Experimental Field Trials

American ginseng (*Panax quinquefolium*) is a shade tolerant herbaceous perennial that has been a valuable, non-timber forest product for the last 300 years. Ginseng is becoming

increasingly rare in the wild mostly due to overharvesting. The increasing market demand for ginseng root and declining population numbers has caused a surge in ginseng cultivation. In this study, we examined slope aspect and soil type to address inconsistencies in the literature regarding optimal locations for ginseng growth. We implemented a three by two factorial design (soil*slope aspect) at a field site in an Appalachian Cove forest system in West Virginia. Soil was transplanted from three forest sites: calvin series (fertile loam that was limed), macove series (fertile loam), and dekalb series (cobbley, sandy loam). Seeds were planted in raised beds at six sites in the fall of 2014. All beds were placed in gaps with approximately 30% light. We predicted that leaf area, height, berries, and survival of two-year-old plants would be significantly greater in limed loam soil on north-facing slopes. Soil had a significant effect on height and leaf area ($p < 0.00001$), while aspect had no effect on any measured variable. On average, plants in the calvin series were 32% taller and had 57% more leaf area than plants in the macove series, and were 38% taller and had 54% more leaf area than plants in dekalb series. Survival, which ranged from 0% to 59% at each of the six sites, was only affected by plot location. Plots on the top of the mountain did significantly better than the mid ($p = 0.029$) and bottom ($P = 0.011$) plots. Berry presence was positively correlated to leaf area ($p < 0.001$; $R^2 = 0.740$). An understanding of how environmental variables affect ginseng's growth and performance will help with the development of successful reintroduction plans.

P44 Patricia Brown, Dr. Roshna Wunderlich

A Comparison of Plantar Pressure Data From Traditionally Unshod and Shod Children

We are comparing foot function in traditionally shod and unshod children to understand the extent to which shoes impact foot growth and development. We hypothesize that the pressures from habitually unshod children will be more evenly distributed and lower overall, as seen in habitually unshod adults (D'Aout, 2009). We collected plantar pressure and kinematic data on 75 unshod children from Ileret, Kenya by having subjects walk over a 1-meter long RSScan plantar pressure mat. The foot was divided into 10 segments and maximum peak pressure, maximum force, impulse, and load rate were calculated for each segment. These data will be compared to plantar pressure data we will collect on traditionally shod children using a similar process but on an EMED plantar pressure mat. While the study is currently in the early stages of data analysis, our goal is to examine morphological and functional differences between shod and unshod children's feet that can be applied to footwear recommendations for children.

P45 Joshua Donohue, Sraavya Poliset, Dr. Ray Enke, Dr. Chris Lantz

Establishment of a mouse model to evaluate microvascular changes in the retina during malaria infection

Malaria is a mosquito-borne disease caused by the protozoan parasite *Plasmodium*. Common outcomes of infection include anemia, fever, chills, sweats, and headaches. In addition, some strains of *Plasmodium* induce a potential fatal neurological condition called cerebral malaria in which parasitized RBCs become sequestered in blood vessels of the brain and cause inflammation. Sequestration and vascular damage also occurs in the retina and the degree of damage correlates with the severity of microvascular brain damage. We wished to establish a retinal whole-mount model that will eventually allow us to examine the potential influence of the cytokine interleukin-3 on the progressive microvascular changes that occur in the retina during infection. To establish this technique in the laboratory, we first sacrificed C57BL/10 mice that were previously injected intravenously with the fluorescent dye Evans blue. Mouse eyes were then enucleated, fixed, and retinal whole mounts were prepared and examined by confocal fluorescence microscopy. Our results show that Evan blue clearly allows the visualization of the retinal vasculature. Future experiments utilizing this technique should allow us to quantify and compare the degree of retinal vascular leakage that occurs in both *Plasmodium*-infected wild-type and interleukin-3-deficient mice.

P46 Quinlin McCormick, Jocelyn Medrano, Dr. Elizabeth Doyle, Dr. Oliver Hyman, Dr. Raymond Enke

Integration of Geospatial Analysis into the JMU Biology Foundations Lab Curriculum

DNA barcoding is a methodology used for identification and classification of organisms using a highly variable portion of the genome universal to all species within a broad taxonomic group. This short DNA sequence barcode is compared to a comprehensive sequence database and used in tandem with morphology to characterize or identify the organism of interest. Barcoding applications include the detection of fraudulently labeled food, identification of new or previously uncharacterized species, and cataloging biodiversity within a geographical region. Here we demonstrate an array of geospatial tools integrated into the DNA Barcoding workflow including GPS, web-based geospatial data hosts, geospatial database development and Google Earth to create interactive maps containing relevant metadata for each sample collected. These methods can be applied in tandem with traditional DNA Barcoding analysis as a part of the new JMU Biology first year curriculum beginning in the Fall 16 semester. Integration of these tools into BIO140 & 150 Foundations Lab activities will provide first year JMU Biology majors with a broad range of experiences to help clarify their interests as well as to hone a diverse skill set to address questions related to ecology, molecular biology and bioinformatics.

