

## St. Louis Ecology, Evolution, and Conservation (SLEEC) Retreat

September 29, 2012

# Principia College, Elsah, Illinois

## Schedule

0830 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 Principia College: Chrissy McAllister (Principia)
- 0915 Scott Mangan (WUStl): Integrating soil-borne organisms into major themes in plant ecology
- 0930 Peter Minchin\*, Adam S. Fitzgerald, and Jennifer L. Laquet (SIUE): The effect of changes in the spatial configuration of fragmented temperate deciduous forests on current patterns of biodiversity
- 0945 Adam Smith (MOBot): Over par—Fairways and sand traps on the migration route to a favorable climate
- 1000 Elizabeth Kellogg\*, Matt Estep, Dilys Vela Diaz, and Jinshun Zhong (UMSL): Phylogeny, Polyploidy and Genome Evolution in the Andropogoneae
- 1015 Dan Warren (SLU): The physiology of overwintering anoxia tolerance in painted turtles
- 1030 Coffee and posters

#### Second morning session

- 1100 Debbie Brock (WUStl): Farming amoebas, like human farmers, protect their crops from competitors
- 1115 Melissa Anthony\* and Jason Knouft: Accounting for multiple scales of spatial autocorrelation in species distribution models—a hierarchical Bayesian framework
- 1130 Maria Pil\* and R. E. Ricklefs (UMSL): Using genetic variation to infer the demographic history of *Coereba flaveola* in the West Indies
- 1145 Kyra Krakos (Maryville): Phenological change and impacts on pollination biology
- 1200 Peter Bernhardt\* and R. Meier (SLU): Charles Darwin's orchids then and *Thelymitra* now!
- 1215 Lunch break and posters; walks in the woods, weather permitting
- 1. Hike to active rattlesnake dens
- 2. Hike to hill prairie
- 3. Tour timber harvest site (& discuss recent Forest Stewardship Council certification)
- 4. Tour mammoth lab & hear about progress on the excavation

#### Afternoon session

- 1400 Kate Waselkov (WUStl): Go East, Young Weed—Population genetics of the invasion of weedy waterhemp across the Mississippi River
- 1415 Cheri Asa (Zoo): The role of captive breeding in recovery of the island fox
- 1430 Iris Levin\* and Patricia G. Parker (UMSL): The secret lives of hippoboscid flies
- 1445 Raelene M. Crandall\* and Tiffany M. Knight (WUStl): Seasonal timing and intensity of fire alters competition between the invasive legume, *Lespedeza cuneata*, and co-occurring native species
- 1500 Wendy Applequist (MOBot): Botany and quality control of medicinal plants
- 1515 Aimee Dunlap (UMSL); Components of change in animal information use

#### 1530 Coffee and posters

#### Keynote address

- 1615 LEONIE C. MOYLE (Indiana University): Genetics and evolution of species diversity in wild *Solanum*
- 1715 Allison Miller: Concluding remarks
- 1830 Dinner (\$20) Audubon Center, 301 Riverlands Way, West Alton, MO 63386

### ST. LOUIS SLEEC FALL 2012 RETREAT

#### **Poster Presentations**

Allington, Ginger R.H. and Thomas J. Valone (SLU), Islands of fertility: an artifact of grazing?

Bogler, David (MOBot), The pollen flora of Missouri

**Baer, Christina** (UMSL), Leaf-tying caterpillars increase abundance of Asiatic oak weevil on deciduous trees through ecosystem engineering

**Beachum, Colin E. and Jason H. Knouft** (SLU), Assessing temperature related variation in routine metabolic rate across the geographic range of the Bluntnose Minnow (*Pimephales notatus*)

**Douglas, Tracy** (WUStl), Is there a conflict between the sexes? Mating type distribution in the social amoeba *Dictyostelium discoideum*?

Geist, Katie (WUStl), Molecular signatures of parent-offspring conflict in seed tissues

**Ghulam, Abduwasit** (SLU), Mapping invasive plant species in tropical rainforest using geoinformatics

Gruhn, Jennifer A. (WUStl and MOBot), Ivan Jimenez, Kenneth M. Hiser, Jun Wen, R. E. Ricklefs, Plant lineages conserve their climate niche over geologic time

**Holmberg, Nels, Sandra Arango-Caro, and James Trager** (MOBot), Long-term vegetation responses to controlled burns used to restore Eastern Deciduous Hardwood Forest

Klein, Laura L., Morphology and introgressive hybridization in North American ground cedar, *Diphasiastrum* 

**Liu, Shih-Hui, Janet Barber, Peter Raven, and Peter Hoch** (SLU and MOBot), Preliminary study of the evolutionary history of polyploidization in *Ludwigia octovalvis* (Onagraceae)

