Biology Graduate Research Symposium
Spring 2012 Program

Friday, April 13th, 2012

Sponsored by
Department of Biological Sciences
& the College of Arts and Sciences

Schedule of Events

Session I Oral Presentations:
9:30-11:50 am; Waggoner 378
Moderator: Dr. Shawn Meagher

Plenary Speaker: Dr. Nohra E. Mateus-Pinilla (DVM, MS, PhD)
Wildlife Veterinary Epidemiologist
University of Illinois - Illinois Natural History Survey
12:00-1:00 pm, Waggoner 378

Session II Oral Presentations:
1:10-1:50 pm; Waggoner 378
Moderator: Dr. Wendell French

Session III Poster Presentations:
2:30-4:30 pm, Waggoner Hall 3rd Floor

5:00-7:00 pm, Potluck Dinner and Awards: Old Bailey House

Organizing committee
Dr. Andrea Porras-Alfaro (chair)
Dr. Shawn Meagher (co-chair)
Dr. Wendell French
Cindy S. Drasities

Graduate students
Joseph Van Dyke
Terri L. Tobias
Laura Hubbard
Tabitha Williams
### Session I: 9:30-11:50 am, Dr. Shawn Meagher, Moderator

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<td>Eric Schroder</td>
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<td>Susan Romano</td>
<td>Indiana Bat (Myotis sodalis) Migratory Routes And Summer Habitat Characteristics Concerning Wind Farms In Iowa And Illinois</td>
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<td>Parasite Decline As A Driving Factor Of Deer Mouse (Peromyscus maniculatus) Postfire Population Growth</td>
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### Session II: 1:10-1:50 pm, Dr. Wendell French, Moderator

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<td>Brian Traughber</td>
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<td>Timothy Spier</td>
<td>Developing Sustainable Watershed Management Through Web-Based Outreach &amp; Education: Spoon River Watershed, Illinois</td>
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<td>1:30</td>
<td>Ben Ade</td>
<td>G/In progress</td>
<td>Richard Musser</td>
<td>Tissue Specific Gene Expression Of Helicoverpa zea In Response To Soybean Herbivory</td>
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Session III: Posters 2:30-4:30

Graduate
10. Allison Treadway  
G/Complete  
Faculty Advisor: Brian Peer  
Maximizing Small Mammal Communities In Roadside Right-Of-Ways In An Agriculturally Dominated Landscape

11. Joseph Van Dyke  
G/In progress  
Faculty Advisor: Ken McCravy  
Comparative Neurology Of Social And Solitary Hymenoptera And The Identification Of Factors Influencing Brain Development

12. Terri Tobias  
G/In progress  
Faculty Advisor: Andrea Porras-Alfaro  
Endophytic Fungi: Mechanism Of Transmission, Potential Applications, And The Effect On Germination And Plant Growth

G/In progress  
Faculty Advisors: Sean Jenkins and James Lamer  
A Population Study Of Blanding's Turtle (Emydoidea blandingii) In A Nearly Pristine Wetland Habitat

14. Kim Gillespie  
G/In progress  
Faculty Advisor: Shawn Meagher  
Does “White Grub” Decrease The Fitness Of Its Bluegill Hosts?

15. Scott Pinker  
G/In progress  
Faculty Advisor: Jeff Engel  
The Effects Of Aging On Habitatuation In Drosophila

16. Jared Ruholl  
G/In progress  
Faculty Advisor: Ken McCravy  
Native Bee Diversity in West-Central Illinois Forests: Determining Methodology and the Effects of Fire

17. Samantha Workman  
G/In progress  
Faculty Advisor: Meshack Afifihile  
The Role Of atTo159 Receptor In The Synthesis Of Polyunsaturated Lipids In Plants That Have Been Exposed To Low Temperatures

Undergraduate
18. Zachary Gossage  
G/In progress  
Faculty Advisor: Andrea Porras-Alfaro  
Fungal isolates from the roots of Geum rossii and Deschampsia cespitosa at the Niwot LTER site

19. Kenny Kusimba  
G/In progress  
Faculty Advisor: Susan Meiers  
Monitoring The Phytolankton Community During A Wetland Restoration At Emiquon Nature Preserve, Havana, IL

20. Eric Haas  
G/In progress  
Faculty Advisor: Jeff Engel  
The Effects Of Aging Upon The Visual System Of Long-Lived Drosophila indy Mutants As Measured By Electrotetroretinography

21. Tabitha Williams  
G/In progress  
Faculty Advisor: Andrea Porras-Alfaro  
In Search For A Killer: Psychrophilic Fungi Associated With Seven Bat Species CommonlyFound In Southern Illinois

22. Brandon Gross  
G/In progress  
Faculty Advisor: Jeanette Thomas  
Determining Critical Habitat Of The River Otters (Lontra canadensis) At The Upper Mississippi River National Wildlife And Fish Refuge Using Trail Camera Monitoring Techniques

23. Khanh Dao  
U/Complete  
Faculty Advisor: Meshack Afifihile  
A Mutant Of Arabidopsis italiana, atTo132/120(+/-) Had Reduced Levels Of A-Linolenic Acid When Exposed To Low Temperature

24. Antonio Rosales  
U/Complete  
Faculty Advisor: Andrea Porras-Alfaro  
Vertically Transmitted Endophytes Isolated From Plants In The Alpine Tundra

25. Myrtha Pierre  
U/In progress  
Faculty Advisor: Wendell French  
Antibiotic Susceptibility Testing of Non-Escherichia coli Thermotolerant Coliforms (KEC) Isolated from Streams Feeding into the Mississippi River in Hancock County, Illinois
26. James Zweep  
U/In progress  
Faculty Advisor: Ken McCravy  
Assessing Bee Habitat Associations In Oak-Hickory And Maple Forests

27. Kara Tracy  
U/Complete  
Faculty Advisor: Meshack Afitlhile  
Cold-Induced Accumulation Of Polyunsaturated Fatty Acids In A Null Mutant Of Arabidopsis thaliana, atToc159

28. Katrina Sandona  
U/Complete  
Faculty Advisor: Andrea Porras-Alfaro  
Effect Of A Dominant Endophytic Fungus, Phialocephala fortinii, On Plant Growth

29. Zachary Andrew  
U/In progress  
Faculty Advisor: Scott Holt  
Leuconostoc Bacteria on Defined Growth Media vs Complex Growth Media

30. Michelle Golz  
U/In progress  
Faculty Advisor: Meshack Afitlhile  
The Expression Of Jar1 Genes In An Arabidopsis Mutant, atToc132/120 (+/-)

31. Donna James  
U/In progress  
Faculty Advisor: Richard Musser  
Analysis Of Transcriptomic Responses To Toxins In Helicoverpa Zea Diets

32. Lauren Zager  
U/Complete  
Faculty Advisor: Andrea Porras-Alfaro  
Study of Chaetomiaceae fungi isolated from Illinois

33. Morris Parker  
U/In progress  
Faculty Advisor: Wendell French  
Antibiotic Susceptibility Testing Of Escherichia Coli Thermotolerant Coliforms (Kec) Isolated From Streams That Feed Into The Mississippi River In Hancock County, Illinois