P47 Elizabeth Rogers, Sybelle Djikeng, Suma Haji, Stephanie Masters, Monica Paneru, Yasmin Shahkarami, Dr. Kyle Seifert

The Antimicrobial Activity of Novel Amphiphiles

Amphiphiles are a diverse class of amphiphatic compounds that have well-documented antimicrobial effects. The diversity in amphiphile structure, coupled with an improved understanding of the effects of structural changes on antimicrobial activity allows for a wide range of potential novel antimicrobial compounds with applications including more efficient surface disinfection.

Several novel series of amphiphiles have been synthesized, and their antimicrobial activity tested on seven different bacteria, including *Pseudomonas aeruginosa* and *Staphylococcus aureus*. This research has revealed a strong correlation between the length of the hydrophobic carbon tails and the antimicrobial activity of these compounds, with twelve carbons per tail being the most effective for the double-tailed series. Additionally, substituting new counter ions such as chloride and iodide has been shown to increase antibacterial activity as well.

P48 Dakota Kobler, Katie Sipes, Dorottya Boisen, Dr. Christine May

Freshwater mussel detection: a research synthesis aimed at filling knowledge gaps to aid in conservation

Freshwater mussels are ecologically important organisms: they remove suspended particles from the water column via filter feeding, which improves the water quality thus making the environment more hospitable for other aquatic organisms. Additionally, mussels are a food source for other animals. Freshwater mussels are thought to prefer habitats with coarse grained substrates; however, due to the legacy of erosive practices such as forestry, farming, and development, mussels also occupying stream stretches dominated by deep layers of fine grained sediments.

The longevity of native freshwater mussel species is threatened due to anthropogenic pollution, habitat destruction, and competition by invasive species. Complicating conservation efforts is the lack of life history information for imperiled species. Furthermore, mussels are difficult to locate because they are cryptic by nature; mussels spend the majority of their lives burrowed in the stream-bed, and when surfaced, their shells are camouflaged against the substrate. The result is that surveying for mussel populations can be time consuming, of limited accuracy, and potentially incomplete all due to surveyors lacking adequate life history information.

In hopes of improving surveying efficiencies by examining current limitations, we investigated differences in visual detection of mussels by substrate, the depth to which mussels can burrow, and the time need to re-surface after a disturbance. Results from an experiment involving novices surveying for mussels in an artificial stream channel suggest there is no bias in visual detection of mussels in sand versus rock-dominated substrates. Preliminary trials on mussel burrowing depth found juvenile mussels were capable of re-surfacing after being buried to

depths up to 35 cm in artificial stream channels. Mussels were found to stay subsurface for ~48 hours after burial, with at least 50% synchronously surfacing on the second day, regardless of burial depth. The maximum cumulative percent of surfaced mussels reached a plateau after the third day since burial. This finding supports the idea that a disturbance could prompt a synchronous rebound of sub-surfaced mussels.

Based on our findings, we suggest that those surveying streams for mussel populations assume no sampling bias between substrates when surveying, to dig at least 35 cm into the substrate, and to survey shortly after a disturbance event such as high flows, to find the greatest amount of mussels present at the surface.

P49 Kendyl Combs, Will O'Connor, Osna Samady, Ryan Samuel, Rebekah Tenney, Dr. Susan Halsell

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

Nociception refers to an organism's perception and reaction to potentially damaging noxious stimuli. While nociception is a beneficial behavioral response to harmful stimuli, humans may suffer from chronic pain in which the pain signals abnormally persist months after any form of trauma, injury or infection. Evolutionary similarities between mammalian and *Drosophila* nociception makes the fruit fly an ideal organism to study the molecular components of nociceptor neurons. This study aims to better understand the molecular mechanisms of pain by studying the proteins hypothesized to be involved in the propagation or transduction of cold nociceptive signals, including the pickpocket DEG/ENaC ion channel family and Innexin gap junction proteins. To establish a role in cold nociception signaling, cell specific RNAi is used to knockdown the protein expression levels. The effect of the knockdown is visualized in larvae using a cold behavior assay to test for the presence or absence of the wild-type cringe response. The assays are recorded and the videos are processed using a computer program to convert the visual images into a quantitative "percent cringe" value for statistical analysis. By comparing the percent cringe of the knockdown to the wild-type, the involvement of the knockdown protein in the cold nociceptive signaling pathway can be inferred.