Lynn, Austin, and Sandra Arango-Caro (MOBot), Ecology of the invasion of border privet (*Ligustrum obtusifolium*) in the Shaw Nature Reserve: habitat suitability with distance to roads and consequences of invasion

Loza, Isabel, J. Sebastian Tello, Iván Jiménez, and Peter M. Jørgensen (MOBot), Rarity in woody plants of the Madidi region (Bolivia)

McAllister, Christine, Russell Blaine, Paul Kron, Brent Bennett, Anna Glotzbach, and Allison Miller (SLU), Environmental correlates of cytotype diversity in big blue stem (*Andropogon gerardii* Vitman)

Michel, Matt J. & Jason H. Knouft (SLU), A local-scale analysis of environmental change on an assemblage of stream fishes

**Miller, Eliot** (UMSL), The Meliphagidae: honeyeater foraging ecology in a phylogenetic context

**Mosby, Lisa, Matthew Albrecht, Elizabeth J. Esselman, Helen Clawitter, and Matt Rhodes** (SIUE), Determination of seed viability in a rare species: the Tennessee coneflower

**Niu, Sophia Qian & Jason H. Knouft** (SLU), Current velocity, prey abundance and feeding rates of benthic and pelagic fish species in Huzzah Creek, Missouri

**Pusadee, Tonapha** (WUStl), Molecular population genetics of adaptive evolution to deep water condition in wild rice (*Oryza rufipogon* Griff.)

**Raines, Patrick** (UMSL), Why we want too much of a good thing: Experimental evolution of supernormal stimuli

**Ranarivelo, Heritiana** (UMSL), Morphometric relationships, phylogenetic correlation, and character evolution in the Afro-Malagasy genus *Psorospermum* (Hypericaceae)

Salick, Jan, and Katie Konchar (MOBot), Himalayan climate change and Tibetan ethnobotany

**Shulkina, Tatyana, and Burgund Bassuner** (MOBot), The Red Book of the Caucasus – a collaboration between the Missouri Botanical Garden, USA and botanists from Armenia, Azerbaijan, Georgia, Iran, Russia, and Turkey

**Siebrasse, Erica, Kate Chiappinelli, Tom Wolsey** (WUStl), The Young Scientist Program: Integrating Science and Inquiry into the St. Louis Public School System

**Sutton, Alexandra, Marian Smith, Paul McKenzie and E. Esselman** (SIUE), Determining the DNA content of a *Schoenoplectus hallii* (Cyperaceae) population in Howell County, MO, using flow cytometry

**Toko, Pagi** (UMSL), Species richness and community composition of moths (Geometridae) along a complete rainforest gradient in Papua New Guinea

Tsunekage, Toshi (UMSL), A comparative study of oxidative stress in avian embryos

**Vigueira, Cindy** (WUStl), Genomic structure and contemporary evolution of weediness in red rice

## ORAL PRESENTATIONS

**Applequist, Wendy** (MOBot): *Botany and quality control of medicinal plants*. The Missouri Botanical Garden's William L. Brown Center focuses on ethnobotany, or human uses of plants. Correct identification is critical to research on medicinal plants, because accidental or deliberate substitution of one plant for another is common both in traditional practice and in the market. Adulteration may reduce the quality or even the safety of herbal products. We recently surveyed selected unprocessed bulk herbs in the U.S. retail market. While most historically adulterated herbs were consistently correctly identified, a few usually included material of other species. Researchers must independently confirm the identity of botanical test materials.

**Asa, Cheryl** (St. Louis Zoo): *The role of captive breeding in recovery of the island fox*. After populations of foxes crashed on 4 of California's Channel Islands, remaining foxes were trapped to establish a captive breeding program on the islands while the reasons for the crash could be

determined and mitigated. The Saint Louis Zoo's Research Dept was enlisted by the National Park Service to monitor reproductive parameters so that reproductive output could be maximized. On 3 islands recovery entailed removal of golden eagles and feral pigs and reintroduction of bald eagles, while on the 4<sup>th</sup>, the threat of distemper had to be mitigated. Within 10 years, all captive foxes were released and population recovery on each of the islands is considered successful.

**Brock, Debbie** (WUStl): *Farming amoebas, like human farmers, protect their crops from competitors*. Agricultural crops raised and tended by humans, ants, termites, beetles, and now the social amoeba *Dictyostelium discoideum*, are public goods that must be defended if the system is to be evolutionarily stable. *D. discoideum* farmers carry both food and non-food bacteria and here we test the hypothesis that non-food bacteria are used to attack non-farming competitors. We found non-food bacteria have both a beneficial effect on *Dictyostelium* farmers while simultaneously harming non-farming competitors offering support for our hypothesis. Investments in crops are vulnerable to exploitation by non-investors, but farming amoebas solve this problem by carrying bacteria that harm non-farming competitors.