34. Danielle Sprout  
U/Complete  
Faculty Advisor: Meshack Afitlhile  
The Attoc159 Receptor Complex Represents A Critical Point In The Biosynthesis Of Jasmonic Acid

35. Memory Cain  
U/In progress  
Faculty Advisor: Rich Musser  
Gene Expression Of Caterpillars After Feeding On Tomato Plants

36. Shiloh Lueschow  
U/Complete  
Faculty Advisor: Andrea Porras-Alfaro  
Morphological, Physiological, and Molecular Characterization of Geomyces Species

37. Courtney Cluney  
U/Complete  
Faculty Advisor: Tim Spier  
Zooplankton Community Dynamics In Spring Lake
The Genomic Response Of Helicoverpa zea After Feeding On Phytohormone Treated Tomato Plants

H. zea is a prevalent insect pest that has a wide geographical distribution and feeds on a wide range of prominent agricultural crops. We investigated caterpillar’s transcriptomic response to tomato plant defense activated by salicylic acid and jasmonic acid. Plants were grown in the lab for eight weeks and then sprayed with salicylic acid or jasmonic acid and allowed to generate defenses over 24 hours. Plants treated with jasmonate stimulated significantly higher levels of anti-nutritive defenses such as protease inhibitors in comparison to salicylate treated plants. Recently molted 6th instar caterpillars were allowed to feed on these phytohormone treated plants for 24 hours. Whole body caterpillars were analyzed through microarray analysis to determine the transcriptomic response and tested for statistical significance with a t-test. 1,331 significantly putative genes were altered from feeding on the plants compared to the control fed caterpillars. Caterpillars that fed on jasmonic acid treated plants showed an up-regulation in genes responsible for digestive enzymes such as proteases and lipases correlating to anti-nutritive defenses. In addition, detoxification, amino acid metabolism, dehydrogenases, and transferases were stimulated. Salicylate treated plants showed an up-regulation in genes responsible for chitinases and immune responses. This is one of the first transcriptomic studies to correlate caterpillar gene alteration to inducible plant defenses. Understanding how H. zea responds to induced plant defenses will provide information for developing biological control.
4. **Student Name:** Audrey Putnam  
**Status:** Graduate Student  
**Email:** asp109@wiu.edu  
**Faculty Advisor:** Dr. Jeff Engel  
**Presentation Type:** Oral presentation  
**Project Status:** In progress

*Effects Of Potassium Ion Current Mutations On Flight Pattern Generators In Drosophila*

Putnam A, Engel J  
Department of Biological Sciences Western Illinois University  

*Drosophila* use twenty-six indirect flight muscles in their thorax to power the wings for flight. The patterns of action potentials which control the indirect flight muscle activity are complex and stereotypic in wild-type flies. This coordination is provided though a flight pattern generator in the central nervous system. Pattern generators are groups of neurons which are able to coordinate complex movements without cycle by cycle feedback by firing action potentials in complex patterns. When not flying, spontaneous action potentials in the indirect flight muscles are rare in wild-type flies. However, *eug* and *shaker* mutant flies are hyperexcitable, due to altered potassium ion currents, and spontaneous action potentials occur within muscles when these flies are at rest. These spontaneous action potential patterns are quite different from what is observed during flight. However, the extent of these mutations’ effects on the flight motor pattern has not been explored. The underlying physiology which creates the hyperexcitability may also affect the pattern generator that controls the motorneurons and flight muscles during flight. The goal of this project is to determine if the flight pattern generator is altered in *eug* and *shaker* potassium channel mutants. This will be determined by recording the patterns of action potentials in pairs of muscles of the flies during flight and rest. The results of this study should indicate the degree of stability of the flight pattern generators in *Drosophila*.

5. **Student Name:** Jeffrey E. Noland  
**Status:** Graduate Student  
**Email:** ie-noland@wiu.edu  
**Faculty Advisor:** Richard O. Musser  
**Presentation Type:** Oral Presentation  
**Project Status:** Complete

*Gene Expression Profile Of Helicoverpa zea In Response To HzSNPV*

Noland, JE, Noland HC, Hum-Musser SM, Musser RO  
Department of Biological Sciences, Western Illinois University  

*Helicoverpa zea* is a widely known agricultural pest that is linked to 1 billion dollars in damage and management annually. Potential biological controls for *H. zea* are baculoviruses such as the *Helicoverpa zea* Single Nucleocapsid Nucleopolyhedrovirus (HzSNPV). We tested the transcriptomic response of *H. zea* as whole larvae, as well as the midgut after a 24 hour period. Examining the midgut allowed for a view into the main site of infection, whereas the whole body showed responses surrounding the infection in addition to the gut. Results for both microarrays were log transformed and analyzed for statistical significance with a t-test. There were 831 significant putative genes in the midgut tissue and 77% of genes were down-regulated and 23% were up-regulated compared to the non-infected control. While in the whole larvae only 179 significantly putative genes altered, 70% of these genes were up-regulated and 30% down-regulated compared to the non-infected control. The low number of genes found in the whole body compared to the gut alone suggested that the virus had not spread much beyond the midgut in the first 24 hours. Several digestive related genes were down-regulated such as aminopeptidases and serine proteases. Immune response and apoptosis related genes were a bit more complicated with genes like antimicrobial peptides being both up and down-regulated. In general, detoxification genes in the midgut were down-regulated as a result of infection. This first transcriptomic study of *H. zea* to HzSNPV that we are aware of provides further ground work to understanding the global physiological changes the virus.

6. **Student Name:** Laura Hubbard  
**Student status:** graduate student  
**E-mail:** ll-hubbard@wiu.edu  
**Faculty Advisor:** Brian Peer  
**Presentation Type:** Oral presentation  
**Project Status:** First Season Complete (second season data analysis in progress)

*The Road Ahead: Characteristics Of Roadside Right-Of-Ways That Influence Bird Abundance And Diversity In An Agricultural Landscape*

Hubbard, L., Treadway, A., McCleery, R., Peer, B.  
Department of Biological Sciences, Western Illinois University  

More than 99% of the original prairie grassland in Illinois has been lost, much of this to agricultural development, making suitable habitat for grassland bird species scarce. Not surprisingly, grassland obligates have declined more than any other group of birds in North America. Much of the grassland that remains is in rural pastures and roadways, with > 300,000 ha of marginal grasslands found adjacent to roads throughout the state. We conducted double observer transect surveys on both sides of 50 randomly selected roadside right-of-ways (ROWs) adjacent to agricultural production (corn and soybeans) in west-central Illinois. We used an information theoretic approach and developed 23 *a priori* models to determine the characteristics of ROWs that influenced bird abundance and diversity. Our best models of avian abundance included ROW width, visual obstruction, and biomass (V*O* *width*). Biomass (β=0.0168, CI: 0.0007 - 0.0329) and VO (β = 0.3046, CI: 0.0345 - 0.5747) were relevant predictors of abundance. Our best models of species richness included ROW width, VO, and biomass. Biomass (β= 0.0107, CI: 0.0012-0.0202) was the only relevant predictor of species richness. Occupancy modeling showed the percent of vegetative cover to be a positive influence on the occurrence of two grassland obligate species, the Eastern Meadowlark (*Sturnella magna*) and the Dickcissel (*Spiza americana*). To enhance the viability of ROWs for grassland birds, we recommend implementing a mowing regime that maximizes the biomass of grassland vegetation to increase nesting cover during the breeding season and increasing the width of ROWs where possible.
7. **Student Name:** Jonathan Vaughan  
**Student Status:** Graduate student  
**E-mail:** pvvaughn@wiu.edu  
**Faculty Advisor:** Shawn Meagher  
**Presentation Type:** Oral presentation  
**Project Status:** Complete  

