11th Biology Student Research Symposium

Schedule of Events

Thursday April 4th, 2013

2:30-3:00 pm Waggoner Hall 3rd Floor
Poster session pre-view and refreshments

3:00-4:00 pm Waggoner 378 Opening Talk
Dr. May Berenbaum, University of Illinois
Sex and the Single Parsnip: Coping with Florivores and Pollinators in Two Hemispheres

Friday April 5th, 2013

11:30 am – 3:30 pm Waggoner 365
BGSA Annual Dessert Competition

12:00 pm-1:30 pm Waggoner Hall 378
Oral Presentations
Moderator: Dr. Susan Romano

1:30 pm-3:30 pm Waggoner Hall, Third Floor
Poster Session

4:00 pm-5:00 pm Waggoner 378 Plenary Speaker
Dr. Jessica Whitham, Brookfield Zoo
The Road to Animal Welfare Research: From Grunts to Greetings to Great Well-Being

5:00 pm-5:30 pm Waggoner Hall 378
Award Ceremony and Refreshments
April 4th, 2013
Plenary Talk

Sex and the Single Parsnip: Coping with Florivores and Pollinators in Two Hemispheres

Dr. May Berenbaum, University of Illinois
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Oral Presentations

12:00 pm-1:20 pm Waggoner Hall 378
Moderator: Dr. Susan Romano

12:00-12:20 pm Lauren A. Kline
Identifying Behavioral Types of Captive Callimicos (*Callimico Goeldii*) at the Chicago Zoological Society’s Brookfield Zoo

12:20-12:40 pm Tabitha Williams
Identification of Fungal Communities in Bats at Risk of White Nose Syndrome in Caves and Mines in Southern Illinois

12:40-1:00 pm Jared Ruholl
Forest bee diversity in relation to habitat and vertical stratification

1:00pm-1:20pm Beth Lane
Host Specificity of White Grub (*Posthodiplostomum minimum centrarchi*) in Spring Lake, McDonough County, IL
Poster Presentations

1:30 pm-3:30 pm Waggoner Hall, Third Floor

   Comparative neuroanatomy of social and solitary Hymenoptera

2. **Alicia Pugh**, Lisa Wen, and Jenq-Kuen Huang
   Amplification Of A Putative L-3 Hydroxacyl-CoA Dehydrogenase Gene From Genomic DNA Of *Micrococcus luteus* WIUJH20 By Polymerase Chain Reaction

3. **Jason Tuter**, Zachary Gossage, Terri Tobias, Sue Hum-Musser, Andrea Porras-Alfaro, Richard Musser
   Defense Response and Growth Regulation of *Zea Mays* is Triggered in Response to *Phialocephala fortinii*

4. **Jamela Thompson**, Sean Jenkins
   Turtle community composition and structure of two remnant wetland complexes on the Upper Mississippi River

5. **Jeffrey Liles**, Sue Hum-Musser
   The Effect of *Serratia marcescens* and *Pseudomonas aeruginosa* bacteria on the Corn Earworm, *Helicoverpa zea* larva

6. **James S. Zweep**, Kenneth W. McCravy
   Assessing Forest Bee Sampling Methodology at Kibbe Life Science Station

7. **Mobayode Desmond Osatuyi**, Sue Hum-Musser
   The Effect of *Bacillus thuringiensis* Israelensis and *Bacillus thuringiensis* kurstaki bacteria on the Corn Earworm, *Helicoverpa zea* larva

8. **Jeff P. Woodyatt**, Sean Jenkins
   Age Structure and Stand Composition of Prairie Glen in Relation to Landscape Position and Recent Prescribed Burning Regime

9. **Katrina Sandonia**, Terri Tobias, Andrea Porras-Alfaro
   Diversity and Potential Risks of Thermophilic Fungi in Corn

10. **Morgan Clark**, Sue Hum-Musser
    The Effect of Ozone on Corn Germination and Insect Pest Growth

11. **Kenny Kusimba**, Susan Meiers
    Seasonal Wildlife Behavior in Urban Chicago, IL
12. **Marina Small**, Terri Tobias, Katrina Sandona, Andrea Porras-Alfaro
Survey of Thermophilic Fungi in Western Illinois Grain Elevators

13. **Neil D. Gillespie**, Sean E. Jenkins, and James T. Lamer
Turtle Community Dynamics and Habitat Factors Influencing Occupancy in the New Crystal Lake Club, Gulfport, Illinois.