**Crandall, Raelene M., and Tiffany M. Knight** (WUStl): *Seasonal timing and intensity of fire alters competition between the invasive legume,* Lespedeza cuneata, *and co-occurring native species.* The success of an invasive plant following fire should depend on the invasive plant's response to fire, aspects of the fire regime, and presence of co-occurring fire-adapted plants, such as native perennial grasses. We tested this concept in old-fields near Saint Louis, Missouri by examining how *Lespedeza cuneata*, an invasive legume, and the native plant community responded to prescribed fires during different phases of *L. cuneata* and the native community's development (May, mid-July, October, January). We found that *L. cuneata* is most successful after high intensity burns in dormant and early growing seasons where dominant, perennial grasses are absent.

**Diaz-Granados, Mauricio, and Janet C. Barber** (SLU and MOBot): *Phylogenetic and biogeographic relationships within the endemic subtribe Espeletiinae Cuatrec. (Asteraceae) of the South American páramos: preliminary results.* The primary goal of my dissertation project (in progress) is to understand the patterns and mechanisms of speciation in the páramos, and the consequences of climate change on the geographic distribution of species. This is being accomplished using the dramatic radiation of the more than 150 species of frailejones (subtribe Espeletiinae, family Asteraceae) of the Andean forest and páramos, which provide a potential model system for investigating these phenomena. The immediate goals of my dissertation project are to: 1) build a digital identification key for the species; 2) reconstruct a robust phylogeny of frailejones using multiple molecular markers; 3) model the geographic distribution of the species in geographical distribution of species under different scenarios of climate change.

**Dunlap, Aimee** (UMSL): *Components of Change in Animal Information Use.* Animals must deal with uncertainty. One way of reducing uncertainty is to use learning to acquire and use information, allowing for plastic behaviors and tracking the changing environment. In theoretical

models, the adaptive function of learning is tied to these patterns of change in the environment. By partitioning change into different components and manipulating their statistical properties, we can predict when and what kind of learning should evolve as well as which cues or signals animals should attend to. I will describe two experimental systems testing these predictions: experimental evolution using Drosophila melanogaster and decision making in foraging bumblebees.

Kellogg, Elizabeth, Matt Estep, Dilys Vela Diaz, and Jinshun Zhong (UMSL): *Phylogeny, polyploidy and genome evolution in the Andropogoneae*. The grass tribe Andropogoneae is a morphologically diverse clade that contains some of our most economically important species (maize, sorghum, and sugarcane), as well as the ecologically important species in temperate and tropical grasslands (e.g., big bluestem, little bluestem and Indian grass of the North American tallgrass prairie), some of the most troublesome agricultural weeds (e.g. Johnson grass), many important forage crops (*Dichanthium* spp., *Bothriochloa* spp., *Andropogon* spp.) and some burgeoning biofuels (*Miscanthus* and *Saccharum*). We have used a set of 5 nuclear markers to generate a phylogeny for 160 taxa from 59 genera. The tribe includes several large polyploid complexes, for which we have been able to identify/verify identify their likely parental donors. By looking at several closely related polyploidy complexes we can investigate the influence of polyploidy in new detail, and explore its implications for genomic and morphological evolution.

**Mangan, Scott A.** (WUStl): *Integrating soil-borne organisms into major themes in plant ecology.* Soil communities are exceptionally diverse and contain taxa that have substantial effects on plant growth, survival, and reproductive output. Plant-soil interactions are often species-specific and can be fundamental in determining plant diversity and distribution through feedback processes. In this talk, I will briefly highlight three recent studies that integrate plant-soil feedback into major themes in plant community ecology. Specifically, I will discuss how plant-soil feedbacks are likely to 1) determine tropical tree diversity and relative abundance, 2) explain the classic diversity-productivity pattern, and 3) set the stage for plant speciation. Collectively, results of these studies suggest that soil communities may offer answers to major questions in ecology.