Parasite Decline As A Driving Factor Of Deer Mouse (Peromyscus maniculatus) Postfire Population Growth  
Vaughn J, Meagher SDepartment of Biological Sciences, Western Illinois University  

Deer mouse populations increase dramatically following fire in coniferous forests. Several hypotheses for this population boom have been proposed, but none of them have been supported upon being tested. A possible, but untested, explanation for this mouse population explosion is a change in levels of parasitism: parasites have negative effects on hosts and if parasite densities decrease after a fire, mouse populations will respond positively. Fire may decrease the population density of intermediate hosts of many parasite species, which could consequently lead to lower levels of infection in their definitive host, mice. Here, I test this hypothesis by examining deer mice collected from burned and unburned traplines one year after a stand-replacing forest fire in northwestern Montana. Mice were dissected and inspected for external parasites and gut parasites. Four species of flea, two species of louse, four species of nematode, and two species of tapeworm were identified. Fisher’s exact tests were used to test for effects of fire on prevalence, and t-tests for effects on intensity (counts per individual host) of all parasite taxa. No significant effect of fire was found on measures of infection in any parasite taxon, with two exceptions: fire had a positive effect on louse intensity and a negative effect on flea prevalence. These results indicate that parasites are not likely the driving factors of deer mouse postfire population growth, and that further research is needed to identify the variables which are.

8. **Student Name:** Brian Traughber  
**Student Status:** graduate student  
**E-mail:** bj-traughber@wiu.edu  
**Faculty Advisor:** Timothy Spier  
**Presentation Type:** Oral presentation  
**Project Status:** Complete  

Developing Sustainable Watershed Management Through Web-Based Outreach & Education: Spoon River Watershed, Illinois  
Traughber B, Spier T  
Department of Biological Sciences, Western Illinois University  

Non-point source water pollution remains one of the most challenging environmental issues. Nutrient pollution causes impairment of drinking water resources, habitat quality, and biodiversity. In the Midwest, excessive agriculture-based nitrate pollution – one form of non-point source pollution – from the Upper Mississippi River basin (UMRB) as well as hydrologic and climatic factors are contributing to a growing hypoxic zone in the Gulf of Mexico. Within the Lower Illinois sub-basin of the UMRB, ecosystem services such as recreation, water quality, and biodiversity have been greatly reduced due to habitat destruction and fragmentation of natural areas. To further support water quality improvement, community-based watershed management has the potential to influence public policy with goals of creating sustainable economies and equitable communities to meet the needs of local stakeholders. Agricultural best management practices (BMP) such as wetlands, grassed waterways, vegetative filter strips, rotational grazing, cover crops, and conservation tillage are important tools for restoring ecosystem services. In order to implement community-based watershed management, outreach and education have been identified as effective tools for BMP implementation in agricultural watersheds. I have developed an educational platform for disseminating data and information via the internet and web-based mapping technology to guide the watershed community and natural resource managers towards a sustainable watershed management plan. For example, a landowner will be able to identify a potential wetland restoration site based on hydric soil maps, riparian buffers, and elevation contours using ArcGIS Explorer, a free GIS online viewer.

9. **Student Name:** Ben Ade  
**Student Status:** Graduate Student  
**E-mail:** JT-Ade@wiu.edu  
**Faculty Advisor:** Richard Musser  
**Presentation Type:** Oral presentation  
**Project Status:** In progress  

Tissue Specific Gene Expression Of Helicoverpa zea In Response To Soybean Herbivory  
Musser, Richard O.  
Department of Biological Sciences, Western Illinois University  

Gene expression of Helicoverpa zea (corn earworm) caterpillar labial salivary gland and midgut tissues were measured in response to being fed on Glycine max (soybean) leaf tissue. Two groups of H. zea caterpillars were used in the experiment, a control group, which was fed an artificial diet, and the experimental group that was fed on mature G. max leaves in vitro. Total RNA was extracted from surgically removed labial salivary gland and midgut tissues of actively feeding caterpillars. Total RNA was then amplified using i7 primers and labeled with fluorescent dyes to produce amplified and labeled cRNA, which was then hybridized on a custom oligo-nucleotide microarray. Microarray analysis showed that a total of 1200 labial salivary gland genes, and 498 midgut genes were significantly altered genes from the midgut tissue are significantly different (P<0.05 t-test), from the soy fed experimental group compared to the diet-fed control group. Between the two tissues, only 8 genes of unknown function were found to be significantly different between both tissues. Among the significantly altered caterpillar salivary gland genes altered were genes, which encode for proteases, metabolic pathways, cytochrome P450 system, and other detoxification and immune system genes. Significantly altered genes from the midgut tissue are primarily related to aiding in the digestion of proteins, starches, and lipids. These data provide an insight into the gene expression of H. zea caterpillars in response to the plant defenses of G. max and gives a more in depth understanding in the regulation between different tissues under similar conditions.
12. Student Name: Allison Treadway
Student Status: Graduate student
E-mail: ar-treadway@wiu.edu
Faculty Advisor: Brian Peer
Presentation Type: Poster presentation
Project Status: Complete

Maximizing Small Mammal Communities In Roadside Right-Of-Ways In An Agricuiturally Dominated Landscape
Allison R. Treadway, Robert A. McCleery2, Laura L. Hubbard, Brian D. Peer
1Department of Biological Sciences, Western Illinois University
2Department of Wildlife Ecology and Conservation, University of Florida

Agricultural practices create landscapes with minimal wildlife habitat. Marginal linear habitats, such as road right-of-ways (ROWS), are potential habitat for wildlife in agriculturally dominated landscapes. To determine features of roads and ROWs that promote wildlife populations, we examined changes in community diversity, community abundance, and occupancy of grassland endemic small mammals on 46 randomly selected ROWs in west-central Illinois. We used an information theoretic approach and developed 21 a priori candidate models to explain community level responses of small mammals. Additionally, we evaluated 10 candidate models to explain occupancy of grassland endemic small mammals. Differences in density of small mammals were best explained by a single model containing ROW width and month. ROW width (β = -0.9684, 95% CI = -0.9995, -0.9372) and month (β = -0.5403, 95% CI = -0.2707, 0.8099) appeared to be important predictors of density. Diversity was also best explained by ROW width (β = -0.0259, 95% CI = 0.0046, 0.0472) and month (β = 0.3192, 95% CI = 0.1281, 0.5104). Occupancy modeling demonstrated a positive influence of ROW widths >11 m in width on the occurrence of 13-lined ground squirrels (Spermophilus tridecemlineatus). Wildlife value of ROWs in an agricultural landscape can apparently be increased by expanding ROW widths.

