

Table of Contents: Poster Abstracts

- P1:** Direct regulation of plant Argonautes by microRNA-targeted transcription factors
- P2:** Utilizing physiological traits as a high-throughput phenotyping selection tool for yield in soft red winter wheat
- P3:** Phloem loading as a driver of plant photosynthetic responses to rising atmospheric CO₂
- P4:** Exploiting maize leaf development to identify networks underlying C₄ differentiation
- P5:** Secondary contact short-circuits allopatric speciation in *Carex furva* (Cyperaceae)
- P6:** Negative density dependence is stronger in resource-rich environments across species and associated with higher diversity
- P7:** MET18 connects the cytosolic iron-sulfur cluster assembly pathway to active DNA demethylation in *Arabidopsis*
- P8:** Genetic characterization of Rpp1-mediated resistance to Asian Soybean Rust using in-depth transcriptomic, small RNA, and genomic analyses
- P9:** An RNA-Seq analysis of oxalate-degrading transgenic soybean in response to *Sclerotinia sclerotiorum* during early infection
- P10:** Combining gas exchange physiology with genetics to understand leaf photosynthesis and transpiration
- P11:** Ecological niche specialization of temperate and tropical forest trees across large-scale diversity gradients
- P12:** Potential novel role of the *Agrobacterium* virulence effector protein VirE2 in modulating plant gene expression
- P13:** Nectary size and nectar loss in the evolution of the selfing syndrome in *Ipomoea lacunosa* (Convolvulaceae)
- P14:** Dynamic regulatory changes in nitrogen utilization genes from a century of selection for seed protein concentration in maize
- P15:** The ecological genetics of critical photoperiod clines in annual monkeyflowers (*Mimulus guttatus*)

- P16:** Next generation weed control system in cotton
- P17:** Leaf-level hyperspectral reflectance as a tool for measuring photosynthetic capacity in C4 grasses
- P18:** Rapid hemispherical photographic phenotyping of productivity and canopy dynamics in a *Setaria* RIL population
- P19:** Functional characterization of maintenance DNA methyltransferases in antiviral defense against cassava-infecting geminiviruses
- P20:** Comparative transcriptomics on the macroevolutionary scale using Caryophyllales
- P21:** Ecological field studies and copy number variation (CNV) analyses shed light on the selective mechanisms maintaining North American white clover cyanogenesis clines
- P22:** Suberin feruloylation is not required for CO₂ concentration in the maize bundle sheath
- P23:** Quantifying the sources of reductant for fatty acid biosynthesis in *Camelina sativa*
- P24:** Histone H1 mutation affects gene imprinting and DNA methylation in *Arabidopsis*
- P25:** Triacylglycerol biosynthesis in seeds of *Camelina Sativa* expressing *Arabidopsis* PLD genes
- P26:** Development of molecular markers for genetic male sterility in *Gossypium hirsutum*
- P27:** Disturbance and dispersal interactively homogenize plant communities: A synthesis of experiments
- P28:** Patterns of colonization in the ebony and persimmon genus (*Diospyros*) in Madagascar and the Mascarene Islands
- P29:** Analysis of mating system and genetic structure in the endangered, amphicarpic plant, Lewton's polygala (*Polygala lewtonii*)
- P30:** Enemy-mediated negative feedbacks as a stabilizing force that maintains diversity of Tallgrass prairies
- P31:** Genome mining for CLE orthologs reveals surprising conservation across angiosperms
- P32:** KAZU buffer for plant DNA extraction

- P33:** Genome sequencing and development of a high-density genetic map for European Hazelnut (*Corylus avellana L.*)
- P34:** Evidence of a robust DNA methylation monitoring sequence in *Arabidopsis*
- P35:** Effect of drought treatments on transpiration rate and stomatal density in *Brachypodium distachyon*
- P36:** A comparison of pollination systems of *Oenothera nealleyi* in pre- and post-drought years
- P37:** Pollinator patterns affecting seed set in *Baptisia alba*
- P38:** Genetic analysis of root system architecture in TeoNILs
- P39:** Preliminary results from an investigation of pollination and floral form change in the Genus *Dalea*
- P40:** A role for long-distance RNA signaling in tomato via graft-induced vigor
- P41:** Transcriptional dynamics of jasmonate responses across the *Setaria viridis* leaf developmental gradient
- P42:** The impact of plant height on the reproductive success of *Campanula americana* in bluff and wetland populations
- P43:** Proteomics & mass spectrometry: Essential tools for systems biology
- P44:** Advocating Translational Genetics/Genomics Conference in St. Louis (ATGC-STL): Connecting genes, connecting people
- P45:** PLD α 1 is a key component and regulator of G-protein mediated signaling
- P46:** QTL by Environment Interactions in the Maize Ionome

Poster Abstracts

Poster 1

Direct regulation of plant Argonautes by microRNA-targeted transcription factors

J. Steen Hoyer¹, Mariah Hassert¹, Jose Pruneda-Paz², Ghislain Breton², Steve A. Kay^{2,3}, James C. Carrington¹.

Email: jhoyer@danforthcenter.org

¹Donald Danforth Plant Science Center, Saint Louis, MO, USA. ²University of California San Diego, CA, USA.

³University of Southern California, Los Angeles, CA, USA.

Argonautes are the central effector proteins of RNA silencing which bind target transcripts in a small RNA-guided manner. Arabidopsis has ten Argonaute proteins, with specialized roles in RNA-directed DNA methylation, post-transcriptional gene silencing, and anti-viral defense. To better understand specialization among Argonautes (AGOs) at the level of transcriptional regulation, we tested a library 1541 transcription factors for binding to the promoters of AGO1, AGO10, and AGO7 using yeast 1-hybrid assays. A ranked list of candidate DNA-binding TFs revealed binding of the AGO7 promoter by a number of proteins in two different miRNA-regulated families with known roles in developmental timing and leaf morphology. We are testing the functional significance of these binding sites for AGO7's role in vegetative phase change and its polar expression pattern. Reverse genetic, transgenic, ChIP, and expression profiling approaches will be used to define the regulatory network involving AGO7, TFs, and the microRNAs that regulate them.

Poster 2

Utilizing physiological traits as a high-throughput phenotyping selection tool for yield in soft red winter wheat

David Chappell and Anne McKendry. Email: dgcvff@mail.missouri.edu

University of Missouri, Columbia, MO, USA.

The objective of this experiment was to determine the efficacy of utilizing high-throughput phenotyping technologies based on measurement of physiological traits as indirect selection criteria for yield and related components. Two replications of 36 soft red winter wheat (*Triticum aestivum* L.) genotypes arranged in a randomized complete block design and selected for high or low yield were planted over the course of two years. Physiological and agronomic traits were measured over both years during four developmental stages. In the combined analysis, spectral reflectance indices based on light in the far red portion of the visible spectrum were the physiological traits most highly correlated with agronomic traits. Coefficients of determination ranged from 0.55 to 0.7 for grain number per square meter, yield, and harvest index when physiological traits were measured during the anthesis (Zadoks 60 to 68) and milk (Zadoks 71 to 77) developmental stages. Significant environmental effects were observed across years, but collecting physiological trait data during anthesis minimized these effects. Experimental results indicate that spectral reflectance indices based on the far-red portion of the visible light spectrum can be effectively utilized by breeding programs as high-throughput indirect selection criteria for agronomic traits, saving time and resources for other purposes.

Poster 3

Phloem loading as a driver of plant photosynthetic responses to rising atmospheric CO₂

Kristen Bishop¹, Elizabeth Ainsworth^{1,2}, Christopher Montes¹. Email: kabisho2@illinois.edu

¹University of Illinois at Urbana-Champaign, Urbana, IL. ²USDA-ARS, Urbana, IL.

Increased atmospheric [CO₂] stimulates photosynthesis of C₃ plants, but at elevated [CO₂], sugars can accumulate in leaves and negatively feedback on photosynthesis. This phenomenon

has primarily been tested in species which use active sugar transporters to load phloem (apoplastic loading). Other species use passive diffusion along a sucrose gradient from leaf mesophyll cells to phloem (passive loading). The hypothesis for this experiment was that passive loaders, adapted to high mesophyll sucrose concentrations, would experience less sugar-mediated feedback of photosynthesis at elevated $[\text{CO}_2]$ compared to apoplastic loaders. To test this, pea and beet (apoplastic phloem loaders) and strawberry and peony (passive phloem loaders) were grown at elevated $[\text{CO}_2]$ in the field in 2013 and 2014. Decreases in photosynthetic capacity were observed in 2014, but not 2013, in all species, corresponding to an increase in soluble sugar content in all species at elevated $[\text{CO}_2]$ in 2014, but not in 2013. When photosynthesis measurements were taken at different CO_2 concentrations (A/c_i curves), the passive loading species transitioned from Rubisco- to electron transport-limited photosynthesis at much higher CO_2 concentrations than apoplastic loading species. A meta-analysis of previous literature was performed to determine whether the field results are consistent for a broader range of species.