**Krakos, Kyra N.** (Maryville), **Peter C. Hoch** (MOBot), **Nicole Miller-Struttman** (UM-Columbia): *Phenological change and impacts on pollination biology*. In order to understand the impacts of human-influenced environmental changes, we have established a long-term floral phenology study in glade, forest, and prairie communities at the Shaw Nature Reserve (SNR) in eastern Missouri, using as a starting point a dataset on flowering at the site developed by Edgar Anderson in 1937-1942 and added to discontinuously since then. Based on this historical record and three years of complete recent observations, we will present analyses documenting both shifts in phenology and more prolonged periods of flowering for many species, especially in the latter part of the season. This extended flowering has led to a 2.5-fold increase in co-blooming species in some communities, with unknown impacts on the pollination biology of those communities. We will discuss these impacts and summarize on-going efforts to analyze the pollination ecology of these communities through intensive pollination studies of selected species, coupled with site-specific micro-climatic monitoring to further refine our understanding.

We specifically seek to clarify if specialist and generalist pollinators respond differently to these changes.

Levin, Iris I., and Patricia G. Parker (UMSL): *The secret lives of Hippoboscid flies*. Throughout their range, frigatebirds are parasitized by a common blood parasite, *Haemoproteus iwa*, that is vectored by a Hippoboscid fly that lives under the feathers of their hosts. We have demonstrated that there is more gene flow among Galapagos populations of flies than among bird hosts. Within island colonies, we inferred fly movement among hosts by analyzing host (frigatebird) microsatellite markers from fly blood meals. Sixty-three percent of the flies had recently switched hosts, and flies infected with *H. iwa* were less likely to have recently moved. Reduced movement of infected flies suggests a cost of parasitism for the fly.

**Minchin, Peter R., Adam S. Fritzgerald and Jennifer L. Laquet** (SIUE): *The effect of changes in the spatial configuration of fragmented temperate deciduous forests on current patterns of biodiversity*. Using aerial photos from 1941 through 2010 we analyzed changes in area and degree of fragmentation of three oak-hickory forest stands in southwestern Illinois. Biodiversity indicators, including richness (S), Simpson diversity (D2), and meanC (a measure of conservation value) were computed from vegetation data collected in 130 random plots. Regression modeling showed that biodiversity is positively correlated with successional age and mean distance from edge and negatively related to distance from nearest 1941 forest and exotic species abundance. Management of forest fragments should concentrate on increasing area and decreasing the sinuosity of fragments and reducing the abundance of exotic species.

**Moyle, Leonie C.** (Indiana University): *Genetics and evolution of species diversity in wild* Solanum. Speciation and adaptation are the two processes that drive diversification. However the mechanistic connection between these two drivers is still surprisingly poorly understood. Focusing on the plant group *Solanum* section *Lycopersicon* (the wild tomatoes) we have been examining the evolution of both reproductive isolation and inter- and intraspecific ecological variation. Using QTL mapping and other techniques, we are dissecting the genetic basis of these two classes of traits, with the aim of both identifying the underlying genes and evaluating and testing theoretical expectations. In parallel, we are examining ecological components of species adaptive divergence, especially in abiotic environmental factors. By examining isolation and adaptive traits from both ecological and genetic perspectives, across an entire clade of species, our goal is to develop an integrated understanding of the connection between adaptation and speciation in driving the evolutionary origin of biodiversity.

**Pil, Maria W., and Robert E. Ricklefs** (UMSL): *Using genetic variation to infer the demographic history of* Coereba flaveola *in the West Indies.* The sizes and distributions of populations vary over time, and episodes of expansion and contraction create characteristic patterns of genetic variation. Consequently, contemporary patterns of genetic diversity open a window onto demographic history. Here, we employ population genetics approaches to infer the demographic history of the bananaquit, *Coereba flaveola*, in the West Indies. The bananaquit is a small nectivorous and frugivorous bird, abundant throughout the archipelago. We analyzed genetic variation in two mitochondrial genetic markers (cytochrome b and ND2) for ca. 23

individuals on each of fourteen islands. Tajima's D, Fu's FS, mismatch distributions and Bayesian skyline plots were used as indicators of population change, supplemented by signature patterns in haplotype networks. The Greater Antillean islands of Jamaica and Cayman Brac Island, and the southernmost Lesser Antillean islands of Saint Vincent and Grenada show evidence of stable populations, whereas the northern Lesser Antillean islands in between have clear signs of expansion. Demographic and phylogeographic patterns support the concept of the taxon cycle in the archipelago.

**Smith, Adam B.** (MOBot): *Over par—fairways and sand traps on the migration route to a favorable climate.* Climate change will encourage migration at different rates in different directions as a function of both the physical and climatic landscape. One measure of migratory pressure from climate change is climate change velocity (CCV), the speed at which a population located at a point in space would have to disperse to maintain the same environmental conditions. To date, work with CCV has assumed that species respond to climatic landscapes as if they were a liquid medium, always choosing the steepest gradient down which to flow. However, the steepest gradient represents the direction of greatest climatic change and so may least amenable to survival and species may not "flow" in just one direction. Here I amend the calculation of CCV to account for movement in directions other than the steepest gradient and represent multiple "flows" from a target site. Vectors of likely movement can be analyzed using tools from hydrology to map flow networks where migrants are likely to travel, as well as areas which accumulate species and might serve as sinks or refugia under future climate scenarios. These networks represent targets for conservation and may help explain the accumulation of biodiversity in hotspots throughout the world.