11. Student Name: Joseph Van Dyke
Student Status: Graduate student
E-mail: jsvd101@wiu.edu
Faculty Advisor: Dr. Ken McCravy
Presentation Type: Poster presentation
Project Status: In progress

Comparative Neurology Of Social And Solitary Hymenoptera And The Identification Of Factors Influencing Brain Development
Van Dyke J
Department of Biological Sciences, Western Illinois University

Larger bodied species generally have larger brains. Increased brain size usually correlates with higher learning potential and increased complex behavior. However, brain tissue is expensive to develop and maintain. Previous studies have predominately focused on energy consumption and metabolism as the factors for complex brain development but these have been constraints, not developmental factors. Even though a species has sufficient energy to develop a complex brain doesn’t mean it needs to do so. Sociality has been correlated with more complex brains in select species and has led to the development of the social brain hypothesis. This hypothesis states that sociality imposes evolutionary pressures above those of solitary relatives. This pressure to deal with the interactions between individuals creates the demand for a larger, more complex brain. This hypothesis is generalized for multiple taxa but has only been heavily studied in vertebrate species. It is currently being tested for its validity in social insects in the order Hymenoptera. Many of these studies, however, are limited to one or two species and there is dispute as to what factors are influencing brain development. The goal of this study is to incorporate multiple species of varying degrees of sociality to give a broader, more detailed representation of what factors influence brain development in insect species.
In Spring Lake, McDonough County, IL, 100% of bluegill (Lepomis macrochirus) are infected with white grub, with an average intensity of <1000 white grubs per fish. These levels of infection are known to cause death in bluegill. A negative correlation between white grub infection and survival of bluegill is expected. I will compare parasitism levels in fish caught in the fall and in the following spring, to determine if white grub reduces over-winter survival rates in bluegill. If infection reduces survival, then the mean parasite load will be lower in spring-caught fish, indicating that heavily infected hosts have died over winter.

The term “parasite” implies a relationship where one organism (the parasite) is harmful to the host; however this level of harm has not been measured in most parasite/host associations. “White grub” (Postthripodiplostomum minimum) is the juvenile (metacercaria) stage of a fluke that inhabits a wide variety of fish species. Because it inhabits a wide variety of organs, such as the liver, kidney, and heart, it is presumably harmful to the fish it infects, but previous studies indicate it causes little harm. In Spring Lake, McDonough County, IL, 100% of bluegill (Lepomis macrochirus) are infected with white grub, with an average intensity of <1000 white grubs per fish. These levels of infection are extremely high, and often, metacercariae nearly replace several important organs. In my Master’s research, I will test whether these extreme intensities are harmful to fish in two ways. First, I will determine if there is a negative correlation between intensity and the “condition” of the fish, predicting that the heavier the infection, the thinner the fish. I will also measure the effects of white grub on bluegill survival. Stressful conditions, such as winter cold, may be necessary to reveal the negative consequences of parasitic infection. Therefore, I will compare parasitism levels in fish caught in the fall and in the following spring, to determine if white grub reduces over-winter survival rates in bluegill. If infection reduces survival, then the mean parasite load will be lower in spring-caught fish, indicating that heavily infected hosts have died over winter.
the effectiveness of these sampling methods in the forest understory. My study has two objectives: 1) to determine which type of trap, or combination thereof, is best used to sample native bee diversity within a deciduous forest, and 2) to determine the effects of prescribed fire on native bee diversity. Samples have been collected from four different plots, two of which were subjected to a controlled burn. Each plot contained four different trap types. The collected specimens will be identified to species level. Species richness, diversity indices, and similarity indices will be used to compare species composition between burned and unburned plots. The multi-response permutation procedure will be used to compare species composition of bees collected by the different sampling methods. Knowledge of the effectiveness of bee sampling methods is essential for useful estimates of bee diversity. With prescribed fire becoming a more common technique in managing forests it is important to understand how this practice could potentially affect bee diversity.

17. **Student Name:** Samantha Workman  
**Student status:** Graduate Student  
**E-mail:** sd-workman@wiu.edu  
**Faculty Advisor:** Meshack Afitlhile  
**Presentation Type:** Poster presentation  
**Project status:** In progress

The Role Of atToc159 Receptor In The Synthesis Of Polyunsaturated Lipids In Plants That Have Been Exposed To Low Temperatures  
Workman, S  
Department of Biological Sciences, Western Illinois University

When plants are subjected to lower temperatures, they synthesize polyunsaturated lipids, which increases membrane fluidity and allow plants to survive the cold. Enzymes that synthesize desaturate chloroplast lipids are encoded by nuclear genes and are therefore synthesized in the cytoplasm and imported into the chloroplasts. The import of proteins into the chloroplasts is facilitated by receptors, which are located on the outer and inner membranes of the chloroplasts. The atToc159 gene family encodes the receptors that are located on the outer membrane of the chloroplasts and these include atToc 159, atToc132, and atToc120 receptors. Studies have shown that in Arabidopsis, the atToc159 receptor complex imports proteins that are required for chloroplast biogenesis. The atToc132 and atToc120 are found in the same complex and are redundant receptors that function in the import of non-photosynthetic or housekeeping proteins. The null mutant of atToc159 has a pale phenotype and can only grow in a medium supplemented with sucrose, which suggests that enzymes involved in chlorophyll biosynthesis are not being imported into the plastids. Since lipids are the major component of the chloroplast membranes, we hypothesize that atToc159 receptor is a major route for the import of enzymes that are required in lipid biosynthesis and desaturation. We anticipate that when grown at low temperatures, a null mutant of atToc159 (pp2-2) will not be efficient in the import of fatty acid desaturases and will therefore accumulate low levels of polyunsaturated fatty acids, such as linolenic acid (18:3). We also expect the mutant to have low expression levels of fatty acid desaturases, which are required in fatty acid desaturation.

18. **Student Name:** Zachary Gossage  
**Student Status:** Graduate student  
**E-mail:** z.gossage@wiu.edu  
**Faculty Advisor:** Andrea Porras-Alfaro  
**Presentation Type:** Poster presentation  
**Project Status:** In Progress

Fungal Isolates From The Roots Of Geum rossii And Deschampsia cespitosa At The Niwot LTER Site  
Gossage, Zachary T., 1 Yeraballi, Sagar1, Suding, Katherine2, Sinsabaugh, Robert1, Porras-Alfaro, Andrea1  
Addresses: 1 Biological Sciences, Western Illinois University, Macomb, IL, 2 Department of Environmental Science, Policy & Management, University of California Berkeley, CA 3 Department of Biology, University of New Mexico, Albuquerque, NM.

