**Poster Abstracts 2016 SLEEC Retreat**

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**Endophytic bacteria on Missouri prairie plants**

There is an increasing number of publications describing the distinction between the rhizosphere and endophytic bacterial communities for many plants. Data generated on endophytic bacterial communities of model organisms may not adequately represent the composition and diversity of the microbiota of agricultural or prairie plant species. We conducted a green-house study using five Missouri prairie plant species to not only characterize the endophytic bacterial community but to also understand the assembly of the communities. We perturbed the microbial community by introducing four different antibiotics to soil collected from the prairie plants. Biomass was used as a final measure of plant performance in the different soils and sequenced the bacterial and fungal communities. We discovered that within live and sterile soils the bacterial communities were drastically different between the plant species but the use of antibiotics did not alter the structure of the bacterial community.

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**Assessment of the relationship between geographic range size, environmental niche characteristics, and body size of freshwater fishes at a regional scale**

Identification of the factors regulating species distributions has important implications for understanding the mechanisms structuring regional patterns of biodiversity. Species-level traits such as niche breadth (i.e. the range of environments occupied by a species) and body size are often predicted to exhibit positive correlations with geographic range size, but these relationships are rarely estimated using data from multiple regions. Here, we test the associations between range size, environmental niche characteristics, and body size among freshwater fishes native to Illinois and Alabama watersheds. While streamflow volume, body size, and spatial variability in streamflow conditions generally exhibited positive relationships with range size, intra-annual streamflow variability was associated with restricted range size. This finding suggests the specific ecological and evolutionary traits of individual lineages, along with local habitat, are important factors in characterizing the relationship between niche measures, body size, and range size.

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**Comparing movements of Timber Rattlesnakes between consecutive years**

Studying the movement patterns of the Timber Rattlesnake (*Crotalus horridus*) can provide important information on how this Illinois Threatened species uses its home range which can then be used to inform management of the species and its critical habitats. Previous research conducted in the forests and prairies of Principia College suggest that there are three main types of movements by Timber Rattlesnakes: Spring and fall migration, Foraging movement patterns, and mating season movement patterns. Each of these movement patterns correlate with specific time periods and influence how far the snakes travel; their rate of travel and the types of habitats used. In this study we continued monitoring the movement of 7 Timber Rattlesnakes that had previously been tracked in 2015. I examined the movements of these snakes in 2016, compare that movement to those of 2015 and examine how the snakes are using their habitats.

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**Parasitism and predation in a tropical community of shelter-building caterpillars**

Preliminary analysis of shelter-building caterpillars in Palo Verde National Park, Costa Rica has identified interactions between caterpillars, their host plants, and their natural enemies. First, caterpillars are relatively specialized on particular host plants: each species eats an average of 1.4 plant species. Second, these caterpillars build a variety of shelters: webs, leaf rolls, leaf ties, leaf folds, and cut-and-fold shelters. Third, caterpillars are attacked by a variety of invertebrate predators and parasitoids. Parasitism varies with shelter type (p = 0.04), with leaf rolls having significantly lower parasitism (3%) and leaf ties having significantly higher parasitism (23%) than other shelter types. Shelter-building caterpillars are one of the most important herbivore groups in forest ecosystems and are frequently considered pests. These results suggest that caterpillar that build different shelters vary in parasitoid vulnerability, which has implications for both natural population dynamics and the use of parasitoids for biological control of pest species.

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**Criteria for Endangered and Threatened Listing do not Predict Population Growth Rate**

Conservation practitioners use state Endangered and Threatened (E&T) species lists as a way to prioritize species for limited conservation resources. Quantitative methods for assessing extinction risk (PVA’s) require long-term data, so E&T assessments are usually based on criteria thought to be associated with extinction risk, such as species’ habitat specificity. However, there is no reason to expect that species restricted to few habitat types are more likely to have declining population trends. Most plant species with Illinois E&T status were listed based on habitat specificity or range size. We are using long-term population monitoring data for 36 rare plants in IL (data from the Chicago Botanic Garden) to determine if these criteria predict local population growth rates. A multiple regression showed that they do not, indicating the need to identify better criteria for assessing population viability when assigning state level E&T status to plant species.