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15. **Myrtha Pierre**, Richard O. Musser, Sue Hum-Musser, Andrea Porras-Alfaro
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20. **Terri Tobias**, Katrina Sandona, Abraham Matlack, Andrea Porras-Alfaro, Andrew Clayton, Joel Gruver
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21. **Shelby Rogers**, Brian Peer
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22. **Blake Bushman**, Tim Spier
Saugeye in Argyle Lake

23. **Zachary R. Andrew**, Scott M. Holt
Growth Rates of *Leuconostoc* Bacteria on Defined Growth Media vs Complex Growth Media

24. **Brooke J. Bryant**, Timothy W. Spier
Alarm Pheromone Response in Red Shiners Using Quantitative Methods

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Plenary Talk

The Road to Animal Welfare Research: From Grunts to Greetings to Great Well-Being

Dr. Jessica Whitham, Brookfield Zoo

4:00 pm-5:00 pm Waggoner 378 Plenary Speaker

Awards Ceremony

5:00 pm-5:30 pm Waggoner Hall 378

Acknowledgments, Dr. Andrea Porras-Alfaro
Brooke Bryant, Graduate Student BGSA, Dessert Awards
Closing Remarks, Dr. Charles Lydeard
Oral and Poster Awards, Dr. Charles Lydeard
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Identifying Behavioral Types of Captive Callimicos (*Callimico Goeldii*) at the Chicago Zoological Society’s Brookfield Zoo

Lauren Kline, Jeanette Thomas, Jason Watters
Department of Biological Sciences, WIU, Brookfield Zoo, Department of Behavioral Research

Although research investigating human personality is booming, researchers studying animal personality types have been more reticent. However, recently more research has been published that successfully identified personality types in a variety of animal species and have used personality information to investigate ecological relationships, mating preferences, and aid in animal welfare in captivity. This study was conducted to identify personality types in the 25 callimicos (*Callimico goeldii*) in a colony at Brookfield Zoo. Research ensued over eight months using focal animals and scan-sampling of behaviors. Principal component analysis elucidated five factors that varied among individuals. Given the behavioral ecology of wild callimicos their neophobic nature in captivity, behaviors of these animals loaded into sensible factors. By becoming familiar with unique behavioral profiles of callimicos in this captive environment, husbandry staff can tailor husbandry to particular individuals in their care.
Identification of Fungal Communities in Bats at Risk of White Nose Syndrome in Caves and Mines in Southern Illinois
Tabitha F. Williams¹, Robert McCleery², Rod McClanahan³, Andrea Porras-Alfaro*¹.
¹Western Illinois University, Department of Biological Sciences, Macomb IL 61455, ²Wildlife Ecology and Conservation PO Box 110430, University of Florida, Gainesville, FL 32611, ³United States Forest Service, Shawnee National Forest, Harrisburg, IL 62946. A-Porras-alfaro@wiu.edu

Bats are indispensable to ecosystem stability; they play an important role in the control of insect populations and plant pollination. White Nose Syndrome, caused by the fungus *Geomyces destructans*, is a new and emerging disease infecting several species of bats in the USA and Canada. The major objective of this research was to identify, characterize and compare psychrophilic fungal communities associated with seven different bat species commonly found in southern Illinois. Following the USGS National Wildlife Center protocols, bats were trapped using harp trap techniques. Swabs were taken from the bats wings and were inoculated *in situ* on petri plates in malt extract agar with antibiotics. Samples were incubated at 6°C to select for psychrophilic fungi. Approximately 20-30 colonies were obtained in each petri dish, averaging four unique morphospecies per swabbed area. From the swab plates about 300 psychrotolerant pure cultures were obtained and 158 samples were identified using the ITS rDNA barcode region. Fungal communities were dominated by Ascomycota (135 isolates) followed by Zygomycota (16 isolates) and Basidiomycota (7). Most commonly identified orders in the Ascomycota include: Capnodiales (32 isolates), Eurotiales (28), Pleosporales (28) and Leotiomycetes incertae sedis (20). Common fungi in bat wings include: *Penicillium*, *Cladosporium*, *Epicoccum* and *Alternaria*. Of the fungi that have been identified 19 isolates are *Geomyces* strains that are closely related and show high genetic similarity to *Geomyces destructans*. This research will increase our knowledge about all fungal communities associated with bats living in caves and mines which are endangered and currently facing local extinctions.
Relatively few studies have examined bee diversity in temperate deciduous forests, particularly in relation to vertical stratification. We investigated differences in bee species composition between early successional and oak/hickory Midwestern forest habitats. Both habitats were sampled using vane traps and pan traps suspended 10 m in the canopy and at 1 m above the ground. A total of 4,611 bees constituting 76 different species were captured, with *Augochlora pura* comprising 66% of the total collection. Species composition was significantly different between the two habitat types and between canopy vs. understory, with *A. pura* both included and excluded from the analyses. Based on indicator species analyses, several species of bees were associated with either the canopy or understory of the two habitat types. *Agapostemon virescens*, *Lasioglossum macoupinense*, and *L. smilacinae* were associated with oak/hickory understory, while *Certina calcarata* and *L. versatum* are associated with oak/hickory canopy. *Lasioglossum coeruleum* and *A. Pura* were the only species associated with the early successional canopy. Our results suggest that substantial spatial variation in bee diversity can occur within Midwestern deciduous forests.
Host Specificity of White Grub (*Posthodiplostomum minimum centrarchi*) in Spring Lake, McDonough County, IL  
Beth Lane, Shawn Meagher  
Department of Biological Sciences, Western Illinois University