Plant-associated fungi are known to play an important role in plant productivity and sustainability of the ecosystem. Endophytic fungal diversity in the alpine tundra is unknown for the majority of the plant species. The main goal of this study was to identify and describe fungal symbionts associated with two alpine tundra co-dominant plants: Geum rossii and Deschampsia cespitosa. Plants were collected at Niwot Ridge long-term nitrogen fertilization experiments in Colorado. In 2008, forty-two plants were collected from four different treatments: control, N fertilized, D. cespitosa removal with N fertilization, and D. cespitosa removal with no N addition; additional plants were collected from control plots in 2010. Roots from each treatment were stained to determine fungal colonization. Roots were surface sterilized and plated on malt extract agar with antibiotics. One hundred and ten pure cultures of endophytic fungi were isolated and identified by sequencing the Internal Transcribed Spacer rDNA. Analysis of the sequences at 97% similarity yielded 25 contigs and 24 unique sequences. Ninety-one percent of the isolates belong to the phylum Ascomycota, with most being of Helotiales, Hypocreales, and Eurotiales orders. Within Helotiales, dominant taxa were closely related to Phialocephala fortinii and Cryptosporiopsis ericae. Within Hypocreales some common taxa included Tolypocladium and Beauveria. Dominant taxa within Eurotiales included isolates related to Penicillium sp. and Aspergillus sp. Endophytic communities showed very little plant specificity suggesting that most taxa are adapted to colonize both of these dominant species.

19. **Student Name:** Kenny Kusimba  
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**Presentation Type:** Poster Presentation  
**Project Status:** In progress

Monitoring The Phytoplankton Community During A Wetland Restoration At Emiquon Nature Preserve, Havana, IL  
Kusimba K., Meiers S  
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“Phytoplankton” is derived from the Greek words “phyto” meaning “plants” and “plankton” meaning “to wander.” Phytoplankton are microscopic organisms that live in aquatic environments, both marine and freshwater with most being unicellular algae. The common taxa amongst these are
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Project Status: In progress  

Effects Of Aging Upon The Visual System Of Long-Lived Drosophila indy Mutants As Measured By Electroretinography  
Haas ET, Engel JE  
Department of Biological Sciences, Western Illinois University  

Like almost all multicellular organisms, Drosophila melanogaster is subject to the effects of aging. Drosophila heterozygous for mutation of the indy gene live up to 85% longer than wild-type controls. Flies homozygous for the indy mutation live longer as well, but have less extension of life span than heterozygotes. This life span extension is reportedly accompanied by no detriment to reproductive ability and physical activity. Do such findings imply that senescence, the decline in Darwinian fitness and the efficacy of physiological systems, is delayed in all tissues of these indy mutants? The electroretinogram (ERG) enables physiological examination of the nervous system generally and the visual system specifically. Changes in the relative intensity of or absence of one of the components of the ERG trace (on-transient, off-transient, and receptor potential) are indicative of physiological changes to the visual apparatus. The ERG traces have also been found to change with the age of the fly. I am using the ERG to examine indy mutants of various ages, and I predict to see a slowed decline in neural and visual function with an increase in life span. I also seek to confirm previous data regarding the life extension effects of the indy mutation by conducting lifespan analysis in our rearing conditions.

cyanobacteria, diatoms, dinoflagellates, green algae, and coccolithophores. Phytoplankton are the base of most aquatic food webs and thus constitute the ultimate food source for the majority of living creatures in these habitats. Due to their rapid growth, phytoplankton are sensitive and readily detectable indicators of biogeochemical and ecological change. They play a key role in wetlands productivity, nutrient dynamics, and the development of wetland ecosystems as a whole, especially before macrophytes become established.

Samples were collected from The Nature Conservancy’s Emiquon Nature Preserve, located between the Dickson Mounds Museum and Havana, Illinois, along the Illinois River. It is one of the largest floodplain restoration projects in the country outside of the Florida Everglades, and is the primary site for TNC’s work on the Illinois River and within the Upper Mississippi River system. This project objective is to understand how the restoration of Emiquon is affecting the phytoplankton community as the wetland is being restored, and understanding how the wetland restoration as a whole is proceeding.

Keywords: phytoplankton, Emiquon, wetland, restoration, Mississippi River system, macrophytes.

21. Student Name: Tabitha Williams  
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Presentation Type: Poster presentation  
Project Status: In progress  

In Search For A Killer: Psychrophilic Fungi Associated With Seven Bat Species Commonly Found In Southern Illinois  
Williams, Tabitha F, McCleery, Robert2, McClanahan, Rod1, Porras-Alfaro, Andrea1  
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Bats are indispensable to ecosystem stability; they play an important role in the control of insect populations and plant pollination. White Nose Syndrome (WNS), caused by the fungus Geomyces destructans, is a new disease infecting bats in the USA and Canada. WNS was first reported in 2006 in New York and has since then spread across the eastern and central United States where it had made its way to the Illinois borders. The major objective of this research was to identify, characterize and compare psychrophilic (“cold loving”) fungal communities associated with different bat species in southern Illinois. Bats were trapped using a harp trapping technique following USGS National Wildlife Center protocols. Swabs were taken from the bat wings and were inoculated in situ on petri plates in MEA (Malt Extract Agar) with antibiotics. Samples were incubated at 6°C to select for psychrophilic fungi. We evaluated seven different bat species, approximately 20 to 30 colonies were obtained in each petri dish, with an average of four unique morphospecies per swabbed area (2-3cm²). From the swab plates about 300 psychrotolerant pure cultures were obtained. DNA extractions, PCR and sequencing reactions were used to identify fungal cultures. Fungal communities were dominated by Ascomycota followed by Zygomycota and Basidiomycota. Common fungi in bat wings include Penicillium corinabludum, Cladosporium spp, Epicoccum, and Alternaria. Most abundant species were isolated multiple times from different bat species and caves. This research will increase our knowledge about all fungal communities associated with bats which are endangered and currently facing local extinctions.

22. Student Name: Brandon M Gross  
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Project Status: In progress  

Determining Critical Habitat Of The River Otters (Lontra canadensis) At The Upper Mississippi River National Wildlife And Fish Refuge Using Trail Camera Monitoring Techniques  
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The North American river otter (Lontra canadensis) has historically experienced both decline and subsequent recovery in North America, particularly in regions bordering the Mississippi River. The recovery of river otter on the upper Mississippi River provides an opportunity to evaluate their...
current localized densities, as well as environmental factors that determine critical habitat of the species. Bushnell Trophy field cameras were placed near land trails with suspected otter activity on designated areas of the Upper Mississippi River National Wildlife Refuge to determine relative site visitation and seasonal variation. Areas chosen for analysis were located on Pool 13 of the Mississippi River and were selected due to their ease of access and unique topographical traits. Reported data is currently preliminary, however several patterns have been observed. Land trails always connected two or more water systems. Site visitation by otters was highly scheduled and site fidelity was often characterized by periods of common visitation followed by complete abandonment of the site. Site abandonment correlated strongly with freezing surface water. Site visitation concentrated on few trails with open water access during frozen periods, and spread back after periods of warm temperatures and ice thaw. Preliminary data also suggests that high use land trails are commonly concentrated on the smallest land division between two water systems; however this is not a strong correlation. Environmental factors that likely drive variation from this pattern are reported. This unique method of determining habitat use by trail camera images will provide insight into determining critical habitat of the river otter along the Mississippi River. Identifying critical habitat is crucial for the future management of this species.

