

The Field Museum and the Chicago Botanic Garden proudly
present the

5th Annual Undergraduate Research Symposium 2013

Research presentations and poster presentations by
undergraduate research interns from the Field Museum
and the Chicago Botanic Garden

Program and Abstracts

Friday, August 16

Simpson Theatre

PROGRAM

- 8:00 – 8:45am** Poster set-up in West Door Lobby in front of Simpson Theatre, mounting board, easels, push pins and tape provided
- 9:00 – 9:15 am** **Opening of the Symposium, Welcome**, (opening remarks by P. Sierwald, K. Angielczyk, J. Fant and D. Larkin)

Session 1:

Moderator: Kenneth Angielczyk
Curator, Field Museum

- 9:15 – 9:30am** **Microsatellite patterns in two *Castilleja* subspecies *affinis* and *neglecta***
Hosin West, University of New Haven, and Chicago Botanic Garden
- 9:30 – 9:45am** **Analyzing the genetic component in caste determination of Neotropical Army Ants**
Andrew Burchill, University of Chicago, and Field Museum of Natural History
- 9:45 – 10:00 am** **The circumscription of the genus *Lecanora* (Fungi: Ascomycota: Lecanoromycetes: Lecanorales)**
Patricia Brandt, University of Chicago and Field Museum of Natural History
- 10:00 – 10:15am** **Bizarre biology: morphogenesis of the freshwater bryozoan *Plumatella vaihiria* (Phylactolaemata)**
Andrea Rummel, University of Chicago, and Field Museum of Natural History
- 10:15 – 11:00am** **Speaker Group Photo, Coffee Break**

Group photo of all speakers and poster presenters in West Door Lobby at 10:35 sharp, please assemble with Stephanie Ware

Coffee Break for all: in West Door Lobby at Field Museum, please do not take food or drink into Simpson Theatre



Session 2:

Moderator: Emily Yates

Seed Bank Coordinator, Dixon National Tallgrass Prairie Seed Bank and Conservation GIS Lab
Manager, Chicago Botanic Garden

- 11:00 – 11:15am** **GIS-based spatial analysis of rare plant populations on gravel hill prairies: Habitat suitability modeling**
Christopher Wright, University of Washington Bothell, and Chicago Botanic Garden
- 11:15 – 11:30 am** **Rooting PhyLoTA: A case study in taxonomically rooting phylogenetic trees**
Joshua Stevens-Stein, University of Chicago, and Field Museum of Natural History
- 11:30 – 11:45pm** **Assessment of the effects of the introduction of *Echinacea pallida* in the pollination of native *Echinacea angustifolia* in western Minnesota**
Dayvis Blasini, Northeastern Illinois University, and Chicago Botanic Garden
- 11:45 – 12:00noon** **Seeding restorations: Evaluating seed viability to improve restoration outcomes**
Jessica Riebkes, Central College, and Chicago Botanic Garden
- 12:00 – 12:15noon** **Does the attempt to restore golden Indian paintbrush to a former habitat or raising the species in isolation have an effect on genetic diversity, and if so to what extent?**
Alexander Shaffer, Northwestern University, and Chicago Botanic Garden
- 12:15 – 1:00pm** **Lunch Break**

Lunch: provided for speakers, poster presenters and mentors in *Lecture Hall II*, ground floor, Field Museum, follow Stephanie Ware, Petra Sierwald and Ken Angielczyk

Audience **Lunch options:** Corner Bakery, first floor; McDonalds, ground floor

Session 3:

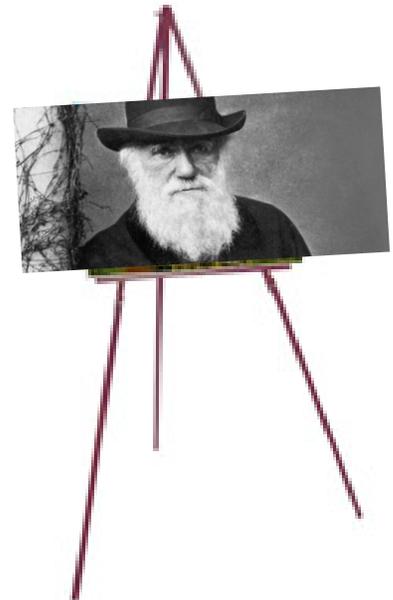
Moderator: David Clarke

Postdoctoral Research Associate, Field Museum

- 1:00 – 1:15pm** **Decomposition and fungal diversity in restored tallgrass prairies**
Mariah Allen, Lake Forest College, and Chicago Botanic Garden
- 1:15 – 1:30pm** **Organic matter stabilization in soil aggregates during grassland restoration**
Jenifer Yost, Lake Forest College, and Chicago Botanic Garden
- 1:30 – 1:45pm** **The role of fungi in soil C-sequestration**
Allison Buiser, Knox College, and Chicago Botanic Garden
- 1:45 – 2:00pm** **Now you setae, now you don't: Comparing millipede morphology up close and personal**
Madeleine Metz, Emory University, and Field Museum of Natural History
- 2:00 – 2:45pm** **Coffee Break and Poster Session**

Poster Session: Poster presenters, please stand by your poster, so that members from the audience can ask questions.

Coffee Break for all: in West Door Lobby at Field Museum, please do not take food or drink into Simpson Theatre



Session 4:

Moderator: Lauren Umek

Graduate student, Northwestern University and Chicago Botanic Garden

- 2:45 – 3:00pm** **A molecular phylogenetic survey of *Borrelia* from migratory birds: Are migratory birds potential vectors for Lyme disease?**
Sarah Kurtis, University of Chicago, and Field Museum of Natural History
- 3:00 – 3:15pm** **The Bats of Kenya: assessing the species limits of cryptic species**
Kyle Reid, Olive Harvey College, and Field Museum of Natural History
- 3:15 – 3:30pm** **A new dicynodont from the late Permian of Tanzania**
Ben Otoo, Amherst College, and Field Museum of Natural History
- 3:30 – 3:45:pm** **How to grow a dinosaur: the histology and femoral ontogeny of the Middle Triassic dinosauriform *Asilisaurus kongwe* and implications for the growth of early dinosaurs**
Christopher Griffin, Cedarville University, and Field Museum of Natural History
- 3:45- 4:00 pm** **Closing Remarks:** Drs Dan Larkin and Jeremie Fant, Chicago Botanic Garden
- 4:00 pm** **End of Symposium**

ABSTRACTS and POSTER TITLES

Title: Micro Plants: Connecting collections to biodiversity research and education [poster presentation]

Xenia Alava, Northeastern Illinois University and Field Museum, Chicago, IL

Dara Arabsheibani, Northeastern Illinois University and Field Museum, Chicago, IL

Charlie D'Lavoy, Northeastern Illinois University and Field Museum, Chicago, IL

Kavita Elliott, Ohio State University and Field Museum, Chicago, IL

Veronica Lopez, Northeastern Illinois University and Field Museum, Chicago, IL

Ramsey Millison, DePaul University and Field Museum, Chicago, IL

Pedro Rebollar, DePaul University and Field Museum, Chicago, IL

Jonathan Scheffel, Harold Washington College and Field Museum, Chicago, IL

Alex Vizzone, Northeastern Illinois University and Field Museum, Chicago, IL

Ariel Wagner, DePaul University and Field Museum, Chicago, IL

Zak Zillen, Northeastern Illinois University and Field Museum, Chicago, IL

Audrey Aronowsky, Field Museum, Chicago, IL

Beth Sanzenbacher, Field Museum, Chicago, IL

Eve Gaus, Field Museum, Chicago, IL

Beth Crownover, Field Museum, Chicago, IL

Arfon Smith, Zooniverse

Brian Carstensen, Zooniverse

Tom Campbell, Northeastern Illinois University and Field Museum, Chicago, IL

Matt von Konrat, Field Museum, Chicago, IL

Title: Decomposition and fungal diversity in restored tallgrass prairies [oral presentation]

Mariah Allen, Lake Forest College, and Chicago Botanic Garden, Glencoe, IL

In prairie restoration, land managers use aboveground methods that focus on the plant community, such as removal of invasive species, reintroduction of native species, and prescribed fire. The soil microbial community plays an essential part in prairies because they decompose organic matter such as leaves and other decaying plant material and make nutrients from that litter available for next year's plant growth. How these aboveground methods of restoration affect the microbial community and the process of decomposition. We explore this question with six fallow agricultural fields and high quality prairie remnants throughout the Chicago region. We placed 60 mesh litterbags containing fall collected grass (*Andropogon gerardii*), forb (*Rudbeckia subtomentosa*) and a legume (*Baptisia australis*) at the sites March-April and collected 3 bags of each species in mid June 2013. The legume has the highest litter quality (lowest C:N) followed by the forb and the grass *Andropogon*. We hypothesize that higher decomposition will be observed with the legume. We analyzed each collected litter sample for total mass loss, moisture, enzyme activity, hyphal productivity, and litter quality. Enzyme activity on most of the collected samples was below detection range, suggesting that little microbial activity occurred following the ~100 days in the field. This statement is also

supported by our observation of minimal- hyphael growth on the litter (0-19% of fields contained hyphae). Legumes contained the most hyphae followed by the grasses, then the forbs.

