



3rd Annual
St. Louis Ecology, Evolution, and Conservation (SLEEC)
Retreat
Saint Louis Zoo Living World

September 28, 2013
Schedule (Asterisks indicate Presenters)

0800 **Bagels and coffee**; signing in; setting up posters and talks

First morning session:

0900 Welcome and Introduction: Bob Ricklefs and Bob Marquis (UMSL)

0905 Greetings from the Saint Louis Zoo: Louise Bradshaw

0915 Jason Knouft* and Huicheng Chien (SLU): The impacts of climate change on the hydrology and biodiversity of the Mobile River watershed

0930 Karen E. DeMatteo*, Miguel A. Rinas, Carina F. Arguelles, Mario S. Di Bitetti, Barbara Davenport, Patricia G. Parker, Lori S. Eggert (WashU): Using noninvasive techniques to expand carnivore conservation in Misiones, Argentina

0945 Stephen Blake*, Fredy Cabrera, Sharon Deem, Susan Flowers, James Gibbs, Jamie Palmer, Wacho Tapia and Martin Wikelski (WashU): Tracking turtles from the volcanoes of Galapagos to Tyson and downtown St. Louis

1000 Kimberly A. Medley*, Mari K. Reeves, Alfred E. Pinkney, Pieter T.J. Johnson (WashU): Amphibian abnormalities: nation-wide patterns and environmental drivers

1015 Adrian Cerezo (STL Zoo): Biodiversity conservation and environmentalism in the era of post-equilibrium ecology

1030 **Coffee and posters**

Second morning session:

1100 Nathan Muchhala* (UMSL), Sönke Johnsen, and Stacey Dewitt Smith. Competition for hummingbird pollination and the evolution of flower color diversity in Andean Solanaceae

1115 Zong-Xin Ren* and Peter Bernhardt (SLU): Do Generalist Pollination and Self-Incompatibility in Yellow Star Grass (*Hypoxis hirsuta*; Hypoxidaceae) Correlate with Charles Darwin's Predictions About the Evolution of Orchid Flowers?"

1130 Christine Edwards (MOBOT): Use of DNA metabarcoding to quantify the diversity of plant species utilized by a pollinator

1145 Monica Carlsen (MOBOT): Contrasting patterns of morphological diversity and climatic preferences in the genus *Anthurium* (Araceae)

1200 Peter Stevens (UMSL): What do species of flowering plants actually DO (other than looking pretty – most of them)? Rethinking aspects of biosphere change and co-evolution

1215 Lunch break and posters

Five tours of Zoo facilities: TBA (Signup at beginning of Retreat)

Afternoon session

1400 Katie Williams* and Justin Fay (WashU): Evolution of ecological dominance of yeast

1415 Michael Hughes (UMSL): Orchestrating transcriptional rhythms in mammals and flies

1430 Suzanne Austin-Bythell (UMSL): Growth and development of New World Passerines

1445 Christine McAllister*, Russell Blaine, Paul Kron, Brent Bennett, Anna Glotzbach, Jennifer Kidson, Heidi Garrett, Blanda Matzenbacher, and Allison Miller (SLU). Environmental correlates of cytotype diversity in *Andropogon gerardii* Vitman

1500 Ivan Jimenez (MOBOT): Assembly of a regional tree flora in the tropical Andes

1515 Coffee and posters**Keynote address**

1615 SUSAN HARRISON (University of California Davis): Historical and ecological causes of phylogenetic diversity in Californian plant communities

1715 Allison Miller: Concluding remarks

1830 **Happy Hour and Dinner** (\$20) Picnic Shelter #6, Wells Drive, Forest Park

ST. LOUIS SLEEC FALL 2013 RETREAT
ORAL PRESENTATIONS

AUSTIN-BYTHELL, SUZANNE (austinbythells@umsl.edu) Department of Biology, University of Missouri-St. Louis, One University Blvd., St. Louis, MO 63121. Growth and development of New World passerines.

Rate of development differs widely among species of birds and is associated with variation in life-history syndromes. Nestling growth patterns vary broadly, reflecting differences in the mode of development, parental investment, sibling competition, adult size, geographic region, and environmental factors that affect energy and nutrient availability. We studied development in temperate and tropical songbirds of the New World to determine how development relates to natural and life-history traits and latitude. We found that tropical species grew more slowly than temperate species yet, paradoxically, the duration of time that young spent in the nest did not differ. Tropical passerines exhibit a greater diversity in the range of life-history phenotypes than temperate species.

BLAKE, STEPHEN (SBLAKEWCS@GMAIL.COM). Department of Biology, Washington University in St. Louis, Saint Louis, MO 63130 USA. Fredy Cabrera, Sharon Deem, Susan Flowers, James Gibbs, Jamie Palmer, Wacho Tapia and Martin Wikelski.
Tracking turtles from the volcanoes of Galapagos to Tyson and down town St. Louis.

Giant tortoises from Galapagos and three toed box turtles from Missouri are not obvious bedfellows to integrate in an ecological research program. Yet conceptually, intellectually, technically, and emotionally they are a surprisingly good fit, and after all, they both have shells! Despite decades of research on both taxa, surprisingly little is known about the ecology, movements, population trends, health and conservation status of these species. In 2009, we developed a research program to determine the movement patterns of Galapagos tortoises and elucidate their causes and consequences. Since then we have deployed over 80 GPS tags onto tortoises from four species on three different islands, and have found that stereotypical migrations, nomadism, and sedentarism may occur depending on environmental conditions. Catholic diet and long distance movements provide giant tortoises with prodigious abilities as seed dispersers. Struck with conceptual parallels between the Galapagos Islands and Forest Park (truly), in 2012 we began studying the movement and health ecology of box turtles in St. Louis. Initial data indicate that Forest Park box turtles are more sedentary and more stressed than to their rural counterparts at Tyson Research Centre. We are using these programs to promote interest in science, conservation, and the outdoors among young people both on Galapagos and St. Louis. Over 400 school-aged young people have directly participated in our research on Galapagos. In St. Louis, numerous school teachers, undergraduates, high school and elementary school students have been exposed formally and informally to turtles, their habitat, and field science.

CARLSEN, MONICA (monica.carlsen@mobot.org). Missouri Botanical Garden, P.O.Box 299, St. Louis, MO 63166. Contrasting patterns of morphological diversity and climatic preferences in the genus *Anthurium* (Araceae).

The genus *Anthurium* (Araceae) comprises ca. 1,000 Neotropical species, distributed from southern Mexico to northern Argentina. The most recent molecular phylogeny of the genus

recovered 18 strongly supported clades that vary in terms of their geographic range size, morphological diversity, and climatic niche width. Using distribution models, molecular phylogenetics and morphological analysis, it was found that clade geographic extent is correlated with climatic niche width, but not with morphological differentiation or species richness. Climatic niche diversity and morphological diversification seem to be decoupled within *Anthurium*. So that, species that belong to clades that have restricted distributions have more similar climatic niche preferences but are more dissimilar morphologically, in comparison with species belonging to widely distributed clades. Interestingly, phylogenetic structure at the subgeneric level (i.e. among major clades) does not seem to play an important role in determining species richness, or be influencing climatic niche width and morphological diversity within *Anthurium*.

CEREZO, ADRIAN, (cerezo@stlzoo.org) Associate Director of Conservation Education Research, Saint Louis Zoo, One Government Drive, St. Louis, Missouri, USA 63110. In harmony with nature: How key principles of conservation ecology can inform the human dimensions of conservation.

Over the last century, the natural science of ecology has evolved to consider nature as a complex, dynamic, non-equilibrium, system of systems. This epistemological shift has allowed a deeper understanding of organisms as well as large-scale phenomena. Perhaps more important, it has shed light on why it is so hard to document, model and predict certain systems and processes. During the same period, the environmentalist movement has grown as the advocacy and social policy counterpart of biology, ecology and conservation science. Yet the conceptual principles of environmentalism have not evolved in alignment with the science. This presentation will highlight some of the misaligned principles and explore why this misalignment is detrimental to promoting effective, long-term conservation solutions. The presentation will then discuss how ecological principles can help improve the interaction between the scientific and the policy/programs aspects of conservation organizations.

DEMATTEO, KAREN E. (KDEMATTEO@aol.com) Department of Biology, Washington University in St. Louis, Saint Louis, MO 63130 USA, Miguel A. Rinas, Carina F. Argüelles, Mario S. Di Bitetti, Barbara Davenport, Patricia G. Parker, and Lori S. Eggert. Using noninvasive techniques to expand carnivore conservation in Misiones, Argentina.

Many of the mammal species found in Misiones, Argentina, the region containing the largest remaining tract of Upper Paraná Atlantic Forest ecoregion, are forest specialists that require an expansive range and are threatened as they navigate a heterogeneous landscape. This varying degree of protection, the network of roads, and widespread human population in the region increases opportunities for human-wildlife conflicts. Ensuring the long-term survival of wide-ranging, landscape carnivores in this ecoregion requires understanding how fragmentation affects movement patterns and estimating connectivity between protected areas. To address these questions, we have been using three noninvasive techniques (conservation detection dogs, genetic analyses of scat, GIS technology) to collect data on five wide-ranging carnivores (jaguar, puma, ocelot, oncilla, bush dog). During the first two phases of the study (2009 and 2011), we collected 588 scats in and around 16 protected areas in central and northern Misiones. Genetic analyses allowed us to examine the degree of genetic differentiation between the two zones and evaluate potential differences in habitat preference among the five species. In the third phase

(2013), we focused our efforts outside of protected areas and collected 329 scats in privately owned forest, agricultural areas, monoculture plantations, and human-occupied areas. These data were missing for the region and are seen as the core data needed to determine the optimal location for a biological corridor that maximizes animal mobility and minimizes human-wildlife conflict between protected areas in the northern and central zones.