Host specificity measures the number of host species a parasite can infect. White grub (*Posthodiplostomum minimum centrarchi*) is a parasite of many sunfish species (Family Centrarchidae), however, we do not know whether it displays specificity for particular centrarchid species. Understanding the host specificity of *P. minimum* could help control infection by this worm. Two centrarchids, bluegill (*Lepomis macrochirus*; *n*=82) and crappie (*Pomoxis annularis*; *n*=89), were collected from Spring Lake in McDonough County, IL. I determined the species, sex, age, length, and white grub burden for each fish. White grub prevalence was significantly higher in bluegill (100%) than in crappie (57%). Mean intensity was significantly higher in bluegill (1,474) than crappie (9), and infection levels increased with host length in both species. White grub in Spring Lake is more infective to bluegill than crappie, which is consistent with other studies that have measured white grub infection levels in sympatric centrarchids. Fish from the genus *Lepomis* have higher infection levels than other centrarchids, but there is also significant variation in infection among *Lepomis* species. Thus, *P. m. centrarchi* is not a generalist that infects all hosts equally well, but shows a high level of “structural” host specificity (that is, different infectivity to different hosts). Further studies are necessary to determine whether host differences in infection level are due to ecological differences that affect exposure to *P. minimum*, or physiological differences that affect host compatibility with this worm.
Comparative neuroanatomy of social and solitary Hymenoptera
Joseph W. VanDyke, Harold H. Edwards, and Kenneth W. McCravy
Department of Biological Sciences, Western Illinois University, Macomb, IL, 61455

Social lifestyles are perceived to be more complex than solitary ones because social demands are considered to impose added pressures leading to an increase in cognitive capability. These pressures lead to an increase in size in brain regions responsible for social behavior. In insects, the mushroom bodies are associated with multisensory integration and learning. Social Hymenoptera are known for their large and elaborate mushroom bodies, suggesting sociality facilitates an increase in mushroom body volume. However, it has been shown that these complex structures arose before sociality in Hymenoptera within ancestral parasitoids. Recent research has also shown that increasing brain size isn’t the only strategy for handling the demands of sociality. In eusocial insects, division of labor may narrow the behavior repertoire of individuals, lessening the need for a larger, more complex brain. I investigate if sociality, parasitoidism, or generalist behavior is associated with larger, more elaborate regions of the brain by relating allometric measurements to species’ social structure and behavior repertoires.
Amplification Of A Putative L-3 Hydroxacyl-CoA Dehydrogenase Gene From Genomic DNA Of Micrococcus Luteus WIUJH20 By Polymerase Chain Reaction
Alicia Pugh, Lisa Wen, and Jenq-Kuen Huang
Department of Chemistry, Western Illinois University

A previously cloned secondary alcohol dehydrogenase from Micrococcus luteus WIUJH20 is homologous (96%) to an annotated NAD+-dependent L-3-hydroxyacyl-CoA dehydrogenase (an enzyme in fatty acid β-oxidation) from M. luteus NCTC2665. Through bioinformatics, we found three annotated genes of L-3-hydroxyacyl-CoA dehydrogenases (L-3-HADH) at different locations in the genome of M. luteus NCTC2665 (accession number, CP001628), one of which corresponds to the secondary alcohol dehydrogenase. The objective of the present research is to amplify, clone, and express the putative L-3-HADH genes with locus tag Mlut_12970 and 2172 bp in length. Here we report the amplification of the gene by PCR using genomic DNA of M. luteus WIUJH20 as template and synthetic primers flanking the gene. The PCR conditions were optimized by including 2% DMSO and altering annealing temperature. Agarose gel electrophoresis was used to analyze the PCR products. The successful amplification of the gene was shown by the presence of a ~2,000 bp in the gel. In the future, this gene will be cloned and protein expressed. The kinetic properties of the enzyme and its substrate specificity will be studied and compared to that of the secondary alcohol dehydrogenase
Endophytic fungi are common plant inhabitants and form complex symbiotic relationships with their plant host. Under optimal growing conditions the fungus can stimulate tolerance to biotic and abiotic stressors. The plant-fungal symbioses can be very fragile and stressed environments can trigger pathogenic activities. These relationships have been widely studied however little is known about how the plant responds to dark septate fungi at the molecular level. *Phialocephala fortinii* is a common dark septate endophyte found in soil around the world. The purpose of this study is to identify genes that are involved in the establishment of the interaction of *P. fortinii* and corn plants. We have inoculated corn seeds with a strain of the fungus. Plants showed a significant increase in germination and growth and the plants did not show signs of physical damage caused by the fungus. RNA was purified from leaf and root tissues to conduct microarray analysis and qRT-PCR. We found at least 1,192 genes that show statistically significant differential expression. Of those 761 genes were down-regulated and 431 genes were up-regulated. In both tissues, genes involved in the expression of plant defenses, growth photosynthesis and stress tolerance were differentially stimulated by the fungus. Though the plants showed no visible damage, plant defense genes were up-regulated suggesting biotic stress from the presence of the fungus. Our data suggests that the plant is regulating the interaction with this particular fungus and additional studies need to be conducted to determine the specific role of defense genes in the presence of endophytes.
Turtle community composition and structure of two remnant wetland complexes on the Upper Mississippi River
Jamela Thompson, Sean Jenkins
Department of Biological Sciences, Western Illinois University