P50 Poster 50 was changed to a talk.

P51 Giavanna Verdi, Kimberly Seamon, Chris Chrzan, Leanna Carter, Jason Lee, Julio Soriagalvarro, Miriam Kabore, Dr. Corey Cleland

Rat hind limb nociceptive withdrawal response to heat and mechanical stimuli depends on position of initial paw but not stimulus location

Rats rapidly withdraw their hind limb in response to noxious stimulation, an example of the Nociceptive Withdrawal Response (NWR). Previous studies in spinalized or lightly anesthetized non-human mammals have shown that the direction of response depends on stimulus location; however studies had not yet been conducted in intact mammals. Our initial goal was to determine whether the location of heat and mechanical stimuli influences the direction of the NWR in intact rats. Based on previous studies we hypothesized that the response would be directly away from the location of the stimulus. Sprague-Dawley rats (n=57), placed on a glass or mesh plate, were stimulated with either localized noxious heat (infrared laser) or mechanical (Von Frey monofilament, 30 g needle) stimuli. Stimulation was directed to one of five small (1mm) spots (three aligned rostral-caudal, three aligned lateral-medial) on the left paw's plantar surface. The initial and final positions of the stimulated paw were recorded with a camcorder (60 fps @ 1080p) underneath the rat, with the difference representing the NWR movement response vector. In response to stimuli, rats rapidly withdrew and replaced (~50ms) their paw on the surface in all possible directions. Unexpectedly, stimulus location did not significantly influence the direction of the response ($p > 0.005$, ANOVA), falsifying our hypothesis. We noticed, however, that the initial paw position was variable, suggesting its location may influence the direction of response. Correlation between the initial location and the change in location rostral/caudally or medial/laterally revealed significant negative slopes ($p < 10^{-6}$, t-test) regardless of stimulus modality. Thus, if the paw was initially rostral, it would move caudal after stimulation; if the paw was initially

caudal, it would move rostral. There are two possible sources of the information that the CNS could have used to determine the initial location of the paw – proprioceptive feedback or efference copy (a copy of the internal command the rat used to place the foot in its current location). To distinguish between these hypotheses, we placed the stimulated paw on an independently movable glass plate and then dissociated proprioceptive.

P52 Ariel Childs, Aubrey Siebels, Kate Reiman, Dr. Corey Cleland

Determinants and mechanisms of the escape response to looming stimuli in crickets, *Acheta domesticus*

Animals respond to aversive stimuli with escape or withdrawal responses. In crickets, wind, which might normally be produced by an approaching predator, has been shown to evoke an escape response in which the cricket turns and then runs or jumps away. Looming stimuli, however, better approximate the combined stimulus modalities (wind, vision and sometimes touch) associated with attack by a predator. Nevertheless, there are a limited number of studies on the response of crickets to looming objects. The goal of this study was to describe the escape response of the cricket (*Acheta domesticus*) to looming stimuli delivered from each of 8 angles around the cricket. Looming stimuli were created by attaching a 3" black polyurethane ball to the end of a 12" air cylinder (45 degrees to vertical) driven by compressed air at a speed of about 90 mm/sec. The direction of "attack" was varied in 45 degree increments around the cricket. The cricket's response was recorded by a high-speed video camera (Redlake/IDT, 650 fps) placed overhead. The top of the head, thoracic-abdominal junction and the tip of the abdomen were tracked over time (Proanalyst, Xcitex) to provide the two dimensional locations and orientation of the abdomen and the head/thorax. Further, the initial locations of the tip of tarsi just prior to movement were recorded. In response to looming stimuli, crickets typically first pointed their proximal antenna toward the looming object and then initiated a turn away from the stimulus. At the completion of the turn, the crickets either walked (89%) or jumped (11%) away. The direction of the turn was almost always (98%) away from the stimulus. Further, the response direction varied with the laterality of stimulus (slope = -0.57; 1.0 would be directly away from the stimulus; $p < 0.0005$). Interestingly, the head/thorax nearly always led the turn. These results demonstrate that the direction of the crickets' escape turn from looming stimuli depends strongly on both the side and the laterality from which the stimulus is delivered.