Title: Which species of tropical canopy tree species access the water source provided by underground caves on the Yucatan Peninsula and are their natural fungal symbionts present in these portions of the root system? [poster presentation]

Kevin Amses, Humboldt State University, and Chicago Botanic Garden, Glencoe, IL

The seasonally dry forests of the eastern Yucatan peninsula represent a synapse between temperate and tropical environments in the Western hemisphere and overlay one the largest known limestone karst systems on the planet. Karst systems are and have been important in the course of human history, because of the availability of clean fresh water they boast, and are responsible for the subterranean geography of the area. This region is disappearing quickly under layers of concrete as resorts are being rapidly constructed and towns quickly expanded to support a constant stream of tourism. Similar threats pose a serious conservation risk to about 97% of the remaining seasonally dry tropical forests worldwide. In contrast to forests in the temperate zone, seasonality is driven by precipitation rather than temperature. Although annual rainfall remains relatively high, precipitation is concentrated in the rainy seasons, which are separated by periods of drought lasting about half of the year. Despite this, many canopy tree species exhibit an evergreen habit. A unique feature of this system that likely contributes to this is that throughout the year, and especially during the dry season, canopy trees utilize extensive, yet difficult to access, underground water sources provided by vast networks of subterranean caverns. It is clear that plants are accessing this water source, as thick bundles of roots descending through the bedrock into open cavern space and radiating toward standing water are commonly observed in caves. Despite the probable importance of access to this below ground water in determining above ground plant community structure, no definitive survey of the plant species that are capable of taking advantage of this resource has yet been published. In this study we use molecular genetic tools to identify the plant species that are present in subterranean root bundles. We expect that the capability to access this water source gives these species a competitive advantage over others and allows them to co-inhabit the canopy in highly mixed stands, and to maintain an evergreen habit throughout the dry season. Additionally, we estimate the thickness of bedrock through which root bundles penetrate to gain access to the caverns and investigate it as a potential driver of root bundle community composition.

Title: Effects of the introduction of non-native *Echinacea pallida* on the pollination of *Echinacea angustifolia* [oral presentation]

Dayvis Blasini, Northeastern Illinois University, and Chicago Botanic Garden, Glencoe, IL

The narrow-leaved purple coneflower *Echinacea angustifolia* (Asteraceae) is the only native *Echinacea* species found in Minnesota tallgrass prairies. Due to high levels of habitat fragmentation in this area, many restoration projects have been developed in these tallgrass prairies recently. Some of these restoration efforts have introduced non-native *Echinacea pallida*. This species could potentially have detrimental effects on the native *Echinacea* species,

as well as on the arthropod communities that depend on this plant. A specific concern is the invasion by hybridization between native and non-native echinacea species. Last year we successfully tested the likelihood of hybridization between *Echinacea pallida* and *Echinacea angustifolia* using artificial crosses and demonstrated that each species accepts interspecific pollen and seedling resulted. Because we did not have any evidence that such hybridization occurs in nature, we identified and contrasted the pollinator species that visit each echinacea species to determine the ultimate possibility of hybridization among these plant species. Simultaneously, we studied echinacea plants in the field to quantify synchrony in the time of flowering between the local and the introduced species. We observed, recorded, and collected pollinators for later identification using high resolution cameras and an existing reference pollinator collection. Because both species are visited by generalist pollinators, we hypothesized that the introduced species was very likely to hybridize with the native species in nature. After one month of pollinator visitation observation, we found that both echinacea species were predominantly visited for the same pollinator species. Also, our data revealed that although *Echinacea pallida* flowers early than *Echinacea angustifolia*, their overall time of flowering is mostly synchronized. The information we gathered from this research is indicating the high possibility of hybridization between these two species in nature. This is particularly important since *Echinacea pallida* has proved to outcompete other echinacea species in different regions of the United States in the past. The information gathered in this research indicates how important it is to use local flora in restoration projects exclusively.

Title: The circumscription of the genus *Lecanora* (Fungi: Ascomycota: Lecanoromycetes: Lecanorales) [oral presentation]

Patricia Brandt, University of Chicago and Field Museum of Natural History, Chicago, IL

Classification of lichen-forming fungi has changed dramatically over the last decades with the help of molecular data. While the classification of lichenized fungi traditionally relied heavily on growth morphology and fruiting body anatomy, molecular data have often shown these characters to be of limited value to circumscribe monophyletic groups. The genus *Lecanora* is a perfect example for a poorly delimiting genus. Results of previous studies suggest that smaller genera are nested within the large genus. To better understand the delimitation of the genus and the relationships of species groups within *Lecanora*, I used a multi-locus approach and extracted DNA from new samples collected worldwide. These molecular data were used to infer a phylogenetic tree of the genus *Lecanora*. Techniques that were applied include DNA extraction, PCR amplification, gel electrophoresis, DNA sequencing, and alignment. Analysis of the molecular data was performed using maximum likelihood and Bayesian tree sampling. The trees showed that specimens sharing characters, such as secondary metabolites or general preferences for substrate, clustered together. Characters of the groups found will be discussed. This study demonstrates that by incorporating more loci in the phylogenetic analysis, the support for clades can be improved and our confidence in the phylogenetic estimate is enhanced. This study will provide a basis for a revised classification of the genus *Lecanora*.

Title: Using X-Rays to Identify Unprepared Fossils From the Eocene Green River Formation of Wyoming [poster presentation]

William Buchman, New Trier High School, and Field Museum of Natural History

The Field Museum houses a large number of unprepared, unidentified and uncatalogued fossil fish specimens from the Eocene Green River Formation. These specimens are uncatalogued because they cannot be identified, and they are unidentified because they are unprepared, i.e. the rock covering the fossil has not yet been removed thus the fossil cannot be seen. The fossil fish collection is arranged systematically, and identifying each specimen would allow us to place them in the cabinet reserved for their taxon. We took x-ray images in order to identify each of these buried fossils. The x-rays allowed us to view detailed images of the fish hidden inside the unprepared slabs. Our initial plan was to use the x-ray images to identify each specimen to species. I began by x-raying slabs we suspected contained *Priscacara serrata* or “Priscacara” (Cockerellites) liops. These species are identified by counting fin rays. The smallest of these fin rays were not dense enough to show up on the x-rays, rendering a species identification impossible. The x-rays did allow us however to make accurate genus level identifications, and to identify the specimens of greatest scientific value in order to prioritize subsequent preparation. We printed out each x-ray on acid-free card stock, and housed them in zip lock bags with their respective specimens. All the newly identified fish fossils will now be catalogued into the Fossil Vertebrate Collection and housed in their appropriate cabinets. The x-rays also allow us to judge whether or not each slab contains a fossil. If a slab did not contain a useful fossil we disposed of it thus freeing up valuable collections space. This procedure has allowed us to make identifications more quickly than through the time consuming process of preparation thus enabling us to catalogue hundreds of unprepared specimens into our vertebrate paleontology collection.

Title: The role of fungi in soil C-sequestration [oral presentation]

Allison Buiser, Knox College, and Chicago Botanic Garden, Glencoe, IL

Saprotrophic fungi are able to enzymatically degrade the three most abundant biopolymers: cellulose, chitin, and lignin, and therefore mediate a globally important flow of carbon. However, little is known about how that carbon is transformed and/or stored in soil organic matter (SOM). Fungi are known to aid in the formation of soil aggregates through a variety of mechanisms, including hyphal growth and production of extracellular mucus-like exudates. Additionally, fungal biomass, specifically cell wall material, has been shown to be more decay-resistant than other microbial biomass. Fungal cell walls are mainly composed of chitin, glucan, and melanin, and it is likely that much of this material is resistant to decay and contributes to SOM storage. To study these contributions, a month long *in situ* degradation experiment was performed in Dixon Prairie at the Chicago Botanic Garden. The degradation of fungal cell wall material from the common soil saprotrophic fungus *Fusarium avenicum* by a natural soil microbial community was investigated. Fungal samples, contained in steel mesh litter bags, were buried approximately 5cm below the soil surface and then collected at eight harvest intervals for chemical analysis using Fourier Transform Infrared Spectroscopy (FTIR). Results show that about 31% of the original *Fusarium avenicum* mass resisted degradation over the one month period. FTIR analysis of the leftover tissue shows significant changes over the course of

the degradation, specifically in the carbohydrate region, potentially indicating breakdown of structural polysaccharides. FTIR analysis shows additional changes that reveal breakdowns of ester-linked groups. Specific peaks in the amide region of the FTIR, potentially from chitin, appear to be stable throughout the degradation sequence.