Turtle community composition was determined in two wetland complexes adjacent to Pools 18 and 19 of the Upper Mississippi River. One of the sites has never been drained or farmed and has greater flora and structural diversity compared to the second site which is a restored area that was drained and farmed in the past. The habitats were sampled included open water marsh, aquatic and emergent vegetation beds in littoral zone, scrub shrub swamp, and channels. The main goal of the study was to determine if site disturbance history and the resulting difference in flora and structural diversity influenced turtle species diversity and community composition. The turtle populations were sampled by trapping turtles using fyke nets, floating hoop nets, and hoop nets. The traps were baited with fish each day, left to soak overnight, and checked in the morning. The species, carapace/plastron length and width, weight, and exact location trapped were recorded for each specimen collected. The shells were also permanently marked to determine recapture rates. The turtles were then returned to the habitat where they were caught after data collection. Trapping took place from June to August 2012. This research established permanently geo-referenced sampling sites which will be sampled on an annual basis by the staff at the Kibbe Life Science Station. This will allow for the continued monitoring of changes in turtle species populations and diversity over time.
Due to an increase in the use of insecticides, more and more pests are becoming resistant to insecticides making them progressively harder to control (Regupathy et al., 1999). This has spurred the development and application of different types of microbial pathogens for the control of pests an alternate form of pest control (e.g. toxic proteins from the bacterium *Bacillus thuriengensis* (Pascual et al., 2012). In this project, we will examine how a common pest the corn earworm, *Helicoverpa zea*, reacts when exposed to two pathogenic bacterial species, *Serratia marcescens* and *Pseudomonas aeruginosa*, by measuring the growth, survival, and the expression of key insect detoxification and metabolic genes. Corn earworm larva at the sixth instar stage will be fed on corn based diet that will be treated with bacterial. After allowing the caterpillar to feed on the treated diet for 24 hours, they will be flash frozen at -80°C and processed for gene expression. In addition, the larva treated with *S. marcescens* and *P. aeruginosa* will have increased mortality rates compared to the control caterpillars. This study will examine the molecular response to insects when exposed to these commonly occurring bacteria.
Assessing Forest Bee Sampling Methodology at Kibbe Life Science Station
Department of Biological Sciences, Western Illinois University

Although native bees play an important role in the pollination of many different plant species, there have been relatively few studies done on their ecological needs, especially bee species that reside in forest habitats. There is also little standardization of sampling methods for forest bees. In this study, I studied the differences in bee species composition collected by four trap types at the Alice L. Kibbe Life Science Station in Hancock County, Illinois. Trapping was done during the months of April to September 2012, using vane traps and white, yellow, and blue pan traps that were suspended 10 m in the canopy and 1 m above the ground. A total of 4,611 bees constituting 76 different species were captured, with Augochlora pura comprising 66% of the total collection. Species composition (species richness and relative abundance) of bees collected using the different trap types was compared using the multi-response permutation procedure (MRPP), a statistical method for comparing the species composition of ecological communities. Indicator species analysis (ISA) was used to test for species that were strongly associated with a particular trap type. MRPP showed little difference between species composition of vane traps and pan traps overall, but ISA found several indicator species, primarily for vane traps.
The Effect of *Bacillus thuringiensis Israelensis* and *Bacillus thuringiensis kurstaki* bacteria on the Corn Earworm, *Helicoverpa zea* larva

Mobayode Desmond Osatuyi, Sue Hum-Musser
Department of Biological Sciences, Western Illinois University

Proteins from the bacterium *Bacillus thuringiensis* (BT) is a common natural insecticide. The ‘Israelensis” strain affects mosquito larvae while the ‘Kurstaki’ strain affects caterpillars. The transcriptomic response of the corn earworm, *Helicoverpa zea* to BT infection will be determined by comparing differential gene expression from three different groups of caterpillars: a control group that fed on untreated caterpillar diet, and two experimental groups that fed diet coated with a culture of each of the two bacterial strains for 24 hours. Quantitative real-time PCR analyses of several caterpillar defense and hormone genes were performed on purified caterpillar RNA. Several genes were significantly altered i.e. down regulated genes and up regulated genes after bacterial infection in the experimental groups compared to the gene expression of the control group. Caterpillar gene expression affected included digestive enzymes, proteases, trypsins, cytochrome P450 and other detoxification and immune system genes. We will also examine the transcriptomic response of the caterpillars using microarray analysis to determine which genes are turned on or off. With this information we will obtain insight on how the caterpillars react to pathogenic attack by these two bacterial strains and provide a better understanding of their effectiveness in insect pest control.
Age Structure and Stand Composition of Prairie Glen in Relation to Landscape Position and Recent Prescribed Burning Regime
Jeff P. Woodyatt, Sean Jenkins
Department of Biology Sciences, Centennial Honors College, and Western Illinois University