P53 Jianga Ou, Dr. Corey Cleland

Escape response of Madagascar cockroaches (*Gromphadorhina portentosa*) to looming and localized heat stimuli

Animals respond to aversive stimuli with escape or withdrawal responses. In crickets, wind, which might normally be produced by an approaching predator, has been shown to evoke an escape response in which the cricket turns and then runs or jumps away. Looming stimuli, however, better approximate the combined stimulus modalities (wind, vision and sometimes touch) associated with attack by a predator. Nevertheless, there are a limited number of studies on the response of crickets to looming objects. The goal of this study was to describe the escape response of the cricket (*Acheta domesticus*) to looming stimuli delivered from each of 8 angles around the cricket. Looming stimuli were created by attaching a 3" black polyurethane ball to the end of a 12" air cylinder (45 degrees to vertical) driven by compressed air at a speed of about 90 mm/sec. The direction of "attack" was varied in 45 degree increments around the cricket. The cricket's response was recorded by a high-speed video camera (Redlake/IDT, 650 fps) placed overhead. The top of the head, thoracic-abdominal junction and the tip of the abdomen were tracked over time (Proanalyst, Xcitex) to provide the two dimensional locations and orientation of the abdomen and the head/thorax. Further, the initial locations of the tip of tarsi just prior to movement were recorded. In response to looming stimuli, crickets typically first pointed their proximal antenna toward the looming object and then initiated a turn away from the stimulus. At the completion of the turn, the crickets either walked (89%) or jumped (11%) away. The direction of the turn was almost always (98%) away from the stimulus. Further, the response direction varied with the laterality of stimulus (slope = -0.57; 1.0 would be directly away from the stimulus; $p < 0.0005$). Interestingly, the head/thorax nearly always led the turn. These results demonstrate that the

direction of the crickets' escape turn from looming stimuli depends strongly on both the side and the laterality from which the stimulus is delivered.

P54 Romie Powell, Benito Blanchfield, Kelly Burke, Elli Flora Samantha Hetrick, Kelcy Jackson, Lilly Nelson, Alex Schmidt, Dr. Justin Brown

Exploration of the Role of Ambient Temperature in the Recovery From Major Surgical Stress

Laboratory animals are routinely surgically instrumented for utilization in experimental protocols. The guidelines for their recovery from surgical stress suggest housing rats between 20°C - 26°C. Previous data suggest that rats prefer ambient temperatures (T_{amb}) of $\sim 27^\circ\text{C}$ (Brown and Le 2011). However, animals are often allowed to recover at normal room temperature ($\sim 22^\circ\text{C}$), which may be comfortable to the researchers but equates to a cold thermal stress for the rats. It is hypothesized that housing rats at ambient temperatures away from their preferred T_{amb} could lead to a thermal stress, which adversely affects surgical recovery.

To explore the role of T_{amb} on surgical recovery, rats will be surgically instrumented with a radiotelemetry probe, which allows non-invasive measurement of core temperature (T_c). In addition, a cannula will be inserted into the brainstem to allow microinjection of drugs as part of a separate project. For >1 week of recovery, the rats will be housed in one of 5 T_{amb} (21°C, 24°C, 27°C, 30°C, 33°C) while T_c , food and water intake, and body weight changes will be measured.

Rats housed at 24°C seemed to struggle to recover a normal T_c while those housed at 33°C recovered quickly and then maintained a slightly elevated T_c compared to control (27°C). Furthermore, rats housed at the extreme T_{amb} (21°C, 30°C and 33°C) also delayed the onset of normal circadian cycling after surgery. The return of body weight to pre-surgical levels was delayed in rats housed at the warm T_{amb} (30°C & 33°C) or the extreme cold T_{amb} (21°C). The effect of T_{amb} on daily food and water intake after surgery was not remarkable except for on the 5th day of recovery in the 30°C and 33°C groups.

These data suggest that the T_c , food/water intake, and body weight of rats maintained at 27°C returned to normal circadian patterns more quickly than those maintained at T_{amb} outside their preferred environment. Rats housed at $> 30^\circ\text{C}$ may have been exposed to a heat stress which affected weight gain and surgical recovery while those housed at 21°C may have been cold stressed and therefore affected their thermoregulatory recovery as evidenced by a delay in the exhibition of a normal circadian rhythm. It is suggested that animals be maintained at or near 27°C during the week following surgical instrumentation to minimize thermal stress. This reduction in animal stress will return the animal to their normal physiologic state and consequently enable more reliable data collection from these animals.