EDWARDS, CHRISTINE (Christy.Edwards@mobot.org). Science & Conservation Division, Missouri Botanical Garden, P.O. Box 299, St. Louis, MO 63166-0299, USA. Use of DNA metabarcoding to identify the diversity of plants utilized by a pollinator.

DNA metabarcoding combines the use of next-generation DNA sequencing, DNA barcodes, and bioinformatic analysis to identify and quantify diversity in a sample. Although this technique has been explored extensively in the field of microbiology, few studies have used this approach to quantify the diversity of plants utilized by a pollinator. In this study, we used DNA metabarcoding to identify the plant resources utilized by nectivorous bats, and compared the results to estimates based on visual identification of pollen. Scat and fur-swab samples were collected from two species of nectar-feeding bats, the Mexican long-tongued bat (*Choeronycteris mexicana*) and endangered lesser long-nosed bat (*Leptonycteris curasoae*), from Arizona, USA. Samples were divided, and plant diversity was quantified in one half of each sample by visual identification of pollen, with the other half analyzed using DNA metabarcoding. DNA metabarcoding was carried out by PCR enrichment for three plant DNA barcodes (*rbcL*, *psbA-trnH*, and *trnL-F*), followed by 454 DNA sequencing of tagged, pooled samples. To identify the diversity of plant species, reads were assembled and compared to the NCBI nucleotide database and to DNA sequences generated from potential food plants collected from Arizona. Visual identification of pollen found that 99.6% was from *Agave* sp., which is thought to be the main food source utilized by the bats. DNA metabarcoding identified a much broader diversity of plant species, indicating that it is a very sensitive approach to quantify the plants visited by bats, potentially allowing for the identification of less frequently utilized food-plant species. However, many of the plant species identified by metabarcoding may not be utilized as food resources and instead may result from incidental transfer or pollen by-catch arising from the broader network of species interactions within the plant-pollinator community. These results suggest that metabarcoding may be a powerful tool to understand the ecology and interactions among species, but that careful analysis of results is necessary to derive accurate and robust ecological conclusions.

HARRISON, SUSAN (SPHARRISON@UCDAVIS.EDU). Department of Environmental Science and Policy, University of California, Davis, One Shields Avenue, Davis, CA 95616. Historical and ecological causes of phylogenetic diversity in Californian plant communities.

Community diversity may be determined from the 'bottom up' by the breadth and partitioning of niche space, or from the 'top down' by historical and evolutionary forces. We used a novel application of phylogenetic and functional techniques to test these contrasting explanations for plant diversity across California. 'Communities' were sets of field plots that sampled alpha (within-plot) and beta (among-plot) sources of variation in diversity. We sampled 93 such communities, nested within 78 larger regions for which species pools were independently estimated, across the California Floristic Province. We found no evidence linking the phylogenetic diversity of communities to within- or among-plot functional diversity. Instead, we

found that community phylogenetic diversity (as well as species richness) depended on that of regional species pools. In turn, diverse regional pools were those with high proportions of species of northerly biogeographic origins, supporting what we call the ‘climatic refuge’ hypothesis. Our study illustrates the value of considering multiple regions as well as multiple types of data (phylogenetic, functional, biogeographic) in analyses of community diversity.

HUGHES, MICHAEL (michael.evan.hughes@gmail.com), Department of Biology, University of Missouri-St. Louis, One University Blvd., St. Louis, MO 63121. Orchestrating transcriptional rhythms in mammals and flies.

The Earth rotates around its axis every 24 hours, generating daily rhythms in light and temperature. Consequently, many organisms have evolved to anticipate and respond to predictable daily changes in the environment. These internal timekeeping mechanisms are known collectively as circadian clocks, and in animals they regulate sleep/wake cycles, as well as activity rhythms, metabolism, and physiology. At a molecular level, circadian clocks drive oscillations in gene expression. The targets of circadian regulation are called ‘circadian output genes’ and are involved in many different molecular and cellular processes. We have used microarray analysis and next-generation sequencing to systematically identify thousands of circadian output genes in different tissues in human, mice, and flies. These data are freely available as a resource to the field, and have been used as the starting point for on-going work on the mechanism of circadian rhythms in humans and flies.

IVÁN JIMÉNEZ¹ (Ivan.Jimenez@mobot.org), Isabel Loza², Sebastián Tello¹, Peter Jørgensen¹, Alfredo F. Fuentes³, Leslie Cayola³, Maritza Cornejo³, Manuel J. Macía⁴, Gabriel Arellano⁵, Tatiana B. Miranda³, Javier³ Quisbert-Quispe³, and Vania Torrez⁶.¹Research and Conservation Division, Missouri Botanical Garden, P.O. Box 299, St. Louis, MO 63166-0299, USA. sebastian.tello@mobot.org, ²Department of Biology, University of Missouri-St. Louis, One University Blvd., St. Louis, MO 63121, ³Herbario Nacional de Bolivia, Campus Universitario Cota-Cota, calle 27, Correo Central Cajón Postal 10077, La Paz, Bolivia. alfrefuentes@gmail.com.⁴Departamento de Biología, Área de Botánica, Universidad Autónoma de Madrid, Calle Darwin 2, 28049 Madrid, Spain. manuel.macia@uam.es, ⁵Real Jardín Botánico, CSIC; Plaza de Murillo 2, 28014 Madrid, Spain and Departamento de Biología, Área de Botánica, Universidad Autónoma de Madrid, Calle Darwin 2, 28049 Madrid, Spain, ⁶Division of Plant Conservation and Population Biology, Department of Biology, University of Leuven, B-3001 Leuven, Belgium.

Tertiary Andean orogeny is widely acknowledged to have determined current spatial patterns of plant diversity across the Neotropics, but debate persists as to how it did so. A prominent hypothesis suggests that, as the Andes rose, newly emerging environments were occupied mostly by immigrating clades of pre-adapted species, and less so by species that underwent *in situ* adaptation. This hypothesis predicts that species turnover across elevational gradients reflects replacement of clades that diverged from each other before the Andean uplift (pre-Andean clades), while species turnover associated to geographic distance within narrow elevation bands

reflects diversification within pre-Andean clades. We tested these predictions by integrating information on lineage divergence times with data on species distribution across a 4,000 m elevational gradient of known geologic history in the Bolivian Andes. Our results supported both predictions, and suggest that Andean uplift resulted in limited adaptive diversification across elevational gradients.

KNOUFT, JASON H. ¹ (knouft@gmail.com), and Huicheng Chien^{1,2}. Department of Biology, Saint Louis University ²Current address: Department of Geography, State University of New York at New Paltz. The impacts of climate change on the hydrology and biodiversity of the Mobile River watershed

The goal of this study is to use a landscape-scale hydrological model to predict current stream flows and the potential impacts of climate change on future stream flows in the Mobile River watershed in the southeastern United States. In-stream flow data generated from hydrological models are integrated with locality data from 118 species of fishes, 16 species of mussels, and 12 species of crayfishes and Maxent, an ecological niche modeling algorithm, to predict the potential impact of changes in streamflow on the distribution of suitable hydrological habitat for each species. Hydrological model predictions based on nine separate downscaled global climate models with three emissions scenarios generally indicate that total annual streamflow will decrease in the future and seasonal streamflow patterns will become more variable. Maxent results indicate a range of potential responses by fishes and crayfishes to changes in flow, while hydrologic variables were poor predictors of mussel species distributions.

MCALLISTER, CHRISTINE (Chrissy.McAllister@principia.edu; Principia College), Russell Blaine, Paul Kron, Brent Bennett, Anna Glotzbach, Jennifer Kidson, Heidi Garrett, Blanda Matzenbacher, and Allison Miller. Environmental correlates of cytotype diversity in *Andropogon gerardii* Vitman

Polyploidization within plant lineages can lead to a mosaic of cytotypes across the range of a species, and the existence of multiple cytotypes within populations is well-documented in plants. Documenting the geographic distribution of cytotypes can be a critical first step in identifying whether abiotic factors are associated with whole genome duplication or habitat differentiation between cytotypes. We examine patterns of cytotype diversity in big bluestem (*Andropogon gerardii*), the dominant species of the tallgrass prairie ecosystem. The most common ploidy levels in *A. gerardii* are hexaploids ($2n = 6x = 60$) and enneaploids ($2n = 9x = 90$), with rare intermediate cytotypes. We estimated ploidy level in 352 plants from 37 populations of *A. gerardii* in 18 states, using flow cytometry with silica-dried leaf samples. Fifteen populations (or 40.5%) showed evidence of mixed cytotypes. The population-level frequency of higher order polyploids (e.g. higher than $6x$) ranged from 0% in the northern portion of the sampled range to 100% in the southern portions of the range. We tested for environmental correlates of cytotypic diversity using seven biologically relevant GIS-based climate layers selected from the 19 BIOCLIM layers (2.5 arc second resolution). A principal component analysis reduced these seven variables to two principal components that together explained 79.8% of the variation in the data. Partial regression analysis indicated that, even after controlling for the effects of geography, high

diurnal temperature range and low summer precipitation were significantly correlated with higher ploidy level.