Undergraduate

23. Student Name: Khanh Dao
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Presentation Type: Poster
Project Status: Complete

A Mutant Of Arabidopsis Thaliana, atToc132/120(+/-) Had Reduced Levels Of A-Linolenic Acid When Exposed To Low Temperature
Danielle Sprout, Kayla Duffield, Melissa Savage, Samantha Workman
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All biological membranes are made of lipid bilayers, which are interspersed with proteins. In plants, some lipids are synthesized exclusively in the chloroplasts, and the synthesis and desaturation of these lipids require enzymes that are synthesized in the cytoplasm. The import of proteins into the chloroplast is facilitated by receptors that are located on both the outer and inner membranes of the chloroplast. In Arabidopsis, receptors on the outer membrane are encoded by the Toc159 gene family and they include atToc159, atToc132 and atToc120 receptors. The atToc132 and atToc120 receptors are found in the same complex and carries out the same function. Plants that lack both atToc132 and atToc120 are not viable, but a mutant that lacks atToc132 and has one functional copy of atToc120 has a pale phenotype, and is referred to as atToc132/120 (+/−). When plants are subjected to cold stress they synthesize more of the polyunsaturatad lipids, which increases membrane fluidity and allow plants to survive the cold. In this study, we evaluated the ability of the mutant to accumulate polyunsaturated fatty acids when subjected to cold stress. After 3 days of being incubated in the cold, the mutant had a 20% reduction in linoleic acid (18:3). This observation suggests that FaD8 enzyme, which converts linoleic acid (18:2) to 18:3 under cold temperature, had a reduced activity. Since high levels of 18:3 were measured in atToc132/120 (+/-) mutant, we propose that FaD8 enzyme was imported into the chloroplasts mainly through the atToc159 receptor complex.

24. Student Name: Antonio Rosales
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Presentation Type: Poster
Project Status: Completed

Vertically Transmitted Endophytes Isolated From Plants In The Alpine Tundra
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Alpine tundra plants are able to survive harsh conditions with the help of endophytes and mycorrhizal fungi. Endophytes are fungi or bacteria that live within plants without causing apparent damage. These symbiotic relationships between plants and endophytic fungi are known to have a direct impact on plant community structure, fitness, and diversity. Endophytes can colonize plants by either horizontal or vertical transmission and little is known about their abundance, taxonomy and function. The objective of this study was to isolate and quantify vertically transmitted endophytes from plant seeds that were collected at the Niwot LTER Site in Colorado. Six plant species (Geum rossii, Erigeron simplex, Artemisia scopulorum, Deschampsia caespitosa, Bistorta bistortoides, and Trietrum spicatum) were studied. Thirty seeds of each plant were surface sterilized and plated on malt extract agar with antibiotics. Fungi were sequenced using the ITS rDNA region. Thirty three endophytes were isolated from the seeds. Ten different morphotypes were present. E. simplex and D. caespitosa show the highest germination rates. Germination rates varied between 67% to 0% and colonization rates varied between 6% to 33%. B. bistortoides seeds did not germinate and showed the highest fungal colonization rates. Preliminary identification of some isolates using ITS-rDNA shows that G. rossii and D. caespitosa seeds are colonized by a fungus closely related to Cladosporium ureadincola. Additional tests need to be conducted to determine the potential role that these seed endophytes may have in plant germination, seed establishment and the structure of plant communities in the alpine tundra.

25. Student Name: Myrtha Pierre
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Faculty Advisor: Wendell L. French
Presentation Type: Poster presentation
Project Status: In Progress

Antibiotic Susceptibility Testing Of Non-Enteririchia Coli Thermotolerant Coliforms (KEC) Isolated From Streams Feeding Into The Mississippi River In Hancock County, Illinois
Pierre, M., French, W.L.

Fecal pollution is determined by the presence of thermotolerant coliform bacteria in water (Crenshaw, 2011). Thomas Crenshaw and Dr. Wendell French conducted a recent study on the degree of fecal pollution in natural water streams feeding into the Mississippi River in Hancock County, Illinois. Over a period of three months, they collected different samples of water aestically to prevent sample contamination, from seven streams that flow into the Mississippi River. The samples were filtrated using the membrane filtration technique and placed on CHROMagar ECC
26. **Student Name:** James S. Zweep  
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**Presentation Type:** Poster  
**Project Status:** In Progress

Assessing Bee Habitat Associations In Oak-Hickory And Maple Forests

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The goal of this study is to examine variation in forest bee species across different forest types and microclimatic conditions. The objectives of this study are 1) to compare bee abundance, diversity, and species composition between oak-hickory and maple forests and 2) to document patterns in bee abundance, diversity, and species composition in relation to forest microclimate. Many bees spend part of their life cycle in forests, but the ecology of forest bees is poorly understood. My research project will investigate bee abundance and species diversity in relation to forest habitat type (oak-hickory vs. maple forests). I will test the hypothesis that maple forests harbor lower bee abundance and species diversity than do oak-hickory forests. This project will be conducted at Alice L. Kibbe Life Science Station between the months of April and September, 2012. Study plots will be established in the two forest types. A variety of bee sampling methods such as understory pan traps and canopy vane traps will be used to sample bees amongst the plots. Microclimatic factors such as temperature, humidity, and wind speed will be measured at the study plots with a portable weather monitor. Statistical analysis tools (multi-response permutation procedure (MRPP), indicator species analysis (ISA), and regression analysis) will be used to measure the patterns between bee abundance, diversity, and species composition in relation to forest habitat type. This study will provide information on the importance of forest management in maintaining bee diversity, and how changes in microclimate affect bees.

27. **Student Name:** Kara Tracy  
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**Presentation Type:** Poster  
**Project Status:** Completed

Cold-Induced Accumulation Of Polyunsaturated Fatty Acids In A Null Mutant Of Arabidopsis thaliana, atoc159

Kara Tracy, Kayla Duffield, Samantha Workman, Danielle Sprout  
Department of Biological Sciences, Western Illinois University

When plants are subjected to low temperatures, their membrane lipids are desaturated to increase membrane fluidity. Chloroplasts are the sites of lipid synthesis, which could be induced de novo by low temperatures. The synthesis of chloroplasts lipids is largely dependent upon enzymes that are synthesized in the cytoplasm and imported into the chloroplasts. The outer and inner membranes of the chloroplasts have a set of receptors that recognize, bind and facilitate the import of pre-proteins into the chloroplasts. These receptors have been identified and studied in Arabidopsis, and the Toc159 receptor is the most abundant and is found in the same complex as Toc33 and the protein channel, Toc75. Studies have shown that mutation in both alleles for Toc159 resulted in plants with an albino phenotype, and they are referred to as plastid protein import deficiency or ppi. The Toc159 receptor is apparently very specific for the import of light-induced proteins, while Toc132/120 receptor complex imports housekeeping proteins. In this study, we tested the ability of ppi2 mutant to accumulate polyunsaturated fatty acids under cold stress, specifically hexadecatrienoic acid (16:3) and linolenic acid (18:3). Our preliminary results indicated that when ppi2 was incubated at 2°C for 3 days, the mutant accumulated less than 5% of linolenic acid (18:3), a polyunsaturated fatty acid that is required to maintain membrane fluidity under cold stress. This data indicates that under cold stress, the activity of fad8 enzyme was highly reduced in the mutant and not in the wild type. Therefore, our preliminary data suggest that the import of fatty acid desaturases (fad) is nonspecific, however fad8 appears to be imported into the chloroplasts mainly through the Toc159 receptor complex.