Title: Analyzing the Genetic Component in Caste Determination of Neotropical Army Ants [oral presentation]

Andrew Burchill, University of Chicago, and Field Museum of Natural History, Chicago, IL

Many organisms exhibit instances of polyphenism, in which a single genotype can result in various, discrete phenotypes, depending on environmental cues. The Neotropical army ant species *Eciton burchellii* provides an excellent study system for polyphenism, because as a eusocial insect, they have a large number of morphological castes present within one colony. The sterile, non-mating workers can be divided into four castes that exhibit functional specialization. Although it is believed that caste determination in army ants is primarily accomplished through different doses of juvenile hormone, recent studies suggest there may be a genetic component as well. Queens are highly polyandrous, and there is evidence that some paternal lineages may have higher propensities for developing into certain castes. In order to address this issue, 240 individuals from 10 colonies in South America were sampled. Back leg lengths were measured and used as a proxy for individual body size and caste. DNA was also extracted and three microsatellite loci were used to assign patriline in the colonies. Interpatriline variation could then be statistically assessed. Approximately 106 patrilines were detected, a larger number than what other studies have estimated, implying that queens may be even more polyandrous than previously believed. Initial analyses suggest that there is no genotypic bias on caste phenotype, although increased sampling is needed for a more robust analysis. In future research, geometric morphometrics could be applied to further characterize morphological variation and caste division in *Eciton burchellii*. Workers born from a single cohort should also be sampled to control for time-related effects and patriline shifting.

Title: Silurian Reef Digitization Project [poster presentation]

Liza Connolly, University of Chicago and Field Museum, Chicago, IL

Nicole Karpus, University of Illinois at Chicago and Field Museum, Chicago, IL

Alex P. Layng, Northwestern University and Field Museum, Chicago, IL

Project: Philogeography and genetic's landscape of *Elaenia ruficeps* (Aves: Tyranidae) [poster presentation]

Camila Duarte, Universidade Federal de Santa Maria (Brazil)

Campinas are open vegetation habitats that are related to white-sand soils and are as islands inserted in a forest matrix. *Elaenia ruficeps* is an Amazonian white-sand specialist species, we use this species as a model to understand the effect of the last glacial maximum (GLM) in their populations. In addition, we seek to elucidate what is the barrier to gene flow species and how the current landscape patterns influences the genetic diversity of populations of *E. ruficeps*. Low genetic variability was found among *E. ruficeps* populations and the intraspecific phylogeny had low resolution. However, the haplotype network showed separations through three Amazonian regions. These were: the Branco and Negro river interfluvium, the Guayanan

shield with Jaú and the regions north and south of the Amazon river. The most important barriers to gene flow between populations seem to be the white water rivers in north of the Amazonas river, and the isolation by distance. Terra-firme habitats do not constitute strong barriers to gene flow. Demographic growth was found in the recent past, at 25,000 years before present approximately. This may be related to a greater connectivity among campinas due the expansion of open habitats during the last glacial maximum. Or it may be related to the genesis of white-sand soil during the same period favoring a population expansion of *E. ruficeps*. Both hypotheses are related to changes of the landscape due to climatic variations during the Pleistocene. *E. ruficeps* did not show population structure at the landscape-scale studied. Aracá and Uatumã landscapes had their genetic diversity explained, in part, by landscape characteristics such as the area of the campina. Thus the genetic diversity of populations is related to historical and current processes in the studied landscapes.

Title: What are the effects of mulching on soil's microbial community in restored habitats?

[poster presentation]

Ben Girgenti, Brown University, and Chicago Botanic Garden, Glencoe, IL

In the Chicago-land area, European buckthorn (*Rhamnus cathartica*, L.) has invaded prairies and woodlands. This is not a unique case, as invasion of nonnative plants is a global issue. Land managers have begun adding carbon to the soil to boost microbial immobilization, which reduces inorganic nitrogen in the soil among other nutrients. Invasives are able to take advantage of high levels of resources much better than natives, so if the resources are reduced, the natives can compete better against invasives. In this experiment, soil cores were taken from four restoration treatments along a hydrological gradient. For each core, a sieved 25g subsample of soil was treated with 5 ml (1g of carbon source/13ml distilled water) of distilled water, glucose, and lignin solution. Respiration was measured using an open plastic vial filled with 5 ml of NaOH and incubated in the dark room at room temperature for 44 hours. Soil moisture and inorganic nitrogen was determined for each soil sample before and after incubation. We report difference in N availability in response to field treatments and N mineralization in response to C addition. Respiration rates were highest with glucose addition compared to lignin and no C addition, but there was no difference among the field treatments. Field plots with buckthorn mulch showed lower respiration rates than all other field treatments following water and lignin addition.

Title: How to grow a dinosaur: the histology and femoral ontogeny of the Middle Triassic dinosauriform *Asilisaurus kongwe* and implications for the growth of early dinosaurs [oral presentation]

Christopher Griffin, Cedarville University, and Field Museum of Natural History, Chicago, IL

The ontogeny of dinosaurs and their closest relatives is poorly understood due to the lack of ontogenetic series from the same species-level taxon. The large numbers of skeletal elements of the silesaurid *Asilisaurus kongwe* recently recovered from the Anisian of Tanzania provides an opportunity to closely examine the ontogenetic trajectory of the earliest known member of Ornithodira and one of the closest relatives to Dinosauria. We examined the histological tissues and the appearance of muscle scars over a series of different lengths of long bone elements.

Five femora, as well as three tibiae, a fibula, and a humerus were thin sectioned to examine osteological tissues. No annual lines of arrested growth (LAG) are present in any of the specimens, and it is likely that *A. kongwe* did not lay down LAGs, although all specimens thin sectioned may be <1 year old. The woven bone present in the cortex is similar to that of the earliest dinosaurs in all elements sectioned. We also observed muscle scar appearance and shape change throughout an ontogenetic series of femora (n = 26) of different lengths (73.8 to 177.2 mm). Femoral muscle scars develop at different ontogenetic stages, and we hypothesize that the majority of femora follow a similar developmental trajectory, e.g. the anterior trochanter and trochanteric shelf develop separately and roughly simultaneously, but fuse later in ontogeny in the most common developmental path. However, we did observe developmental polymorphism in the order of appearance and shape of muscle scars, e.g. there is high morphological variability in the fourth trochanter throughout most of the series, and although fusion of the trochanteric shelf and the anterior trochanter is only common in larger specimens, it is present in the second smallest specimen and conspicuously lacking in one of the largest specimens. The ontogenetic pattern of *Asilisaurus* femora provides a baseline for understanding growth in early dinosaurs. This developmental trajectory provides an alternate explanation for the robust/gracile dichotomy found in early dinosaurs (e.g. *Coelophysis*, *Syntarsus*) that commonly has been interpreted as sexual dimorphism. The shared femoral scar features found in *Asilisaurus* and early dinosaurs suggest this ontogenetic pathway may be pleisiomorphic for Dinosauria.

Title: Characterizing phenotypes in *Pseudomonas aeruginosa* mutants under different oxygen conditions [poster presentation]

Lisa Guan, University of California, Berkeley, and Chicago Botanic Garden, Glencoe, IL

Biofilms are ubiquitous in the natural world, inhabiting living and nonliving surfaces. They play a role in environmental cleanup, crop disease, and a wide variety of bodily infections. Bacteria that form biofilms are especially difficult to eradicate due to their sticky quality and increased antibiotic resistance. Biofilm communities also support bacteria resistance to environmental stress. *Pseudomonas aeruginosa*, an opportunistic bacteria, frequently infects cystic fibrosis patients and forms biofilms in the lungs. Here we show that *Pseudomonas aeruginosa* biofilm formation and colony morphology is influenced by redox-active phenazines. Phenazines act as electron acceptors and alter the intracellular redox state, affecting biofilm and colony phenotypes. The amount of oxygen availability dictates the degree of dependency on phenazine. The results show that in situations of oxidative stress, phenazines can support survival through the formation of biofilms.