MEDLEY, KIMBERLEY, A. (kimberly.medley@colorado.edu). Department of Biology, Washington University in St. Louis, Saint Louis, MO 63130 USA, Mari K. Reeves, Alfred E. Pinkney and Pieter T.J. Johnson. Amphibian abnormalities: Nation-wide patterns and environmental drivers of disease.

A central principle in disease ecology is that environmental conditions often moderate the likelihood and severity of disease occurrence. The relationship between environment and amphibian abnormalities—including missing, extra, or deformed limbs—is poorly understood at a broad spatial scale. Recent work has revealed abnormalities often cluster in space, but vary substantially through time and within spatial clusters. This pattern suggests that broad-scale underlying risk factors combine with dynamic local phenomena to drive abnormalities. Regional-scale studies support several hypotheses for causes of amphibian abnormalities, including infection by the trematode parasite *Ribeiroia ondatrae*, eutrophication, contaminants, and sub-lethal predation (as main effects or interactions). We combined multiple modeling techniques to evaluate the relative roles of broad-scale, local, and temporally variable environmental factors on multiple types of amphibian abnormalities using a 10-yr, nationwide dataset of amphibians (48,081 frogs) collected on U.S. National Wildlife Refuges. After accounting for spatial structure, all non-traumatic abnormalities at 314 sites were most strongly influenced by land cover and nitrates, and secondarily by road density surrounding sites. Land cover was strongly influenced by agricultural land use, so these results together suggest a role for eutrophication in abnormal amphibian development. Road runoff can contain chemicals, which points towards an additional role for contamination. We followed up these analyses by evaluating models for skeletal malformations, a type of abnormality that can result from parasite infection that disrupts limb formation. For this abnormality type, the most important predictors were nitrates and parasite infection, followed by climate and land cover. This complex suite of predictors suggests a role for parasite infection for malformations, but also highlights the complexity of the issue. Parasite infection plays a role, but may be exacerbated by additional environmental factors. Nitrate and land use effects point toward eutrophication, while climate suggests a role for developmental timing. Together, these results suggest that exposure time combined with additional factors (e.g. parasites, contaminants) that are coincident in space and time may drive the dynamics of amphibian abnormalities, and lend insight into factors that may assist in disease mitigation.

MUCHHALA, NATHAN¹ (n_muchhala@yahoo.com), Sönke Johnsen², and Stacey Dewitt Smith³, ¹ Department of Biology, University of Missouri – St. Louis, St. Louis, MO 63121² Department of Biology, Duke University, Durham, NC 27708³ Department of Ecology and Evolutionary Biology, University of Colorado, Boulder, CO 80309. Competition for hummingbird pollination and the evolution of flower color diversity in Andean Solanaceae.

Angiosperms display a remarkable diversity of flower colors across species. Competition for pollinators could select for such diversification if local color differences discourage switching between species during foraging bouts. In this study we combined morphometric analyses, field

surveys, and models of pollinator vision with a species-level phylogeny to test the role of competition in color diversification among Iochrominae (Solanaceae), a hummingbird-pollinated Andean clade. We found that flower color as perceived by pollinators is significantly overdispersed within communities. This pattern is not due to phylogenetic history: phylogenetic community structure follows random expectations, and flower color itself lacks phylogenetic signal. Other plant traits display moderate levels of phylogenetic signal and are randomly distributed across communities. These results support the hypothesis that the multiple shifts from the ancestral purple to white, red, yellow, and orange flowers occurred as a response to interspecific competition for pollination in regions of high sympatry.

REN, ZONG-XIN¹ (RENZONGXIN@MAIL.KIB.AC.CN), Peter Bernhardt² and Hong Wang¹.
¹Key Laboratory of Biodiversity and Biogeography, and Germplasm Bank of Wild Species, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China. ²Department of Biology, St. Louis University, St. Louis, USA. Do generalist pollination and self-incompatibility in yellow star grass (*Hypoxis hirsuta*; Hypoxidaceae) correlate with Charles Darwin's predictions about the evolution of orchid flowers?

Hypoxis hirsuta is an early vernal-flowering but nectarless herb providing pollen as its only reward for generalist pollinators. While flowers at our site were visited infrequently by a few pollen-eating flies (primarily Syphidae), beetles (*Acmaeodora* spp.) and a butterfly (*Falcapica midea*), the majority of pollinators were small, native bees. Collections of pollen-collecting females represented 21 species in the Andrenidae, Apidae, Halictidae and Megachilidae. Pollen load analyses indicated that most bees carried grains of *H. hirsuta* mixed with pollen of co-blooming species secreting nectar. Results of controlled hand-pollination series showed that bagged hand-self-pollinated, bagged emasculated but not pollinated and bagged control flowers produced capsules with undeveloped or no seeds. In contrast, 77.3% of hand mediated, cross-pollinated pistils developed into capsules containing mature seeds. Fruit set in open, insect-pollinated flowers was 72.4%. Epifluorescence analyses showed that most germinating grains failed to penetrate the stigmatic surface > 24 hours after hand self-pollination. In contrast, the ovaries of hand cross-pollinated pistils contained pollen tubes entering their ovules by 24 hours. Early acting self-incompatibility (SI) is rare in petaloid monocots and the system in *H. hirsuta* parallels the breeding system described in some species in the Melanthiaceae. Recent, molecular phylogenetic analysis shows that the Hypoxidaceae is the sister family of the Orchidaceae but most orchid lineages are dominated by self-compatibility despite high species diversity. Self-incompatibility in orchids has been reported most commonly in sub-family Epidendroideae with several early-acting SI taxa. Generalist pollination and SI in *Hypoxis* may correlate with floral evolution in orchids from radial symmetry to bilateral symmetry. Future research is needed to compare the pollination and breeding system between the basal orchid subfamily Apostasioideae and Hypoxidaceae as they share similar flower color and presentation.

STEVENS, PETER (stevensp@umsl.edu) Department of Biology, University of Missouri-St. Louis, One University Blvd., St. Louis, MO 63121. What do flowering plants actually DO (other than looking pretty – most of them)? Rethinking aspects of evolution and biosphere change.

The metric most commonly used to evaluate success is species number, indeed, other data are hard to come by. However, available estimates of measures like primary productivity and especially above- and below-ground carbon sequestration paint a different picture of evolution. Members of a few, relatively small clades largely other than asterids dominate considerable areas of the earth's surface, often in more or less extreme conditions outside tropical rainforest. Examples are angiosperms living in mangrove, marine and estuarine conditions, those with C₄ photosynthesis, and seed plants with ecto- and ericoid mycorrhizae. In communities with such plants carbon sequestration is massive and long-lasting. Add changes in wood formation, stomatal functioning, and venation density, and seed plants in general may have driven major elements of biosphere evolution, in particular, changes in atmospheric CO₂ concentration, rainfall, and rock and soil weathering regimes. Integrating such aspects of seed-plant evolution with historical change is a challenge. Thus grasslands and their unique C-sequestering mollisols are recent (<10 m.y.), but the origin of C₄ photosynthesis can be dated to 20 m.y. or so earlier, and at least some ectomycorrhizal associations are still older, and understanding their ecological history is more difficult. But one may well ask, do seeds, flowers, and species numbers really matter?

WILLIAMS, KATHRYN M.¹ (kathrynmrwilliams@gmail.com) and Justin C. Fay² Evolution, Ecology, and Population Biology Program¹ and Dept. of Genetics², Washington University in St. Louis, MO. Evolution of Ecological Dominance in Yeast

Selective pressures from the environment interact with community dynamics to influence the evolution of adaptations and the ecological success of species. Frequently, a single species is able to invade and dominate a new habitat. However, the evolution and genetic basis of such ecological dominance is often unknown. In the vineyard, the yeast *Saccharomyces cerevisiae* dominates multiple other species as grape juice ferments to wine. One suspected mechanism that enables *S.cerevisiae* to dominate is the Crabtree effect, or the preferential fermentation of glucose to ethanol in the presence of oxygen. This trait evolved following whole genome duplication (WGD) in yeast and is expected to be advantageous in high-glucose environments such as in grape juice because it produces toxic ethanol. If the ability to dominate in grape juice evolved during the transition to a predominately fermentative lifestyle in yeast, then post-WGD yeast species are expected to exhibit an intrinsic fitness or competitive advantage relative to pre-WGD yeast species in high-glucose environments including grape juice. We tested this hypothesis using monoculture and co-culture assays of multiple pre- and post-WGD yeast species in high-glucose laboratory medium and Chardonnay grape juice. Inconsistent with our hypothesis, we found no intrinsic fitness difference between pre- and post-WGD yeast species overall. Yet, *S.cerevisiae* was able to dominate nearly all other pre- and post-WGD yeast species except for its sibling species, *S.paradoxus*. Compared to *S.cerevisiae*, all species were equally fit in high-glucose laboratory medium, while multiple species exhibited a fitness defect in Chardonnay grape juice. Our results show that evolution of the ability to dominate in grape juice did not coincide with WGD in yeast, but may have evolved much more recently in the lineage

that gave rise to *S.cerevisiae* and *S.paradoxus*. Our results also indicate that both differences in intrinsic fitness and competitive ability facilitate *S.cerevisiae*'s ecological dominance.