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**Assessment of Bluff Prairie Health using Grass and Forb Diversity and Density**

While nearly all native prairies in Illinois have been destroyed due to farming and over-grazing, bluff prairies have naturally been preserved because of their location on steep slopes and rocky soil. However, the absence of disturbance (i.e. fire) allows woody encroachment, altering resource availability and has been shown to decrease diversity in prairie and savanna systems. Principia College once had high-quality examples of bluff prairies on its 4-mile stretch of southwest-facing bluffs. This study assessed the quality of restored and unrestored remnant bluff prairies located on Principia College property near Elsah, Illinois. Herbaceous vegetation, seedling, shrub, and tree data was collected from 79 plots. Grass and forb diversity and density were correlated with canopy closure and whether the plot had been restored or not. We found a significant negative correlation between plant species diversity and closed canopy and a significant positive correlation between herbaceous species diversity and restored plots.

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**Home Range Analysis of Timber Rattlesnakes (*Crotalus horridus*) in Central Illinois**

An animal’s home range is defined as the geographic area in which an animal carries out its regular activities and interacts with its environment. The home range of timber rattlesnakes includes its hibernacula, movement corridors and its foraging areas. Identifying the habitats that the snakes use within their home range is important in their conservation. Timber rattlesnakes are considered a keystone species in the oak-hickory forest found along the southern and western margins of Illinois. Principia College campus is located along the bluffs above the Mississippi river and includes several rattlesnake hibernacula and large tracts of forest habitats. Eleven rattlesnakes were radio tagged and tracked using VHF telemetry over the summer and fall of 2015 and the summer of 2016. Home range size and habitat use of seven snakes tracked in consecutive years were compared.

Brant, Rachel (rbrant@slu.edu) Saint Louis University (with Gerardo Camilo).

**The phenology of the eusocial sweat bee, *Halictus ligatus,* in an urban environment**

It has been proposed that social bees respond to urbanization more obviously than solitary species. We selected the social sweat bee, *Halictus ligatus*, which has shown to respond to varying environmental conditions by altering its phenology. We hypothesize that *Halictus* will exhibit different phenology patterns, consistent with resource availability, across locations within St. Louis. Geographic areas were assigned as treatments based upon resource availability, as well as the management type. Because development of the tegula is directly proportional to resource availability, we measured the intertegular width of females *H. ligatus.* Larger individuals were found in May, while the smallest were found during the summer months, consistent with workers collecting pollen for the brood. There are also differences among north and south, which is likely a difference in resource availability across the city. How this differentiation can lead to better performance in a city environment remains to be investigated.

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**Evolutionary history of the genus *Camelina* (Brassicaceae)**

*Camelina* (Brassicaceae) is a small genus of interest as biofuel with proposed origin in the Irano-Turanian region. Floras from the region of species diversity differ in number of species recognized and the morphological characters used to define them. Despite taxonomic uncertainty, five species appear in all treatments of the genus: *C. hispida, C. laxa, C. microcarpa, C. rumelica*, and *C. sativa*. As a first step in determining taxonomic units in the group we are employing a phylogenetic approach to understand species relationships. Over three summers, we collected species in *Camelina* from the proposed region of origin in Turkey, Georgia, and Armenia from ~150 distinct locations. To assess phylogenetic relationships among these collections, we sequenced the internal transcribed spacer (ITS) region of nuclear ribosomal DNA for maximum likelihood phylogenetic analysis. Results from this work suggest a history of hybridization among currently recognized *Camelina* species. In addition, we are documenting differences in genome size among our collections using flow cytometry. Results from this work confirm that diploids, tetraploids and hexaploids exist in the genus. In ongoing work, we are employing next-generation sequencing to provide a more robust, high-resolution phylogeny based on analyses of thousands of phylogenetically informative genome-wide SNPs.

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**Global inventory and evaluation of wild, perennial herbaceous cereal, pulse and oilseed species for pre-breeding and domestication**

The Perennial Agriculture Project - Global Inventory (PAPGI) is a collaborative project between Saint Louis University, the Missouri Botanical Garden, and The Land Institute (Salina, Kansas). This project aims to inventory perennial, herbaceous members of the Asteraceae, Fabaceae, and Poaceae families, to generate a web-searchable database, and to develop a short list of perennial candidate crops with potential uses in perennial polycultures. For the short list of candidate species, the on-line global inventory will record ecological, ethnobotanical information as well as morphological and reproductive traits. The inventory uses specimen-based information, geographic locality references, and elevation. The innovative approach of this project is to leverage existing resources at the Missouri Botanical Garden including Tropicos, as well as other related global databases, to expedite the identification of wild species with potential to be developed into perennial crops for use in perennial polycultures that mimic natural ecosystems, advancing food and ecosystem security.