Oak hickory woodlands are recognized as disturbance driven ecosystems, whose composition and structure, prior to European settlement, were in a large part determined by the frequency, severity and seasonality of fire and how these factors interact with landscape position and topography. More recently these woodlands have been fragmented due to, timber harvesting, agriculture and urban development. The overstory composition and structure of remaining remnants are shifting from being dominated by oaks (*Quercus* spp.), to being dominated by fire intolerant and shade tolerant species such as sugar maple (*Acer saccharum Marshall*) as a result of a decrease in frequencies of fire disturbances and closed canopy conditions. Recent research indicates that this shift in overstory composition and structure has led and will continue to lead to the disappearance of native shade intolerant and fire dependent woody species, as well as a loss in diversity amongst forest flora species. This study will examine the effects of landscape position and recent prescribed burn history on the age structure, species composition and seedling composition and abundance of the woodland stands in Prairie Glen at the Alice L. Kibbe Life Science Station. This paper will focus on a wide range of woody understory, mid, and upperstory species including; oaks (*Quercus* spp.), hickories (*Carya* spp.), ashes (*Fraxinus* spp.), redbud (*Cercis canadensis L.*), grape (*Vitis* spp.), and numerous others. Information obtained by this study may serve to promote a further understanding of woodland stand dynamics in respect to anthropogenic effects, specifically fire suppression.
Diversity and Potential Risks of Thermophilic Fungi in Corn.
Katrina Sandona, Terri Tobias, Andrea Porras-Alfaro
Department of Biological Sciences Western Illinois University

The Midwest United States has been under extreme drought conditions for the past two years which could cause changes in the composition of microbial communities in corn. The high temperatures and low humidity conditions are favoring the colonization of grain by thermophilic fungi in corn storage facilities and very little is known about the diversity of thermophilic/thermotolerant fungi or the health risk they may represent for farmers and consumers. The objective of this project was to isolate and identify thermophilic and thermotolerant fungi from corn grain stored in bins during drought season and determine potential interactions between thermophiles and known mycotoxin producing fungi. Corn samples were collected from local farmers during the summer and winter season. The corn that was collected had been dried to 15 percent moisture. The corn was plated and incubated at 50°C and the fungi were isolated and identified using ITS rDNA primers. The number of spores in the corn silos was very high, more than 90% of grains show colonization by thermophilic fungi. Multiple species of thermophilic fungi were isolated and identified including: *Thermomyces lanuginosus*, *Aspergillus fumigatus*, *Thermoascus crustaceus*, and *Rhizomucor pusillus*. Many of the species isolated were true thermophiles with optimal growth temperature at 50°C. Mycotoxin production will be measured for the thermophilic isolates and for grain exposed to known mycotoxin producers and thermophilic isolates. This study raises new concerns of high abundance of previously undocumented actively growing fungi in corn which could represent a new food safety risk.
The production of corn is extremely important to the United States for food, seed, and other non-industrial purposes. Due to industrial development and pollution, levels of ozone gas at ground-level are increasing. While ozone in the upper atmosphere protects us from damaging UV radiation, ground-level ozone is a health hazard and harmful to crop production. Because of its structure, ozone is very reactive and can damage plants and lower crop yield. We will test the effects of ozone on three types of sweet corn. One variety, Ruby Queen Hybrid, contains a red pigment called anthocyanin, which is an antioxidant. Because of its antioxidant properties, corn with anthocyanin could germinate more quickly and resist tissue damage due to anthocyanin acting as a defense against the ozone. The two other varieties lack anthocyanin. It is expected that these types of corn will take longer to germinate and have more damage. The corn seeds will be exposed to ozone in a chamber. In addition, we will examine gene expression using microarray hybridization and quantitative PCR. These tests will tell us how the plant is responding to the treatment with ozone by telling us which genes are turned on or off. We will also test caterpillar feeding preferences and growth by allowing the “corn earworm” caterpillar to feed on the different types of corn. The information from this project will allow us to determine the impact of increasing ozone on an important crop, as well as its effects on a major crop pest.
Seasonal Wildlife Behavior in Urban Chicago, IL
Kenny Kusimba, Susan Meiers
Department of Biological Sciences, Western Illinois University and Urban Wildlife Institute, Lincoln Park Zoo, Chicago, IL