POSTER PRESENTATIONS

ADU-OPPONG BOAHEMAA (WashU), Claudia Stein and Scott A. Mangan. Do root associated bacteria mediate plant-soil feedbacks?

Interactions between plants and their associated belowground microbes have been shown to serve as strong forces that structure plant communities through plant-soil feedbacks. Although much attention has been placed on the importance of mutualistic and pathogenic fungi as drivers of plant-soil feedbacks, far less is known about the roles in which root-associated bacteria mediate this process. In an experimental prairie at the Tyson Research Center, we are evaluating the strength and direction of plant-soil feedback dynamics among four native and one invasive forb species. Plants are grown in the greenhouse with either their own soil biota or biota of other species. We are applying a cocktail of antibiotics to half of the treatment combinations to reduce bacterial abundance and isolate their effects on feedback dynamics. Preliminary census results indicate negative feedbacks among native species and that the effect of bacteria on plant growth is species specific.

ALLINGTON, GINGER, Missouri Botanical Garden Seed Bank: Germplasm conservation of the Missouri flora...and beyond.

Ecosystems around the globe are facing intense pressure from habitat loss, changing climate and invasive species, all of which threaten the viability of plant populations. With the strains on natural ecosystems increasing every year, many conservation organizations are looking for ways to supplement on-the-ground plant conservation efforts. One valuable tool in the conservation toolbox is seed banking. Seed banks are long-term storage facilities where seeds are dried and stored at low temperatures in order to preserve them for the future. This year the Missouri Botanical Garden launched a new Seed Bank program to collect and conserve seeds from the entire Missouri eco-regional flora. We will collect seeds from multiple populations across the range of each species in the state, in order to capture and protect representative genetic diversity within species. Germplasm conservation enables us to preserve a high amount of genetic diversity of a large number of species within a relative small amount of space. These resources will be available in the future for reintroductions, restorations and research.

BAER, CHRISTINA (cbaer89@gmail.com; UMSL) Larval shelters of the silver-spotted skipper vary in shape depending on host plant

Caterpillars of the silver-spotted skipper (*Epargyreus clarus*) construct shelters on a variety of fabaceous host plants by tying leaves or portions of leaves with silk. While these shelters can be easily classified into different types depending on the number leaves involved or the number of cuts on a leaf, quantitative analysis of shelter shapes independent of shelter size has been extremely limited. I applied geometric morphometric analysis to first- and second-instar skipper *E. clarus* shelters built on *Desmodium glutinosum* and *Robinia pseudoacacia* and found that shelters built on different host plants have significantly different shapes. Furthermore, there is a host plant × instar effect on shelter shape: first- and second-instar shelters on *D. glutinosum*

differ in shape but those on *R. pseudoacacia* do not.

BALLEN, LINDA B. (lballen@siue.edu) and Peter R. Minchin (SIUE). Evaluating the success of bottomland forest restoration in the Upper Mississippi Valley.

Agricultural development, changes in hydrology, and urbanization in the Upper Mississippi Valley has significantly reduced the area of bottomland forest (BLF), which provides vital ecosystem services. Since 1995, the US Army Corps of Engineers has attempted to restore BLF on a range of sites by planting root production method (RPM) seedlings of flood-tolerant oaks and pecan. My research evaluates restoration success, utilizing a chronosequence of nine restoration sites with ages ranging from 1-23 yr to assess trajectories of tree growth and changes in forest composition, structure, and diversity relative to mature BLF reference sites. Data collection is currently in progress.

BENNETT, BRENT, Sarah Bruemmer, Jayne Gardiner, Christine Bedore (Principia). Electroreception in bonnethead sharks, *Sphyrna tiburo*

Sharks detect *changes* in voltage (electric gradient) with specialized receptors called Ampullae of Lorenzini, which terminate at the skin surface in an array of pores. Pore distribution and density differ for each elasmobranch species. Higher pore density is associated with higher resolution, similar to pixels from a camera. Pore number does not change over ontogeny so larger animals may have lower resolution. Gel-filled canals that connect pores to the subdermal receptor elongate with growth, which is thought to increase sensitivity. Therefore, as a shark grows, it may lose spatial resolution capabilities, but may increase in sensitivity. We compared sensitivity of adult bonnethead sharks *Sphyrna tiburo* to neonates to determine if behavioral sensitivity changes with size. Few if any studies have done behavioral electroreception tests with adult sharks. We found no difference in sensitivity, but larger sharks did seem to have decreased resolution evidenced by inaccurate biting at the center of the dipole.

CALLEN, STEVEN, Justin Zweck, Tracy Zander, Allison Miller, Peter Bernhardt (SLU). Sexual reproduction and self-compatibility of the invasive vine kudzu (*Pueraria montana*) in Missouri roadside populations.

Self-fertilization in plants provides the means to reproduce when compatible mates are lacking, such as during biological invasions. A transition from a self-incompatible (SI) to a self-compatible (SC) mating system may promote invasion success by providing enhanced seed production. Current understanding of mating system shifts during invasion is limited, particularly for perennial invaders that reproduce both sexually and clonally. We performed controlled, hand-pollination experiments in two populations of the perennial, clonal vine kudzu (*Pueraria montana*) to investigate the potential role of SC in facilitating invasion. The SI index was 0.267 at one site (partial SI) and 1.00 at the other (full SC). Pollen tubes reached the ovules in both self- and cross-pollination treatments, suggesting kudzu possesses a late-acting, partially-SI mating system. As these populations experience a high probability of self-pollination and

demonstrate partial to full SC, this may signify a SI to SC shift, potentially contributing to its invasional success.

CALLEN, STEVEN, and Hong Wang (SLU). The good side of invasive species: Experimenting, establishing collaborations, and exchanging cultures in China

The National Science Foundation's East Asian and Pacific Summer Institute Fellowship (EAPSI) aims to provide the Fellow with a first-hand research experience outside the United States; an introduction to the science, science policy, and scientific infrastructure of their location; and an orientation to the society, culture and language of the host country. My research, which focuses on the evolution of mating system for perennial, clonal invasive plants, benefitted from the EAPSI fellowship as it provided me with the opportunity to perform an investigation on the mating system of an invasive species (kudzu) in its native range. The results from this study will then be compared to a similar study conducted in the introduced range to determine if there has been a mating system shift upon its introduction into a novel environment. Aside from conducting research, I also established and strengthened international collaborations and exchanged culture with the local people.

DIERKES, DARON (UMSL – History). The Engelmann Project

The George Engelmann Correspondence Project at the Missouri Botanical Garden is working diligently to add the personal letters and papers of the 19th century botanist George Engelmann to the Biodiversity Heritage Library. This builds upon a previous project at the garden which digitized some of the specimens from the Engelmann Herbarium for the Tropicos database. Reuniting specimens and letters that originally traveled together is a challenge, but having both online is a step in that direction. The project is also enhancing and pushing existing digital infrastructure to deal with problems specific to archival materials, and especially to correspondence.

DUBOIS, ANDREW M. (Maryville U.), Gregory R. Ruthig and Christopher O'Connor. Delayed hatching of Axolotl (*Ambystoma mexicanum*) in response to water mold.

Life-history theory predicts that organisms will transition between life-history stages at times that provide the greatest fitness advantage. Several amphibian species accelerate their egg hatching when they are exposed to a threat of mortality in the egg stage, whereas other amphibians delay hatching when there is a threat of mortality in the larval stage. We exposed embryos of the aquatic salamander, *Ambystoma mexicanum*, to a pathogenic water mold. We incubated embryos in the presence or absence of water mold. We observed a delay in hatching of *A. mexicanum* in the presence of the pathogen. Eggs were also larger at the time of hatching in the presence of the pathogen. Hatched larvae from the infected treatment were of similar size to the control larvae, which hatched 1.5 d earlier. However, larvae that we exposed to water molds in our experiment did not suffer significantly higher mortality than control larvae. *A. mexicanum* may have evolved delayed hatching as a defense mechanism against larval infections in the field, but water molds may only be pathogenic under stressful environmental conditions.

FAY, JUSTIN (Washington U), Ping Liu, Sofia Dashko, Lorena Butinar², Melita S. Lemut, Uros Petrovic, Jure Piskur. Yeasts of the European Wild.

Saccharomyces cerevisiae has long been used for the production of beer, bread and wine and numerous strains have been isolated, selected and distributed for such purposes. Yet, *S. cerevisiae* is also isolated from sources unrelated to the production of food and beverages and has consistently been found in association with tree exudate and association substrates. Isolates of *S. cerevisiae* form a number of genetically differentiated groups, defined by either the geographic location or the ecological source from which they were obtained. One strongly differentiated group includes numerous strains isolated from vineyards, grapes and grape must and is thought to have a European origin based on a small number of non-vineyard isolates from Europe. To determine whether there are wild populations of *S. cerevisiae* in Europe we have sampled oak bark and soil in vineyard and non-vineyard locations in Slovenia. Following enrichment we identified 25/173 (14%) yeast isolates as *S. cerevisiae* and 90/173 (52%) as *S. paradoxus*. We plan to use RAD-seq to answer questions about *S. cerevisiae* population structure in Europe.