Poster 4

Exploiting maize leaf development to identify networks underlying C4 differentiation

Yingying Cao^{1,2}, Indrajit Kumar¹, Andrea Eveland¹, Thomas P. Brutnell¹. Email: ycao@danforthcenter.org

¹Donald Danforth Plant Science Center, Saint Louis, MO, USA. ²Henan Agriculture University, Zhengzhou, Henan, China.

Maize (*Zea mays*) is one of the most important food, feed and fuel crops in the world and is also one of the most productive. Like many of the world's most productive plants, maize utilizes C4 photosynthesis to fix carbon using two anatomically and biochemically distinct cell types. Two features of C4 plants are close vein spacing and a photosynthetically active inner bundle sheath (BS) with large, numerous starch-filled plastids that are arranged centrifugally around the cell. In contrast, mesophyll cell plastids are arranged randomly in the cell and do not accumulate starch. The maize leaf is an ideal system to study C4 differentiation as it is subdivided into two organs, a low vein density sheath and a high vein density blade. The *lg1* mutant blurs the normally distinct boundary between sheath and blade tissues and provides an opportunity to follow the differentiation process by extending the transition from C3-like to C4 tissue. Several hormones have been implicated in the control of vein patterning, a key C4 trait, but little is known of the regulatory network that controls this differentiation process. Here I describe our preliminary data utilizing RNAseq analysis to define the network of genes associated with C3 and C4 tissues at the boundary of blade and sheath in wild type and the *lg1* mutant.

Poster 5

Secondary contact short-circuits allopatric speciation in *Carex furva* (Cyperaceae)

Enrique Maguilla¹, Marcial Escudero², Andrew L. Hipp^{3,4}, Modesto Luceño¹. Email: emagsal@gmail.com

¹Universidad Pablo de Olavide, Seville, Spain. ²Universidad de Sevilla, Seville, Spain. ³The Morton Arboretum, Lisle, IL, USA. ⁴The Field Museum, Chicago, IL, USA.

Carex furva (Cyperaceae) is a chionophylous species endemic from the Iberian Peninsula, inhabiting high siliceous mountains from 1800 to 3100 m above sea level. The highly specific habitat requirements have led to a disjunct distribution of the species in the high altitudes of the Mediterranean mountains. Moreover, this species is expected to be highly sensitive to changes on its habitat caused by direct human activities and/or climate change. We have performed an exhaustive study of the species including sampling through the full distribution range, morphological measurements of herbarium specimens, the amplification and sequencing of the plastid regions (*atpI-atpH* and *psbA-trnH*), a genomic study using RADseq, and divergent times

estimation analysis using DNA regions (ITS, ETS and trnL-F). The combination of our results led us to detect an incipient allopatric speciation process supported by morphological and molecular data that seems to be short-circuited by a recent secondary contact, a north-to-south gene flow event.

Poster 6

Negative density dependence is stronger in resource-rich environments across species and associated with higher diversity

Joseph A. LaManna, Maranda L. Walton, and Jonathan A. Myers. Email: jlamanna@wustl.edu

Washington University in Saint Louis, MO, USA.

Negative density dependent recruitment is thought to increase species diversity by more strongly limiting population densities for common than for rare species. The strength of negative density dependence can also change along biogeographic-scale productivity gradients, potentially increasing diversity in more productive regions. Yet whether the strength of negative density dependence increases along landscape-scale productivity gradients remains untested, leaving the effects of these gradients on biodiversity unclear. We therefore tested for increases in the strength of negative density dependent recruitment and diversity along a resource availability gradient for 28 woody-plant species across two life stages (seedling and sapling). We also tested if negative density dependence promotes species co-existence by favoring rarer species. Negative density dependence was stronger in resource-rich than in resource-poor environments across species at both life-stages, which corresponded to higher diversity in resource-rich environments despite no overall increases in biomass. In addition, negative density dependent sapling recruitment was stronger for common than for rare species. These results suggest that productivity gradients at the landscape scale can alter the strength of negative density dependent recruitment, increasing diversity in resource-rich environments. Moreover, we provide evidence that negative density dependence promotes species co-existence by favoring the recruitment of rarer species.

Poster 7

MET18 connects the cytosolic iron-sulfur cluster assembly pathway to active DNA demethylation in *Arabidopsis*

Cheng-Guo Duan^{1,§}, [Xingang Wang](mailto:Xingang.Wang@purdue.edu)^{1,§}, Kai Tang¹, Huiming Zhang², Satendra K. Mangrauthia^{1,4}, Mingguang Lei¹, Chuan-Chih Hsu³, Yueh-Ju Hou¹, Chunguo Wang^{1,5}, Yan Li⁶, W. Andy Tao³, Jian-Kang Zhu^{1,2,*}. Email: wang758@purdue.edu, jkzhu@purdue.edu

¹Department of Horticulture and Landscape Architecture, Purdue University, West Lafayette, IN 47907, USA.

²Shanghai Center for Plant Stress Biology, Shanghai Institute of Biological Sciences, Chinese Academy of Sciences, China. ³Department of Biochemistry, Purdue University, West Lafayette, IN 47907, USA. ⁴Biotechnology Section, Directorate of Rice Research, Hyderabad 500030, India. ⁵College of Life Sciences Nankai University, Tianjin, China. ⁶Ecological Security and Protection Key Laboratory of Sichuan Province, Mianyang Normal University, Mianyang, Sichuan 621000, China. [§]These authors contribute equally to this work.

DNA demethylation mediated by the DNA glycosylase ROS1 helps determine genomic DNA methylation patterns and protects active genes from being silenced. However, little is known about the mechanism of regulation of ROS1 enzymatic activity. Using a forward genetic screen, we identified an anti-silencing (ASI) factor, ASI3, the dysfunction of which causes transgene promoter hyper-methylation and silencing. Map-based cloning identified ASI3 as MET18, a component of the cytosolic iron-sulfur cluster assembly (CIA) pathway. Mutation in *MET18* leads to hyper-methylation at thousands of genomic loci, the majority of which overlap with hyper-methylated loci identified in *ros1* and *ros1dml2dml3* mutants. Affinity purification

followed by mass spectrometry indicated that ROS1 physically associates with MET18 and other CIA components. Yeast two-hybrid and split luciferase assays showed that ROS1 can directly interact with MET18 and another CIA component, AE7. Site-directed mutagenesis of ROS1 indicated that the conserved iron-sulfur motif is indispensable for ROS1 enzymatic activity. Our results suggest that ROS1-mediated active DNA demethylation requires MET18-dependent transfer of the iron-sulfur cluster, highlighting an important role of the CIA pathway in epigenetic regulation.

Poster 8

Genetic characterization of Rpp1-mediated resistance to Asian Soybean Rust using in-depth transcriptomic, small RNA, and genomic analyses

Xing Wu, Alexandre Garcia, Gautam Naishadham, Matthew Hudson, Steven Clough. Email: xingwu2@illinois.edu
University of Illinois at Urbana-Champaign, Urbana, IL, USA.

Asian Soybean Rust (ASR) is an important disease of soybean. Geneticists have found that there are at least six different resistant genes. The work presented here focuses on rust resistance gene *Rpp1*. An RNA-Seq analysis was conducted to explore the difference in transcriptome level regulation between different *Rpp1* resistant and susceptible genotypes when inoculated with an *AvrRpp1* containing isolate of ASR. The susceptible genotype being used is a dominant susceptible to *Rpp1*, which we hypothesize is the result of a silencing effect by na-siRNA. Therefore, we are comparing the mRNA transcript levels with the expression of small RNA from all the genotypes. Both edgeR and GFOLD statistical programs were used to explore the pattern of differential mRNA expression, and 1662 genes were determined to be differentially expressed among three soybean lines. The small RNA analysis program Shortstack identified 56852 *de novo* small RNAs, 451 of which are predicted as microRNAs. In addition to the expression studies, we are attempting to clone the *Rpp1* region from the three genotypes by screening genomic DNA fosmid libraries that have been made at an average of 3X genome coverage. Results of this research might identify *Rpp1* and will provide further detail on the molecular interactions between soybean and this important pathogen.

Poster 9

An RNA-Seq analysis of oxalate-degrading transgenic soybean in response to *Sclerotinia sclerotiorum* during early infection

Wei Wei. Email: Weiwei8@illinois.edu
University of Illinois at Urbana-Champaign, Urbana, IL, USA.

Oxalic acid (OA) is a main virulent factor for *Sclerotinia sclerotiorum*, which is the causal agent for Sclerotinia stem rot. OA has been suggested to play multiple roles during disease development, especially in the early stage of infection when this necrotrophic pathogen and host maintain a temporarily co-existing relationship. This study involves RNA-seq of infected leaf tissue from a susceptible soybean line (AC-Calibri) and the same genotype transformed with the gene oxalate oxidase (OxO) at 4h and 8h post inoculation. The goal of this project is to get a better understanding at transcriptome level of how soybean and *S. sclerotiorum* interact with each other during early infection, as the previous earliest time point studied by a transcriptomic analysis was 12 hpi. 1009 soybean genes showed differential expression in at least one of the comparisons between different lines, time points and treatments, with a cutoff of FDR <0.02. Gene expression patterns of the two soybean lines and of *S. sclerotiorum* responding to them had been depicted and displayed as heat maps. The pattern shows that OxO induces basal defense in a faster and stronger manner during early infection stages.