Urban areas are dominated by built-up structures which influence the structure, composition, and succession of plant communities and the wildlife associated with them. Urbanization alters wildlife behavior due to habitat disturbance with human activities such as construction and other land use changes. To assess seasonal wildlife behavior across rural to urban city of Chicago, IL, three transects were established at DesPlaines River/Milwaukee Avenue to the northwest of the city of Oak Park, Roosevelt Road to the west of Eisenhower Express way, and the ship canal to the southwest of Lawndale. Transects originated at the center of the Chicago “Loop” and extended 50 km from the urban core. Samples were collected using remote -triggered trail cameras in winter, spring, summer, and autumn 2012. Transects were sectioned into 10 segments extending 5 km along each transect. Four cameras were placed in each 5 km segment along transects. Three visits were made to each site lasting 15 minutes of data collection; images were downloaded from the cameras (date, time, species present, activity, location of the camera trap, and number of individuals of each species). During the visits, camera batteries were changed out. T-tests will be used to determine whether there is a significant difference in the presence of species in transects along the urban gradient. Bivariate logistic regression models and Spearman’s rank correlation will be used to determine the relationships between the occurrence of wildlife species at the sites and the relationships between species richness for native and invasive species. This study will provide insight into management decisions and potential mitigation of challenges that human activities impose on wildlife.
The Midwest United States is the largest grain producer in the country. Drought conditions and high temperatures during the summer may promote the growth of specific groups of fungi known as thermophiles. Thermophilic fungi can thrive in high temperatures between 45 and 50°C. The presence of these unique fungi in corn grains could represent an unknown potential health hazard to local farmers and the general public. The main objective of this project was to identify and quantify thermophilic fungi in western Illinois grain elevators. Fungi were cultured on Emerson agar or MEA and incubated at 50°C. Fungal DNA was amplified using ITS rDNA fungal primers and species were identified using NCBI BLAST analysis. So far, we have obtained 15 isolates (5 morphotypes) from ground corn, 45 isolates from unsterilized corn grains (18 morphotypes) and 34 isolates from sterilized corn grains (4 morphotypes) that were all collected from western Illinois corn storage bins. Preliminary identification showed the corn is colonized by multiple thermophilic fungal species including *Thermomyces lanuginosus*, *Aspergillus fumigatus*, *Thermoascus crustaceus*, and *Rhizomucor pusillus*. We expect this research will help us document a new unknown potential risk to farm worker’s health and food safety.
The decline in reptile populations has become a growing concern among scientists in recent years. Understanding reptile community dynamics and species specific habitat preferences allows for a better understanding of how to stabilize and increase declining reptile populations. One area, the New Crystal Lake Club, located along Pool 19 of the Mississippi River in Gulfport, IL is a privately owned, 1500 acre wetland habitat with no sampling history of reptile species. A mark and recapture study of the turtle species, along with significant aquatic habitat sampling, at 27 sites was conducted during the 2011 and 2012 summer seasons. Sampling data was then used to determine the turtle community composition, population dynamics (population size, sex ratio, age structure), species specific habitat preferences (water quality, vegetation type, habitat type), and home range estimates for each species within the club. The presence of an endangered species, the Blanding’s turtle (*Emydoidea blandingii*), was also noted, which prompts further studies into the condition of this particular population, as little is known about most of the Blanding’s turtle populations within Illinois.
Leuconostoc is a non-pathogenic, aero-tolerant anaerobic bacterial genus that lives on vegetation. Leuconostoc plays an important role in industrial and food fermentations. The goal of this project is to determine if a defined nutrient source can serve as a suitable alternative to a complex nutrient source for growth of Leuconostoc. A complex nutrient source is commonly used to support growth of Leuconostoc for physiological and genetic research studies related to polymer production. Complex nutrient source, however, is made with beef and yeast extracts and its exact chemical composition is unknown. This gives inconsistent results when doing research. The composition of every chemical component in defined nutrient source, on the other hand, is known. This gives consistence results, which is very desirable for genetic or physiological-based research. To accomplish the research goal, Leuconostoc species will be cultivated for 12 hours in a defined nutrient source and a complex nutrient source. Bacterial growth in each nutrient source will be determined through two methods called viable plate count (quantitative) and spectrophotometry (qualitative). Growth rates (μ h⁻¹) and bacterial colonies formed per milliliter of culture broth (CFU/ml) will be calculated from the quantitative viable plate count. Spectrophotometry is used as a real-time growth assessment to monitor the progress of each growth experiment. Data indicating that there is no statistical difference in growth between each nutrient source would support the use of defined as a suitable alternative to complex. In addition, data indicating an increase in growth for the defined would also support its use as an alternative to complex.
Transcriptome Profile of *Helicoverpa zea* Caterpillar that Feed on Maize Plants (*Zea mays*) Treated with *Phialocephala fortinii*

