



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

September 28, 2012

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*, Sönke Johnsen, and Stacey Dewitt Smith (UMSL)
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

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*.

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.

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.

MATTEO, 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.

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?

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.

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.

HENRIQUEZ, CLAUDIA L. (WashU), 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.

Temporal ambient temperature variations correlate with thoracic temperatures and abundance across butterfly families, genera and species in Guyana

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.

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.

SCHULER, MATTHEW (WashU). 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 result 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).

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 to 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.

WOODS, LAUREN (WashU). 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.

ZELLE, KATHLEEN (WashU), 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