28. **Student Name:** Katrina Sandona  
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**Presentation Type:** Poster presentation  
**Project Status:** Complete

Effect Of A Dominant Endophytic Fungus, Phialocephala Fortinii, On Plant Growth  
Sandonia Katrina 1, Tobias Terri 1 , Suding Katherine 1 , Sinsabaugh Robert 1, Porras-Alfaro Andrea 2  
1. Department of Biological Sciences, Western Illinois University 2. Department of Environmental Sciences, University of California, Berkeley 3. Department of Biology, University of New Mexico

Plants in the alpine tundra rely on symbiotic relationships they have with microbial communities to endure the harsh conditions of that environment. Endophytes are fungi that live within a plant and little is known about the function of these fungi. The objectives of this experiment were to isolate fungi found in plant seeds and roots from the alpine tundra and determine their potential function on
commercial plants. Seeds and roots were surface sterilized and plated on malt extract agar. Isolates were identified using ITS rDNA and Phialocephala fortinii was selected for germination experiments. The fungus SS37 was plated in five culture jars containing malt extract agar with antibiotics, after a week six surfaced sterilized seeds of Zea mays (corn) and Glycine max (soybean) where planted in each jar. Five jars with no fungus were used as controls. The seeds were allowed to grow for one week. Plants were then removed from the jars; the roots and stems were measured. The fungus Phialocephala stimulated the growth of corn seeds with an average number of roots of 8.4 with respect to 2.4 for the control. While the soybeans with the Phialocephala had an average number of roots of 8.6 while control had an average of 1.9. Phialocephala significantly promoted the growth of two commercial plants. The use of endophytic fungi has potential to reduce the need for fertilizers and additional studies are necessary to understand the nature of the symbiotic relationships between plants and endophytes.

29. Student Name: Zachary R. Andrew  
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Faculty Advisor: Scott Holt  
Presentation Type: Poster  
Project Status: In Progress  

Leuconostoc Bacteria on Defined Growth Media vs Complex Growth Media

This project will determine the growth rates of Leuconostoc mesenteroides bacteria on defined growth media (known chemical composition) compared to that of a complex growth media (unknown chemical composition). Complex media is used for genetic and physiological research, but gives inconsistent results due to its unknown composition. Defined media, however, gives more consistent results (desirable) due to its known chemical composition. Two different carbohydrates will be used in testing these growth rates; glucose and sucrose. The bacteria will be inoculated into each type of media and incubated for a period of twelve hours. To determine the growth rate, samples will be collected from each media type every two hours during the 12-h growth cycle. Samples collected will be subcultured on agar petri plates and incubated at 30°C for 48 h to allow for colony formation. Colonies will be counted and colony forming units (CFU) per milliliter will be determined. The CFU/ml data will be log10 transformed and plotted versus time using Microsoft Excel. The slope of the log phase of growth (initial increase in growth) will be determined using a regression line or trend line. This slope will then be multiplied by a predetermined constant of 2.303, giving the growth rate (μ). Values for μ will then be tested for significant differences using the statistical analysis ANOVA. Tukey test will be used to identify significant differences between specific μ values if the ANOVA test indicates differences exist. Statistical analysis will determine if growth rates between different media are significant.

30. Student Name: Michelle Golz  
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Faculty Advisor: Dr. Afshihile  
Presentation Type: Poster  
Project Status: In Progress  

The Expression Of Jar1 Genes In An Arabidopsis Mutant, atToc132/120 (+/-)

Golz, Michelle A  
Department of Biological Sciences, Western Illinois University

Jasmonic acid (JA) is a plant hormone that accumulates at high level in plants that are wounded or eaten by herbivores. JA synthesis begins in the chloroplast and is completed in the peroxisomes, after which JA is transported to the cytoplasm where jasmonate resistant enzyme 1 (JAR1) conjugates isoleucine (Ile) and JA to form JA-Ile. The initial steps in the JA pathway, which occur in the chloroplasts, require nuclear-encoded and cytoplasm synthesized enzymes, which are imported into the chloroplasts in a process that is facilitated by receptors. In Arabidopsis, several chloroplast receptors have been identified and studied in details and these include the Toc159 family of receptors such as atToc159, atToc132 and atToc120. The atToc132 and atToc120 are found in the same complex and they recognize, bind and import housekeeping proteins. In this study, we will evaluate the ability of the atToc132/120 (+/-) mutant to synthesize 12-oxo-phytodienoic acid (OPDA), an intermediate in the JA pathway that is transported from the chloroplasts to the peroxisomes. If the mutant does not accumulate OPDA, then JA will not be synthesized and JAR1 will have no substrate to conjugate to Ile. In this study, we will measure the abundance of mRNA for JAR1 and JA responsive gene, PDF1.2 in both the wounded and unwounded tissues of the mutant and wild type.

31. Student Name: Donna James  
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Presentation Type: Poster  
Project Status: In progress  

Analysis Of Transcriptonic Responses To Toxins In Helicoverpa Zea Diets

The polyphagous eating habits of the corn earworm, Helicoverpa zea (Boddy), are underscored by its status as a major agricultural pest with a wide geographic distribution and host plant repertoire. To study the transcriptomic response to toxins in diet, a microarray analysis was conducted on 6th instar caterpillars feeding on artificial diet, or tobacco plants Nicotiana tabacum (L.) plants. The mid-guts of the caterpillars were dissected from the caterpillars after 24 hours of feeding on the respective treatments and placed immediately in trizol. Then total RNA was purified, amplified and labeled a placed onto a caterpillar microarray chip. 100bs of genes were altered in the transcriptome reflecting an abundant expression of proteases, cytochrome P450 and immune-related genes which are likely in part adaptive to feeding on the more toxic and more difficult to digest tobacco leaves in comparison to the artificial diet. My study provides a beginning to understanding the broad regulation of genes associated with feeding on plants and their defense responses.
The objective of this study was to characterize growth requirements of fungi in the Chaetomiaceae family that were isolated at 6°C for potential use in biofuel production. Chaetomiaceae fungi were isolated from wing swabs from bats in Southern Illinois at 6°C in malt extract agar. A total of six isolates identified using ITSrDNA were evaluated. Growth was also evaluated at three different temperatures, 6, 25, and 50°C. Three replicates of each fungus were plated on malt extract agar (MEA) and fungal growth was evaluated every week. All isolates showed optimal growth at 25°C with an average diameter of 5.92 cm after a week. The majority of isolates were able to grow at 6°C with an average of 1.89 cm after a week. At 50°C the isolates were unable to grow, many showed signs of contamination. This experiment shows that the Chaetomiaceae fungi isolated from bats are psychrotolerant with optimal growth at 25°C.