Title: Phylogeny of the genus *Artocarpus* (Moraceae) using plastid markers [poster presentation]

Robert Harris III, Carleton College, and Chicago Botanic Garden, Glencoe, IL

The Moraceae family contains 37 genera and 1,050 species. These genera are distributed throughout tropical climates, particularly Southeast Asia and Oceania. *Artocarpus*- the third largest genus- is particularly interesting because it contains several economically important fruit bearing plants including breadfruit (*A. altilis*) and jackfruit (*A. heterophyllus*). Morphological classifications of the genus *Artocarpus* have shown different results than those of genetic

studies. Evolution of inflorescence structure, pollination syndromes, and other features have clouded the taxonomy of the genus at the subgenus level and below. We addressed the question: is the morphological classification supported by genetic data? We evaluated two plastid regions for 137 taxa representing a comprehensive sampling of *Artocarpus* as well as several closely related outgroups. We analyzed the data using Bayesian inference and compared the trees to previous work. Polytomies persisted in both trees and monophyly of traditional subgenera were not supported. The addition of more DNA regions may help resolve the trees and inform a revision of the genus.

Title: Comparing genetic diversity in *Cirsium pitcheri* populations [poster presentation]

Rosalba Herrera, Loyola University, and Chicago Botanic Garden, Glencoe, IL

Preserving the genetic diversity within threatened species requires understanding and maintaining the genetic structure. *Cirsium pitcheri*, which is commonly known as pitcher's thistle, is an endemic species of the Great Lakes that grows in sand dunes. The populations studied were collected from Wisconsin from 2005-2013. There are nine known populations of *Cirsium pitcheri* in Wisconsin. Previous genetic studies found that the two Wisconsin populations included had the highest and lowest genetic diversity, and highest and lowest inbreeding co-efficient. The objective of the study was to add additional samples to get a improved picture of the genetic health of *Cirsium pitcheri* in Wisconsin. Thirty-six samples were collected from the Sturgeon Bay Canal that were used and analyzed by seven different primers in order to measure the number of alleles and its' frequency between the samples. The average number of alleles per population for Sturgeon Bay Canal (avg. alleles 3.714) was closer to the Whitefish Dunes site (avg. alleles: 3.429) than Kohler Andrae (avg. alleles 1.286). The results also demonstrated the high level of genetic diversity (He: 0.414) in the Sturgeon Bay Canal site as well as Whitefish Dunes site (He: 0.463) compare to the Kohler Andrae site (He: 0.133). In Sturgeon Bay Canal site (F: 0.051) and Whitefish Dunes site (F: 0.061) have low inbreeding results compare to Kohler Andrae site (F: 0.274). Sturgeon Bay Canal and the Whitefish Dunes having similar results in the average number of alleles, genetic diversity, and inbreeding suggest that Kohler Andrae site is the anomaly in Wisconsin. A more detailed investigation may be required to determine why this population is genetically depauperate.

Title: A molecular phylogenetic survey of *Borrelia* from migratory birds: Are migratory birds potential vectors for Lyme disease? [oral presentation]

Sarah Kurtis, University of Chicago, and Field Museum of Natural History, Chicago, IL

Lyme disease is one of the most common vector-borne illnesses in North America. It is caused by the bacteria *Borrelia burgdorferi* and is transmitted by the blacklegged deer tick, *Ixodes scapularis*. Lyme disease's current spread and homogenization does not correspond to the historic barricaded gene flow of the blacklegged tick, suggesting that vertebrate vectors are potentially responsible for the expansion and increased prevalence of the disease (Humphrey et al., 2010). Possibly responsible vertebrate vectors include the white-footed mouse and other mammalian tick hosts. However, the dispersal abilities of these hosts are narrow compared to those of migratory birds, capable of flying twice across North America every year. North American birds, like their mammalian counterparts, are potential tick and Lyme disease bacteria hosts and can transmit the disease to uninfected ticks (Ginsberg et al., 2005). Our study

investigates whether migratory birds are important vectors in the expansion of Lyme disease in North America. To determine the prevalence of Lyme disease, we sampled around 500 migratory bird specimens from mainly Chicago, Illinois. Migratory birds sampled included mainly ground feeders such as *Catharus thrushes* along with a few species of sparrows and mimids. We collected and extracted the DNA from a skin and liver tissue from each specimen since we suspected Lyme disease bacteria to inhabit these tissues. We planned to screen all tissue samples for the bacteria via polymerase chain reaction amplification, purification, and sequencing of the *flaB* gene, a gene specific to *B. burgdorferi*. Currently, we are working on PCR optimization before completely screening all tissue samples for Lyme disease. Thus far, we have not discovered any tissues positive for Lyme disease, but this does not disprove our hypothesis. This result could be due to a faulty PCR protocol or that we have not screened a sufficient number of samples to make an informed conclusion. We will determine the percent of infected tissues and bird samples for Lyme disease and conduct a phylogenetic analysis of the relationship between *Borrelia* strain and migratory bird species. We can then determine whether migratory birds are important vectors for Lyme disease.

Title: Optimizing ecological niche models for *Cynometra bauhiniifolia* [poster presentation]

Matthew Lichty, Knox College, and Chicago Botanic Garden, Glencoe, IL

Correlative ecological niche models (ENM), also known as species distribution models, have found wide application in ecology and evolutionary biology. These techniques combine information regarding species presence (and sometime absence) at a location with environmental data to generate a map of the species's abiotically suitable habitat. However the resultant model's quality depends critically on the quality of input data. Here, we present preliminary results examining the effect of occurrence data quality on model output. We used two occurrence datasets to generate our models. One, downloaded from the Global Biodiversity Information Facility (GBIF) consisted of all records of the neotropical legume *Cynometra bauhiniifolia* contained in their database (n=82). The other dataset consisted only of occurrence records whose identifications we were able to verify and which we carefully georeferenced using multiple sources (n=39). Environmental data consisted of two sets of 19 bioclimatic variables downloaded from WorldClim; one corresponded to current climatic conditions while the other corresponded to conditions at the last glacial maximum. All models were generated using the program Maxent; settings were left at default with the exception of regularization multiplier, which was set to 2.0, and the number of replicates, which was set to 4. Comparisons between the two model sets indicated that the model generated using the GBIF dataset predicted a more extensive suitable area for the species in both time periods, totaling more than twice the area predicted as suitable by the smaller data set. In addition, there was significant variance in the area predicted as suitable between replicates within each modeling run. These findings suggest that researchers should carefully vet all occurrence data being used for modeling, especially for taxonomically confusing species. Further, different subsets of the same data can generate substantially different predictions. ENMs are a promising tool, but methodological refinement must keep pace with their implementation.

Title: Climate Change Adaptation Strategies for an Urban Environment [poster presentation]

Jessica Magolan, Elmhurst College and Field Museum, Chicago, IL

Lydia Nichols-Russell, University of Maryland and Field Museum, Chicago, IL
Muzit Gebretensae, Loyola University and Field Museum, Chicago, IL
Mary Szabo, Loyola University and Field Museum, Chicago, IL

Title: Digitizing the Field Museum's Oldest Collection [poster presentation]

Kaitlyn A. McCain, University of Chicago and Field Museum, Chicago, IL
Melissa C. Clark, Bryn Mawr College and Field Museum, Chicago, IL
Elizabeth M.K. Dybal, Arizona State University and Field Museum, Chicago, IL
Rebecca Friedlander, University of Vermont and Field Museum, Chicago, IL
Nathan Isaacs, University of Chicago Lab School and Field Museum, Chicago, IL

Title: Optimizing microsatellite markers in 4 species of *Oenothera*: *O. brachycarpa*, *O. hartwegii*, *O. serrulatus*, and *O. lavandulifolius* [poster presentation]

James Medina, Oberlin College, and Chicago Botanic Garden, Glencoe, IL

Neutral genetic diversity within plants is often used to track important evolutionary process including gene flow, species and population divergence, and evolutionary ancestry. By comparing the genetic diversity within and among five species of evening primrose (*Oenothera*), we can track the influence of major factors such as gene flow and diversification, to adaptive traits such as flower morphology, floral scent, flower color (white or yellow), pollinator community (bee or hawkmoth pollinated), and geographic distribution (narrow or widespread). In order to measure genetic diversity among these species, we need to first find marker regions that amplify consistently for each species. DNA from four species of *Oenothera* - *O. serrulatus* (suspected), *O. lavandulifolius*, *O. hartwegii*, and *O. brachycarpa* was extracted using the CTAB method for plant tissue. Using polymerase chain reactions (PCRs), 12 chloroplast microsatellite primers developed for *O. harringtonii* were tested on samples of each of these species. In addition, 55 chloroplast microsatellite primers developed for *O. biennis* were tested on both the four species listed above and on *O. harringtonii*. Seven of the 12 primers developed for *O. harringtonii* and 14 of the 55 primers developed for *O. biennis* successfully amplified in all five species. These primers will be useful for future studies investigating gene flow within and among populations of these species, studies of their genetic structure, parentage studies, and investigating the influence of various factors on genetic diversity.