FRANSEN, HILARY, Adam Eckert, and Scott Eckert (Principia). Heart rate measurements of nesting leatherback sea turtles (*Dermochelys coriacea*) in response to tourism activities at Matura Beach, Trinidad

Evaluating impact of tourism activities is critical to the sustained management of any sea turtle nesting colony, where tourism is present. This issue is particularly difficult to assess with the largest sea turtle, the leatherback (*Dermochelys coriacea*) because this species does not appear to frighten or abort nesting attempts easily. To determine if heart rate could be used as an involuntary response measure of leatherback sea turtle reaction to tourism activities, we measured heart rates for 160 leatherbacks nesting at Matura Beach, Trinidad. We designated specific nesting phases as emerge, body pitting, digging, oviposition, covering, camouflage, and return. Control heart rates were calculated with leatherbacks not exposed to any unusual stimuli. Experimental heart rates were measured to test the leatherbacks' reactions to light, touch, and sound stimuli, as well as the presence of tourists. Heart rates varied by nesting phase, in both control and experimental turtles. There was no statistically significant difference in heart rates between experimental and control turtles except for during the camouflage phase in response to touches. Data was also collected that quantified the number of tourists, tourist flashes, and tourist touches during select nesting events to determine if an involuntary heart rate response was dependent on the specific level of stimuli. There were no statistically significant differences. My hypothesis that the heart rate of leatherbacks will change based on activity levels (nesting phases) is supported by this study, however the hypothesis that there would be a measurable involuntary heart rate response to tourism stimuli was confirmed. I propose that leatherbacks may not exhibit a flight response to perturbations.

GREG, MATTHEW¹, Laura Klein¹, David Bogler², Iván Jimenez², and Allison Miller¹
¹ St. Louis University, ² Missouri Botanical Garden. Morphometric analysis of leaf variation in three North American grape species (*Vitis acerifolia*, *V. riparia*, and *V. rupestris*).

Species within the genus *Vitis* (Vitaceae) are the foundation of wine, table grape, raisin, and grape juice industries. Although grapevine cultivation is based primarily on the European

grapevine *V. vinifera*, North American *Vitis* species play an important role in grape production as well. In some ways, grapevines are unusual crops because cultivated varieties often consist of two genetically distinct entities that are grafted together: the above-ground part of the plant (the scion) produces the stem, leaves, flowers, and berries, and the below-ground part (the rootstock) forms the lower stem and roots. Widespread grafting in grapevine dates back to the mid-1800's when insects in the genus *Phylloxera* devastated the French grape industry. Starting with this crisis, North American grapevines have been key genetic resources for the development of biotic and abiotic stress resistant rootstocks, as well as hybrid grape varieties. Today, vineyards in France and other regions consist of European *V. vinifera* grafted to North American *Vitis* species, including the river grape (*V. riparia*), the rock grape (*V. rupestris*), and their hybrid derivatives. Despite their importance for grape growing, relatively little is known about morphological variation in natural populations of *Vitis* species used for rootstocks. The purpose of this study is to identify morphological traits associated with drought tolerance by documenting leaf variation in a small clade of three species whose natural distributions differ with respect to abiotic conditions. The study focuses on *V. acerifolia* and *V. rupestris*, which are found in dry areas and gravel beds respectively, and their close relative, *V. riparia*, which is found primarily in moist soils. Natural variation in leaf morphology is preserved through plant specimens housed in herbaria. Leveraging the collection at the Missouri Botanical Garden herbarium, we apply comprehensive morphological indices developed by the International Organization of Vine and Wine (OIV) to characterize variation in 25 leaf characters in at least 10 accessions each of *V. acerifolia*, *V. riparia* and *V. rupestris*. The resulting data are used in univariate and multivariate analyses to describe leaf morphological variation in the three species, and to identify traits that differentiate these close relatives. This study represents an important step in describing natural variation associated with adaptation to dry environments in species used for rootstocks by the global grape industry.

HENDRIX, MELISA, and Kyra Krakos (Maryville U). The pollination systems of *Ruellia strepens* and *Ruellia humilis* (Acanthaceae)

A self-compatible breeding system reduces the reliance on pollinators, but can result in a loss of genetic variation and lowered reproductive success. Flowering species that are self-incompatible rely entirely on pollinators for full seed set, and multiple environmental factors can impact that plant-pollinator interaction. The common species of *Ruellia* found throughout Missouri are *Ruellia strepens* and *Ruellia humilis*. This study looked at reproductive behavior and what factors influence reproductive success in *R. strepens* and *R. humilis*. Individual plants ($n = 10$) of each species were evaluated and measured for growth and development, flowering, fruiting and pollinator species. To determine the main pollinators, plants were observed in 20 minute intervals ($n = 130$). Visitation duration, foraging patterns, and stigma contact were recorded. Pollen loads from a sample of visitors were collected and analyzed for amount and type. The main pollinators were determined by combining visitation rate and pollen load average. Breeding system was determined with hand pollination experiments ($n = 56$) Treatments included: 1. open (no manipulation), 2. control (anthers removed), 3. self-pollinated, 4. cross-pollinated. Stigmas were collected for each treatment and the presence of pollen tubes were determined using fluorescent microscopy. Insects were collected to determine primary pollinators and gauge the movement of pollen. Our results indicated both species of *Ruellia* require specific habitats to survive. *R. strepens* prefers indirect sunlight and moist soil along the

edges of open woods, borders of streams and ponds. *R. humilis* prefers direct sunlight and dry or well drained soils in glades, prairies and fields. *R. strepens*' flowers open during the early morning dark hours, allowing pollination by moth species while *R. humilis*' flowers open after sunrise, allowing pollination by bees and other generalists such as Long-tongued bees, including Anthophorid bees and Leaf-Cutting bees. Both *Ruellia* species are self compatible, but most seed set is due to outcross pollen. Self-pollination produced small fruit and low seed set in *R. strepens* and *R. humilis*, while cross-pollination in both species produced larger fruit and a higher yield of seed. If a decline in bees or other generalists persist, some species of *Ruellia* could be at risk.

HENRIQUEZ, CLAUDIA L. (Washington U), Tatiana Arias, Chris J. Pires, Thomas B. Croat and Barbara A. Schaal. The Good, the Bad and the Ugly: Plastid and mito phylogenomics of Araceae.

The biogeography, chromosome number evolution, and evolutionary history of the plant family Araceae have become much clearer in recent years. The still poorly resolved backbone of the family phylogeny, however, precludes answering questions about the early evolution of the family. With the advent of next generation sequencing, phylogenetic analyses can now be based on thousands of informative nucleotides, which greatly enhance our confidence in the resulting phylogeny. We used reference-based assemblies of Illumina data for 37 genera from across the backbone of the family to resolve the remaining questions in the deep phylogeny of Araceae. Reference-based assemblies were performed using the chloroplast and mitochondrial genomes of two species of Araceae from Genbank. Sequences from the chloroplast genome produced strongly supported phylogenies, using both coding sequences alone and the entire genome. In contrast, the mitochondrial genome proved to be much more problematic in terms of assembly and the resulting alignment had very limited phylogenetic signal. Better supported clades in the new study are: 1) Tribe Spathiphyllae is sister to the rest of Monsteroideae; 2) The Unisexual Flowers clade, with the bisexually-flowered genus *Calla* within, is recovered with strong support; 3) *Anubias* and *Montrichardia* form a clade sister to the *Zantedeschia* clade; and 4) *Zantedeschia* is sister to the Old World *Anchomanes* clade. However, despite the strong statistical support for almost all nodes in the chloroplast phylogenies, the placement of the bisexually-flowered genus *Calla*, and the rheophytic genus *Schismatoglottis* within the Unisexual Flowers clade remains unclear.

HOEFT, ADAM, and Kyra Krakos (Maryville University). A comparative study on the reproductive biology of two Missouri native *Tradescantia* spp. (Commelinaceae)

The genus *Tradescantia* contains some 71 species, all possessing the ability to form hybrids. The occurrence of hybridization is assumed to be common and will occur whenever populations are in relative close proximity. Hybridization is enhanced by the self-incompatibility of most species in the genus and perennial nature of the plants. Because of this increased frequency of cross pollinations and the potential of numerous hybrids, the question of continuance of species status becomes an important concern. The purpose of our study focused on the reproductive biology of *Tradescantia ohioensis*. and *T. subaspera* var. *montana*, two native Missouri species that inhabit drastically distinct ecosystems. Specifically, we compared plant morphology and pollination systems of each species with previous studies to look for variation across species ranges over a seasonal breeding period. This study was conducted at a restored prairie habitat and upland woods in eastern Missouri during the months of May through July for 2012 and 2013. Timed

pollinator observations were conducted throughout the flowering season, and both number and identification of floral visitors were recorded. A sample of stigmas from open flowers were collected during the same time to determine insect visitation rate to flowers. These samples were compared against pollen tube data from three other treatment methods that included cross pollination, self pollination, and pollen supplementation. Our results indicate that these species are utilizing partially overlapping pollination systems and are not experiencing pollen limitation. Both species are self-incompatible, which agrees with previous studies conducted. Observations show that bees of the family group Halicadae are the main pollinator group for both species, while *T. ohioensis* was also visited by secondary pollinator groups such as beetles, syrphid flies, *Bombus* spp., and *Apis* spp. The identification of halictid bees as the main pollinators does not agree with previous observations made for the genus 50 years earlier. While these two species share numerous overlapping characteristics, the identification of a natural hybrid has yet to be discovered at this study site. Further tests are being conducted to observe if cross pollination of these two species does in fact produce viable offspring.

