University of Georgia

Department of Plant Biology Student Symposium

August 21st and 22nd, 2017

Georgia Center

Please join us!

Plant Biology Welcome Reception

Georgia Center Magnolia Ballroom
4:00pm – 6:00pm
Immediately following the Symposium

Food and drinks will be served as we honor award winners, welcome new graduate students and enjoy another great slideshow salute to PBIO faculty and staff.

Acknowledgements

Thank you to the PBIO office staff for their assistance in making this event possible. We would like to particularly acknowledge Stephanie Chirello for organizing many of the logistical aspects of the symposium.

Thank you to our invited speakers Phil Gibson and Luanna Prevost.

Finally, thank you to Douda Bensasson, Wolfgang Lukowitz, and Xiaoyu Zhang for judging graduate student posters and Karolina Heyduk, Jonathan Gent, and Suxing Liu for judging graduate student talks.

2017-18 PBGSA Officers

President: Maria Soto

Vice President: Torey Burns

Secretary: Callie Oldfield

Treasurer: Patrick Smallwood

Peer Development Mentor: Rishi Masalia

Symposium Schedule

AUGUST 21ST

8:30-9:00 Beverages Served, Hang Posters

9:00-9:05 Alumni Speakers Welcome – Master's Hall

9:05-10:00 Alumni Speakers – Master's Hall

Phil Gibson
Associate Professor of Microbiology and Plant Biology,
University of Oklahoma

Luanna Prevost
Assistant Professor of Integrative Biology,
University of South Florida

10:05-10:35 Coffee Break

10:35-11:15 Panel Discussion – Master's Hall

AUGUST 22ND

1:00 – 2:00 Graduate Student Session I – Master's Hall

Kristen Engle - *Single and pairwise expression of Arabidopsis GAUT proteins in HEK293 cells identifies multiple pectin biosynthetic galacturonosyltransferases and potential interactions between them*

Ilkay Doerter - *Understanding the role of septin AspD in the early vegetative growth of Aspergillus nidulans*

Callie Oldfield - *Coarse woody debris and soil respiration 6 years post-tornado in a southern Appalachian forest blowdown*

Rishi Masalia - *It's not Helianth-you, or Helianth-me, but rather Helianthus and how much water we use to grow our food*

2:00 – 3:00 Poster Session, see below

3:00 – 4:00 Graduate Student Session II – Master's Hall

John Spiekerman - *Response of seashore paspalum to short-term salt stress*

A. Kelly Lane - *Exploring benefits and limitations of combining transcriptomic data from different species for WGCNA in order to answer questions related to morphine biosynthesis*
Andries Temme - *Unravelling traits, genes, and trade-offs in low nutrient stress tolerance of cultivated sunflower (Helianthus annuus)*

Karolina Heyduk - *Evolution of PEPC in independent origins of CAM*

4:00 – 6:00 New Student Reception – Magnolia Ballroom

Posters

Graduate Students

Peter Pietrzyk - *Automated phenotyping of root hair traits from microscopy images*
Maria Soto – *FUT4 and FUT6: Arabinogalactan-specific fucosyltransferases in Arabidopsis thaliana*
Alex Mela - *Stress-Response Regulation of Septin AspE in Cell Wall Integrity and High Osmolarity/Glycerol Pathways in A. nidulans*
Rishi Masalia - *Stressful situation? Find some common ground*
Nathan Taitano - *Genotyping-by-sequencing in chile peppers from Oaxaca, Mexico yields insights into evolutionary history of different chile pepper use-types*
Bill Ricci - *Surveying Chromatin Features for the Identification of Intergenic Transcriptional Regulatory Elements in Maize*
Torey Burns - *Drought Resistance Not Lost in Cultivated Sunflower (Helianthus annuus)*
Nick Morffy - *Investigating SMAX1 Degradation in the Karrikin Signaling Pathway*

Will Jordan - *TET-mediated epimutagenesis of the Arabidopsis thaliana methylome*

Undergraduate Students

Liana Mosely - *Comparing the incomparable: a methodological investigation of water limitation treatments*
Ella Vardeman - *Flora of Stone Mountain based on Digitized Specimens at GA Herbarium*

Rosemary Wills - *Predicting Taste of Wild Yeast in Craft Beer due to 4-VG Production*

Nicole Reisinger - *Testing the Repeatability of Sunflower Biomass Accumulation*

Sydney May - *Soil respiration 6 years after wind disturbance and salvage logging at Boggs Creek*