Poster 10

Combining gas exchange physiology with genetics to understand leaf photosynthesis and transpiration

Allison R. Kolbe¹, Thomas P. Brutnell², Asaph B. Cousins¹, [Anthony J. Studer](mailto:astuder@illinois.edu)³. Email: astuder@illinois.edu

¹*School of Biological Sciences, Washington State University, Pullman, WA, USA.* ²*Donald Danforth Plant Science Center, Saint Louis, MO, USA.* ³*University of Illinois at Urbana-Champaign, Urbana, IL, USA.*

Current global challenges highlight the need for sustainable agricultural systems and increases in crop yields. A deeper understanding of how crops balance CO₂ uptake for photosynthesis with transpirational water loss will enable the development of crops to meet global food, feed and fuel demands. In 2015, nearly 89 million acres of corn were planted in the United States (USDA), and each acre transpires 3,000-4,000 gallons of water a day (USGS). Even a modest reduction in transpiration while maintaining rates of photosynthesis would constitute large water savings. Time course experiments performed on maize mutants revealed subfunctionalization of duplicated gene copies of *carbonic anhydrase* in specific grass lineages. These genes play a role in carbon fixation and also in stomatal movement in response to changing CO₂ and light conditions. The vast natural genetic variation within maize is also being leveraged to identify leaf traits that affect photosynthesis and transpiration. Preliminary experiments show that significant variation exists between maize lines for traits related to carbon fixation. Furthermore, these phenotypes are robust across environments, suggesting fundamental differences in primary metabolism within a single species. These findings will facilitate the optimization of maize and other crops that can better adapt to the changing global climate.

Poster 11

Ecological niche specialization of temperate and tropical forest trees across large-scale diversity gradients

[Dilys Vela Díaz](mailto:veladd@go.wustl.edu), Marko Spasojevic, Jonathan A. Myers. Email: veladd@go.wustl.edu

Washington University in Saint Louis, MO, USA.

Local-scale interactions among species are often invoked to explain differences in species-composition among high-diversity and low-diversity plant communities. In high-diversity communities, species may partition resources more finely to reduce competition, resulting in smaller niche breadths across environmental gradients. Although variation in species niche breadths among plant communities may provide insights into large-scale diversity gradients, this hypothesis has only been tested at local scales. To test this prediction at large scales, tree species-composition data and environmental data (soil & topography) from 13 forest plots in The Center for Tropical Forest Science-Forest Global Earth Observatory (CTFS-ForestGEO) were used to quantify niche breadths of 2391 tree species. These plots are distributed globally and span low-diversity (e.g. Czech Republic with 11 species) to high-diversity (e.g. Papua New Guinea with 581 species) forests. Average species niche breadth varied significantly among the 13 plots. Within both temperate and tropical regions, species had smaller niches in more diverse communities. This pattern was driven primarily by topographic gradients in temperate regions and soil gradients in tropical regions. These results suggest that local-scale interactions among species can influence niche breadths and offer new insights into the processes that create and maintain large-scale diversity gradients.

Poster 12

Potential novel role of the *Agrobacterium* virulence effector protein VirE2 in modulating plant gene expression

Rachelle Lapham, Lan-Ying Lee, Stanton B. Gelvin. Email: rbuuck@purdue.edu
Purdue University, West Lafayette, IN, USA.

VirE2 is an *Agrobacterium* effector protein that is essential for plant transformation. VirE2 likely coats single-strand T-DNA after it enters the plant cell to protect it from degradation and may assist nuclear import of T-DNA. VIP1 and VIP2 are host transcription factors that interact with VirE2 and are involved in activating plant defense responses. The “Trojan Horse” model posits that T-DNA-bound VirE2 binds VIP1 and uses VIP1 nuclear localization to deliver T-DNA into the nucleus. Recently, our lab showed that VirE2 holds at least a portion of the VIP1 pool outside the nucleus. In addition to VirE2’s proposed structural role in T-DNA trafficking, VirE2 may therefore prevent VIP1 and VIP2 nuclear localization during *Agrobacterium* infection. We shall investigate this model by placing VirE2 under the control of an inducible promoter in *Arabidopsis* and performing RNAseq under non-induced and induced conditions to determine its effect on plant gene expression. We shall identify VIP1 and VIP2 target genes using chromatin immunoprecipitation sequencing (ChIPseq) and determine the VIP1 and VIP2 transcriptomes in the presence or absence of VirE2. We shall also image the intracellular localization of VIP1- and VIP2-fluorescent protein fusions before and after induction of VirE2.

Poster 13

Nectary size and nectar loss in the evolution of the selfing syndrome in *Ipomoea lacunosa* (Convolvulaceae)

Irene T. Liao, Mark D. Rausher. Email: irene.liao@duke.edu
Department of Biology, Duke University, Durham, NC, USA.

In flowering plants, the shift from outcrossing to self-fertilization is one of the most common evolutionary transitions. This transition is associated with changes in several morphological characters, collectively known as the selfing syndrome. While one study demonstrates that natural selection drives reduced flower size in selfers, evidence for other syndrome traits is lacking. We are examining this issue by determining whether nectar loss is the result of selection or drift in *Ipomoea lacunosa* (Convolvulaceae). This morning glory has a 95% selfing rate and exhibits selfing syndrome characters (reduced floral size, pigment loss, little nectar) compared to its outcrossing sister species. As initial steps to address this question, nectary (nectar producing organ) size was measured to establish if correlations exist among nectary size and other floral traits. To determine if candidate genes underlying nectar production and nectary development are involved in nectar loss in *I. lacunosa*, we 1) assessed RNA expression differences in these homologs between the two species and 2) tested the co-segregation of molecular markers and nectar volume in an F2 mapping population. This will lay the groundwork for molecular and field experiments for examining the evolutionary forces driving nectar loss in the evolution of the selfing syndrome.

Poster 14

Dynamic regulatory changes in nitrogen utilization genes from a century of selection for seed protein concentration in maize

Jennifer Arp, Christine Lucas, Han Zhao, Farag Ibraheem, Martha Schneerman, Juliann Seebauer, Michael Zinder, Michael Gapinske, Fred Below, Stephen Moose. Email: jarp2@illinois.edu
Department of Crop Sciences, University of Illinois at Urbana-Champaign, Urbana, IL, USA.

Begun in 1896, the Illinois Long Term Selection Experiment (ILTSE) is the longest running

genetic experiment in higher plants, with more than 110 cycles of divergent recurrent selection producing known extremes for grain nitrogen concentration. The ILTSE is a unique resource for maize functional genomics because of its genetic variation for N uptake, utilization, and growth response to N, each of which is influenced by many genes. Based on RNA sequencing of the high and low protein inbred lines, 7% of genes on average are differentially expressed in the leaf, earshoot or seeds. Similarly, only 5% of SNP loci were found to be fixed for different alleles between the high and low protein populations. Meanwhile, surprisingly high levels of allelic diversity remain within the population. Continued response to selection using this standing variation may be an effect of canalization. The asparagine cycling system is an example of a change that allowed cryptic variation to become important for continued response to selection. Two genes involved were tested using near isogenic lines to determine the effect on seed protein. Genes found to be important in the ILTSE population could be utilized to improve nitrogen use efficiency in breeding maize and other crops.

Poster 15

The ecological genetics of critical photoperiod clines in annual monkeyflowers (*Mimulus guttatus*)

Nicholas Kooyers, Benjamin Blackman. Email: njk5k@virginia.edu
University of Virginia, Charlottesville, VA.

Plants use environmental cues to orchestrate the developmental transition to flowering in a way that maximizes survival and reproduction in native environments. While the flowering gene regulatory network is well-characterized, genetic variants that allow widespread plants to adapt to local seasonal conditions have rarely been identified. This research explores how variability in photoperiod response allows adaptation to drastically different seasonal environments in an obligate long-day plant, *Mimulus guttatus*. Utilizing samples collected along ten altitudinal gradients, this work identifies parallel clinal patterns in critical photoperiod where high elevation populations require longer daylengths to flower. The genetic basis for variation in photoperiod response within transects is simple, 1-3 QTL control nearly all of the variation in each cline. By assessing patterns of differential expression under photoperiod conditions restrictive to flowering for high elevation plants, strong candidate genes located within each QTL have been identified including multiple FT homologs and MAF-like genes. Furthermore, a reciprocal transplant study conducted in native environments at low and high elevation demonstrates that these QTL are highly adaptive, as they impact the ability to flower and fitness. In combination, these results demonstrate how genetic perturbations to the flowering gene regulatory network can result in locally adaptive gene-by-environment interactions.

Poster 16

Next generation weed control system in cotton

Rita Varagona, Clayton Larue, Marianne Malven, Sherry LeClere, Ron Brinker, Ty Fowler, Richard Voth, Paul Feng. Email: rita.j.varagona@monsanto.com; clayton.t.larue@monsanto.com
Monsanto Company, 700 Chesterfield Pkwy. W, Chesterfield, MO, USA.