Cloyed, Carl (ccloyed@lc.edu). National Great Rivers Research and Education Center, One Confluence Way, East Alton, IL 62024 (with Tracie Hayes, Anthony Dell, and Eoin O'Gorman).

**Using a geothermal stream system to test the effects of body size and temperature on locomotor performance in the snail, *Radix balthica***

How an organism moves is central to its ecology, influencing many ecological processes and properties. Body size and temperature are known to be key determinants of movement. To test the effects of temperature and body size on movement, we used a geothermally heated watershed in Iceland, where individual streams varied systematically in their water temperature. Using automated tracking stations that our lab developed, we tracked the in situ movements of 191 snails from seven streams. As predicted, larger snails had higher average velocities, as did snails from warmer streams. However, the largest snails occurred in streams with intermediate temperatures and these snails had the highest velocities. We propose this is due to a combination of longer lifespans in cooler streams and a greater amount of resources available in warmer streams. In streams with intermediary temperatures, snails live longer, eat more, and can therefore obtain larger body sizes and move faster.

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**The use and analysis of *Paeonia officinalis* from the records of Anna Maria Luisa de’ Medici in the Medici Archives in Florence, Italy**

This is an historical ethnobotanical study focusing on the use of *Paeonia officinalis* by Anna Maria Luisa de’ Medici (1667-1716). In Florence, Italy, the Medici Archives house the correspondence and documentation of the ruling house of Medici in the 15th and 16th century. Recent translations have provided documentation of the use of P. officinalis as a key recipe promoted by Anna Maria as a treatment for childhood fevers. In this study we document the pre-Linnean taxonomy of *P. officinalis*, compare past and present medicinal uses, and examine the known biochemistry of this species. This research was conducted both in collaboration with the Medici Archives and at the Missouri Botanical Garden Raven Library. We find that the use of P. officinalis has multiple sources of folk medicine documentation, and has biochemical properties consistent with potential efficacy for medicinal effects

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**Linking trait variation to trophic interactions in natural and created pond communities**

Ecologists increasingly acknowledge the important role that individual trait variation can play in shaping species interactions in wildlife communities. Nevertheless, empirical demonstrations linking individual traits to species interactions remain rare. We conducted a series of controlled experiments to a.) measure trait variation of an amphibian predator, larval spotted salamanders (*Ambystoma maculatum*), and their prey, gray tree frogs (*Hyla versicolor*), b.) determine how individual traits influence the strength and outcome of predator-prey interactions between these two species, and c.) assess how trait variation and predator-prey dynamics differ in naturalized versus recently-created pond communities. We developed a novel video-based experimental system, which we utilized to quantify behavioural and morphological traits of over a thousand larvae from various natural and recently-created ponds in Eastern Missouri.

Haas, Alexis (ahaas2@live.maryville.edu) (with Adam Rork and Kyra N. Krakos)

**A Comparison of Morphology and Breeding System of *Camassia scilloides* Between Different Habitats**

The reproductive biology of a plant species can be habitat specific. This study compares the reproductive biology of *Camassia scilloides*, a MO native species, in glade and wetland populations. Morphological measurements, visitation pattern observation and hand pollination experiments were conducted in each habitat. Results show that glade and wetland plants significantly differ in height, flower number and stamen length. In both habitats the main pollinating visitor was Halictidae. The glade population of *C. scilloides* is self-compatible, not negatively impacted by geitonogamy and not experiencing pollen limitation. Our results do not indicate that variation in morphology impacts pollination services. Further studies are needed to establish possible temporal variation of the pollination in the two habitats.

Herron, Sterling, Claudia Ciotir, and Allison Miller, *Department of Biology, Saint Louis University*

**Comparison of annual and perennial herbaceous legumes (*Glycine, Lupinus*, and *Phaseolus*) for response to natural and artificial selection**

The vast majority of global seed crops consist of annual monocultures, but this agricultural method is unsustainable in its loss of nonrenewable topsoil. The adoption of perennial crops offers several advantages: retention of soil, water, and nutrients by roots, as well as fewer fertilizer and pollutant inputs into soil. Legumes (Fabaceae) offer the additional advantage of fixing nitrogen in the soil, an essential plant macronutrient. This project seeks to answer: what are the patterns of variation in agriculturally relevant traits (e.g., seed size, yield, seedling vigor, flowering time) when comparing congeneric herbaceous annuals and perennials in *Glycine* (soybean), *Phaseolus* (common bean), and *Lupinus* (lupine), both in how they have been affected by 1) natural selection and 2) artificial selection. This will help determine reasons for original anthropogenic domestication of annual crops, as well as if the phenotypic variation necessary to become a viable crop is present in herbaceous perennial legumes