P55 Kristianna Bowles, Amanda Crandall, Jessie Doyle, Rhiannon English, Megan Moore, Joseph Noel, Cole Roberts, Nathan Robinson, Katherine Stanley, Erin Thady, Dr. Bruce Wiggins

A comparative stream water quality survey of a Smith Creek restoration using benthic macroinvertebrates

Rainbow Hill Farm is located on Smith Creek, a 35-mile tributary of the North Fork of the Shenandoah River. In 2006, stream restoration began at Rainbow Hill in which trees were planted in the fields surrounding the stream and cattle fenced out. In 2010, a study was initiated that utilized the quality of aquatic macroinvertebrate assemblages within the stream to determine the success of the restoration. Both the restoration area (Rainbow Hill Farm) and an upstream, unrestored area (Depoy Farm) were analyzed using the HBI, VA-SCI, and Shannon Diversity Index. We hypothesized that the water quality at Rainbow Hill would be higher than that of Depoy because of the restoration efforts, and that the stream health within the restored area would improve over time. The mean VA-SCI values for the restored area were significantly better than the upstream area (58.6 and 53.5 respectively ($p=0.021$)). The mean index values for the restored sites were also better for the HBI and Shannon Diversity Index, but not significantly. The slope of the regressions of time of restoration versus metrics was not significantly different than 0 for both upstream and restored. Continued biomonitoring of the stream is encouraged to see changes in water quality.

P56

Stanley Peyton, Zackary Zayakosky, David Taves, Dr. Pradeep Vasudevan, Dr. Alice Besterman, Dr. Michael Pace, Dr. Joanna Mott

Isolation and enumeration of *Vibrio vulnificus* and *Vibrio parahaemolyticus* from coastal Virginia

Vibrio vulnificus and *V. parahaemolyticus* are gram-negative, halophilic bacteria that commonly reside in estuarine waters but are also commonly associated with infections in humans. While gastroenteritis due to the consumption of raw fish and shellfish is common for both organisms, *V. vulnificus* can also produce wound infections leading to severe septicemia, and in some cases, death. Because of the increasing incidence of infections due to these two organisms, recent research efforts have focused on potential reservoirs and environmental conditions that can increase human exposure to and infection with these species of bacteria. This study was conducted in order to locate, isolate and analyze reservoirs that potentially harbor both species of *Vibrio* commonly identified near commercial water sources. Water, sediment, algae, fecal and invertebrate samples were collected from the mud flats of coastal Virginia. These were processed and analyzed by means of dilution, vacuum filtration, and plating on selective media in order to accurately quantify the abundance of *Vibrio* spp. on the coastal flats. Sample isolates will then be confirmed *Vibrio* species by PCR, and this will give an accurate estimate to the abundance of *Vibrio* on the Virginia coastline. Future studies may include other qualitative analyses of the *Vibrio* isolates such as Antibiotic Resistance Analysis (ARA).

P57Dustin Phillips, Daniel Breyse, Kimber Mapili, Elizabeth Dunlap, Dr. Janet Daniel
Investigating the Response of the STP1 k/o and WT *Arabidopsis thaliana* in Response to Various Environmental Stresses

Sugar Transport Protein-1 (STP1) is a H⁺/monosaccharide co-transporter found in the common model organism *Arabidopsis thaliana*. Its role in the proper growth and function of the plant is not well known, so the purpose of our investigation is to better understand how STP1 contributes to the overall condition of the plant. This was accomplished by investigating how the wild type (WT) plant and a knock-out (k/o) respond to varying environmental stresses. Previous research suggests that when exposed to different levels of NaCl, the k/o grows slightly better in higher NaCl concentrations than the WT. Starch assays were run on leaves from both strains following a period of darkness in order to qualitatively observe a difference in the starch consumption between the WT and the k/o. The WT and k/o plants were also exposed to a diagonal NaCl gradient to identify a possible difference in the halotropic response between the two. Qualitative differences in the starch content were noticed, as the k/o plants showed a higher starch content. In addition, the k/o seemed to respond better to higher NaCl concentrations, and had longer roots and stems as well as more leaves than the WT. In total, results suggest that the STP1 k/o plant exhibits an alternate phenotype when grown in higher NaCl concentrations. This may indicate higher salt stress resistance.