Rhett Parr - *Effects of Salvage Logging on Tree Biomass*

Grace Zheng - *The effect of soil nutrient on the leaf nutrition and root mycorrhizal colonization in the gynodioecious wild geranium, Geranium maculatum*

Elizabeth Umanah – *The Development of Recombinant Campylobacter Vaccines to Combat Food Poisoning*

Garrett Vollino - *A phylogenetic analysis of Pyractomena fireflies*

Brandon Davis - *An investigation of environmental variables and dispersal patterns of North American Photinus fireflies*

Pearl Shah - *Characterizing the species distributions of North American Pyractomenafireflies.*

Olivia Bauer

Presentation Abstracts

Single and pairwise expression of Arabidopsis GAUT proteins in HEK293 cells identifies multiple pectin biosynthetic galacturonosyltransferases and potential interactions between them.

Kristen Engle[1,2], Robert Amos[3], Jeong-Yeh Yang[3], Melani Atmodjo[3], Kelley Moremen[3], Debra Mohnen[2,3]
[1]Department of Plant Biology, The University of Georgia, Athens, GA
[2]BioEnergy Science Center, Oak Ridge, TN
[3]Department of Biochemistry and Molecular Biology, The University of Georgia, Athens, GA

Pectin is a plant cell wall polysaccharide that affects biomass recalcitrance (1,2). The mechanism of its effect on recalcitrance is not known, but likely is due to covalent and non-covalent interactions between pectin and other cell wall polymers (3,4) making extractability of these polymers from biomass difficult. The synthesis of homogalacturonan (HG) and possibly rhamnogalacturonan-I (RG-I) is attributed to the 15 member GAlactUronosylTransferase (GAUT) family in Arabidopsis thaliana (3). GAUT1 has HG biosynthetic (HG:GalAT) activity and functions in a protein complex with GAUT7, which anchors GAUT1 in the Golgi (5,6). To determine if other GAUTs have HG biosynthetic activity by themselves or in a complex, we expressed all GAUTs individually and in pairwise fashion in the Gateway-compatible Human Embryonic Kidney (HEK293) cell expression system. Successfully expressed GAUTs were tested for oligogalacturonide acceptor (OGA)-dependent HG:GalAT activity. We discovered that, in addition to GAUT1, four additional individual GAUTs demonstrate HG:GalAT using radioactive and mass-spectrometry methods. Additionally, pairwise expression of each GAUT suggest that additional GAUT complexes are possible, and these complexes are currently being investigated. This work identifies new pectin biosynthetic enzymes. Understanding the role of specific GAUTs in cell wall biosynthesis will increase our understanding of the role of pectin in recalcitrance and our ability to manipulate pectin in crop species to improve biomass for biofuel production.

Understanding the role of septin AspD in the early vegetative growth of Aspergillus nidulans.

Ilkay Doerter
Dept. of Plant Biology, University of Georgia, Athens, GA

Basic research on septin dynamics in the model organism Aspergillus nidulans helps us better understand the cellular and molecular mechanisms of these cytoskeletal elements and can help develop new therapeutic approaches against propagating diseases. Under right conditions Aspergillus nidulans spores emerge a germ tube to conquer new growth medium. Thereby fungal hyphal tips grow into the food substrate forming a hyphal network with evenly spaced lateral branches. This basic process requires a fine and precise coordination of biochemical and cellular processes. We performed single deletions of the genes encoding for the core septins in A. nidulans (AspA-D). In the absence of AspA, AspB and AspC we could observe an abnormal increase of lateral branches, which is also known as hyperbranching. The knock-out of the fourth core septin gene AspD did not result in obvious phenotypic changes whereas fluorescence microscopy revealed abnormal nuclear structures that worsened with each mitotic division. In contrast to WT the average distance between two neighboring nuclei was greatly reduced in the ΔaspD mutant background, whereas the nuclei themselves were slightly elongated. Time-lapse analyses with a strain expressing AspD-GFP fusion protein showed septin bars contacting both nucleus and cell cortex. Shortly after nuclear division the septin bar located between the two newly divided nuclei suggesting that the septin AspD plays a role after mitosis. In addition, the disruption of the septins revealed an increased number of cells harboring an odd number of nuclei. This may point to an asynchronous nuclear division cycle of the multinucleated fungus in the absence of core septins. We asked the question whether septins could be part of a checkpoint that regulates nuclear division by monitoring cell cycle progression. We treated WT and septin deletion mutants with benomyl, which depolymerizes microtubules and inhibits spindle formation thereby activating the spindle assembly checkpoint. In contrast to the other cells all ΔaspD mutants showed changes in conidiospore density and color, a sectoring phenotype, which is the result of chromosome missegregation. This supports the idea that the SAC checkpoint did not function properly in the absence of AspD. We were able to construct a strain, which expresses both AspB-CFP and AspD-GFP and could confirm that at least two distinct septin heteropolymer populations co-exist in A. nidulans. Future time-lapse analyses will show if these two populations play different roles during nuclear division in A. nidulans.