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**Amphibian Diversity and Abundance in Old Artificial Ponds on the SIUE Campus**

Amphibian populations are used as indicators of environmental quality, and declines in both diversity and abundance are well documented. We surveyed two ponds located in close proximity (<150m) to each other on the SIUE campus from June - November 2015 and from March 2016 to the present. At each pond, three drift fences (0.36 x 5m) with pitfall and funnel traps were installed. Six minnow traps were placed along pond margins at the same approximate depth. Ponds were similar in overall diversity. Seasonally, ponds differed in abundance, with higher numbers of amphibians in the open pond during summer. During our survey period, both ponds were used by a variety of amphibians, and breeding individuals of most species were evident. Despite differences in pond features, similar species were present in both ponds. Future work will assess changes in water levels and composition and their effects on abundance and diversity.

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**Temperature influence on mating behavior of male and female *Enchenopa binotata* (Hemiptera: Membracidae)**

Environmental conditions can affect a variety of behaviors that have an important fitness consequence. Male mate-signaling and female preferences are examples of behaviors that can potentially impact sexual selection in small ectothermic organisms. *Enchenopa binotata* (Hemiptera: Membracidae) communicate using substrate-borne vibrations that are sent through the plant and can be influenced by temperature. Females select males based on the frequency (Hz) of a male’s signal. Using recorded live males and females across temperature, data collected showed male signals and female preference are not exactly aligned. With over 100 Hz in variation for both male signal frequency and female preference, it can be suggested that temperature has an influence in *E. binotata’s* mating behavior.

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**Exposure to an acidic environment during early development affects morphological development in *Danio rerio****.*

Exposure of vertebrate embryos to environmental stress during development can result in various anomalies. Due to anthropogenic activities, all of the earth's water systems are becoming acidic. This change represents a new environmental stress to aquatic vertebrates and their developing progeny. Research is beginning to examine the effects of an acidic environment on fish development. However, very little is known about the outcomes of exposure to acidity during specific time periods of development. Here we use the model organism, *Danio rerio*, to investigate the effects of exposure to an acidic environment on morphology during specific intervals of early development. We have collected data that indicates exposure to an acidic environment during early development results in significant morphological changes in larvae. Ongoing experiments will examine the morphological changes of acidic environmental exposure in intervals within this time period of fish development.

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**Current and future species distribution modeling of stream-dwelling crayfish species using hydrologic, topographic, geologic, and land cover data**

In the face of anthropogenic global change, it is critical to understand what climatic and physical factors are important in regulating species’ current distributions in order to predict how their distributions may be altered. In this study, species distribution models (SDMs) for ten stream dwelling crayfish species were modeled with a Maximum Entropy approach across the Mobile River Basin. Models were generated using current hydrologic, topographic, geologic, and land cover data and were projected into the future with future hydrologic data (all variables model). Species’ distributions were also modeled utilizing just hydrologic data (flow only model). SDMs were generally significant when using both the all variables and flow only models, but geologic and land cover data were found to be most important in regulating suitable habitat. This demonstrates that seemingly significant SDMs can be generated even when factors most important in determining areas a species can occupy are not considered.

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**Breaking the Bonds of Domestication: Adaptation Shapes the Weedy Rice Genome**

Weedy crop relatives are a common, problematic and under-studied byproduct of the domestication process. In the case of rice, weedy strains have evolved multiple times in different world regions from different domesticated varieties and wild relatives. We generated whole genome sequence assemblies for 38 weedy rice accessions representing the two major US strains (straw hull, SH; and black hull awned, BHA); these were analyzed together with published whole genome sequences for diverse cultivated and wild Oryzas. Weeds differ in their relationships to cultivated rice; BHA weeds are genetically similar to S. Asian aus varieties while SH strains are most similar to SE Asian indicas. Differences among weeds in their level of genetic similarity to their closest crop relatives suggest differences in timing of weed origins during the history of rice cultivation. This inference is supported by candidate gene analysis of domestication loci, which indicate BHA weeds likely diverged earliest.

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(with Allison Miller).