P58Jillian Breault, Dr. Amanda Storm, Dr. Christopher Berndsen, Dr. Jonathan Monroe
See printed program for title and abstract.**P59**Sheikh Hossain, Megan Hines, Dr. Amanda Storm, Dr. Jonathan Monroe
Searching for Potential Binding Partners of *Arabidopsis* Beta-amylase 9 Using Yeast 2-Hybridization

In almost all plants, starch is a major carbon and energy storage compound. Starch is made as the product of photosynthesis while plants are in the presence of light and is degraded at night. Our lab is especially interested in the cellular mechanism of starch degradation in plants and for our studies we use *Arabidopsis thaliana* as a model due to its practicality in lab settings. Beta-amylases are primary responsible for the hydrolysis of starch in plants and a total of nine Beta-amylases genes are encoded in *Arabidopsis thaliana*. These nine genes are identified as BAM1-9. BAM9 is specifically located in the chloroplast where starch is located and BAM9 is present in all flowering plants but it is not catalytically active. However, it is proposed that BAM9 may have an altered activity as a regulator as it was published that BAM9 was very strongly expressed in the transition between daytime and nighttime. Since regulatory proteins

function by interacting with other proteins, the yeast two-hybrid system will be utilized to obtain more information about which protein may interact with BAM9. The protocol for yeast Two-hybrid has multiple steps. As a first step, yeast cells have been transformed with a BAM9 bait plasmid and the bait vector has been validated to proceed with the rest of the yeast two-hybrid protocol. Next, the cDNA library screening will be performed where our specific yeast cells with the bait is transformed with a library that encodes for potentially interacting proteins. We will look for the expression for reporter genes that indicates interaction. The next step is to eliminate false positives by a series of control experiments. Lastly, bioinformatics analysis will be used to identify the protein(s) that interacted with the bait protein and activated transcription of the reporter genes. Obtaining more comprehensive information about protein-to-protein interactions will not only aid our understanding of BAM9's activity but also help us to understand the regulatory processes in which BAM9 may part take.

P60 Milos Lesevic, Grace Bauer, Dr. Terrie Rife

Examining Peroxisome Proliferator-activated Receptor Gamma Coactivator 1-Alpha (PGC1-a) Gene Transcription in Neurodegenerative Disease

Peroxisome proliferator-activated receptor gamma coactivator 1 alpha (PGC1-a) is a transcriptional coactivator involved in metabolic regulation. Misregulation of this gene's expression levels has been correlated to the development of numerous neurodegenerative diseases such as Huntington's disease (HD), Parkinson's Disease (PD) and Alzheimer's Disease (AD). All of these diseases are characterized by the aggregation of the proteins alpha-synuclein and tau. There is increasing evidence that one of the normal roles of these proteins in the cell is in controlling transcriptional regulation. Literature and preliminary studies in our lab show that PGC1-a changes in expression upon increasing cellular alpha-synuclein, and another study also shows that alpha-synuclein can directly bind to the PGC1-a promoter. However, the site at which alpha-synuclein binds to PGC1-a is still unclear. We have preliminary evidence in our lab that purine-pyrimidine repeats may play a role in NOS1 regulation by tau and alpha-synuclein and this promoter has a TG repeat of 50 bp. CHIP studies, in the literature, suggest that alpha-synuclein binds a consensus sequence (CCTTCCCC). We hypothesize that alpha-synuclein will bind to one of these two or both of these consensus sites. We will also test to see whether tau may be able to regulate the PGC1-a gene. In order to test the transcriptional effects of alpha-syn and tau on the PGC1-a promoter we will design several promoter constructs with deletions in either one or both of the sequences of interest, and then clone the constructs into luciferase expressing plasmids. These transcripts will be transfected into human neuroblastoma cells with varying levels of tau and alpha-synuclein. By monitoring luciferase activity we will be able to determine how the PGC1-a promoter responds to changes in tau or alpha-synuclein expression in these cells.

P61 Samantha Webster, Dr. Patrice Ludwig

Initial measurements of barnacle survivorship on alternative substrates

Oyster reef depletion due to habitat destruction has risen 85% in the last 130 years. One strategy for restoration and conservation of these reefs is using artificial substrates. Research suggests that juvenile oysters are able to "strike" to concrete structures, however, there is a lack of understanding on the effect of other sessile animals using these substrates and the oysters that grow on them. For instance, barnacles and other invertebrates rely on oyster reefs for their habitat. Barnacles attach on to both real oyster and artificial substrates in order to grow and survive. I investigated the effect of substrate on survivorship of barnacles using photo analysis. The survivorship of the barnacles' declines over time regardless of substrate. Initial counting shows no significant difference in the survivorship of the barnacles on the different substrates. This research can help determine whether artificial substrates versus natural oyster shell has an effect on barnacles' and other surrounding invertebrates' survivorship. Further research is needed to know what aspects of the substrate affects the survivorship of barnacles.