HUISMAN, KELSEY,¹ and David Bogler².¹ Northern Michigan University ² Missouri Botanical Garden. Conservation genetics of the rare species *Delphinium exaltatum* (Ranunculaceae) of the Appalachian mountains and the Ozark highlands of Missouri.

Delphinium exaltatum is a rare tall perennial late-blooming Larkspur species with populations throughout the Appalachian mountains and the Ozark highlands of Missouri in Shannon County, making the Missouri populations disjunct by more than 600 km. Several Missouri populations occur within the National Scenic Riverways on land that is managed for glades and savanna. Fire suppression in *D. exaltatum* habitats has allowed over shading to occur and the encroachment of nonnative plant species, and leaf litter which inhibits seed germination. The effects of fire management on the genetic diversity of this species are unknown. This species is ranked globally threatened (G3) and imperiled (S2) in the state of Missouri, making *D. exaltatum* a cause for conservation concern. In this study we are using Single Nucleotide Polymorphisms in PEP Carboxylase intron 4 sequences as population markers to explore the relationships, levels of genetic variation and differentiation within and among populations of *D. exaltatum* from the Appalachian mountains and the Ozark highlands of Missouri.

HULSEY, RYAN, and Kyra Krakos (Maryville U.). The chambered stigma and its role in the reproductive biology of *Chamaecrista fasciculata*.

Buzz pollination is a highly specialized form of pollination in which a pollinator gains access to pollen by vibrating the anthers, causing pollen to be expelled. *Chamaecrista fasciculata* is a buzz pollinated prairie species with a specialized stigmatic chamber. Preliminary studies indicated that pollinator vibrations may be necessary to move pollen both out of the anthers and also when deposited into the stigmatic chamber. This study seeks to address the role of the stigmatic chamber in the pollination of *C. fasciculata*. We asked the following questions: 1) Who are the main pollinators of *C. fasciculata*? 2) Does the plant use secondary pollinators? 3) Does the chambered stigma mandate buzz pollination for pollen deposition? 4) In a growing season with low precipitation, how is seed set impacted? We used both pollinator observations and pollen load analysis to determine which insect visitors were involved in transferring pollen between plants. Exclusion experiments and hand pollinations were used to determine if *C. fasciculata* was able to receive pollen from secondary pollinators. Florescent microscopy was used to count the number of pollen tubes and determine reproductive success. Our results agree with previous

studies that show *Bombus* is the main pollinator group. Our results indicate that pollen must be vibrated into the chamber, as well as vibrated out of the anthers for successful fertilization. The plant does not use secondary pollinators, and requires a specific functional group of large bees for successful reproduction. Although small halictid bees were carrying pollen, they are most likely not secondary pollinators because of the chambered stigma requirements. The highly specialized nature of the plant most likely does not pose a risk to the species, due to the generalist nature of *Bombus*.

KARSLAKE, ELIZABETH (elizabethkarlake@yahoo.com) and G. R. Bourne. Department of Biology, University of Missouri-St. Louis, St. Louis, MO 63121-4400. Preference decisions of leaf-cutting ants *Atta cephalotes* already transporting leaves.

I explored the question—why do leaf-cutter ants (*Atta cephalotes*) take crop leaves when surrounding forests have more available leaves? By presenting ants with a smorgasbord of forest and crop leaf samples when they were already transporting leaves to their nests, I found significant preference differences among colonies. Although, there were no differences for discovery or handling times of forest or crop leaf species, the observed preferences for crop leaves may be due to lower levels of defensive compounds in crop species. Furthermore, ants from particular colonies should favor leaves based on previous experience; such that ants reduce digestive costs to fungi which can detoxify some secondary compounds that may kill or reduce the fitness of ants eating the fungi.

KESSLER, MIMI (Mimi.Kessler@asu.edu) Tsevenmyadag, Natsagdorj, Nyambayar, Batbayar, and Smith, Andrew (Arizona State University). Geographic variation in Great Bustard migration: results of satellite telemetry in Mongolia.

The range of the Great Bustard (*Otis tarda*), the heaviest bird capable of flight, stretches from the Iberian Peninsula to Manchuria. Populations of the Asian subspecies of Great Bustard (*Otis tarda dybowskii*) are endangered and their movement patterns have not previously been investigated, hampering conservation efforts. We used satellite telemetry to monitor the movements of Great Bustards breeding in northern Mongolia. While European Great Bustards are sedentary or make relatively short seasonal movements, our data revealed that Mongolian Great Bustards migrate 2000 km one-way to winter in central China. We have also found that these birds spend approximately one-third of the year at migratory stopovers in variable locations. Bustards are subject to high rates of mortality at these migratory stopovers, primarily due to poaching. These findings present challenges for the conservation of the Asian subspecies of Great Bustard. Due to the variable nature and high number of stopovers, the standard solution of protected areas is likely to be ineffective. Further, due to this long-distance migration, conservation of this subspecies will require international cooperation.

LIU, SHIH-HUI, Peter C. Hoch, Peter H. Raven, Janet C. Barber (MOBOT and SLU). Polyploid evolution in *Ludwigia* section *Macrocarpon* (Onagraceae): preliminary insights.

Polyploidy has long been recognized as a crucial force in plant evolution and has also been suggested as a contributing factor in invasiveness. While the understanding of polyploid evolution of a few model organisms is being improved, the role of polyploidy in the evolution of non-model organisms remains poorly understood. Increased variation of traits in polyploid taxa

may enable them to adapt to different habitats and contribute to invasion success. The pan-subtropical genus *Ludwigia* L. (Onagraceae), currently comprising 82 species in 23 sections, exhibits extensive polyploidy and plays important roles in ethnobotany and ecology. Earlier studies have clearly established that *Ludwigia* is monophyletic and is sister to the remaining genera in the family, but a robust reconstruction of evolutionary relationships within *Ludwigia* is incomplete. In this study, we are continuing the phylogenetic study of *Ludwigia*, especially focusing on characterizing polyploid evolution in section *Macrocarpon* based on both molecular and morphological data. Section *Macrocarpon* is an ideal group for studying polyploid evolution because it includes self-incompatible diploid taxa (*Ludwigia bonariensis* and *L. lagunae*; $n=8$) with limited distributions, as well as a self-compatible (sometimes autogamous) polyploid species (*L. octovalvis*; $n=8, 16, 24$) with worldwide distribution that has become invasive in some regions. In the past two years, we have extended earlier phylogenetic studies of *Ludwigia* using the same chloroplast and nuclear DNA markers for 29 additional taxa of *Ludwigia* and one additional outgroup, with a focus on increased sampling within section *Macrocarpon*. Our current phylogenetic tree includes about 40% of species and half of sections in *Ludwigia* and strongly supports section *Macrocarpon* as monophyletic. Moreover, our morphological analyses suggest that tetraploid and hexaploid *L. octovalvis* can be identified by their pollen sizes, though there is considerable variability in other traits.

MAHARAJ, GYANPRIYA (gyanpriya.maharaj@mail.umsl.edu), and G. R. Bourne. (UMSL). Temporal ambient temperature variations correlate with thoracic temperatures and abundance across butterfly families, genera and species in Guyana.

Our study provides baseline evidence of how temporal ambient temperature at an equatorial site is related to butterfly physiology, behaviors and abundance. We found similar moderate positive correlations between ambient and body temperatures for the nymphalids, *Anartia jatrophae*, *Heliconius sara* and *H. melpomene*. However, a stronger positive correlation was evident for *Lemonias emylius*, a riodinid. Butterfly activities and abundance patterns showed species specific temperature ranges with greatest abundance and most intense activity for *A. jatrophae* at a range of 25.7–37.7°C, *H. sara* 23.3–31.0°C, *H. melpomene* 25.4–32°C and *L. emylius* 28.0–33°C. Only *L. emylius* displayed sexually dimorphic behavioral patterns in relation to ambient temperatures—hotter males, cooler females. Overall, our results are indicative of open habitat to shade seeking behaviors of the studied species.

MOURA, TANIA M.¹; David Bogler²; V. F. Mansano³; A. M. G. A. Tozzi¹. ¹ Universidade Estadual de Campinas, Brasil. ² Missouri Botanical Garden. ³ Jardim Botânico. Rio de Janeiro, Brasil. Phylogeny of *Mucuna* (Leguminosae: Papilionoideae: Phaseoleae), based on ITS marker.