Coarse woody debris and soil respiration 6 years post-tornado in a southern Appalachian forest blowdown

Callie A. Oldfield and Chris J. Peterson
Dept. of Plant Biology, University of Georgia, Athens, GA

Severe wind disturbances can rapidly change carbon pools and fluxes forests, causing a site to switch from a carbon sink to a source in a matter of minutes. Moreover, salvage logging after a disturbance can resulting in disturbed and compacted soil, altered woody debris carbon pools, and seedling mortality, all of which may further alter carbon dynamics beyond that caused by the disturbance itself. We measured down dead wood and soil respiration in the summer of 2017 at Boggs Creek Recreation Area in northeast Georgia, the site of a severe tornado in 2011. Down dead wood and soil respiration were compared in control (intact forest), salvaged, and unsalvaged areas. Megagrams per hectare of down dead wood was significantly higher in the unsalvaged condition than the control or salvage logging condition (ANOVAs, $p<0.05$ in both cases). Conversely, the volume of down dead wood was not significantly different in the control when compared to the salvage logging condition ($p=0.99$). Soil respiration was significantly higher in the salvage logged condition than the control ($p<0.05$), but was not significantly different between the unsalvaged condition and the control ($p=0.30$) or the unsalvaged condition and the salvaged condition ($p=0.58$). This research shows that wind disturbances have a lasting impact on the amount of down dead wood in a forest, and salvage logging may lead to greater soil respiration years after the initial disturbance, both of which will influence the time elapsed before a disturbed forest switches from carbon source to carbon sink. Further research is needed to determine the duration of these effects, along with the carbon consequences for other forest carbon pools.

It’s not Helianth-you, or Helianth-me, but rather *Helianthus* and how much water we use to grow our food.

Rishi Masalia
Dept. of Plant Biology, University of Georgia, Athens, GA

Cultivated sunflower (*Helianthus annuus*) is an important oilseed crop often grown in rainfed regions. As such, droughts, particularly those occurring the seedling stage, may be devastating for stand establishment and potential crop yield. As such, a better understanding of the genetic pathways regulating drought resistance will enable breeders to develop varieties with improved resistance during young seedling stages. To assess drought resistance we phenotyped 288 genotypes in the sunflower association mapping population, and performed a genome-wide association study (GWAS) utilizing 609,914 SNPs to identify significant marker/trait associations across two seedling vigor and eight root architecture traits. We used polyethylene glycol 6000 (PEG-6000; 8.25%) to create a consistent drought across all stressed individuals Significant differences between both treatments were identified with individuals exposed to PEG-6000 exhibiting deeper rooting and specific root length. The GWAS uncovered 14 QTL at 12 chromosome regions distributed across seven traits, six of which were related to roots and belowground architecture. After assessing the extent of linkage disequilibrium, 310 genes were identified in the 14 QTL, while 55 of these genes have not been previously characterized, a few candidates emerged including Ha14_00019263-RA and Ha3_00037001-RA, which correspond to MIRO2 and DREB26, two known water response genes in *Arabidopsis thaliana*. Moreover, each QTL region was investigated for evidence of genotype-by-environment (GxE) interactions. Seven of these QTL exhibited significant GxE, five of which have the common and rare allele conferring different phenotypic effects under PEG-6000 conditions. QTL with strong effect alleles identified in this study as well as those exhibiting GxE will be useful for marker assisted breeding efforts to improve drought resistance in sunflower seedlings and enhance gene discovery for drought resistance.