**Single nucleotide polymorphism discovery via genotyping by sequencing to assess population genetic structure and recurrent polyploidization in *Andropogon gerardii***

Autopolyploidy, or whole genome duplication within a single lineage, can result in multiple cytotypes within a species. The geographic distribution of these cytotypes may reflect the evolutionary history of autopolyploid formation and subsequent population dynamics including drift and selection. In this study, we used a population genomic approach to investigate the potential recurrence of autopolyploidization in *Andropogon gerardii*, a widespread North American grass with two predominant cytotypes (6x and 9x). Genotyping by sequencing was used to identify single nucleotide polymorphisms (SNPs) in individuals collected from across the geographic range of *A. gerardii*. Two independent approaches to SNP calling were used; SNPs generated using these pipelines were analyzed independently with genetic distance and clustering. Analyses of the two datasets showed very similar patterns of population-level clustering of A. gerardii individuals, and 6x and 9x individuals from the same geographic area clustered together, suggesting multiple origins of the 9x cytotype.

McAllister, Christine (Principia College), Sarah Clewell, Kathrines Biang, Bess Bookout, and ElThe grass tribe Andropogoneae consists of approximately 1200 species, including some of the most economically important grasses (e.g. maize (*Zea mays*), sugarcane (*Saccharum officinarum*) and sorghum (*Sorghum bicolor*)) and ecologically important grasses (e.g. *Andropogon gerardii, Sorghastrum nutans, Schizachyrium scoparium, Themeda* spp.) in the world. Despite the economic and ecological significance of these species, little is known about factors contributing to their success – namely, reproductive strategies and structures. Our goal was to characterize diversity in diaspore morphology in the tribe in order to ultimately examine this variation in an evolutionary context. We documented spikelet morphology in 187 species across six genera and explored relationships between morphological variation and climate.

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**Research-PGR: Adapting Perennial Crops for Climate Change: Graft Transmissible Effects of Rootstocks on Grapevine Shoots**

The goal of this study is to use grafted grapevines to unravel the complex interactions between root, scion, and environment that result in shoot system phenotype. While we know rootstock and environment contribute to scion phenotypic variability, no studies to date have been designed to delineate the relative contributions of these factors and their interaction. This endeavor requires globally sampling the phenotype of a common scion, which we propose to do physiologically, morphologically, metabolically, ionomically, and molecularly in a common scion grafted to varying rootstocks in a common garden, to rigorously isolate genetic, graft-transmissible effects (Aim 1). To sample the environmental plasticity of rootstock-mediated scion phenotypes, we target industry-relevant rootstock and scion genotypes planted in transects across disparate California climates (Aim 2). We analyze under-sampled rootstock genetic recombination events to understand GxE effects modulating graft-transmissible phenotypes in a clonally replicated segregating vineyard planted in four locations (Aim 3). Throughout our proposal, collaborations, research opportunities, and industry training are provided through a collaboration with our industry partner E. & J. Gallo Winery, as well as cross-disciplinary training in multiple EPSCOR states and educational outreach (Aim 4).

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**A functional approach to understanding patterns of bee species distribution across an urban environment**

Urbanization is on the rise worldwide and in the face of global pollinator declines, can have a large impact on ecosystem functioning and services. Yet, little is known about how bee species respond to urbanization. To assess this, we sampled community gardens within the urban core of St. Louis City. Sampling was done in a systematic fashion, weekly from mid-May to late September 2013-2016. We sampled at a rate of 0.25 person per hour hectare for all bee species using aerial nets. Species were then separated by functional traits. Over 100 bee species representing 5 families and 31 genera were collected. Early-mid July to late August was the peak of species abundance and diversity. Bee species richness declined from north to south across the city. Highest species richness was found in the north side where empty lots surrounded sites.

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**Pollen Diversity in the Mint Family (Lamiaceae s.l.)**

The mint family is a large, and easily recognizable family of angiosperms. Many members of this family are used as medical and culinary herbs. There have been many recent molecular and morphological studies that support transfers of some members of the family Verbenaceae into Lamiaceae. Our goals for this study were to examine the range of pollen morphology in Lamiaceae and several outgroups to see if there is any support to these transfers while also exploring the diversity of pollen ornamentation in Nepetoideae. We collected anther samples from living specimens from the Missouri Botanical Garden and preserved them in 75% EtOH. The specimens were placed into paper envelopes and run through a 80%,90%, and 95% EtOH, critical point dried, placed on microscope stubs, and sputter coated with gold. Our study demonstrates there is significant variation in pollen of Lamiaceae sensu lato, and in the hexacolpate pollen of Nepetoideae. This study demonstrates that the pollen morphology is in disagreement with these recent transfers of taxa like *Vitex* and *Callicarpa*.