Mucuna is a Pantropical genus with ca. 100 sp. The genus presents a large morphological diversity and three different pollinator syndromes. This work evaluates the phylogenetic relationships among representatives of *Mucuna* based on ITS marker. Given the difficulty with amplifying *Mucuna* herbarium specimens, we used two primers to study this genic region. 28 taxa of *Mucuna* representing all its morphological diversity and geographic distribution were sequenced; 19 specimens as external groups were also analyzed (representatives of *Apios*, *Desmodium*, *Kennedia* and *Rhynchosia* were included in the analysis). The matrix was aligned using ClustalX and the analysis was conducted in Paup 4.0 through parsimony and maximum

likelihood methods, with 10,000 and 1,000 bootstrap resampling, respectively. The results show *Mucuna* as a monophyletic genus. Two principal clades were revealed for *Mucuna* comprising the two subgenera: *M. subg. Mucuna* and *M. subg. Stizolobium*. Our results imply that the infrageneric classification of *Mucuna* must be revised. Also, they confirmed *Kennedia* and *Desmodium* (Desmodieae) as sister groups of *Mucuna*.

PRIEST, GALEN (galenpriest@gmail.com, UMSL). Effects of ecosystem engineering by wood-boring beetles on trees and arboreal ant communities in the Brazilian Cerrado.

Ecosystem engineering is a ubiquitous yet frequently overlooked process in ecological communities. To date the role of ecosystem engineers in structuring communities and shaping ecological processes is not well understood. This is in part due to an absence of studies investigating the direct mechanistic links between engineer diversity, engineered resource abundance and heterogeneity, and utilizer communities. This study addresses these direct links by investigating how wood-boring beetle communities modulate cavity resources available to arboreal ants on six tree species in the Brazilian Cerrado with the goal of understanding how ecosystem engineers directly structure communities through the creation of heterogeneous resources.

RANARIVELO, HERITIANA S. (hsrq98@mail.umsl.edu) (UMSL). Molecular phylogenetics and variation of morphological characters within the Vismieae (Hypericaceae), with an emphasis on the Afro-Malagasy genus *Psorospermum*.

Vismieae Choisy (1821) are included within Hypericaceae (St. John's wort family). The tribe comprises two genera, *Vismia* and *Harungana* (Stevens 2007) that are morphologically very similar. *Harungana* is considered to be synonymous with the Afro-Malagasy genus *Psorospermum*; *Harungana* has a drupe, but *Psorospermum* has a berry. However Ruhfel *et al.* (2011) found that *Psorospermum sensu* Stevens (2007) is paraphyletic and (*Harungana* + African *Vismia rubescens*) are sister to American *Vismia*. Other African *Vismia* and all *Psorospermum* form another clade. The phylogeny of Vismieae still remains uncertain. The hypotheses I test are: (1) *Psorospermum* forms a distinct African clade with most other African Vismieae, (2) this African clade is sister to (*Harungana madagascariensis* + *Vismia rubescens*) and all the American *Vismia*, (3) the Malagasy *Psorospermum* form a clade. I conducted a molecular phylogenetic analysis based on chloroplast DNA *ndhF*, *trnK-matK*, *psbA-trnH*, *trnStrnG* and nuclear DNA *ITS* to test phylogenetic hypotheses and to plot morphological characters onto the tree. My preliminary results suggest that the relationship ((*Harungana madagascariensis* + *Vismia rubescens*) + American *Vismia*) is robust. However a clade (Malagasy *Psorospermum* + other African Vismieae) is poorly supported. Malagasy *Psorospermum* is monophyletic, but with weak bootstrap support (50%); it includes 2 major clades with high support (>90%) but relationships between species within each clade are unresolved. *Psorospermum chionanthifolium* is polyphyletic and *P. cerasifolium* is paraphyletic. It is likely that hairy staminodes is a synapomorphy of the clade American Vismieae. The character hairy style is likely to be a synapomorphy of the clade (*Vismia rubescens* + *Harungana madagascariensis*). And big, curved and brown embryo is likely to be a synapomorphy of the Malagasy clade. Additional morphological characters, like inflorescence morphology, are as yet unstudied.

RHODES, ZACHARY D.¹, David Bogler², Elizabeth A. Hooper¹, and George Yatskievych².

¹ Truman State University. ² Missouri Botanical Garden. Description of a New African Fern Species Belonging to *Triplophyllum* (Tectariaceae).

A single herbarium specimen collected in 2008 in Gabon, Africa, was suspected to represent an un-described species of fern. Morphological features of this specimen were studied to compare features of the new species to that of related genera (*Tectaria*, *Ctenitis*, *Triplophyllum*). The morphological analysis of the new fern was supplemented with a comparison of spore size and morphology from the same related genera. Based on the data collected, the specimen was determined to be a new species, and is being described as new to science under the name *Triplophyllum parvum*

ROIS, LISA (lisa.rois@mail.umsl.edu; UMSL). Progress in understanding the relatedness of populations of the endangered American burying beetle.

The American Burying Beetle has been facing great conservation challenges ever since its unexplained disappearance from most of its natural historical range and its dramatic decrease in overall population size. Captive populations are critical for the success of reintroduction and reestablishment in the wild. The goals of this project are to: (1) use microsatellite markers in a population genetics framework to describe genetic differences among remaining natural populations of *Nicrophorus americanus*; (2) determine relatedness among individuals in the captive St. Louis Zoo population; and (3) assess the genetic health of the captive population relative to variation found in naturally occurring populations. In order to answer these questions, it was important to first establish a feasible and practical DNA extraction protocol utilizing old, unpreserved samples. After determining the protocol that yielded high quality DNA and was least invasive we are able to move forward and answer our questions concerning the population genetics of this endangered species.

SCHULER, MATTHEW (Washington U). More individuals drive the species energy-area relationship.

Two well-supported patterns in biodiversity studies are that species richness increases with area and with energy. Although area and energy are known to interactively influence richness, the degree to which these interactions results from proportional sampling of more individuals in larger and/or more productive habitats, or from disproportional shifts in the relative commonness and rarity of species has not been examined. Here, we used a diverse assemblage of zooplankton (crustaceans and rotifers) in experimental ponds to disentangle the role of total and relative abundances in driving the interactive effects of area and energy on richness. We found that higher rates of energy flow increased species richness in large, but not small, ponds; and, the total abundances of individuals mirrored those results. By using a rarefaction technique (Probability of Interspecific Encounter), we found that richness patterns resulted from changes in the total, but not relative, abundance of individuals. Overall, our results emphasize the need to consider shifts in total and relative abundances underlying biodiversity patterns and suggest that energy will have a smaller influence on biodiversity as habitats become smaller (e.g., through habitat loss).

SCOTT, ADAM (amviot@gmail.com) Directed percolation in a neutral phenotype evolution model.

Characterization of phase transitions is a fundamental problem in systems whose macroscopic behavior is driven by its microscopic dynamics. Although different models may at first appear drastically different by model rules or model interpretation, at continuous phase transitions, these models have order parameters that scale according to their universality class. One such universality class is directed percolation (DP). Our recent work has shown phase transition behavior in an agent-based model of phenotypic evolution as the parameter for maximum mutation size (mutability) is varied. Here, we present preliminary results that indicate that the transition of the system from an absorbing state of extinction to a fluctuating active state of survival demonstrates that the model belongs to the directed percolation universality class.

SOARES, LETICIA (leticiasoares@mail.umsl.edu), and Robert Ricklefs (UMSL). Temporal dynamics of avian malaria parasites in the Lesser Antilles

We take advantage of the unique biogeographic history in the Lesser Antilles to investigate the temporal dynamics of avian haemosporidian (malaria) parasites. Due to sea level variations up until 10-20 kya, five island pairs in the archipelago were interconnected, likely homogenizing parasite assemblages. Using pair-wise comparisons, we infer losses of malaria lineages in five abundant host species distributed across four island pairs. St. Kitts and Nevis have dissimilar parasite assemblages infecting bananaquits, Lesser Antillean bullfinches, common ground doves, and grassquits; black-whiskered vireos are parasitized by the same single lineage on both islands. In contrast, black-whiskered vireos have non-homogeneous assemblages when comparing Antigua and Barbuda, whereas the parasite assemblages of Lesser Antillean bullfinches' are highly similar in these islands. We hypothesize that whether avian malaria parasite assemblages on formerly connected island pairs are dissimilar or not could be determined by: 1) island-related effects (i.e. variations in area and degree of connectivity over time); and 2) variations in resistance to malaria parasites among host populations.

SPAGNOLO, SARA (sspagno@siue.edu), Carol Bryant, Kurt Schulz, Peter Minchin and Betsy Esselman (SIUE). Assessing Quality of a Regenerated Prairie Using Floral and Faunal Indices.

There is a possibility that successional processes may result in quality prairie communities. This study attempted to ascertain the quality and plant community structure of an old growth field in Macoupin County, Illinois. Vegetation and insect surveys were conducted during the growing season of 2012. Two distinct plant communities were observed, each described by a small number of species dominating the composition. FQI (Floristic Quality Index) was calculated to be 34.48, and AQI (Auchenorrhyncha Quality Index) was calculated at 54.09. Both of these indices suggest that the field is of medium to high quality according to INAI grades.