Next generation weed control systems in cotton are needed to help manage difficult broadleaf and glyphosate-resistant weeds. U.S. farmers have used dicamba on 237 million acres in the past 10 years. Dicamba-tolerant crops would provide an additional tool for farmers to use in their weed control systems. The gene for dicamba monooxygenase (DMO) was isolated from a soil bacterium (Herman et al. 2005) and used as the starting material to make dicamba-tolerant cotton. Stacked with the phosphinothricin acetyl transferase gene (BAR, Wohllenben et al.,

1988), cotton plants were tested to determine the expression elements necessary to make the plants fully tolerant to sprays with dicamba and glufosinate. To make a complete product, this vector stack has been deployed as a trait stack with genes for glyphosate-tolerance and insect-control genes. Extensive testing shows that the DMO enzyme deployed as a transgene that targets DMO to the plastid, conveyed in a vector stack, can provide excellent tolerance to the dicamba herbicide. This poster will discuss the development of the Bollgard II® XtendFlex™ Cotton product.

Poster 17

Leaf-level hyperspectral reflectance as a tool for measuring photosynthetic capacity in C4 grasses

Rachel E. Paul¹, Darshi Banan¹, Andrew D.B. Leakey^{1,2}. Email: leakey@illinois.edu

¹Department of Plant Biology and ²Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, IL, USA.

Modern genomic and genetic tools are not being fully leveraged to improve the photosynthetic capacity of food and fuel crops due to a phenotyping bottleneck. Currently available techniques for measuring photosynthetic performance are not capable of both accurately estimating photosynthetic capacity and achieving the required high throughput for phenotyping a population. Recently, optical, near-surface reflectance spectroscopy has been proposed and tested as a method for high-throughput screening of photosynthetic capacity in C3 trees and crops. This approach was tested during the summer growing seasons of 2013 and 2014 in C4 grasses using a family of 180 phenotypically diverse recombinant inbred lines (RILs) resulting from a cross of *Setaria viridis* and *S. Italica*. Photosynthetic capacity measured by leaf gas exchange and leaf reflectance spectra (350-2500nm) varied significantly across a subset of the population. Partial Least Squared Regression was used to model the relationship between photosynthetic capacity and leaf optical properties. This model was then applied to spectra measured on all 180 RILs in 4 different environments (high planting density, low planting density, well-watered, and water-limited) in order to test genotype by environment interactions in quantitative trait loci mapping of photosynthetic capacity in this model C4 grass.

Poster 18

Rapid hemispherical photographic phenotyping of productivity and canopy dynamics in a *Setaria RIL* population

Darshi Banan¹, Mark Holmes¹, Hannah Schlake¹, Rachel E. Paul¹, Max J. Feldman², Ivan Baxter², Andrew D.B. Leakey¹. Email: banan.darshi@gmail.com

¹University of Illinois at Urbana Champaign, Urbana, IL, USA. ²USDA-ARS, Donald Danforth Plant Science Center, Saint Louis, MO, USA.

Crop genetics and breeding is limited by the ability to accurately gather useful phenotypic information from large, diverse populations of crop genotypes. Most significantly, rapidly and non-destructively assessing the productivity and allometry of crop plants at high frequency during a growing season in the field remains a significant challenge. Hemispherical photography has proven utility in forestry research as a tool to evaluate the growth, structure, and light interception of a canopy. But, high-resolution digital cameras with fish-eye lens have been large and relatively expensive. This study tested the use of a small digital camera (GoPro Hero3+) customized with a fully hemispherical lens and miniature self-leveling gimbal to rapidly assess leaf area index, biomass production and radiation interception efficiency for quantitative trait loci (QTL) analysis in a diverse population of 186 recombinant inbred lines (RILs) generated by crossing *Setaria viridis* with *S. italica*. Plant area index estimated from hemispherical

photographs correlated strongly with leaf area index ($r^2 = 0.85$), stem biomass ($r^2 = 0.76$) and total vegetative biomass ($r^2 = 0.84$) in an initial validation experiment where LAI varied over time and genotypes from 0.3 – 3.6. Using these trait regressions, canopy hemispherical photography was then analyzed from the full population of RILs. QTL analysis will be presented comparing loci identified from conventional biomass harvests and the rapid hemispherical photographic phenotyping.

Poster 19

Functional characterization of maintenance DNA methyltransferases in antiviral defense against cassava-infecting geminiviruses

PK Kuria^{1,2,3}, DW Miano⁴, EM Ateka¹, JM Onguso¹, JC Carrington³, NJ Taylor³. Email: pkuria@danforthcenter.org

¹Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya. ²Kenya Agricultural and Livestock Research Institute, Nairobi, Kenya. ³Donald Danforth Plant Science Center, Saint Louis, MO, USA. ⁴University of Nairobi, Kenya.

Mitigation of Cassava mosaic disease (CMD) and its causal geminiviruses centers on introgression of resistance imparted by the polygenic (CMD1) and the dominant monogenic locus (CMD2). However, the mechanism(s) of resistance imparted by CMD1 and CMD2 remain unknown. Genotypes carrying CMD1 or CMD2 respond to CMD infection through potent antiviral defense leading to symptom recovery. Viral DNA methylation conditioned by DNA methyltransferases is key in DNA virus defense. CMT3 and MET1 orthologs were isolated and characterized from diverse cassava genotypes. Amino acid analysis revealed conservation of *Manihot esculenta* CMT3 and MET1 among different cassava genotypes. Virus induced gene silencing of *ManesCMT3* and *ManesMET1* by EACMV-UG resulted in >50% downregulation and uncovered important functions in cassava plants morphogenesis. Developmental abnormalities, plants lethality and high virus titer was evident after downregulation of *ManesCMT3* and *ManesMET1* in CMD resistant and susceptible genotypes. CMD2 genotype (TME3) recovered from *ManesCMT3* induced phenotype after 35 dpi, while the CMD1 genotype (TMS30572) did not, indicating different modes of geminiviruses resistance. Suppression of *ManesMET1* abolished symptom recovery in all cassava genotypes demonstrating CG methylation as defense mechanism against cassava-infecting geminiviruses.

Poster 20

Comparative transcriptomics on the macroevolutionary scale using Caryophyllales

Ya Yang¹, Michael J. Moore², Samuel F. Brockington³, Stephen A. Smith¹. Email: yangya@umich.edu

¹Department of Ecology & Evolutionary Biology, University of Michigan, Ann Arbor, MI, USA. ²Department of Biology, Oberlin College, Oberlin, OH, USA. ³Department of Plant Sciences, University of Cambridge, Cambridge United Kingdom.

Studying gene and genome evolution in a comparative framework in non-model plants has been difficult due to availability of data sets and difficulties in homology and orthology inference. To fill in this gap, a large data set have been assembled including transcriptomes from 169 species across the hyperdiverse plant clade Caryophyllales (including cacti, beets and carnivorous plants), targeting species representing key lineages and/or key adaptive transitions. Each of these transcriptomes contains sequences from ~15,000 protein coding genes, ~5000 of which are consecutively expressed across the Caryophyllales. Homology and orthology inferences were carried out using multiple tree-based approaches. By analyzing both the homolog tree topology and synonymous distance among paralogs, at least 20 paleopolyploidy events were located, some of which are associated with shift in habitat types and diversification rates. Further investigation is underway characterizing molecular evolution of genes associated

with adaptive traits, such as the gain and losses of the betalain pigmentation, cold and salt tolerance, and plant carnivory.

Poster 21

Ecological field studies and copy number variation (CNV) analyses shed light on the selective mechanisms maintaining North American white clover cyanogenesis clines

Sara J. Wright, Daniel Cui Zhou, Linda Small, Kenneth M. Olsen. Email: sarajeanes@wustl.edu

Department of Biology, Washington University in Saint Louis, MO.

White clover (*Trifolium repens*) is a widespread legume that has repeatedly evolved climate-associated clines in cyanogenesis, the ability to produce hydrogen cyanide upon tissue damage. Cyanogenic plants predominate in warmer and more arid climates. Two genes, *Ac* and *Li*, encode the two biochemical components needed for cyanogenesis, and both loci have evolved deletion alleles, thus creating four possible cyanotypes: *Ac+Li+* (cyanogenic), and *Ac+li-*, *ac-Li+*, and *ac-li-* (acyanogenic). Both *Ac* and *Li* exhibit copy number variation (CNV; from 0-7 copies). We used field experiments, wild population sampling, and genetic analyses to assess the selective and genetic factors that shape cyanogenesis cline evolution. A higher proportion of cyanogenic seedlings survived in a field plot vs. the greenhouse, resulting in increased frequency of the *Li+* allele in the field. Cyanogenic plants experienced significantly less herbivory than acyanogenic plants in a common garden of 161 genotypes sampled across 18 sites from Florida to Vancouver. Common garden fitness analyses are underway. Using wild plants sampled from four climatically distinct North American locations, we found a positive correlation between *Ac* CNV and aridity, and a positive correlation between *Li* CNV and minimum winter temperature; these results suggest local climatic adaptation through selection on CNVs.