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**Strong correlation between codon usage bias and gene functions across the entire genome of *Drosophila melanogaster* suggesting that synonymous mutations are not usually neutral**

Synonymous mutations are usually assumed evolutionarily neutral. However, codon usage bias, the phenomenon that some codons are used more often than their synonymous codons, may undermine this assumption. Recent studies have shown that introducing synonymous mutations to specific genes can modify their functions. In addition, our analysis on the protein coding genes across the entire genome of *Drosophila melanogaster* revealed that 1. the correlation between gene functions and codon usage exists in most genes and is not a special case; 2. specific set of nonsynonymous codons contribute more to codon usage bias; 3. codon usage patterns of genes correlate to their organ-specificity, sexual dimorphism, molecular functions, and genomic locations; and 4. recently diverged paralogs can have fairly different codon usage biases. These findings suggest that "synonymous mutations as evolutionarily neutral" is a risky assumption. Evolutionary neutrality does not depend on how mutations happen, but how they influence gene functions.

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**Cross species selection scans identify components of C4 photosynthesis in the grasses**

C4 photosynthesis evolved multiple times independently in the angiosperms and over 22 times in the grasses suggesting that the ancestral genomes were primed for the acquisition of C4 traits. However, the identification of the genes and networks associated with the transition from C3 to C4 have to date remained elusive. To accelerate the pace of gene discovery in the grasses, we have exploited the close phylogentic relationship of the panicoid grasses and deep genomic sequencing to identify signatures of adaptive evolution. Importantly, this approach does not rely on any a priori knowledge of the genes that contribute to biochemical or anatomical innovations associated with C4 photosynthesis. Enabled by the collinearity of grass genomes and the recently sequenced genome of *Dichanthelium oligosanthes*, this analysis identified both known and novel components that likely underlie C4 traits, including traits that are shared among all C4 panicoids and those that are specific to one lineage.

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**Phylogenomic Analysis of 16 *Fundulus* Species using RNA-seq Data**

Phylogenies provide researchers with a tool for rigorous hypotheses testing within an evolutionary framework. As emerging models for evolutionary studies, fishes of the *Fundulus* genus are receiving increased attention in phylogenetic analyses. Proposed relationships among the fundulids have been based on a variety of organismal and molecular characters. However, deeper evolutionary relationships among clades remain poorly understood. The lack of a well-resolved deep phylogeny for *Fundulus* remains a major impediment to a variety of studies. This study will resolve interspecies relationships using a multi-gene approach based on RNA sequencing data. The data are available from a separate gene expression study by Whitehead and Duvernell (unpublished). Currently, data analysis has progressed through read filtering and trimming, de novo transcriptome assembly, and orthologous gene identification. Multiple sequence alignment, maximum likelihood and Bayesian phylogenetic inference is in progress.

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**Do soil microbes mediate or amplify the effects of foliar enemies under differing precipitation regimes?**

Plants are often dependent on associations with beneficial soil organisms to increase nutrient uptake (e.g. arbuscular mycorrhizal fungi). However, plants are also attacked by multiple enemies, both above and below the ground. These mutualistic and antagonistic interactions can have strong impacts on individual plant growth and survival, which have important ecosystem level consequences. Using experimental native tallgrass prairie communities at the Tyson Research Center, we tested whether soil microbes influence the damage caused by aboveground pathogens and herbivores under drought and no drought conditions. We show that soil microbes do influence the damage caused by aboveground enemies. However, the direction of the effects varied strongly depending on the plant species involved. Our results highlight the importance of multi-pathogen interactions in influencing plant performance under differing precipitation regimes.

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**Analysis of Spatiotemporal Scent Variation in a Rare Glade Species, *Manfreda virginica***

Plants and animals communicate in a variety of ways, including the emission and subsequent detection of floral organic volatiles (FOVs). Such volatiles released by flowers may serve as important cues to both mutualists and antagonists, signaling the presence of rewards and defenses (Pichersky & Gershenzon 2002; Raguso 2015). FOVs may play a role in pollinator attraction that exceeds that of visual cues such as flower color or display size (Byers et al. 2014). Different floral organs may release assorted compounds that may vary across flowering time, which may convey information to pollinators. Such spatiotemporal variation in scent is rarely quantified (Burdon et al. 2015). The rare, protandrous Missouri glade endemic, *Manfreda virginica*, provides a unique opportunity to study spatiotemporal scent variation. We hypothesize that *M. virginica* alters its FOV emission profile as it transitions from one reproductive stage to another as a function of time.