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*Phialocephala fortinii*, a non-pathogenic strain of endophyte, is an organism that inhabits plant tissues and establishes a symbiotic relationship with the plant. Previous studies have indicated an increase in growth rate in *Zea mays* (corn) plants treated with the fungi *P. fortinii*, as well as the stimulation of detoxification and digestive enzymes of the plants. However, the effect of fungus treated plants on caterpillars is still unknown. Because insect feeding causes significant crop losses worldwide, it is important to study the effects of fungus-treated corn on insects. The experiment will consist of three caterpillar treatments that will feed for 24 hours. A group of caterpillars that feed on fungus-treated plants, caterpillars that feed on a control diet, and caterpillars that feed on non-fungus treated plants. A molecular method—microarray analysis will be used to analyze caterpillar total RNA to determine which genes are turned on or off. In addition, quantitative real-time polymerase chain reaction (qPCR) will be used to confirm the microarray analysis. If any change is observed, we will analyze the level at which the fungus *P. fortinii* can alter the genetic expression of *H. zea* caterpillar. The results of the study will help determine whether *P. fortinii* can be considered an effective biological control agent for *Z. mays* plants. This might produce a natural plant growth promoted as well as a natural pesticide.
Parasites are organisms that live in or on another host organism by taking its nutrients, causing harm to the host. Parasites are associated with almost every species on earth. There are many factors that will affect a parasite’s success, including environmental conditions, host age, and sex. In my research project I will observe spatial variation and the effects of microclimate on parasitism of Australian cockroaches by pinworms. Australian cockroaches are large insects found in many locations throughout the world. Within their hindgut, parasitic pinworms are found. Pinworms are small roundworms that infect the digestive tract of most animals. I will trap cockroaches in three different rooms in the greenhouse with three different microclimates, including the moderate, dry, and humid environments. After collecting the cockroaches, I will begin by recording which greenhouse room they were collected in, their age, sex, weight, and femur length. I will then dissect each cockroach and record how many pinworms were found and identify the species of the pinworms. I plan to trap and dissect Australian cockroaches once a week for the entire semester. My specific objective is to observe how microclimatic factors play a role in the parasitism of Australian cockroaches. My hypotheses are: 1) that pinworms will be more abundant overall in the tropical room where more humid conditions will allow greater pinworm survival and reproduction, and 2) relative abundance of the two pinworm species will vary with room and environmental conditions, which may affect pinworm survival and competition differently for the two species.
A cold-acclimated mutant of *Arabidopsis thaliana* that is defective in the major chloroplast receptor, Toc159 has reduced levels of linolenic acid.