Poster 22

Suberin feruloylation is not required for CO₂ concentration in the maize bundle sheath

Rachel Mertz^{1,2}, Patricia Ellsworth³, Lwanga Nsubuga³, Susanne von Caemmerer⁴, R. Howard Berg¹, Asaph Cousins³, and Thomas P. Brutnell¹. Email: rmertz@danforthcenter.org

¹Donald Danforth Plant Science Center, Saint Louis, MO, USA. ²Department of Plant Biology, Cornell University, Ithaca, NY, USA. ³School of Biological Sciences, Washington State University, Pullman, WA, USA. ⁴Research School of Biology, Australian National University, Canberra, Australia.

C₄ grasses often outperform C₃ species under hot, arid conditions due to superior water and nitrogen use efficiencies and lower rates of photorespiration. A method of concentrating CO₂ around the site of carbon fixation in the bundle sheath (BS) is required to realize these gains. In NADP-malic enzyme (NADP-ME)-type C₄ grasses such as maize, suberin deposition in the BS cell wall is hypothesized to act as a diffusion barrier to CO₂ escape and O₂ entry from surrounding mesophyll cells. Suberin is a heteropolyester comprised of acyl-lipid-derived aliphatic and phenylpropanoid-derived aromatic components. Suberin is synthesized by a large network of biosynthesis and regulatory genes, which remain mostly uncharacterized in monocots.

To disrupt aromatic suberin synthesis, we mutated two paralogously duplicated, unlinked maize orthologues of Arabidopsis *ALIPHATIC SUBERIN FERULOYL TRANSFERASE*, *ZmAsfta* and *ZmAsftb*, using closely linked *Ds* transposons. Characterization of loss-of-function double mutants revealed a 50-96% reduction in suberin-specific aliphatic monomers without a stoichiometric decrease in aromatic monomers in juvenile leaves. However, we observed attenuated accumulation of osmiophilic material in the BS suberin lamellae by TEM, as well as separation of the suberin lamellae from the cell walls. We investigated whether arabinoxylan

could act as a competing sink for hydroxycinnamates to mask the aromatic suberin deficiency and found no significant changes. There were no other morphological phenotypes in photosynthetic tissues under ambient conditions. Furthermore, there was no significant effect on net CO₂ assimilation at sub-ambient, ambient, or elevated CO₂ levels, and no effect on ¹³C isotope discrimination relative to wild type. Likewise, although similar monomer deficiencies were apparent in double mutant root suberin, there was no effect on germination in saline soil, nor was there a growth defect relative to wild type during flooding stress. Thus, *ASFT* is required for normal suberin ultrastructure in maize, but not for barrier function, contrary to its *Arabidopsis* and potato homologues.

Poster 23

Quantifying the sources of reductant for fatty acid biosynthesis in *Camelina sativa*

Thuy B. Truong and Douglas K. Allen. Email: ttruong@danforthcenter.org

USDA-ARS/Donald Danforth Plant Science Center, Saint Louis, MO.

Camelina sativa has great potential value as an oilseed crop. On a dry weight basis, its oil content ranges anywhere from 30 to 40%. This oil contains a high percentage of polyunsaturated and monounsaturated fats, making it beneficial for use in food and feed application. A number of industrial goods such as cosmetics, soaps, and detergents can be made from *Camelina* oil. Additionally, *Camelina* may serve as an important source for future biofuels. A challenge for scientists is understanding how these oils are produced in *Camelina*. Three major components are needed for oil production: a carbon source, reducing equivalents, and energy. It has been hypothesized that the oxidative pentose phosphate pathway (OPPP) is responsible for generating most of the reducing equivalents, i.e. NADPH for fatty acid synthesis, though no definitive study exists. Our current work indicates that OPPP provides a minimal amount of NADPH for fatty acid synthesis. Determining the sources of reducing equivalent for oil production will be important to efforts aimed at metabolically engineering *Camelina* for industrial uses.

Poster 24

Histone H1 mutation affects gene imprinting and DNA methylation in *Arabidopsis*

Matthew Rea¹, Wenguang Zheng¹, Qiang Han¹, Tzung-Fu Hsieh², Wenyan Xiao¹. Email: wxiao@slu.edu

¹Department of Biology, Saint Louis University, Saint Louis, MO, USA. ²North Carolina State University, Raleigh, NC, USA.

Gene imprinting, that paternal or maternal alleles are differentially expressed, regulates development in mammals and plants. DNA methylation is regarded as a main cause of imprinting by silencing parental alleles. It has been shown that DEMETER (DME), a DNA glycosylase, demethylates DNA and impacts gene imprinting in *Arabidopsis*. In *Arabidopsis*, there are three histone H1 variants (H1.1, H1.2, and H1.3) containing the conserved histone H1 globular domain. The Xiao Lab found that DME interacted with histone H1.2 *in vitro*. However, it was not known whether histone H1 played a role in regulating gene imprinting. The genetic analysis of the loss-of-function histone *h1* mutant was conducted, and the results showed that the maternal histone *H1* allele was needed for DME-mediated gene expression at imprinted loci, such as *MEDEA* (*MEA*). Mutations in histone *H1* also increased DNA methylation in the maternal *MEA* promoter in endosperm. A reciprocal genetic cross between the *h1* triple mutant and wild type was conducted. The results of DNA methylomes of embryo and endosperm from the offspring revealed that *h1* triple mutant affected the methylation level of most of DME targets, which means that histone H1 probably participates in DME-mediated DNA demethylation.

Poster 25

Triacylglycerol biosynthesis in seeds of *Camelina sativa* expressing Arabidopsis PLD genes

Wenyu Yang, Geliang Wang, Philip Bates, Xuemin Wang, Doug K. Allen. E-mail: wyang@danforthcenter.org
USDA-ARS and Donald Danforth Plant Science Center, Saint Louis, MO.

Oil from *Camelina sativa* seeds has been used for biofuel and biochemical production. Triacylglycerol (TAG) as oil in oilseeds can be synthesized in several pathways. Here we show when Arabidopsis PLD ζ genes (*AtPLD ζ 1* and *AtPLD ζ 2*) are expressed in *Camelina* seeds, TAG synthesis is enhanced, resulting in ~3% more oil in mature seeds. In addition, fatty acid composition in various lipid classes is changed and turnover rates of some lipid metabolic pathways are altered. Pool sizes, labeling with ¹⁴C-acetate and ¹⁴C-glycerol and changes in fatty acid composition and acyl location were used to describe the changes in metabolism that accommodate enhanced lipid production. We found: (i) increases in diacylglycerol (DAG), the precursor to TAG, and reduced total phospholipid content during seed development, (ii) elevated 18:3 (linolenic) and 20:1 (eicosenoic) fatty acids with concomitant reductions in 16:0, 18:0 and 18:2, (iii) enhanced flux to DAG in the overexpression line, (iv) and reduced acyl editing due to the PLD ζ activity. These results indicate that diverting carbon from PC in acyl editing to PA plays a central role in oil accumulation in *Camelina* seeds, and by modifying the flux rate of acyl editing PC to PA higher oil level in seeds can be achieved.

Poster 26

Development of molecular markers for genetic male sterility in *Gossypium hirsutum*

Humphrey Wanjugi, Xuehui Feng, Don Keim, Issa Coulibaly, Yan Fu, John Schwarz, Scott Huesgen, Seungho Cho.
Email: humphrey.wanjugi@monsanto.com

Monsanto Company, 800 N. Lindbergh Blvd., Saint Louis, MO, USA.

Genetic male sterility (GMS) in cotton mediated by two homozygous recessive genes, ms5ms5 and ms6ms6, is expressed as non-dehiscent anthers and unviable pollen grains. Sequence analysis on ms5 and ms6 loci in *Gossypium hirsutum* was conducted to reveal genomic variation at these two loci between GMS and wild-type *G. hirsutum* inbred lines, and sequence polymorphism linked to ms5 on A12 and ms6 on D12 was revealed. A haplotype marker set that consisted of four SNPs targeting both ms5 and ms6 gene regions was developed and validated for association with GMS in cotton. Predictability of GMS phenotype by this haplotype SNP set was over 99 %. GMS haplotype marker set can serve as a high throughput molecular breeding tool to select GMS individuals and improve hybrid production efficiency.

Poster 27

Disturbance and dispersal interactively homogenize plant communities: A synthesis of experiments

Christopher P. Catano¹, Timothy L. Dickson², Jonathan A. Myers¹. Email: ccatano@wustl.edu

¹Washington University in Saint Louis, MO, USA. ²University of Nebraska, Omaha, NE, USA.

Intensifying human impacts on the biosphere are altering the frequency and severity of disturbances worldwide. Of particular concern for plant communities is whether such changes will homogenize species composition across space – a phenomenon called biotic homogenization. However, the effects of disturbance on spatial variation in species composition (β -diversity) appear to be idiosyncratic and the underlying mechanisms are not yet generalizable. Theoretically, disturbance can decrease β -diversity through convergent selection of disturbance-tolerant species, resulting in biotic homogenization. Alternatively, disturbance can increase β -diversity through deterministic sorting of species across environmental gradients. Observed idiosyncratic responses could be explained by failure to account for stochastic effects of

disturbance on species richness and interactions between disturbance and dispersal. We tested these hypotheses by synthesizing results from 22 factorial-field experiments that manipulated local disturbance and dispersal in plant communities distributed across North America and Europe. Our results suggest disturbance increases plant β -diversity through deterministic assembly processes, but acts synergistically with dispersal to homogenize composition within landscapes through stochastic increases in species richness. This novel synthesis lends insights into how plant community assembly may be altered by changes in disturbance and dispersal – two processes heavily influenced by human-driven environmental change and relevant for habitat restoration.