Title: Now you setae, now you don't: Comparing millipede morphology up close and personal [oral presentation]

Madeleine Metz, Emory University, and Field Museum of Natural History, Chicago, IL

While millipedes (Arthropoda: Diplopoda) are critical for vegetative decomposition in forest nutrient cycling, they have not yet been extensively researched employing modern technologies such as scanning electron microscopy. This means their morphological structures are not well documented and the function of these structures is poorly understood, hindering the analysis of millipede ecology, evolutionary history, and basic biology. This project focused on creating a morphological atlas using scanning electron microscopy to gain insight into millipede phylogeny, biodiversity, and ecological niches. Male and female specimens from two orders and four families were dissected using a light microscope; samples were cleaned, dried, and

mounted, then imaged using a scanning electron microscope. These images were compared for shared and variable morphological features with the goal to identify apomorphic characters indicating the monophyly of various taxa, e.g., for the order, family, or genus. Some of the more complex structures in millipedes are the antennae, the gnathochilarium (a lower-lip type structure), the mandibles, and the copulatory organs. These differences are caused by several evolutionary processes: the variations in copulatory organs have evolved due to sexual selection, while the mandibles, the gnathochilarium, and the antennae are altered by natural selection from different habitats and food sources. We found mandible modifications when comparing an arboreal and a terrestrial species in the same family, indicating that this change is an individual adaptation to a disparate habitat. However, we also found apomorphic differences between orders—all members of the Spirobolida sampled so far possess a large separate tooth at the edge of the pectinate lamella. These are only a few of the connections we have found, but there is a clear need for greater sampling across orders and families. Without this information, it will be impossible to expand on arthropod evolution or understand millipedes' role in different ecosystems.

Title: Conservation genetics of birds in Africa's Albertine Rift [poster presentation]

Daniel Montgomery, Indiana State University and Field Museum of Natural History, Chicago, IL

Title: Nutrient availability of white lady slipper orchids (*Cypripedium candidum*) affects presence of mycorrhizal partners [poster presentation]

Geralde Powell, Wellesley College, and Chicago Botanic Garden, Glencoe, IL

Over the past century, research has shown an important relationship between orchids and mycorrhizal fungi. This relationship is important for supplying the nutrient insufficient “dust seeds” with carbon and other nutrients for germination. As photosynthetic plants become adults, this relationship changes. Plants are no longer totally nutrient dependent on their fungi, but often rely on the fungi for limiting nutrients including phosphorus, nitrogen, and carbon. We studied the white lady's slipper orchid, *Cypripedium candidum*. *C. candidum* is a terrestrial orchid found mainly in wet prairies, bogs, and fens in temperate regions of the Northern Hemisphere. Our study used soil and root samples collected across four sites in the Chicago Region. We performed microscopies of root samples to examine evidence of endomycorrhizal colonization within root cortical cells. We completed soil nutrient analyses using a LECO dry combustion system, KCl extractions, and concentration readings using an Epoch spectrophotometer. Using statistical analyses, we compared colonization rates and nutrient abundance among sites. Although total colonization rate was low, we found that the most nutrient rich habitats had the highest rates of colonization. We did not record colonies that appeared to be more than 75% digested. Our results show how soil nutrients affect the presence of mycorrhizal colonization. These results can be used to improve cultivation and conservation methods for this species.

Title: Describing a New Cryptodont Dicynodont from the Permian of Tanzania [oral presentation]

Ben Otoo, Amherst College, and Field Museum of Natural History, Chicago, IL

Dicynodonts (Therapsida, Anomodontia) are a group of non-mammalian synapsids that lived during the Permian and Triassic periods of Earth history (roughly 270-210 million years ago.)

They were the first widely successful group of terrestrial herbivores, ranging from marmot-sized to hippo-sized, and were key parts of their ecosystems. A thorough understanding of dicynodont diversity and phylogeny is crucial to understanding terrestrial faunas and ecosystems during the Permo-Triassic interval, which included the largest mass extinction in the history of life at the end of the Permian, 252 million years ago. Here we present a new dicynodont from the early Late Permian (Wuchiapingian Stage, about 257-255 million years ago) of the Ruhuhu Basin of southwestern Tanzania, *Batagonda trilovops*, gen. et sp. nov. We described the morphology of the holotype specimen, NMT RB156, noting its mixture of characteristics. For example, the morphology of the temporal bar and shape of the snout resemble those of dicynodonts of the clade Cryptodontia; however, the morphology of the secondary palate and the preserved portions of the jaw symphysis are unique. Of particular interest is the fact that the holotype is a juvenile. We included the specimen in a recent phylogenetic data matrix for dicynodonts, and analysis of this dataset recovered *Batagonda* as the most basal member of the large clade Bidentalia. In addition, we also ran several experiments in recoding phylogenetic characters to gain more insight into this unexpected placement. These experiments show that certain alternative placements of *Batagonda* on the cladogram are only slightly longer, and that the placement of the species has important implications for the optimization of particular characters. This new species represents a rarely sampled group of dicynodonts from a time and locality that have just recently become subject to sustained, rigorous study. Aside from adding to the diversity of the Permian Ruhuhu fauna, *Batagonda* has interesting implications for dicynodont evolution and biogeography.

Title: The Bats of Kenya: assessing the species limits of cryptic species [oral presentation]

Kyle Reid, Olive Harvey College, and Field Museum of Natural History, Chicago, IL

The diversity of mammal fauna in east Africa has captured the interest of biologists for centuries. The world-famous “Big Five” grab the attention of people far and wide. However, hidden in plain sight is a group of animals which offer a treasure trove of evolutionary, ecological, and economic knowledge -- the bat! Bats represent a quarter of Kenya’s >400 mammal species. As one of the few mammalian orders capable of echolocation and the only one capable of true flight, bats quickly specialize and separate to adapt to their environment. Only recently have scientist begun to realize the economic and ecological benefits of bat species. Bats contribute to a healthy ecosystem via pollination of flowers, seed dispersal and consuming herbivorous insects. Consumption of insects in Kenya, where agriculture is subsistence based, may be one of their most important contributions to humanity. Our study gathered and tested morphometric information within the genus *Epomorphorus*. Using 27 variables and the *Epomorphorus* collection at the Field Museum, we performed univariate and multivariate analysis to discover which measurements were of greatest influence in distinguishing two species. After gathering this information, we compared it with the current species key to confirm or deny the existence of cryptic species. We found that when distinguishing between species with skull morphometrics, skull length and braincase breadth have the biggest impact. However, *Epomorphorus wahlbergi* and *Epomorphorus haldermanni* continue to be separated by non-morphometric features. This project will evolve. With the continued addition of data to the project, we expect to gain further insight into this misunderstood order. Access to new habitats will greatly increase our capability to accurately

determine the many forms of the Chiroptera.

Title: Congruence between molecular phylogeny and phenotype features of the lichen genus *Pseudocyphellaria* in Hawaii: does morphology predict monophyletic species? [poster presentation]

Brendon Reidy, Northeastern Illinois University, and Field Museum of Natural History, Chicago, IL

Hawaii is home to some of the most striking evolutionary radiations of plants on earth. Besides 1386 species of vascular plants, the archipelago also hosts 880 species of lichens, of which 15%-25% are thought to be endemic. At present, there are few modern taxonomic or comprehensive molecular studies of Hawaiian lichens, and as such most species classifications have been conducted using morphological characteristics of known non-endemic species. We focused on the genus *Pseudocyphellaria* in order to see if observed morphological traits agreed with listed species, and if not, whether observed differences could predict a phylogenetic classification. We collected *Pseudocyphellaria* specimens of five distinct morphospecies: *P. intricata*, *P. argyracea*, *P. aurata*, *P. pickeringii*, and *P. crocata*. All specimens underwent DNA sequencing to determine whether the traditional morphological classification was consistent with molecular analysis. Once sequenced, the specimens were scanned and grouped according to their morphological characteristics by the first author as part of an internship project, with no knowledge of the molecular results. The groups were compared with both the phylogenetic tree and the traditional classification to determine accuracy in species classification, and to analyze if morphological differences between Hawaiian specimens and those used for traditional classifications could be used to provide a more precise species concept. The molecular data revised the species concept of Hawaiian *Pseudocyphellaria*. The five reported and collected, supposedly widespread taxa represent eight species, only one identical with a previously listed name and four new and endemic. The revised species concept is congruent with morphology, evidenced by the fact that the first author, an inexperienced student, could observe morphological differences that predicted the correct species with nearly 70% accuracy, whereas the traditional concept of listed taxa, established by the world authority in the genus, agrees with the correct species only 60%.