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**Evaluation of Plant Structure Relationships vs. Lifespan in the legume genus *Vigna.***

Perennial agriculture is a proposition to identify wild perennial relatives of domesticated annual crops for the purpose of integrating them into commercial food production. Harvesting from perennial plants would reduce soil erosion, water usage, and the need for fertilizers. This study aims to identify any differences in vegetative versus reproductive output between annual and perennial species using the model genus *Vigna* which has both annual and perennial species to compare. Furthermore, this study investigates the relationship between vegetative and reproductive structures within a species to find any differences in how perennial and annual plants might respond to artificial selection. Results showed some indicators of the annuals having larger vegetative structures than the perennials and an overall positive correlation between vegetative and reproductive structures for both annuals and perennials.

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**A comparative study of the impact of introduced honeybees on morphology and pollination in *Veronicastrum virginicum* in prairie and wetland habitats**

A habitat can experience change due to environmental or man-made circumstances. Both types of change can be stressful on plants and cause differences in morphology, (plant size and structure measurements) in populations of species. Plant morphology has a close relationship with function and systematics of a plant (Kaplan et al. 2001). This variance of morphology can lead to alterations in the main pollinators of the species. The introduction of non-native species can also alter main pollinators of a species. In 2016, Purina beehives for commercial purposes are being introduced in land adjacent to Shaw Nature Reserve (SNR). This introduction of non-native honeybees could have a profound impact on the native pollination systems at SNR. This new data that will be collected with the introduction of non-native pollinators will be compared to previous years data without the installation of the beehives so we can have a better understanding of the importance of native pollinators in a population

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**Pollinator foraging patterns and reproductive success of *Baptisia alba***

The flowering structure of a plant may impact the quality of the seed set if the pollinator has a particular pollination pattern (Arista et al. 1999). In this study, we examine how the foraging patterns of the current pollinators impact the reproductive success of *Baptisia alba* at Shaw Nature Reserve. We combined pollinator observations and pollen load analysis to determine main pollinators. We recorded pollinator foraging patterns. Our results show that *Bombus* are responsible for 83.03% of the total pollen flow in these populations*. Bombus* did not consistently forage in a bottom to top pattern on *B. alba*. We hand treated flowers to test for reproductive success in autogamous self, cross, and geitonogamous pollination. Our results indicated no statistical impact on reproductive success between self and cross pollen (p=0.845), cross and geitonogamous pollen (p=0.501), or cross pollen and open flowers (p=0.103). Therefore, we conclude that the foraging pattern of the main pollinator *Bombus*, although most likely increasing geitonogamous pollen deposition in flowers at the top of the inflorescence, are not impacting the reproductive success of *B. alba*.

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**Observing woody invasion on bluff savannah’s using forest dynamics**

Savannah landscapes have played an important role in balancing out the ecosystem and providing a microhabitat for many species. For the last few decades, there has been an increase in abundance of woody stems on the bluff hill prairies, which affect the growth rates of the trees near the invaded areas. Over the study, we had 75 plots located on the Principia College landscape where approximately 1,000 samples were collected. The results showed that Amur Honeysuckle, *Lonicera maackii*, had the highest relative density of any other species along with Fragrant Sumac, *Rhus aromatica*. It is hypothesized that due to a lack of fire disturbance and restoration in the last few decades, has allowed these species that are successful in mesic habitats, to thrive and grow undisturbed. Active restoration methods such as controlled fires and woody stem cutting are suggested to help with thinning out the density of woody stems.

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**A comparison of the effects of continuous versus patchy geographic distributions on the structuring of genetic variation in two bat-pollinated, wind dispersed *Agave* species (Agavaceae)**

Many factors may affect the structuring of genetic variation in plants, including their pollinators, seed dispersers, the continuity of their geographic ranges, and even their history of past cultivation by humans. We examined whether *Agave parryi*, which has a more patchy distribution and a history of past anthropologic use, would show stronger structuring of genetic variation relative to *Agave palmeri*, which has a more continuous geographic distribution and no past cultivation history, or instead whether their pollinators and seed dispersal mechanisms (predominantly bat-pollinated and wind-dispersed) would increase gene flow and reduce the structuring of genetic variation. Results show no discernible structuring of genetic variation in *A. palmeri*. In contrast, *A. parryi* formed 3 distinct genetic clusters corresponding to geographic locations. One genetic cluster contained several populations sampled at lower elevations and showed lower levels of genetic diversity, which may be indicative of anthropogenic origins.