Response of seashore paspalum to short-term salt stress

John Spiekerman
Dept. of Plant Biology, University of Georgia, Athens, GA

Soil salinity is a major detriment to crop productivity with 6% of worldwide soils and 20% of irrigated land being affected by salt stress. Additionally germplasms for most cultivated species lack the necessary salinity tolerance traits to select upon for improvement. Thus identifying traits that confer salinity tolerance in a halophyte is beneficial for future introgression of these traits into salt-sensitive crop species. Seashore paspalum is a highly salt tolerant turfgrass with the ability to survive in environments with saline levels near that of ocean-strength seawater. However, the mechanisms contributing to this high salt tolerance are unknown. Furthermore, it is closely related to important cereal crops including maize, sorghum, Setaria, and millets, which are all highly salt sensitive. Using multiple seashore paspalum accessions that differ in salinity tolerance, short-term “salt shock” screens were conducted and tolerance was assessed via biomass, leaf firing, and leaf sodium and potassium measurements. Our results show that short-term “salt shock” screens are sufficient for distinguishing salt tolerant and sensitive genotypes.

Exploring benefits and limitations of combining transcriptomic data from different species for WGCNA in order to answer questions related to morphine biosynthesis

A. Kelly Lane
Dept. of Plant Biology, University of Georgia, Athens, GA

While many plant-derived pharmaceuticals can be found in a variety of species, morphine is only produced in opium poppy (*Papaver somniferum)* and a proposed subspecies (*Papaver setigerum)* making it a unique and evolutionarily intriguing alkaloid. Morphine is a benzylisoquinoline alkaloid (BIA), which is a large class of plant secondary metabolites that contains a number of currently used and hypothesized plant based pharmaceuticals. Knowledge of morphine biosynthesis can be used as groundwork for exploration of this large alkaloid class. Understanding the evolution of the morphine biosynthesis pathway can provide insights into larger patterns of diversification across plant secondary metabolites, allow for hypothesizing regulators of morphine biosynthesis, and indicate new metabolites worthy of further investigation. Weighted Gene Correlation Network Analysis (WGCNA) has been a framework for research in both plants and animals leading to novel and rich descriptions of species evolution, evolution of biological traits, and identification of candidate genes for biological processes such as stress response. Therefore WGCNA is potentially a powerful tool for use in opium poppy. By capitalizing on evolutionary difference through comparative analysis with closely related species we can create a list of candidate genes for regulation of morphine biosynthesis, which has been insufficiently explored and better understand evolution of these metabolites. However, WGCNA requires large amounts of data, which makes it an intractable technique for many systems and laboratories. We will explore the possibility of combining data from two closely related species, opium poppy and its subspecies, in order to maximize the utility of WGCNA. There are many challenges to this approach and we explore the limits of WGCNA when it comes to pooling data from multiple species. We aim to systematically evaluate the potential for combining species transcriptomic data in order to increase the power of WGCNA to answer specific questions relating to morphine biosynthesis.

Unravelling traits, genes, and trade-offs in low nutrient stress tolerance of cultivated sunflower (Helianthus annuus)

Andries A. Temme, Kelly L. Kerr, Rishi R. Masalia, Kaleigh Davis, John M. Burke, Lisa A. Donovan

Background/Question/Methods

One of the key concepts in functional ecology is the notion of trade-offs in functional traits. Traits beneficial in one environment might be detrimental in another and vice versa. In cultivated crop systems high yielding varieties generally show a far stronger decrease in productivity under adverse conditions than their low wild progenitors. This raises the question of which suite of traits is beneficial under optimal and adverse conditions and whether there are inherent trade-offs in performance depending on traits. By using inbred lines of cultivated sunflower as a model we investigated whether there is a genetic basis to trade-offs in performance and whether traits can be used to predict that trade-off

To address this question we evaluated a morphologically and genetically diverse population of 287 inbred cultivated sunflower genotypes, suitable for genome-wide association studies. Plants were grown in 7.5L pots with either 80g (high nutrients) or 8g (low nutrients) of slow release fertilizer (NPK 15-9-12) and harvested at budding (R2 stage). At harvest, we measured several morphological traits, biomass accumulation, biomass allocation to leaves, stem and roots, plant height, specific leaf area, specific root length/volume, as well as leaf chemical traits, nitrogen content and chlorophyll content.

Results/Conclusions

All genotypes responded to nutrient stress with decreased above ground biomass (mean 40.6% decrease). However, higher performance in high nutrients did not necessarily predict poorer performance in low nutrients. Based on above-ground biomass ranking, genotypes could be categorized into four main groups, resistant (consistently high ranking), susceptible (large rank decrease), tolerant (large rank increase) and feeble (consistently low ranking). Principal component analysis of 23 biomass independent traits of 20 genotypes clearly assignable to each group definition showed groups separating along PC1 (explaining 23.7% at high nutrients, 33.3% at low nutrients). Genotypes PC1 score at high nutrients was a good predictor of above-ground biomass at high nutrients (R2:0.85) but less so at low nutrients (R2:0.52), PC1 score at low nutrients mirrored this, indicating shifts in beneficial traits.