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Fatty acids are synthesized exclusively in the chloroplast and the resulting 16:0-ACP and 18:1-ACP are esterified to glycerol-3-phosphate to yield different lipids. When plants are subjected to cold stress, desaturation of membrane lipids favors the formation of polyunsaturated fatty acids, linolenic (18:3) and linoleic (18:2) acids, which increase membrane fluidity and allow plants to survive the cold spells. The synthesis of chloroplast lipids is dependent upon enzymes, which are synthesized in the cytoplasm and imported into plastids in a process that is facilitated by Toc159 family of receptors, which are located on the outer envelope membrane. A cold-acclimated mutant of *Arabidopsis thaliana* that is defective in Toc159 receptor (ppi2-2) has reduced levels of 18:3. However, levels of 18:2 are comparable in the mutant and wild type. This observation suggests that fad8 enzyme, which function in the cold to convert linoleic acid into 18:3 is functional in both the mutant and wild type. The decrease in 18:3 is likely a result of high turnover of chloroplast lipids, which are rich in 18:3. The candidate lipid is monogalactosyldiacylglycerol (MGDG), which is found in the thylakoid membranes and is rich in both 16:3 and 18:3. Separation of lipid classes and the determination of lipid content are being carried out in order to identify lipid classes with reduced levels of 18:3.
Characterization and Optimization of Isolation Methods for the Genus Geomyces
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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. Geomyces species can be difficult to isolate from cave soils because other Zygomycota and Ascomycoa fungi will colonize the plate at a much faster rate. The main goal of this research was to determine optimal conditions to culture Geomyces from the soil. Currently, a collection of more than 20 Geomyces isolates will be tested to determine if incubation of soil samples at different temperatures and the use of Rose Bengal as well as keratin baits will facilitate the isolation of Geomyces strains. Preliminary characterization of Geomyces strains indicated that the majority of isolates are psychrotolerant, only G. destructans is a true psychrophile. None of the current isolate collection show the curved conidia exhibited by G. destructans even though samples show similarity levels for the ITS region between 97 and 99%. We expect to develop a novel method to optimize isolation of Geomyces species from soil samples. The documentation of closely related fungi and optimal conditions for isolation and growth of Geomyces could have important implications for management of WNS.
The effects of aging can be seen in most organisms. However, many of the causes and effects of aging are not yet fully understood. I will look at the effects of aging on habituation in *Drosophila*. I will do this by studying a jump-and-flight escape response. It is achieved via the giant fiber pathway, a heavily studied neural pathway, which can be stimulated visually or through artificial electrical stimulation. I will use electrophysiological methods to record the resulting action potentials in the muscles responsible for jumping and flying in the escape response. I will look at the changes in habituation, which is a decrease in response to the repeated stimulation over time, and dishabituation for different aged flies. I predict that older flies will habituate quicker and have longer recovery times than younger flies due to weaker synaptic transmission in older flies. However since habituation arises from activity-dependent synaptic plasticity, it may actually happen slower in older flies due to their weaker synaptic transmission.
Comparison of Fungal Diversity in Organic and Conventional Soybean Nodules
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Biological nitrogen fixation is a well-known function of the tripartite symbiotic relationship between legume-rhizobia-mychorrizal fungi. There is an abundance of research examining the function of this relationship. However, endophytic fungi also exist within legume nodules and very little is known in regards to this symbiotic relationship. The objective of this study is to determine the fungal diversity within root nodules taken from the legume Glycine max. Soybean nodules were collected from two farm plots within close proximity of each other, the Allison Organic Research Farm and a neighboring conventional farm. Twenty-five nodules from 10 roots from 10 plants per farm were surface sterilized using 95% ethanol. Nodules were plated on malt extract agar and incubated at 25°C. These isolates were identified using ITS rDNA primers. Organic soybean roots contained a significantly higher number of nodules than conventional soybean roots. Fungi were isolated in pure culture on malt extract agar with antibiotics. A total of 34 fungal endophytes were isolated from the soybean nodules. Eighteen fungal endophytes (6 morphotypes) were isolated from conventional soybean nodules. Sixteen fungal endophytes (9 morphotypes) were isolated from the organic soybean nodules. Dominant orders included Pleosporales in conventional soybean nodules and Hypocreales in the organic soybean nodules. Our preliminary data indicates that there is a shift in fungal community composition associated with the nodules due to conventional farming practices.
Avian brood parasites lay their eggs in the nests of other birds and rely upon these “hosts” to raise their young for them. In North America, most hosts accept parasitic cowbird eggs and raise the parasites as if they were their own. One hypothesis that has been proposed to explain the widespread acceptance of parasitism by hosts is that cowbirds force hosts to accept their young through mafia tactics. This hypothesis suggests that cowbirds revisit host nests to ensure that the host has not rejected their egg. If the cowbird discovers that their egg or nestling is missing, they retaliate by destroying host eggs or nestlings. In the famous words from the movie The Godfather the cowbird “makes the hosts an offer they can’t refuse”. My study will examine whether such interactions are occurring with cowbirds and several of their hosts, including the Northern Cardinal, Dickcissel, American Robin, and Chipping Sparrow. The objective of my study is to determine whether these hosts accept cowbird parasitism due to mafia tactics. I will experimentally remove naturally laid cowbird eggs from half of the parasitized host nests to simulate rejection by the hosts. If female cowbirds are employing mafia tactics, I expect that there will be a higher frequency of nest destruction in those from which the cowbird eggs have been removed. Video cameras will be placed at nests to observe cowbirds laying eggs in nests, and also returning to nests and destroying host eggs if they indeed engage in mafia behavior.
Saugeye in Argyle Lake
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Argyle Lake is small (38 ha), yet contains a thriving saugeye population due to a stocking program implemented by the Illinois Department of Natural Resources (IDNR) since 1992. Lake surveys have been conducted each year to help assess the stocking program and establish harvest regulations. This management program has yielded a strong population of saugeye representing multiple age classes. Site managers implemented a fall drawdown in September 2012 in attempt to control gizzard shad (*Dorosoma cepedianum*) and bluegill (*Lepomis macrochirus*) populations. Saugeye were obtained during IDNR annual sampling, using trap nets in the spring and fall as well as nighttime pulsed DC electrofishing during the fall. Supplemental sampling was conducted using pulsed DC electrofishing on a monthly basis from March - October. Upon capture, total length (mm) and weight (g) were recorded, and all saugeye were implanted with a T-Bar style floy tag. Ninety-six saugeye were randomly selected and aged by counting otolith annuli. Stomach contents from up to 30 saugeye were extracted during each sampling trip using the gastric lavage method. Contents were later identified to species, measured (length), separated by prey groups, dried to full desiccation and weighed to determine the dry mass proportion of the various groups in each diet. These values were then used to establish an Index of Relative Importance (IRI) for each prey type. The results from the dietary analysis will give an insight into saugeye feeding habits and their potential as a biological control for gizzard shad and/or bluegill in small reservoirs.
Growth Rates of *Leuconostoc* Bacteria on Defined Growth Media vs Complex Growth Media.

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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.
In nature, prey species benefit by avoiding predators, and thus many predator avoidance strategies have evolved. Successful predator avoidance behaviors have high selection rates because avoiding predators is a life or death situation. In fish, two different types of predator cues are found that elicit predator avoidance responses: visual and olfactory cues. The fish alarm pheromone response is an olfactory cue released upon injury to fish skin cells. Alarm pheromones induce a species-specific fright response in surrounding fish; for example, behavioral responses to the pheromone such as rapid darting or tighter schooling mislead the predator which helps the prey avoid being eaten. I used a video camera to quantify the behavioral response to alarm pheromones of Red Shiners *Cyprinella lutrensis* in a laboratory setting. Although alarm pheromone response has been shown in many fish species, it has yet to be documented in the Red Shiner. I used software to measure distance between fish and movement of individual fish both before and after exposure to an alarm pheromone. Alarm pheromone responses were elicited by the Red Shiner in this study including an increase in mean swimming velocity \((t=-3.73; \ p=0.02; \ df=4)\) and an increase in distance among fish \((t=-4.19; \ p=0.01, \ df=4)\) after being exposed to the alarm pheromone. This study provides evidence for an alarm pheromone response in the Red Shiner and also a more quantitative method for measuring the fish alarm pheromone response. Future studies will include the effects of water quality (pH and temperature) on the alarm pheromone response.
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