33. **Student Name**: Morris Parker  
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**Faculty Advisor**: Dr. Wendell L. French  
**Presentation Type**: On-going  
**Project Status**: Antibiotic Susceptibility Testing Of *Escherichia Coli* Thermotolerant Coliforms (KEC) Isolated From Streams That Feed Into The Mississippi River In Hancock County, Illinois

Parker M, French W  
Department of Biological Sciences, Western Illinois University

The number of thermotolerant coliform bacteria present in water determines fecal pollution. During a three month period (June 2010-August 2010) Dr. Wendell French and Thomas Crenshaw collected 54 samples from eight different streams that all feed into the Mississippi. These samples were aseptically collected from the eight streams sites labeled A-G. These samples were serially diluted to a 10^1 and then vacuumed filtered onto Whatman membrane filter paper. After filtration, these membranes were placed on CHROMager ECC and placed into incubator at 41°C OR 45°C. After a 24-hour incubation period, the cultures were removed and enumerated. This was done to determine the optimum growth temperature of the thermotolerant coliforms (Crenshaw, 2011; Alonso et al., 1999) Since the degree of susceptibility of microorganism vary in between species and strains (Tortora et al., 2007). It is important that the isolates collected from the Mississippi be tested with antibody susceptibility test. The main objective of our study is to determine the level of sensitivity/resistance as well as multidrug resistance among the different strains of *E. coli* isolated from a previous study of this experiment. The reference strain of *E. coli* (ATCC8739) will be used as a negative control for comparison.
conjugated to isoleucine to yield JA-Ile. Enzymes in the JA pathway are synthesized in the cytoplasm and imported into the chloroplasts in a process that is facilitated by membrane receptors. Receptors on the chloroplasts outer membrane are encoded by atToc159 gene family, which consists of atToc159, atToc132 and atToc120. The atToc159 receptor is specific for the import of light-induced proteins, and mutation in this receptor yield plants with an albino phenotype, and are called pp2. In this study, we have evaluated the ability of pp2 to accumulate mRNA that encode for enzymes that function in the JA pathway, and for the JA induced gene, PDF1.2 and jasmonate repressor, JAZ-1. Our data show that in the wounded wild type, levels of mRNA for LOX-2, AOS, OPR-3 and PDF 1.2 were increased several-fold, while expression of JAZ-1 was comparable in the unwounded and wounded tissues. This suggests that in wounded tissues as JAZ proteins are being targeted for degradation, more JAZ proteins are synthesized. In the mutant, levels of mRNA were several-fold lower than in the unwounded wild type. This observation suggests that the activities of enzymes that function in the JA pathway were impaired in the mutant. Interestingly, the expression of PDF1.2 was suppressed in the wounded tissue, which suggests that JA or JA-Ile did not accumulate to appreciable levels in the mutant. The results of this study indicate that atToc159 receptor is required in the synthesis of JA.

35. **Student Name:** Memory Cain  
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**Presentation Type:** Poster  
**Project Status:** In progress

**Gene Expression Of Caterpillars After Feeding On Tomato Plants**

Gene expression was measured for whole *Helicoverpa zea* caterpillars, (tomato fruitworm) after feeding on tomato plants. For our experimental treatment, newly emerged 6º instar *H. zea* caterpillars fed on tomato plants for 24 hours while the control group continued to feed on artificial diet. The caterpillars were harvested and flash frozen with liquid nitrogen. A technique known as quantitative real-time polymerase chain reaction (qPCR) was performed to determine gene expression in caterpillars in response to feeding on tomato leaves. We selected genes that were previously shown to be stimulated. Those genes were determined in a prior microarray experiment performed in the Musser lab. In that study caterpillar digestive genes such as proteases, and lipases were stimulated. In addition, detoxifying genes such p450s were stimulated. In my study I verified gene expression as determined by the prior microarray study and further showed there was a significant difference between the caterpillars that fed on tomato plants and those that fed on artificial diet. After conducting this project a clearer understanding of how the caterpillars responds to herbivory will emerge.

36. **Student Name:** Shiloh Lueschow  
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**Project Status:** Complete

**Morphological, Physiological, And Molecular Characterization Of Geomyces Species**

Geomyces * destructans* is a fungus responsible for the mycoses in bats known as White Nose Syndrome (WNS), which has already killed millions of bats and may be driving some species towards extinction. Different *Geomyces* species are commonly found in the natural environment such as soils and caves, but it is not clear why *G. destructans* shows greater pathogenicity. *G. destructans* is considered a psychrophilic fungus (optimal grow is at low temperatures), but little is known about the growth requirements of other closely related *Geomyces* strains and species. The main goal of this research was to characterize the growth rates of various *Geomyces* isolates from Illinois and compared them to the pathogen *G. destructans*. Fourteen *Geomyces* isolates including *G. destructans* were plated on sabouraud dextrose agar. The isolates were obtained from bats in Illinois before arrival of WNS. Isolates were incubated at 25 and 6º C. Growth rates were measured weekly to determine differences between the various isolates and *G. destructans*. *Geomyces destructans* showed no growth after three weeks at 25º C. The other *Geomyces* isolates obtained from bats in Illinois showed growth after the first week at 25º C. In all cases except for *G. destructans*, the isolates grew better at 25º C than at 6º C. Excluding *G. destructans*, the growth rate range for 25º C was 56.3mm/week to 94mm/week. The growth rate range for 6º C was 36mm/week to 55mm/week. Our study suggest that the psychrophilic (cold loving) nature of *G. destructans* may be an important factor influencing its pathogenicity.

37. **Student Name:** Courtney Cluney  
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**Presentation Type:** Poster  
**Project Status:** Complete, currently writing thesis.

**Zooplankton Community Dynamics In Spring Lake**

Cluney, C. Spier, T  
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Spring Lake serves as the fresh water reservoir for Macomb, IL and provides local recreation such as fishing and boating. Due to increased sedimentation distributed as a gradient across Spring Lake, the lake has high sediment (and thus nutrient) loads at the extreme west end and lower nutrient and sediment levels are found at the east end (near the dam). My project explored the relationship...
between the sediment and the composition of the zooplankton community. By correlating my data with the sediment gradient from the west to the east, I hoped to find a relationship between zooplankton at Spring Lake and the nutrient load. To accurately correlate the zooplankton community and sedimentation, I sampled the zooplankton at five sites spread across Spring Lake monthly during the Spring of 2011 by pumping 100 liters of water through a 63µm filter, which retained the zooplankton. Samples were preserved and analyzed with a dissecting microscope to identify and enumerate the zooplankton in each sample. I used the data to examine the changes of the zooplankton community across time, space, and compare them to sedimentation in the lake. A large zooplankton population was found at the extreme west end of Spring Lake where sedimentation is highest compared to the east end (near the dam). Dr. Spier and I suspect the excess sediment serves as camouflage to hide zooplankton from predators. My data will serve as baseline data for future research to better determine the relationship between sedimentation and the zooplankton community.