SPASOJEVIC, MARKO J. (WashU), Elizabeth Yablon, Jonathan A. Myers, Brad Oberle, Maranda Walton and Amy E. Zanne. Community assembly mechanisms differ between saplings and adults: The importance of ontogeny in trait-based ecology.

The ecological-filter concept has become a backbone of trait-based ecology and has proved useful for understanding mechanisms underlying deterministic community assembly. The

relative importance of different deterministic assembly mechanisms are typically inferred based on plant functional traits measured on adults, yet these traits are known to vary among life stages (e.g., seedlings, saplings, adults). This variability among life stages suggests that the strength and directionality of deterministic assembly mechanisms may differ between different life stages. To test this hypothesis, we examined patterns of functional diversity in saplings and adult trees along ecological gradients that varied in soil-resource availability and canopy tree density in a stemmapped, temperate oak-hickory forest dynamics plot at the Tyson Research Center, Missouri. We predicted that sapling functional diversity would correlate more strongly with tree density and adult functional diversity would correlate more strongly with soil resources. Using data from 299 20x20-m quadrats (12-ha), we calculated communityweighted mean (CWM) trait values and functional dispersion (FDis) for two leaf traits (leaf size and specific-leaf area [SLA]) of saplings and adults in each quadrat. We found that CWM leaf size and SLA were positively related to tree density for both saplings and adults, but were negatively related soil resources for adults only. Functional dispersion patterns were less consistent with adult FDis of leaf size negatively related to soil resources and sapling FDis of leaf size positively related to tree density and adult FDis of SLA positively related to soil resources and tree density and sapling FDis of SLA influenced by neither. Our results support the hypothesis that ontogenetic shifts in the relative importance of different assembly processes play a role in structuring plant communities and provide insights into how different mechanisms of deterministic assembly vary through ontogeny.

TISINAI, SHELBY, John Lovseth, and Scott Eckert (Principia). Bat activity and diversity in a selectively logged oak-hickory forest.

Bats are an extremely important species in many ecosystems. In forest ecosystems their ecological role may range from insect pest control to seed dispersal. Principia College supports more than 2,000 acres of mature oak-hickory forest. This forest is under active management, which includes an FSC certified timbering program that is structured to maintain a healthy forest ecosystem. In this study the activity and diversity of bats in six different timber harvest units (THUs) in the Principia College forest were measured using a Pettersson D500x bat detector from June 26 to July 30, 2013. Furthermore, continuous forest inventory (CFI) plots were installed at the six sites measured for bat activity and diversity to gain perspective on the tree species present and the tree species with the greatest importance in the areas immediately around the measurement sites. With a general trend of decreasing bat diversity in areas that have been harvested, but the opposite trend regarding bat activity, the data collected provide insights into how each of the six THUs vary in regards to forest dynamics and bat activity and diversity. Furthermore, the data reveals how bat activity and diversity are affected by the management plans in place.

WOODS, LAUREN (Washington U). The influence of metacommunity size on species diversity scaling in protist communities.

I used protist communities to examine how the number of patches in a metacommunity, or metacommunity size, can affect the scaling of species diversity. I expected that metacommunity size would alter species diversity scaling by affecting immigration and extinction dynamics

within communities. Metacommunities were established from a regional pool of protist species collected at Washington University's Tyson Research Center (Missouri, USA). I created 4 metacommunity treatments with 4 replicates each. Control and small metacommunities consisted of 4 patches, or communities, large metacommunities were comprised of 12 patches, and habitat destruction metacommunities were initially established with 12 patches but later reduced to only 4 patches. Small, large, and habitat destruction metacommunities were connected through bi-weekly dispersal events in which 4% of each patch was removed, mixed together, and dispersed equally back into all of the patches of a metacommunity. Control patches were not connected by dispersal and were used to monitor temporal community dynamics in the absence of dispersal. Metacommunities were sampled every 2 weeks over a 10-week period to quantify within community immigration and extinction dynamics. I found that the local diversity in large metacommunities increased overtime when compared to the other treatments. However, metacommunity size did not affect species diversity at the regional scale of four dishes. Metacommunity size did affect species composition. Small metacommunities varied more between replicates in their species composition than large metacommunities. Future analyses will identify if differences in species composition can be attributed to changes in community immigration and extinction dynamics.

XINSHUAI, QI (Washington U), C.C.Vigueira, B.K.Song and K.M.Olsen. Genotyping-by-Sequencing reveals independent evolutionary origins of Asian and US weedy rice.

Weedy rice, also known as red rice, is a close relative of cultivated rice (*Oryza sativa* L.) that infests rice fields worldwide. It mimics and competes aggressively with cultivated rice, reducing crop yields and contaminating harvests with its unpalatable seeds. While found only in crop fields, weedy rice possesses many characteristics of wild *Oryza* species, including freely shattering seed and seed dormancy. Understanding the weed's evolutionary relationship to domesticated and wild *Oryza* species can contribute to the development of strategies to control it. Moreover, the comparison of weedy rice origins among different world regions provides an optimal model to study the genetics of de-domestication and parallel evolution. In previous work, we found that the two major US weed strains are derived from two Asian domesticated rice varieties: *indica* and *aus*. Here we compare those findings to weeds in two regions of East Asia: Southeast Asia, where wild *Oryza* populations grow near rice fields; and Korea, where no wild *Oryzas* occur. With 224 weedy, wild and domesticated *Oryza* samples, we used genotyping-by-sequencing (GBS) to obtain 10,089 single nucleotide polymorphisms (SNPs), which we used in population structure analyses. We find the following: 1) Malaysian weedy rice closely resembles *indica* crop varieties; 2) weedy rice in Cambodia, Thailand, Vietnam and Indonesia is more heterogeneous, with genetic contributions from *aus*, *indica*, and wild *Oryzas*; and 3) Korean weeds fall into two genetically distinct classes, resembling *indica* and *japonica* crops. Thus, in comparison with US weedy rice, the Asian weeds are more diverse, and their evolution is clearly influenced both by local crop varieties and wild populations.

ZELLE, KATHLEEN (Washington U), Annie Altman, Jan Bello, Jocelyn Millar and Yehuda Ben-Shahar. Pheromonal communication and prezygotic isolation in *Drosophila melanogaster*.

Theories and experimental data support a role for both prezygotic and postzygotic processes in maintaining species isolation. While some of the genetics that support postzygotic isolation are well-understood, experimental data that explain the genetic mechanisms that drive prezygotic behavioral species boundaries are limited. Many animals produce species and sex-specific chemical mating signals, which are used during sexual encounters to identify potential mates and maintain prezygotic isolation. During courtship, male *Drosophila melanogaster* rely heavily on input from multiple sensory modalities to detect these signals. Contact chemosensation is specifically important during sexual decision-making as it allows individuals to sense the cuticular pheromones of potential mating targets. In recent years, several members of the *gustatory receptor* (*Gr*) family have been implicated in pheromone sensing in insects. Typically, *Gr* genes are expressed in sensory neurons located in the proboscis, legs, wing margins, and female ovipositor. However, we find that many *Gr* genes are also expressed atypically in the fly abdomen. We find that one of the abdominally-expressed genes, *Gr8a*, is expressed in both sensory neurons and in the pheromone producing cells (oenocytes). Consequently, we hypothesize that *Grs* that are also expressed in oenocytes may be functioning in both the sensory response to pheromones and their synthesis. In agreement with our hypothesis, preliminary data indicate that *Gr8a null* flies have altered cuticular pheromone profiles and show abnormal mating behaviors. Our findings suggest that specific gustatory receptors function not only in the perception, but also in the production of pheromones used during sexual encounters and may represent key evolutionary factors that contribute to the maintenance of species barriers in insects.

ZWECK, JUSTIN (SLU). Pollination and interspecies isolation in two sympatric prairie clovers.

Dalea candida and *D. purpurea* (Fabaceae) are sister taxa co-occurring in prairies and glades across the central U.S.A. Aside from their differently colored flowers these species strongly resemble each other and have overlapping flowering periods. Both possess spike inflorescences of many small flowers. Furthermore, their sexual organs are not enclosed within keel petals, unlike those *Dalea* species which have retained zygomorphy. We compared the breeding systems and pollination ecology of sympatric, co-blooming populations of these two species in order to investigate the consequences of keel-less flowers and reproductive boundaries to interspecific hybridization. *D. candida* and *D. purpurea* shared 48% of flower-visiting insects representing 4 orders (Hymenoptera, Coleoptera, Diptera, Lepidoptera). The majority of visitors belonged to the bee families Apidae and Halictidae. A broad size range (length 4.34 mm-19.45 mm) of insects carried pollen, and there was no significant relationship between insect length and pollen presence for either *Dalea* species. Hand pollinations showed that pollen tubes reached the ovary in self, cross, and interspecies treatments. As previous studies showed limited seed set following self-pollination, we conclude that both species possess late acting (ovarian-type) self-incompatibility systems, as in other legumes. A form of late-acting incompatibility may also explain the lack of known hybridization between *D. candida* and *D. purpurea*, as so many pollinators are shared when these species bloom together. Evolution of the open, keel-free form of *D. candida* and *D. purpurea* flowers has permitted pollination by a wide range of generalist foragers. We hypothesize that pollination in *Dalea* species maintaining zygomorphy requires pollinators specialized in size and behavior.