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**Isolating Orchid Mycorrhizal Fungi from Spiranthes vernalis for Subsequent Seed Germination and Reintroduction**

The Spring Ladies’ Tresses orchid’s (*Spiranthes vernalis*) range extends widely throughout eastern North America. Although the taxon’s distribution is reportedly widespread the species is considered threatened or endangered in many areas throughout its range. One goal for any conservation program is to successfully increase population numbers, possibly by re-introduction of plants into existing populations. It is commonly known that orchids form unique relationships with mycorrhizal fungi and the association is often essential for orchid seed germination and enhanced seedling survival and growth rates. The intent of this study is to isolate and identify mycorrhizal fungi associated with at least one established adult Spring Ladies’ Tresses orchid, although others may be sampled as well, from a southern Illinois population. To date (September 2014), fungi assignable to the ubiquitous genera *Ceratobasidium* and *Tulasnella* have been isolated from pelotons in a mature plant, and efforts are now underway to further identify these strains using genome and transcriptome sequencing. Identification and isolation of the fungi will allow in vitro germination experiments and possibly the subsequent reintroduction of seedlings to aid in the conservation of the species.

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**MacArthur's niche hypotheses revisited: the role of niche space, niche breadth and niche overlap in explaining global patterns of species diversity**

Changes in species diversity across temperate and tropical ecosystems are among the most striking patterns of biodiversity. One leading hypothesis is that geographic variation in niche-assembly mechanisms results in higher diversity in the tropics. Theory predicts that tropical communities have greater niche space, more specialist species with smaller niche breadths, or greater niche overlap among species compared to temperate communities. These three niche properties are not mutually exclusive, but are generally examined independently in comparative studies of temperate and tropical diversity. We tested these hypotheses among 15 CTFS-ForestGEO forest-dynamics plots. We found that species in tropical communities have larger niche breadths and greater niche overlap. This suggests that tropical tree species may be less dispersal limited or more weakly influenced by local environmental heterogeneity or interspecific interactions than temperate tree species. Our results suggest that geographic variation in the strength of local niche-assembly mechanisms contributes to global patterns of biodiversity.

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**3D Phenotyping and QTL Mapping in a Cultivated Rice × Weedy Rice Mapping Population**

Cultivated rice (*Oryza sativa*) is aggressively outcompeted for limiting resources by its weedy relative, weedy rice. There is evidence that differences in root system architecture (RSA) result in higher nutrient uptake in the weed, leading to this competitive advantage. To better understand the underlying genetic components of RSA in this system, we grew 376 plants (representing 189 F8 RILs) from a cultivated × weedy rice mapping population in gellan gum media for 13 days. We employed a semi-automated 3D imaging and phenotyping pipeline to phenotype plants at 117 RSA traits. Seventeen traits mapped to nine discrete QTLs (non-overlapping LOD intervals). Interestingly, three RSA traits mapped to the same chromosome (although to different locations) as RSA QTLs identified in a previous study using the well-known Bala × Azucena cultivated rice mapping population. A basic understanding of the complexity in RSA is of high importance in mediating weed competition in this system.

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**A comparative study of the nocturnal and diurnal reproductive biology of three *Asclepias* species**

*Asclepias* species, the milkweeds, are known for their specialized relationship with monarch butterflies. Our study focused on the differences in morphology and nectar of *Asclepias* and if the species utilizes nocturnal pollinators. We measured how main pollinators and morphological traits differed between the three species over two years. We found that *Apis* was the main pollinator for all three species. *A. syriaca* showed a slight variation in a larger inflorescence, smaller corolla span, and larger height compared to the other species (p<.05). These differences did not impact visitation by pollinators significantly. The umbel span showed no variance between years. We measured nectar day and night and found nectar production was greater at night for *A. syriaca*. Although noctuid moths visit *Asclepias*, they are not pollinators, and most likely nectar robbers. In this study, *Asclepias* does not have a dual pollination system and relies on diurnal pollinators for reproductive success.