Title: Seeding restorations: Evaluating seed viability to improve restoration outcomes [oral presentation]

Jessica Riebkes, Central College, and Chicago Botanic Garden, Glencoe, IL

Tallgrass prairie restorations are occurring across the Great Plains in an effort to re-establish this once dominant landscape. Restored prairies often have fewer species than remnant prairies, so improving species establishment is essential to improving restoration outcomes. A fundamental part of establishing species is ensuring that the seed used is viable and matched to the conditions of the restoration site. Unfortunately, there is no universally accepted method to test seed viability prior to use in a restoration. To address this, we utilized three different viability testing methods (x-ray, tetrazolium, germination) on four prairie forb species (*Eryngium yuccifolium*, *Lespedeza capitata*, *Liatris aspera*, *Ratibida columnifera*) to measure differences in viability calculations. Two accessions of each species were used, allowing us to compare seed collected in the same year from two different states. Additionally, we tested whether pretreatment could improve germination outcomes. Results showed that viability estimates did not significantly differ by testing method for 3 of our 4 study species, with the

exception being *E. yuccifolium* ($p < 0.0001$). In this species, x-ray yielded significantly greater viability estimates than tetrazolium tests ($p = 0.0123$) or germination tests ($p = 0.0000$). Viability estimates differed significantly between accessions in three species (*E. yuccifolium*, *L. capitata*, *L. aspera*) ($p < 0.0001$). Pretreatment yielded significantly higher viability estimates in *L. capitata* ($P < 0.0001$) and in one accession of *L. aspera* ($p = 0.0011$) and *E. yuccifolium* ($p = 0.0004$) in the germination study. We suspect that *E. yuccifolium* may have yielded different results for each viability testing method because its pretreatment was not enough to break dormancy, among other factors. These results confirm that restoration practitioners should calculate seed requirements based on viability measures on a per species basis. For many species, the method used to calculate viability can be determined by available equipment and expertise, but for species with unknown dormancy requirements or those that may lose viability when stored, multiple methods may be needed.

Title: Bizarre biology: morphogenesis of the freshwater bryozoan *Plumatella vaihiria* (Phylactolaemata) [oral presentation]

Andrea Rummel, University of Chicago, and Field Museum of Natural History, Chicago, IL

Bryozoans are a diverse phylum of aquatic small colonial invertebrates whose development, phylogenetic relationships, and reproductive biology are understudied and poorly understood compared to most other metazoan taxa. Within the same genetic individual - the colony - structural individuals called zooids are budded asexually. As zooids in some bryozoan groups are highly polymorphic, the study of these animals could shed light on the origin and evolution of polymorphism and functional specialization, the unique life histories of bryozoans, and the factors influencing colony growth and form. Morphogenesis in bryozoans is complex, potentially involving: embryonic development of a larva, catastrophic metamorphosis, iterative budding, and an asexually produced diapausal statoblast that subsequently germinates. Gene expression is a powerful tool for exploring the implications of these broad questions; we aim to construct a cDNA library for a species of phylactolaemate bryozoan, *Plumatella vaihiria*, to complement an existing library for a cheilostome bryozoan, *Bugula neritina*. With *B. neritina* and then *P. vaihiria*, we plan to investigate the expression of regulatory genes in bryozoans, and their role in patterning body plans in individual zooids and heterozooids, and colony morphology. In addition to this molecular work, we intend to collect a series of images and histological sections detailing the morphogenesis, budding, and sexual reproduction of *P. vaihiria* as a model phylactolaemate bryozoan. Although the project is still in its initial stages, images of statoblast germination and ancestrula formation have been gathered, and techniques for rearing phylactolaemate bryozoans in the laboratory are being perfected.

Title: Fitness and heritability in *Echinacea angustifolia* and *E. pallida* hybrids [poster presentation]

Marie Schaedel, Carleton College, and Chicago Botanic Garden, Glencoe, IL

Native populations in fragmented tallgrass prairie experience reduced levels of fitness owing to a loss of genetic diversity and mean heterozygosity. In western Minnesota, state and federal policies target public land for prairie reconstruction to improve habitat for game and waterfowl. Some restoration projects translocate nonnative species that swamp extant populations through the introgression of genes via intraspecific hybridization. This study estimates variation in fitness and narrow-sense heritability in the 1 year-old progeny resulting from experimental

crosses between the native purple coneflower *Echinacea angustifolia* and an introduced species, *E. pallida*. Research was conducted at a state wildlife refuge in which *E. pallida* was planted adjacent to an existing population of *E. angustifolia*. I measured morphological traits (height, leaf number, trichome density, leaf width and length) of the progeny resulting from all possible cross combinations of the two species planted in an experimental plot. Survival rates ranged from 0.86 (± 0.04) for *angustifolia x angustifolia* progeny, to 0.97 (± 0.02) for *pallida x angustifolia* progeny. After accounting for mortality using an aster analysis, the *pallida x angustifolia* cross-type had the greatest leaf number (2.06 ± 0.14). *Pallida x pallida* offspring possessed the greatest trichome density, with the hybrid progeny representing an intermediate between the mean parental values. Of the traits under study, trichome density was the most heritable ($h^2=0.92$ for *pal x ang*), and height was moderately heritable ($h^2=0.27$ for *pal x ang*). The observed differences in the fitness and genetic variance of the juvenile hybrids foretell a dramatic impact on the population dynamics and evolution of native *E. angustifolia* communities in which *E. pallida* has become established.

Title: Does the attempt to restore golden Indian paintbrush to a former habitat or raising the species in isolation have an effect on genetic diversity, and if so to what extent? [oral presentation]
Alexander Shaffer, Northwestern University, and Chicago Botanical Garden, Glencoe, IL

A host of genetic factors should be taken into account when attempting reintroduction or restoration projects. Such factors include the adaptive significance of a seed source, genetic similarity of seed source to former inhabitant (if available), and genetic diversity of seed source. Ten microsatellite primer pairs were tested on *Castilleja levisecta*. The microsatellite primers have been tested on other *Castilleja* species with varying results. The ten markers were chosen after showing successful amplification and presence on gel electrophoresis (1.5% agarose). Markers were tested on 5 populations comprised of 32 individuals each; 3 wild populations in Washington, 1 nursery population, and 1 restoration population in Washington. The nursery population is derived from a mix of 4 wild populations (three that are tested in this study), and the restoration population is grown from the seed production bed at said nursery. The amplified PCR products were tagged with a fluorescent M13 dye and were run on a Beckman Coulter CEQ 8000 Genetic Analysis System in which the number of base pairs for each amplified product is measured. Preliminary results show an increase in allelic richness (also called genetic diversity) between the wild populations compared to both the restoration population and the nursery population. This phenomenon is most likely due to the mixing of seed sources in the nursery; combining all of the wild sources genomes into one population. It is still difficult to say whether these plants are more “fit”, but several studies have shown a high positive correlation between genetic diversity and fitness.

Title: Rooting PhyLoTA: A case study in taxonomically rooting phylogenetic trees [oral presentation]

Joshua Stevens-Stein, University of Chicago, and Field Museum of Natural History, Chicago, IL

The Open Tree of Life project seeks to produce an online, open, and comprehensive phylogenetic tree of the 1.8 million known species, an invaluable resource to the scientific community and to lay education. Two of the difficulties facing the project, however, are the compilation of all published phylogenetic data and the incorporation of those results in a unified

format. One of the larger and previously unmined and unrefined databases of such phylogenetic data is the PhyLoTA Database, containing 22,165 eukaryotic trees produced by all-against-all BLAST searches and sequence clustering algorithms. Unfortunately, the nature of the analyses (generating trees by clustering with no outgroup) provided only unrooted trees. The focus of PhyLoTA analyses to the NCBI taxonomy and a more general focus on phylogeny in biological classification in recent decades suggested that the NCBI taxonomy could prove informative in rooting these trees. Using the Python packages Ivy and Graph-Tool, we examined each PhyLoTa tree in graph format and determined whether the taxa concerned, from most to least inclusive, formed clades within the larger tree, extracting and saving any such subtrees, the root being the branch connecting this subtree to the rest of the tree. Of the original 22,165 trees with 1,420,989 leaves, 14,338 of these trees yielded 24,371 subtrees with 713,260 leaves. These subtrees are due for inclusion in the Open tree of Life. The code used will shortly be public access, for use in similar endeavors. Though analysis on the subtrees produced has thus far been cursory, it will be telling about the nature of the evolving relationship between taxonomy and phylogeny, and particularly the degree of correspondence between the two over the entire tree of life.