P62 Madeline Henwood, Shaw Camphire, Sophie McGinnies, Dr. Terrie Rife

The effect of alpha-synuclein on gene expression in human cell lines SK-N-MC and HeLa

Parkinson's Disease is the 16th leading cause of death in the United States. One hallmark of the disease is the aggregation of the protein alpha-synuclein into Lewy bodies. Unfortunately, scientists are unclear as to the role of alpha-synuclein in the cell and thus how Lewy bodies may play a role in PD development. Because of the cytoplasmic location of Lewy Bodies, many scientists have attempted to understand the cytoplasmic role for this protein, but its role in the cytoplasm remains elusive. More recent research suggests that alpha-synuclein binds to DNA in the nucleus. Papers have identified several genes PPARGC1A, SLC4A5, CDC42, and NEDD4 that alpha-synuclein appears to bind to. Work in our lab suggests that alpha-synuclein may be a transcription factor and regulate the expression of the NOS1 gene. We suggest that changing alpha-synuclein expression will down regulate the expression of all five of these genes. Experiments to test our hypothesis were performed by transfecting the human cell lines SK-N-MC and HeLa with and without the alpha-synuclein overexpression plasmid and isolating the RNA from these cell lines. Reverse transcription and quantitative PCR will be used to quantitate expressional changes of these plasmids. The findings of this study will lead to a greater understanding of alpha-synuclein's role in the mechanism of PD pathogenesis.

P63 Ryan Hilton, Dr. David McLeod

Quantification of Tubercle Patterns As a Means To Decipher the *Limnometes* Complex

The use of morphology and genetic sequencing is often used to decipher the phylogeny of species. Molecular phylogenetic tools provides a discrete line of evidence regarding the relationships between organisms, whereas the morphological techniques historically used in species delimitation can be confounded by convergent evolution and overall similarities seen in cryptic species complexes. Unlike molecular data, morphology is currently the only practical means for examining live specimens under field conditions. Within the context of a molecular phylogeny, study explores differences in the gross morphology of frog skin as a means for confirming species boundaries in a cryptic species complex. Using the Southeast Asian fanged frogs of the *Limnometes kuhlii* complex as a model, we use 3D imaging technologies to quantify dermal tubercle density, height, volume, and shape to determine species-specific patterns.

P64 Joshua Gerard Mata, Grace Dimond, Sarah Miller, Dr. David McLeod

Curation of a natural history collection: Completed, current, and future projects in the JMU Natural History Collection

Natural history collections exist to maintain specimens for use in scientific research and education. Specimens from these collections are particularly important for use in the identification and description of new species, understanding biodiversity in a historical context, and for the ability capturing data from specimens that may no longer exist in the wild. The JMU Natural History Collection, housed in the Bioscience building, contains a small number of fluid preserved and dry collections. These collections include osteological and insect specimens and whole organisms stored in ethanol and other fluid preservatives. From 2015–2016, a team of students and faculty have worked to raise the quality of the collection to the standards and best-practices of modern museums. The goal of this effort is twofold: First, to ensure the quality and usefulness of these valuable collections, and second, to increase the visibility of the collections and encourage the use of them by students and faculty. To date, the fluid preserved specimens have been organized taxonomically and we are now working on the dry insect collection. Future efforts will include the curation of study skins, birds and mammals, and the osteology collections. Ultimately, all collections will be cataloged and databased, allowing the JMU Natural History Collection to become an even greater resource for both learning and research purposes.