**Waselkov Kate** (WUStl): *Go east, young weed: population genetics of the invasion of weedy waterhemp across the Mississippi River*. Since European contact, the expansion of agriculture across much of the US has created the potential for native species to evolve into crop field invaders. One such species is the Midwestern riverbank pioneer *Amaranthus tuberculatus,* waterhemp. We genotyped 40 populations across the species' range with 10 SSR markers. Population genetic analyses show that waterhemp was diverging into two taxa, on either side of the Mississippi River, until agricultural intensification around the 1950s allowed the western variety to spread eastward as a corn and soybean weed. Present-day agricultural populations are largely derived from this expansion, with much less introgression from local populations than might be expected for a dioecious, wind-pollinated species.

#### POSTER ABSTRACTS

**Douglas, Tracy** (WUStl): *Is there a conflict between the sexes? Mating type distribution in the social amoeba* Dictyostelium discoideum. Sexual conflict occurs when individuals of opposite sexes have conflicting evolutionary interests concerning reproduction. This conflict can sometimes drive the evolution of skewed sex ratios. Much of what we know about sex ratios comes from analyses of two-sex systems. In *Dictyostelium discoideum*, the potential for conflict between the sexes increases with the addition of two more sexes, one of which is selfmating. Here we analyze the distribution of mating types both across the species and within

individual populations to look for areas in which one sex dominates, suggesting that sex ratios here are under some type of selection.

**Geist, Katie** (WUStl): *Molecular signatures of parent-offspring conflict in seed tissues.* When the genetic interests of mothers and their offspring are unequal, parent-offspring conflict evolves because offspring are selected to garner more resources for themselves than mothers are selected to provide. The genetic conflicts that lead to parent-offspring conflict are hypothesized to occur in angiosperms because the genetic backgrounds of the seedcoat, endosperm, and embryo are distinct. However, data supporting this conflict are lacking. Conflict over resource provisioning in seed tissues could generate signatures at the molecular level, which we have tested for in tissue-specific genes expressed during seed development and genomic imprinting genes in the facultatively-outcrossing *Arabidopsis thaliana*.

**Pusadee, Tonapha, and Barbara Schaal** (WUStl): *Molecular population genetics of adaptive evolution to deep water condition in wild rice* (Oryza rufipogon *Griff.*). Our goal is to better understand the evolution of wild rice (*Oryza rufipogon*) to deep-water conditions of flooding. The gene *SK2* influences internode elongation and CIPK15 responsible for seed germination under water, which adapts cultivated rice to flooding. We examine DNA sequence variation in these candidate genes to determine the type and strength of selection in comparison to the neutrally evolving *p-VATPase* B-subunit. A total of 51 wild rice populations were collected in a range of natural habitats in Cambodia, Laos, Myanmar, and Thailand. We determine if these sequences show a signature of selection in native populations and if specific alleles at these loci are associated with dry or flood prone habitats.

Siebrasse, Erica, Kate Chiappinelli, Tom Wolsey (WUStl): *The Young Scientist Program: integrating science and inquiry into the St. Louis public school system.* YSP provides many channels for the Washington University community to help inspire young scientists and provide valuable resources for a school system in need. YSP is a volunteer run organization that reaches hundreds of St. Louis school children grades 6-12, primarily underrepresented minorities. Opportunities to participate include summer mentorship of students (Summer Focus) or teachers (Teacher Researcher Partnership) in the lab, generation of inquiry based teaching kits to provide teachers with hands on activities that supplement their teaching requirements (Teaching Kits), a recycling program to donate used lab equipment to local schools, and much more.

**Vigueira, Cindy** (WUStl): *Genomic structure and contemporary evolution of weediness in red rice.* Red rice is an aggressive, weedy form of cultivated rice (*Oryza sativa*) that infests crop fields and is a primary factor limiting rice productivity worldwide. Capitalizing on the relatedness of red rice with a genomic model species, this project addresses the evolution of weediness through three main objectives. 1) Use QTL mapping and genomic divergence scans to determine the genetic basis of weed-adaptive traits. 2) Determine whether the weed's origin and population structure differ among world regions. 3) Determine how newly imposed selective pressures related to use of herbicide resistant cultivars have affected the contemporary evolution red rice.