Poster 28

Patterns of colonization in the ebony and persimmon genus (*Diospyros*) in Madagascar and the Mascarene Islands

Alexander Linan^{1,2}, George Schatz², Porter P. Lowry II², Allison Miller¹, Christine Edwards². Email: linanag@slu.edu

¹Saint Louis University, Saint Louis, MO, USA. ²Missouri Botanical Garden, Saint Louis, MO, USA.

Islands of the Indian Ocean contain some of the richest plant diversity on earth. One taxon that is particularly diverse in the Indian Ocean region is the genus *Diospyros* (Ebenaceae), which has its center of diversity in Madagascar and the Mascarene Islands (Mauritius, Reunion, and Rodrigues) with ~254 of ~700 total species endemic to these islands. Despite this endemic diversity, the number of colonization events and biogeographic patterns of colonization of these areas by *Diospyros* remain debated. Madagascar has a long, rich geological and biogeographic history that has given rise to a multitude of plausible colonization scenarios, including both vicariance and dispersal, whereas the volcanic Mascarene Islands are relatively young and were likely colonized by dispersal of taxa from Africa or Madagascar. In this study, we seek to identify the number of times Madagascar and the Mascarenes were colonized and possible progenitor species. We conducted phylogenetic analyses of four chloroplast markers across broad taxon sampling of the Mascarenes, Africa, and Madagascar. Preliminary phylogenies indicate that the Mascarenes were colonized twice by *Diospyros*, from Madagascar and Africa. By laying down this phylogenetic framework, future work can be done to examine patterns of population genetic diversity in Mascarene *Diospyros*.

Poster 29

Analysis of mating system and genetic structure in the endangered, amphicarpic plant, Lewton's polygala (*Polygala lewtonii*)

Joel F. Swift¹, Stacy A. Smith², Eric S. Menges², Burgund Bassüner¹, Christine E. Edwards¹. Email: Joel.Swift@mobot.org

¹Center for Conservation and Sustainable Development, Missouri Botanical Garden, Saint Louis, MO, USA. ²Plant Ecology Program, Archbold Biological Station, Venus, FL, USA.

Polygala lewtonii is a federally endangered, amphicarpic plant with a mixed mating system and three types of flowers: 1) aboveground, chasmogamous flowers (i.e., open-pollinated; CH), 2) aboveground cleistogamous flowers (i.e., closed, selfing; CL) and 3) CL flowers on belowground stems (amphicarpy). Aboveground seeds are ant-dispersed, whereas belowground seeds are dispersed via rhizomes. Individuals of *P. lewtonii* were collected at both range-wide and fine geographic scales and genotyped using 11 microsatellite loci. We analyzed patterns of genetic diversity and structure to understand: 1) the predominant mating system (selfing or outcrossing), 2) the amount of reproduction occurring above and belowground and the movement of pollen and seeds across the landscape, and 3) the optimal strategy to conserve the

full range of genetic variation. *P. lewtonii* reproduces predominantly through selfing, but reproduction is occurring by each of the flower types. Patterns of genetic structure indicate that some outcrossing is occurring but both pollen and outcrossed seeds are moving limited distances. Since genetic variation is structured at a fine spatial scale, protecting many populations is necessary to fully conserve the genetic variation in *P. lewtonii*. Conservation seed banking, accompanied by research on seed germination requirements, may also effectively protect genetic variation in *P. lewtonii*.

Poster 30

Enemy-mediated negative feedbacks as a stabilizing force that maintains diversity of Tallgrass prairies

Claudia Stein, Scott Mangan. Email: cstein@wustl.edu

Department of Biology and Tyson Research Center, Washington University in Saint Louis, MO, USA.

Interactions between plants and their soil-borne enemies are hypothesized to serve as strong stabilizing forces that maintain species diversity and determine relative species abundance. However, direct competitive interactions among plants may be equally important to the assembly of plant communities. The Mangan Lab established a series of experiments to test the relative importance of plant-microbial interactions and competitive effects as mechanisms for the maintenance of diversity in a prairie ecosystem. In a greenhouse study, we assessed the performance of seedlings when invading either conspecific monocultures or each of five heterospecific monocultures, in the presence or absence of live soil biota. The results show strong evidence for system-wide negative feedback, but only when live soil microbes remained in the soil. Plant seedlings performed more poorly when invading conspecific monocultures than when invading heterospecific monocultures. When soil organisms were eliminated, the strength of system-wide negative feedback diminished; seedling growth of none of the species was suppressed when grown in their own communities, suggesting that intraspecific competition was weak. Instead, our results support that negative interactions between plants and their specialized soil microbes dominated and are likely sufficient to maintain local diversity.

Poster 31

Genome mining for CLE orthologs reveals surprising conservation across angiosperms

David Goad¹, Matthew Box², Michael McKain², Elizabeth Kellogg². Email: dgoad@wustl.edu

¹*Washington University in Saint Louis, MO, USA.* ²*Donald Danforth Plant Science Center, Saint Louis, MO, USA.*

The Clavata3/ESR like (CLE) genes make up a large family of signaling molecules that are extensively processed after translation. They are important in diverse plant processes, including maintenance of meristem stem cell populations, vascular tissue differentiation, ovule development, and pollen/pistil interactions. CLE genes are composed of three regions: an N-terminal signal domain; a highly conserved C-terminal domain that acts as the active end product after cleavage from the rest of the pre-propeptide during processing; and a central variable domain with low sequence conservation that may play a role in processing. Despite this gene family's importance, little work has previously been undertaken to identify CLEs outside of a few model species, and relationships among orthologs remain confused. In this study, CLEs are identified in a wide range of plant species using HMMER and are unambiguously assigned to orthologous groups using CLANS. Alignments of these ortholog groups revealed a surprising level of conservation in the variable domain but large between-group variation. These findings suggest that CLEs from diverged ortholog groups may be processed by different mechanisms. Further studies are needed to assess the level of functional conservation in these groups.

Poster 32

KAZU buffer for plant DNA extraction

Kazuhiro Kikuchi, Thomas P. Brutnell. Email: kkikuchi@danforthcenter.org
Donald Danforth Plant Science Center, Saint Louis, MO, USA.

We developed KAZU buffer, a novel and safe buffer for a science chemical-free plant DNA extraction in a high-throughput format. It is faster and safer compared with traditional CTAB DNA extraction for plant material. We distributed KAZU buffer to Donald Danforth Plant Science Center (DDPSC) and Boyce Thompson Institute for Plant Research (BTI). We received feedback from five users from DDPSC and two users from BTI. Similar DNA extraction methods have been developed for direct PCR amplification. For example, Sigma-Aldrich sells the Extract-N-Amp tissue PCR kit, which two users compared with our KAZU buffer method. KAZU buffer is currently sold by Kerfast (<http://www.kerfast.com/p-2122-kazu-dna-extraction-buffer.aspx>).

Poster 33

Genome sequencing and development of a high-density genetic map for European Hazelnut (*Corylus avellana* L.)

Erik R. Rowley^{1,2}, Robert VanBuren¹, Douglas W. Bryant¹, Henry D. Priest^{1,3}, Shawn A. Mehlenbacher⁴, Todd C. Mockler^{1,2,3}. Email: erowley@danforthcenter.org

¹Donald Danforth Plant Science Center, Saint Louis, MO, USA. ²Department of Botany and Plant Pathology and Center for Genome Research and Biocomputing, Oregon State University, Corvallis, OR, USA. ³Division of Biology and Biomedical Sciences, Washington University in Saint Louis, MO, USA. ⁴Department of Horticulture, Oregon State University, Corvallis, OR, USA.

European hazelnut (*Corylus avellana* L.) is of global agricultural and economic significance, with genetic diversity existing in hundreds of accessions. Breeding efforts have focused on maximizing nut yield and quality and reducing susceptibility to diseases such as Eastern Filbert Blight (EFB). We present the first sequenced genome among the order Fagales, the EFB-resistant diploid hazelnut accession 'Jefferson' (OSU 703.007), and the characterization of millions of polymorphisms among seven diverse hazelnut accessions. In addition, thousands of new genetic markers derived using Genotyping by Sequence (GBS) were placed on the hazelnut genetic linkage map, a five-fold increase over the previous map. These genomic resources will aid in the discovery of molecular markers linked to genes of interest for hazelnut breeding efforts.

Poster 34

Evidence of a robust DNA methylation monitoring sequence in Arabidopsis

Russell Julian¹, Mingguang Lei¹, Jian-Kang Zhu^{1,2}. Email: julianr@purdue.edu

¹Purdue University, West Lafayette, IN. ²Shanghai Center for Plant Stress Biology, Shanghai Institutes for Biological Science, Chinese Academy of Sciences, Shanghai, China.