Title: Corrosion Casts: A Novel Application of Pu4ii Resin for Visualizing Eggshell Pore Morphology [poster presentation]

Mark Swanson, Illinois Wesleyan University and Field Museum of Natural History, Chicago, IL

Jason Murphy, Illinois Wesleyan University

William Jaeckle, Illinois Wesleyan University

R. Given Harper, Illinois Wesleyan University

Title: Microsatellite patterns in two *Castilleja* subspecies *affinis* and *neglecta* [oral presentation]

Hosin West, University of New Haven, and Chicago Botanic Garden, Glencoe, IL

The focus of this project is on the genetic variation within the subpopulation of *Castilleja affinis* ssp *neglecta*, a federally listed endangered species. Leaf samples were obtained from four of the seven known sites. Two of the sites were open space areas now used as parks; American Canyon Park and Middle Ridge in Tiburon Peninsula. The other two areas were land management areas; Nicasio Ridge managed by National Park service and Golden Gate National Recreation Area and Paintbrush Hill managed by Creekside Center for earth observation. The genomic DNA was extracted from silica dried leaves using a modified CTAB DNA extraction technique from (Doyle and Doyle, 1987). Samples were screened with microsatellite primers developed for *Castilleja sessiliflora* in Fant et al (2013). Gel electrophoresis was used to determine which markers worked before the samples were run on a Beckman Coulter 8000 to determine fragment size and degree of polymorphism. Over thirty primers were screened and nine were used for fragment analysis. The primers showed genetic variation in the fragment sizes across the species. The results were difficult to interpret because this species is hexaploid with an n=36. This consequently gave six peaks per which made data analysis complex.

Title: Voices from the Calumet [video presentation]

Clair Wild, University of Chicago and Field Museum, Chicago, IL

Emily Jan, Northwestern University and Field Museum, Chicago, IL

Title: GIS-based spatial analysis of rare plant populations on gravel hill prairies: Habitat suitability modeling [oral presentation]

Christopher Wright, University of Washington, Bothell, and Chicago Botanic Garden, Glencoe, IL

This GIS-based spatial analysis of rare gravel hill prairie plant species was developed to characterize the habitat of known populations and identify potential suitable habitat. Habitat loss is the leading cause of species extinction, and the identification of suitable habitat for rare plant species may provide the opportunity for the introduction of new populations and may also be a tool to assist land managers in determining management strategies. Utilizing information collected by the Plants of Concern monitoring program, data related to two gravel hill prairie plant species, *Cirsium hillii* and *Asclepias lanuginosa*, was used to create Multi Criteria Evaluation models. By extracting data relating to soil attributes, land cover, hydrology, and distance metrics, gravel hill prairie habitat was classified and models were generated to identify suitable habitat based on variable weighting structures. Using the greater Chicago area as the study area extent, six models were produced identifying varying amounts of highly suitable ($\geq 90\%$) habitat. High suitability areas ranged from 5.6 to 117 km². Thirteen natural areas with occurrences of one or both of these species were analyzed and suitability scores compared. Suitability scores ranging from 20-100% were reported from the six models. The modeling resulted in comparable suitability scores for each natural area regardless of the model chosen. Preliminary population analysis was initiated comparing stem densities between the sites characterized as most and least suitable. Future analysis can include metrics of population health and spatial extent in order to better understand the relationship between site suitability and population dynamics.

Title: Organic matter stabilization in soil aggregates during grassland restoration [oral presentation]

Jenifer Yost, Lake Forest College, and Chicago Botanic Garden, Glencoe, IL

As urban development continues to replace or transform native grasslands, restoration has become increasingly critical for maintaining soil organic matter accrual. This study explores whether urban soils can be restored to C-accruing grasslands. Soil cores were taken from 15 different prairies under five types of management around the Chicagoland Area. The soils were then wet-sieved into micro- (53 – 250 μm) and macro- (> 250 μm) aggregate size classes. Soil aggregate C content increased significantly between early- (< 5 years) and later-stage (> 10 years) model restorations (those resembling pristine prairies), and aggregate C levels in model restorations approached those in prairie remnants. Stable isotope $\delta^{13}\text{C}$ signatures indicated that C₃ forbs were increasingly significant contributors to micro- and macroaggregate C accrual in restored grasslands and macroaggregates in pristine prairies whereas microaggregates in the pristine prairie showed $\delta^{13}\text{C}$ signatures typical of C₄ plants. Lignin phenol analysis by TMAH thermochemolysis GC-MS showed differences in lignin source and degradation state between macro- and micro-aggregates and also among different management types. Our findings suggest that: C accrual occurs with urban grassland restoration; markers of restoration success and perception of a high quality restoration are reflected in C accrual; and management type rather than simply the duration of management are important in promoting C accrual.

2013 FMNH REU Projects

2013 FMNH REU participants, projects and college/university

REU participant: *Patricia Brandt*, pbrandt@uchicago.edu, junior, University of Chicago
Project: Diversity of tropical lichens
Advisor: Dr. Thorsten Lumbsch (Botany, curator)

REU participant: *Andrew Burchill*, andrewburchill@uchicago.edu, junior, University of Chicago
Project: The evolution of nomadic swarm raiders: Determining the genetic component of army ant castes
Advisor: Dr. Corrie S. Moreau (Zoology/Insects, curator) and Max Winston (graduate student)

REU participant: *Christopher Griffin*, chrisgriffin@cedarville.edu, junior, Cedarville University
Project: How to Grow a Dinosaur
Advisor: Dr. Kenneth Angielczyk (Geology, curator) and Dr. Sterling J. Nesbitt (postdoctoral fellow)

REU participant: *Madeleine Metz*, mmmetz@emory.edu, sophomore, Emory University
Project: One-thousand legs: up close and personal
Advisor: Dr. P. Sierwald (Zoology/Insects, curator)

REU participant: *Ben Otoo*, botoo14@amherst.edu, junior, Amherst College
Project: Describing a New Cryptodont Dicynodont from the Permian of Tanzania
Advisor: Dr. Kenneth Angielczyk (Geology, curator)

REU participant: *Joshua Stevens-Stein*, jstevensstein@gmail.com, sophomore, University of Chicago
Project: The Open Tree of Life: toward a global synthesis of phylogenetic knowledge
Advisor: Dr. Richard Ree (Botany, curator)

REU participant: *Kyle Reid*, Kreid15@student.ccc.edu, sophomore, Olive Harvey College
Project: The Bats of Kenya: assessing the species limits of cryptic species
Advisor: Dr. Bruce Patterson (Zoology/Mammals, curator) and Dr. Paul Webala

REU participant: *Andrea Rummel*, arummel25@gmail.com, junior, University of Chicago
Project: Colonial Animals: One genetic individual and many bodies
Advisor: Dr. Scott Lidgard (Geology, curator)



REU Site: Access to Global Biodiversity Studies for Undergraduates (supported by the National Science Foundation, DBI: 08-49958: PIs Petra Sierwald and Peter Makovicky; DBI 11-56594: PIs. Petra Sierwald and Kenneth Angielczyk, see at: <http://fieldmuseum.org/about/c-r-research-experiences-undergraduates-reu>)

2013 FMNH Affiliated Summer High School, undergraduate and graduate Interns

High School Intern: *William Buchman*, willbuchman@gmail.com, New Trier High School
Advisor: William Simpson (Geology, collections manager)

Undergraduate intern: *Melissa C. Clark*, Bryn Mawr College
Advisor: Dr. Philipp Heck (Geology, curator)

Undergraduate Intern: *Liza Connolly*, University of Chicago
Advisor: Paul Mayer (Geology, collections manager)

Undergraduate Intern: *Charlie D'lavoy*, Northeastern Illinois University
Advisors: Dr. Matt von Konrat (Botany, collections manager and adjunct curator) and Dr. Thomas Campbell (Botany, Field Museum and Northeastern Illinois University)

Intern *Camila Duarte* (kmicaduarte@gmail.com), Universidade Federal de Santa Maria (Brazil)
Project: Microsatellite analysis of Rufous-capped *Eleania*, a bird endemic to the white sand forests of Amazonia
Advisor: Dr. John Bates (Zoology/Birds, curator)

Undergraduate intern: *Clarisse de Figueiredo* (cmendese@bowdoin.edu).
Project: Microsatellite analysis of Rufous-capped *Eleania*, a bird endemic to the white sand forests of Amazonia
Advisor: Dr. John Bates (Zoology/Birds, curator)

Undergraduate intern: *Elizabeth M.K. Dybal*, Arizona State University
Advisor: Dr. Philipp Heck (Geology, curator)

Undergraduate intern: *Rebecca Friedlander*, University of Vermont
Advisor: Dr. Philipp Heck (Geology, curator)

Undergraduate intern: *Muzit Gebretensae*, Loyola University
Advisor: Dr. Abigail Derby Lewis (Science Action, conservation ecologist)

Intern: *Charles Griggs* (cgriggs@middlebury.edu)

Undergraduate Research: Field Museum of Natural History: : Projects and Advisors

Advisor: Dr. Corrie Moreau (Zoology/Insects, curator)

Intern: *Nathan Isaacs*, University of Chicago Lab School

Advisor: Dr. Philipp Heck (Geology, curator)

Undergraduate Intern: *Nicole Karpus*, University of Illinois at Chicago

Advisor: Paul Mayer (Geology, collections manager)

Undergraduate Intern: *Emily Jan*, Northwestern University

Advisor: Alison Paul (Science Action, urban conservation educator)

Undergraduate intern: *Sarah Kurtis* (smkurtis@uchicago.edu), sophomore, University of Chicago

Project: A molecular phylogenetic survey of *Borrelia* from migratory birds: Are migratory birds potential vectors for Lyme disease?