P65 Frank May, Jenna Salter, Dr. Katrina Gobetz

Examples of the Trelawny research experience: potential reservoirs for pathogenic bacteria and revolutionary ecological study of box turtles

Several experiments have been done with pathogenic bacteria, but many focus on which strains are most harmful to humans. Research in the Mott Lab aims to identify potential reservoirs for certain bacteria of the *Vibrio* genus. To determine how pathogenic bacteria disperse through an ecosystem, samples of water, sediment, marine snails, and bird droppings

from a region of mudflats were collected. After collection, samples were tested for the presence of *Vibrio* by plating onto media with high salt content, a condition favoring this genus. Plausible samples of the two target species, *V. parahaemolyticus* and *V. vulnificus*, were isolated and underwent PCR to confirm identity of the growing plaques. Establishing *Vibrio* reservoirs in an ecosystem can enable an understanding of how they survive and new ways to inhibit and treat them. Another method to identify organism distribution in an ecosystem is using Arduino-based technology to study habitat preference of Eastern Box Turtles (*Terrapene carolina*). Microprocessors and remote data collection could revolutionize wildlife studies, as location, temperature, etc. are transmitted remotely to a personal device without physically tracking the animal. After surveying land, we will collect data using repeaters and microprocessors placed on the turtle carapace. Transmitted data can be utilized to remotely measure activity patterns and habitat parameters. Results from our research site, undergoing reforestation, potentially improve conservation methods for *T. carolina* in various habitats. Remote tracking could be used in outreach, where K-12 students could “track their own turtle.”

P66 Joshua Gerard Mata, Phoebe Cook, Dr. Idelle Cooper

Color variation within the Beautiful Hawaiian damselfly, *Megalagrion calliphya*

From size differences, ornamentation, and color variation, sexually dimorphic traits are almost always believed to have originated through some form of sexual selection, with studies often overlooking the effect of ecological selection on these traits. The Beautiful Hawaiian damselfly, *Megalagrion calliphya*, contains sexual dimorphism in their coloration. Males are always a bright red while females are green but also have an additional red-colored morph that appears to mimic the males'. The aim of this study is to see whether these colorations change over time, and how that might vary over elevation. Damselflies were caught, marked, and scanned at various sites and elevations on the island of Hawaii. Then measured the color of the scans using Photoshop. Our preliminary results show that females and males get redder over time, perhaps due to exposure to solar radiation. The findings of this study could lead to a greater understanding of sexual dimorphism as it would document the change over time of a trait within only one gender that's acted on by ecological selection.

P67 Noah Greenman, Kaitlyn Staples, Dr. David McLeod

Bad to the Bone: Frogs with Fangs and Claws

The genus *Limnonectes* comprises 66 species distributed throughout Southeast Asia in which the males are generally characterized by the presence of odontoid processes, a feature that gives them the colloquial name of “fanged frogs”. The genotype *Limnonectes kuhlii* has long been considered a single species with a distributional range from Indochina to the Sundashelf. Recent work has revealed that this “species” is in fact a complex of more than 24 species that appear morphologically similar, yet show great genetic variation. One clade from Borneo possesses a unique morphological synapomorphy that separates it from other member of the complex; an ability to extend its distal phalanx as a claw. Though unique in the *L. kuhlii* complex, this feature appears to be a case of convergence and is found in distantly related frog genera from Africa (*Astylosternus* and *Trichobatrachus*). Using 3D modeling we examined this unique morphology along with another, closely related clade in the *L. kuhlii* complex from Laos that does not possess the digital claw.

P68 Monifa Williams, Zachary Schuhmacher, Patrick Kilkenny, Dr. Roshna Wunderlich

Form and Function of Intrinsic Foot Muscles

Intrinsic foot muscles originate and insert within the foot. Intrinsic foot muscles are thought to be active during walking and running, and may support the longitudinal arch of the foot. Atrophy of these muscles has been associated with foot pain, foot deformities, and falling in the elderly 1,2,3. There is no standard for assessing the strength and size of these muscles, and methods that have assessed foot muscle strength and function focus on muscles that flex the toes. However, preliminary evidence from our laboratory suggests that the intrinsic muscles that abduct and adduct the toes are important for balance, turning, and may be implicated in disease processes associated with foot muscle atrophy.

The goal of our experiment is to develop a method to measure toe abduction strength and ultimately assess the function of all of the intrinsic foot muscles. We will use

Polydimethylsiloxane (PDMS) with tracer particles as a substrate in which the toes can move, displacing the tracer particles and facilitating visualization of in small toe movements. Once we can measure toe strength effectively, we will design an experiment to measure toe muscle function using electromyography during daily activities such as walking, running and turning.

BIOSYMPOSIUM 2016 - Author Index
Numbers refer to (T)alks, (P)osters, (G)raduate talks

T1-T8: TH 1-4:30pm *Biosci 2007*
T9-T14: FRI 9-noon *Biosci 2007*
P1-P14: TH noon-2pm *2nd Fl. Foyer and hallway*
P31-P63: FRI 2-4pm *2nd Fl. Foyer and hallway*

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