Securing our food supply while dealing with less arable land, growing world population, and increasingly variable climate patterns requires a thorough study of how plants manage stress. Genes, including those involved in stress response, reside in genomes where transposable elements (TEs) abound. To keep TEs and inactive genes transcriptionally silent, plants mark them by DNA methylation. An important pathway for gene and TE silencing uses RNA-guided methyltransferases to methylate DNA (RdDM pathway). Conversely, activating silent genes involves the removal of DNA methylation, initiated by demethylases such as repressor of silencing 1 (ROS1). Little is known about how plant cells regulate the level of methylation and demethylation activities. The Zhu Lab previously described a DNA methylation monitoring

sequence (MEMS) in the *ROS1* promoter of Arabidopsis. The level of DNA methylation in MEMS is responsive to both RdDM and ROS1-dependent active demethylation. The results suggest the *ROS1* promoter functions like a thermostat (i.e., methylstat) to sense DNA methylation levels and regulates DNA methylation by controlling *ROS1* expression. A survey of *ROS1* promoter polymorphism among Arabidopsis ecotypes revealed an indel hotspot approximately one nucleosome in length. The significance of this variation in relation to MEMS function is being investigated.

Poster 35

Effect of drought treatments on transpiration rate and stomatal density in *Brachypodium distachyon*

Skyler Mitchell, Stuart Marshall, Stephanie Turnipseed, Luke Burnham, César Lizárraga, Rob Alba, Todd C. Mockler. Email: smitchell@danforthcenter.org
Donald Danforth Plant Science Center, Saint Louis, MO, USA.

Drought avoidance in *Brachypodium distachyon* was investigated by measuring transpiration rate and stomatal density. Nineteen accessions were grown vegetatively for 8 weeks, shoots were excised, and transpiration was monitored gravimetrically. Transpiration varied 2.6-fold (21.4–55.9 ul H₂O/g/hr) for control plants. Accessions BdTR8i, BdTR3c, ABR1, and Koz-3 had the lowest transpiration rates, while S6D, Gaz-5, Bd1-1, and Gaz-8 had the highest rates among control plants. Transpiration varied 2.1-fold (31.6–68.0 ul H₂O/g/hr) for drought-treated plants. Accessions Adi-3, Gaz-5, Mig3, and Gaz-8 had the lowest transpiration rates, while Bd21-0, S6D, BdTR3c, and Bd30-1 had the highest rates among drought-treated plants. Transpiration varied 6.6-fold (11.3–74.3 ul H₂O/g/hr) for drought-recovery plants. Accessions Gaz-5, Gaz-8, ABR7, and Koz-3 had the lowest transpiration rates, while Bd30-1, G31i4, S6D, and CSR6 had the highest rates among drought-recovered plants. Stomatal density ranged from 126–177 stomata/mm² in control plants. Accessions Mig3, Bd1-1, Mon3, and Bd3-1 had the least stomata/mm², while Bd21-0, Gaz-8, CSR6, and Bd30-1 had the most stomata/mm². Drought treatment increased stomatal density ($p < 0.05$) by 16.9% and 23.9%, respectively, for Bd1-1 and Gaz-8. Accessions thought to be more drought resistant transpire at higher rates (with fewer stomata, in some cases) than those thought to be drought sensitive.

Poster 36

A comparison of pollination systems of *Oenothera nealleyi* in pre- and post-drought years

Grant Czaplá¹, Ryan C. Hulsey², Adam Rork¹, Hannah Best¹, Sakara Alejo¹, Dr. Kyra N. Krakos^{1,2}. Email: gczapla1@live.maryville.edu

¹Maryville University, Saint Louis, MO. ²Missouri Botanical Garden, Saint Louis, MO.

Pollination systems can change in response to environmental factors. These changes may be from a generalist to a specialist pollination system or a shift to a different main pollinator. These changes may be detrimental to the reproductive success of the species. In this study we focus on the pollination systems of *O. nealleyi* in pre (2009) and post (2015) drought years. We compared detailed pollination data from 2009 and 2015 in the same populations in Alpine, TX. We used hand pollination studies to determine if the species is currently experiencing pollen limitation. Our results indicated a shift from the majority of pollen flow moved by noctuid moths in 2009, to 100% of the pollen flow moved by bees in the day in 2015. However, *O. nealleyi* is not experiencing pollen limitation ($p = 0.909$) in 2015. The change in pollination systems may reflect how a species can maintain reproductive success even through climate changes.

Poster 37

Pollinator patterns affecting seed set in *Baptisia alba*

Kyra N. Krakos^{1,2}, Adam Rork¹, Emily Shipley¹. Email: eshiple1@live.maryville.edu
¹Maryville University, Saint Louis, MO. ²Missouri Botanical Garden, Saint Louis, MO.

The flowering structure of a plant may impact the quality of the seed set if the pollinator has a particular pollination pattern. In this study, the foraging patterns of the current pollinators impacting the reproductive success of *Baptisia alba* at Shaw Nature Reserve was examined. It combines pollinator observations and pollen load analysis to determine main pollinators. The researcher recorded pollinator foraging patterns. They compared seed sets (n=11 plants) for flowers at the bottom and top of the inflorescence to determine impact of potential geitonogamous pollen deposition by pollinators. The results show that *Bombus* are responsible for 89.6% of the total pollen flow in these populations. *Bombus* consistently forage in a bottom to top pattern on inflorescences like *Baptisia alba*, which have multiple flowers. The results indicated no statistical difference ($p=.6172$) between top and bottom seed sets. Therefore, it concludes that the foraging pattern of the main pollinator *Bombus*, although most likely increasing geitonogamous pollen deposition in flowers at the top of the inflorescence, is not impacting the reproductive success of *B. alba*.

Poster 38

Genetic analysis of root system architecture in TeoNILs

Zhengbin Liu¹, Eric Floro¹, Sherry Flint-Garcia^{2,3}, Christopher Topp¹. Email: zliu@danforthcenter.org
¹Donald Danforth Plant Science Center, Saint Louis, MO. ²Division of Plant Science, University of Missouri, Columbia, MO. ³Plant Genetics Research Unit, USDA-Agricultural Research Service, Columbia, MO.

Root system is essential for acquirement of water and nutrients and anchoring shoots to the ground; however, it has never been regarded as one breeding target due to the difficulties of selection in crop breeding programs. Recently, several studies suggested that the future of crop improvement may lie in the genes of the past, including one focused on the dynamic responses to low nitrogen by roots in corn (*Zea Mays* L.) and its ancestor teosinte (*Zea Mays* subsp. *parviglumis*). In addition, given the changes associated with maize domestication, including changes in competition, habitat, and cultivation practices, one unexplored hypothesis is that domestication may have not only altered maize shoot architecture but may have also changed the morphology and physiology of the root system. Gaudin et al (2014) supported this hypothesis with the evidence that changing the expression level of Teosinte Branched 1 (Tb1) could alter the size of the root system via altering the number of crown roots and lateral roots. However, the genetic basis of root system architecture for maize and teosinte has not been reported. To mine the beneficial alleles from teosinte and to facilitate the comparison of maize and teosinte, TeoNILs were developed. TeoNILs are introgression lines with one common/reference parent, B73, and a second parent from ten different accession of teosinte. With shovelomics phenotyping technique and GBS (genotyping by sequencing) data, here we reported the genetic analysis of root system architecture with TeoNILs. A few QTLs controlling root system architecture (RSA) were identified. Meta-analysis of previously measured leaf traits in the TeoNILs showed a colocalized QTL between leaf morphology and RSA, which may be attributable to genetically co-regulated changes in leaf morphology or the root shoot communication. Together, our results not only improved on the utility of a valuable genetic resource but also shed light on the complex, genetic basis for differences in root system between natural populations.

Poster 39

Preliminary results from an investigation of pollination and floral form change in the Genus *Dalea*

Justin Zweck¹, Peter Bernhardt². Email: jzweck@slu.edu

¹Maryville University, Saint Louis, MO, USA. ²Missouri Botanical Garden, Saint Louis, MO, USA.

Dalea is a fascinating plant genus in the legume (Fabaceae) family due to its striking variation in floral form. While some species possess the papilionoid floral form typical of most legumes, in which the sexual organs are enclosed by the petals, others have lost this form, having their anthers and stigma exposed and exerted beyond the petals. We tested the hypothesis that this shift in floral form has been accompanied by a shift in pollination system and also recorded natural rates of pollination of species with each floral form at the Appleton-Whittell Research Ranch from August-September 2014. Specifically, we investigated whether papilionoid *Dalea* feature a more specialized pollination system than non-papilionoid *Dalea*. Insects found pollinating non-papilionoid species *D. albiflora* and *D. candida* represented a broad range of taxa, including beetles, wasps, flies and bees. In contrast, only bees were found pollinating papilionoid *D. formosa*, and only 3 insects were captured over ~33 hours of observation on the three papilionoid species studied. Natural rates of pollination varied between floral forms as well. While unbagged flowers had significantly more pollen grains on their stigmas than those covered with a bag to prevent insect visitation in non-papilionoid *D. albiflora*, there was no significant difference in pollen deposition on bagged vs. unbagged flowers of papilionoid *D. formosa*, *D. nana*, and *D. pogonathera*. Together, these preliminary data are consistent with a shift from bee pollination in papilionoid *Dalea* towards a more generalized pollination system in non-papilionoid *Dalea*. Additionally, differences in natural rates of pollination during the study period suggest that the generalized strategy can be beneficial when bee abundance is low. Although further research is required, this preliminary study may shed light on the selective pressure promoting loss of the papilionoid floral form in *Dalea*.