Advisor: Dr. Jason Weckstein (Zoology/Birds), funded through an REU supplement to NSF DEB-1120054 to J. Weckstein

Undergraduate intern: *Alex Layng*, Northwestern University

Advisor: Paul Mayer (Geology, collections manager)

Undergraduate intern: *Jessica Magolan*, Elmhurst College

Advisor: Dr. Abigail Derby Lewis (Science Action, conservation ecologist)

Undergraduate intern: *Kaitlyn McCain*, University of Chicago

Advisor: Dr. Philipp Heck (Geology, curator)

Undergraduate intern: *Jessica Mohlman*, jmohlman@fieldmuseum.org, Northland College

Advisors: Rebecca Collins, Alan Resetar (Zoology/Herpetology)

Undergraduate intern: *Daniel Montgomery*, Indiana State University

Advisors: Dr. John Bates (Zoology/Birds, curator) and Josh Engel (Zoology/Birds, research assistant)

Undergraduate intern: *Lydia Nichols-Russell*, University of Maryland

Advisor: Dr. Abigail Derby Lewis (Science Action, conservation ecologist)

Undergraduate Intern: *Brendon Reidy*, brendon.reidy@gmail.com, Northeastern Illinois University

Project: Congruence between molecular phylogeny and phenotype features of the lichen genus *Pseudocyphellaria* in Hawaii: does morphology predict monophyletic species?

Undergraduate Research: Field Museum of Natural History: : Projects and Advisors

Advisors: Robert Lücking (Botany, collections manager and adjunct curator) and Bibiana Moncada (Universidad Distrital Colombia)

Undergraduate Intern: *Jonathan Scheffel*, Harold Washington College

Advisors: Dr. Matt von Konrat (Botany, collections manager and adjunct curator) and Dr. Thomas Campbell (Botany, Field Museum and Northeastern Illinois University)

Intern: *Lynika Strozier* (lstrozier@fieldmuseum.org)

Advisor: Dr. Corrie Moreau (Zoology/Insects, curator)

Undergraduate intern: *Mark Swanson* (mswanso2@iwu.edu), Wesleyan University

Project: Microsatellite study of Midwestern Barred Owls

Advisor: Dr. John Bates (Zoology/Birds, curator)

Undergraduate intern: *Mary Szabo*, Loyola University

Advisor: Dr. Abigail Derby Lewis (Science Action, conservation ecologist)

Undergraduate Intern: *Ariel Wagner*, DePaul University

Advisors: Dr. Matt von Konrat (Botany, collections manager and adjunct curator) and Dr. Thomas Campbell (Botany, Field Museum and Northeastern Illinois University)

Undergraduate Intern: *Claire Wild*, University of Chicago

Advisor: Alison Paul (Science Action, urban conservation educator)

FMNH 2013 Phylogenetic workshop

Instructors: Dr. David Clarke (dclarke@fieldmuseum.org)

Ben Winger (bwinger@fieldmuseum.org)



CHICAGO BOTANIC GARDEN

2013 CBG REU participants, projects and college/university

REU participant: *Mariah Allen*, (allenma@mx.lakeforest.edu), senior, Lake Forest College
Project: Decomposition and fungal diversity in restored tallgrass prairies
Advisor: Dr. Louise Egerton-Warburton and Lauren Umek

REU participant: *Kevin Amses*, (kra20@humboldt.edu), senior, Humboldt State University
Project: Which species of tropical canopy tree species access the water source provided by underground caves on the Yucatan Peninsula and are their natural fungal symbionts present in these portions of the root system?
Advisor: Dr. Louise Egerton-Warburton and Benjamin Morgan

REU participant: *Dayvis Blasini*, (d-blasini@neiu.edu), senior, Northeastern Illinois University
Project: Effects of the introduction of non-native *Echinacea pallida* on the pollination of *Echinacea angustifolia*
Advisor: Dr. Stuart Wagenius

REU participant: *Allison Buiser*, (allisonbuiser@gmail.com), freshman, Knox College
Project: The role of fungi in soil C-sequestration
Advisors: Dr. Neal Blair, Dr. Louise Egerton-Warburton and Dr. Kathryn Schreiner

REU participant: *Lisa Guan*, (lisaguan@berkeley.edu), senior, University of California, Berkeley
Project: Characterizing phenotypes in *Pseudomonas aeruginosa* mutants under different oxygen conditions
Advisors: Dr. Yunho Lee and Dr. Yun Wang

REU participant: *Robert Harris III*, (harrisr@carleton.edu), freshman, Carleton College
Project: Phylogeny of the genus *Artocarpus* (Moraceae) using plastid markers
Advisor: Dr. Evelyn Williams and Dr. Nyree Zerega

REU participant: *Rosalba Herrera*, (rherrera@luc.edu), freshman, Loyola University
Project: Comparing genetic diversity in *Cirsium pitcheri* populations
Advisor: Dr. Jeremie Fant

Undergraduate Research: Chicago Botanic Garden: : Projects and Advisors

REU participant: *Matthew Lichty*, (mlichty@knox.edu), junior, Knox College
Project: Optimizing ecological niche models for *Cynometra bauhiniifolia*
Advisors: Dr. Patrick Herendeen and Aleksandar Radosavljevic

REU participant: *Geralle Powell*, (gpowell@wellesley.edu), sophomore, Wellesley College
Project: Nutrient availability of white lady slipper orchids (*Cypripedium candidum*) affects presence of mycorrhizal partners
Advisors: Dr. Pati Vitt and Anne Nies

REU participant: *Jessica Riebkes*, (riebkesj1@central.edu), senior, Central College
Project: Seeding restorations: Evaluating seed viability to improve restoration outcomes
Advisors: Dr. Andrea Kramer and Rebecca Barak

REU participant: *Marie Schaedel*, (schaedem@carleton.edu), junior, Carleton College
Project: Modeling fitness and heritability in hybrid offspring of *E. pallida* and *E. angustifolia*
Advisor: Dr. Stuart Wagenius

REU participant: *Hosin West*, (HWest1@unh.newhaven.edu), senior, University of New Haven
Project: Microsatellite patterns in two *Castilleja* subspecies *affinis* and *neglecta*
Advisors: Dr. Jeremie Fant, Dr. Krissa Skogen and Laney Widener

REU participant: *Christopher Wright*, (wright.christop@gmail.com), senior, University of Washington-Bothell
Project: GIS-based spatial analysis of rare plant populations on gravel hill prairies: Habitat suitability modeling
Advisors: Rachel Goad, Susanne Masi and Emily Yates

2013 CBG Affiliated Summer High School and Undergraduate interns

Intern: *Ben Girgenti*, (btgirgenti@gmail.com), sophomore, Brown University
Project: What are the effects of mulching on soil's microbial community in restored habitats?
Advisors: Dr. Louise Egerton-Warburton and Lauren Umek

Intern: *James Medina*, (jmmedina@oberlin.edu), junior, Oberlin College
Project: Optimizing microsatellite markers in 4 species of *Oenothera*: *O. brachycarpa*, *O. hartwegii*, *O. serrulatus*, and *O. lavandulifolius*
Advisors: Dr. Jeremie Fant and Dr. Krissa Skogen

Intern: *Alexander Shaffer*, (alexandershaffer2015@u.northwestern.edu), junior, Northwestern University

Undergraduate Research: Chicago Botanic Garden: : Projects and Advisors

Project: Does the attempt to restore golden Indian paintbrush to a former habitat or raising the species in isolation have an effect on genetic diversity, and if so to what extent?

Advisor: Dr. Jeremie Fant

Intern: *Jenifer Yost*, (yostjl@lakeforest.edu), senior, Lake Forest College

Project: Organic matter stabilization in soil aggregates during grassland restoration

Advisors: Dr. Louise Egerton-Warburton and Lauren Umek



REU Site: Plant Biology & Conservation Research Experiences for Undergraduates
- From Genes to Ecosystems. (Supported by NSF awards DBI-0353752, DBI-0648972, and DBI-1062675) - See at:
<http://www.cbgreu.org/#sthash.XSNARY7C.dpuf>



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