Poster 40

A role for long-distance RNA signaling in tomato via graft-induced vigor

Margaret Frank, Daniel H. Chitwood. Email: mfrank@danforthcenter.org

Donald Danforth Plant Science Center, Saint Louis, MO, USA.

Grafting has been used to increase yield, especially in the context of biotic and abiotic stress, for over 2000 years. Although recent experimental evidence suggests that non-cell autonomous long-distance signals may play an important role in the mechanism through which grafting impacts plant growth and physiology, the precise identity of these signals and the mechanisms by which they act to affect yield remain largely unexplored. In tomato, the grafting of elite fruit producing shoots (scions) onto vigorous, interspecific hybrid root systems significantly increases yield. Here, we present data showing that grafting-induced vigor can be reciprocally transferred between the root and shoot systems of an interspecific hybrid (*Solanum lycopersicum* x *S. habrochaites*) and domesticated (*S. lycopersicum*) tomatoes. We combine these measurements with RNA-seq profiles from reciprocally grafted root and shoot systems in order to identify non-cell autonomous graft-transmissible transcripts that may serve as molecular signals through which grafting-induced vigor is conferred.

Poster 41

Transcriptional dynamics of jasmonate responses across the *Setaria viridis* leaf developmental gradient

Christine Shyu, Indrajit Kumar, Kimberly Maxon-Stein, Dustin Mayfield-Jones, Thomas P. Brutnell. E-mail: cshyu@danforthcenter.org

Donald Danforth Plant Science Center, Saint Louis, MO, USA.

The wound hormone jasmonate (JA) and its derivatives regulate a broad range of responses from growth and development to defense against biotic and abiotic stresses. Though the core JA signaling pathway has been largely characterized in Arabidopsis, differences in JA responses between monocots and dicots have been reported, suggesting the need for characterization of the JA pathway in grass systems. The grass leaf provides an attractive platform for spatiotemporal studies where the leaf develops and matures from the base to the tip, displaying a continuous developmental gradient. In this study, a wound treatment was applied to the leaf developmental gradient using the emerging grass model *Setaria viridis* to characterize the transcriptional dynamics of JA responses in a high-resolution spatiotemporal manner. Preliminary results suggest that wound responses initiate at mature leaf segments and progress towards young developing segments over time. Clustering analysis of the RNA-seq data also led to identification of 14 novel basic helix-loop-helix transcription factors that co-express with known JA-responsive genes. Outcomes from this research provide insight into the dynamics of JA responses and open new avenues to understanding the molecular mechanism of JA signaling in grass systems, which comprise the world's most important food, feed, and bioenergy crops.

Poster 42

The impact of plant height on the reproductive success of *Campanula americana* in bluff and wetland populations

Adam Wilson¹, Kyra N. Krakos^{1,2}. Email address: awilson3@live.maryville.edu

¹Maryville University, Saint Louis, MO, USA. ²Missouri Botanical Garden, Saint Louis, MO, USA.

An increase in plant height could result in an increase in pollination which could increase the reproductive success of a plant. In this study, we examine how height may impact the pollination system of *Campanula americana* in bluff and wetland habitats. We measured morphological traits and pollination systems in both habitats. We looked at the main pollinators of *C. americana* and if they preferentially pollinated based on height. Our results indicate that there is no morphological difference in traits ($p > .05$) across all traits measured. Pollinator observation results and pollen load analysis showed *Bombus* is the main pollinator for both habitats. There is no correlation between height and the amount of pollen a plant receives in either *Bombus* or Halictidae system. *C. americana* has a pollination system and morphology that is consistent across habitat differences.

Poster 43

Proteomics & mass spectrometry: Essential tools for systems biology

Bradley S. Evans. Email: bevans@danforthcenter.org

Donald Danforth Plant Science Center, Saint Louis, MO, USA.

Nowadays mass spectrometry (MS) is well established as an integrated tool for studying biological systems, in particular in the identification and quantification of perturbations from the environment, such as host-microbe interaction and the adaptative and/or defensive mechanisms induced. Protein and metabolite contents, which are the final products of the genome expression, correlate intrinsically with how the different species and strain genotypes will respond with the interacting environment. Qualitative MS-based tools are routinely used in defining protein-

protein interaction networks, protein signaling pathways, metabolic phenotyping and metabolite pathway and structure elucidation. Quantitative methods can reveal the dynamics of cellular networks in response to modifications with the environment. Though proteomic approaches are more advanced, approaches are rapidly developing for the study of metabolites and metabolic networks with the emergence of higher resolution mass spectrometers. The Proteomics & Mass Spectrometry Facility (PMSF) has been involved in facilitating the progress of various research projects for profiling proteins and small molecules from different species and strains under various conditions. Over the past year, the PMSF has gone through a series of instrumental upgrades. The main tools used for protein and small molecule analyses and the new state of the art equipment at the PMSF are presented here.

Poster 44

Advocating Translational Genetics/Genomics Conference in St. Louis (ATGC-STL):

Linking genes, Linking people

Joseph Bradley, Davinelle Daniels, Chelsea Pretz. Email: atgcstlsymposium@gmail.com
Harris-Stowe State University, Saint Louis, MO, USA.

“Advocating Translational Genetics/Genomics Conference in St. Louis (ATGC-STL)” symposium hosted by the Historically Black College and University of Harris-Stowe State University, aims to pioneer early exposure to quality research in genetics and to promote genetic literacy of students at the high school, undergraduate, and graduate levels. The symposium will offer activities for a wide range of genetics scholars and provide the opportunity for students to present their work in the genetics field, interact with university faculty, and obtain information on undergraduate and graduate level opportunities in genetics research. Underrepresented St. Louis public high school students will be chosen to attend the symposium. These students will be introduced to a diverse array of current genetics research and will be guided through the poster session and oral presentations by experienced undergraduate student volunteers. The ATGC-STL committee aims to foster an environment that enables emerging scientists to explore the field of genetics research. ATGC will be held Saturday, February 27, 2016.

Poster 45

PLD α 1 is a key component and regulator of G-protein mediated signaling

Swarup Roy Choudhury, Sona Pandey. Email: srchoudhury@danforthcenter.org
Donald Danforth Plant Science Center; St. Louis, Missouri, 63132,

Heterotrimeric G-proteins comprised of G α , G β and G γ proteins are important signal transducers in all eukaryotes. In plants, G-proteins are involved in the regulation of multiple biotic and abiotic stresses as well as many developmental processes, even though their repertoire is significantly limited compared to that in the metazoan systems. One G α , one G β and three G γ proteins represent the heterotrimeric G-protein complex in Arabidopsis and a single regulatory protein, RGS, is one of the few known biochemical regulators of this signaling complex. This quantitative disparity between the number of the signaling components and the range of processes they regulate is rather intriguing. We now present evidence that phospholipase D α 1 protein is a key component and regulator of G-protein complex, especially during ABA signaling. We also show that the same G-protein subunits and their regulators exhibit distinct biochemical and genetic interactions depending on the specific signal. Such biochemical plasticity and interaction specificity likely compensates for the lack of multiplicity of individual subunits, and helps to fine-tune the plants' response to constantly changing environment.

Poster 46

QTL by Environment Interactions in the Maize Ionome

Alexandra Asaro¹, Greg Ziegler², Cathrine Ziyomo¹, Owen Hoekenga³, Brian Dilkes⁴, Ivan Baxter². Email: aasaro@wustl.edu

¹Donald Danforth Plant Science Center, St. Louis, MO, USA. ²United States Department of Agriculture, Agricultural Research Service, Plant Genetics Research Unit, Donald Danforth Plant Science Center, St. Louis, MO, USA. ³Genomics Consultant, Ithaca, NY, USA. ⁴Purdue University, West Lafayette, IN, USA

Plant elemental profiles are determined by interactions between a plant's genetic background and its growth environment. In order to investigate genotype by environment interactions, we analyzed the maize (*Zea mays* L.) kernel ionomes of intermated B73 x Mo17 (IBM) recombinant inbreds grown in multiple locations. We measured the levels of 20 mineral nutrients in seeds from ten experiments in six locations over five different years using inductively coupled plasma mass spectrometry (ICP-MS). Quantitative trait locus (QTL) mapping of these element composition data and a set of 4,217 biallelic markers was implemented with the R packages R/QTL and QTLRel. We evaluated several different methods identifying QTL by environment interactions (QEIs). We also performed a principal components analysis (PCA) on the elemental composition data and then used these principle components in place of the elemental phenotypes for QTL mapping. Analysis of PCs identified additional loci affecting the ionome that were not detected in single element scans, suggesting pleiotropic alleles with multi-element effects. Overall, we were able to identify 492 QTL and several instances of QEI, indicating that elemental profiles are highly heritable and responsive to the environment. Weather data and other location-specific variables were analyzed to identify potential environmental drivers of ionic variation.