These results suggest that in cultivated sunflower there is no inherent trade-off in nutrient stress tolerance. Moreover, performance is linked to different traits in treatments. Ongoing genomic analysis focuses on determining the genetic basis of these traits under high and low nutrient conditions. The lack of an inherent trade-off to nutrient stress resistance highlights the potential for breeding more resilient crops, easing demands on food production due to rising population levels and climate change.

Evolution of PEPC in independent origins of CAM

Karolina Heyduk, Jeremy N. Ray, Saravanaraj Ayyampalayam, James Leebens-Mack.

The subfamily Agavoideae in the Asparagaceae has three independent origins of Crassulacean acid metabolism (CAM), a photosynthetic modification that allows plants to thrive in water-stressed environments. CAM plants differ from C3 relatives in that they fix atmospheric CO2 via PEPC rather than RuBisCo during the night, when transpiration rates are lower. Although PEPC is expressed in all plants, the timing of expression is switched to late afternoon/dark period in CAM plants, and overall abundance of transcripts is much higher than in C3 species. While multiple origins of CAM have been documented across the flowering plant phylogeny, the mechanism and genetic modifications by which C3 plants transition to CAM are not well understood. Here, we used comparative transcriptomics to describe gene expression changes associated with two independent shifts from C3 to CAM within the Agavoideae: one within the genus Yucca and one on the ancestral lineage leading to Agave. Yucca has two main subgenera which diverged roughly 5 Mya from a C3 ancestor – CAM evolved in one of these lineages encompassing approximately half of extant Yucca species. CAM also evolved independently in the ancestor of Agave sensu lato. We constructed gene trees for a number of CAM genes and mapped temporal expression patterns across the orthologs. Gene tree analysis reveals that the two independent origins of CAM are using alternative version of the PEPC gene family, suggesting convergent evolution of CAM in the Agavoideae. Subsequent studies of additional genes will be required to full describe the number of convergent or parallel changes to the genomes of these CAM lineages.

Graduate Poster Abstracts

Automated phenotyping of root hair traits from microscopy images

Peter Pietrzyk, Chartinun Chutoe, Patompong Saengwilai,
Alexander Bucksch
Dept. of Plant Biology, University of Georgia, Athens, GA

Improving nutrient and water uptake in crops is one of the major challenges to sustain a fast-growing population that faces increasingly nutrient limited soils. Root hairs, which are specialized epidermal cells, compromise up to 70% of the total root surface area. Therefore, it is likely that root hairs are important for nutrient uptake from the soil. Microscopy provides a mean to record root hairs as digital images. However, quantifying root hairs in microscopy images remains a bottleneck because of a high degree of geometric complexity in their spatial arrangement. We present a methodology to automatically quantify phenotypic traits of root hairs in digital microscopy images. Our method uses a machine learning approach that is trained to classify root hair versus other root components and the image's background. Image statistics of six training images were used to automatically classify root hair images taken with the same imaging protocol. Since root hairs may cross each other or form blobs of two or more hairs, we define metrics to distinguish these cases computationally. As a result, we measure the root hair traits number, length, density, diameter, orientation and overall complexity. We investigated root hair traits of six Thai rice varieties. First tests with the new machine learning method suggest that our measured traits distinguish between genotypes in our study and pave the way towards identifying the genetic control of root hair traits. We plan to further extend the study to maize and common bean under suboptimal nitrogen, phosphorus and potassium conditions.

FUT4 and FUT6: Arabinogalactan-specific fucosyltransferases in Arabidopsis thaliana

Maria Soto

Dept. of Plant Biology, University of Georgia, Athens, GA

Plant cell walls are composed of several complex sugars, including some with a long linear backbone substituted with an array of side-chains. Fucose is a sugar which is commonly found on side-chains in numerous species of plants, and can also be found in bacteria, and human proteins, among others. Fucose in the cell wall is found most commonly as a terminal branch modification on the sidechains of cell wall polymers such as xyloglucan (XyG) and arabinogalactan protein (AGPs). *Arabidopsis thaliana* fucosyltransferase 1 (AtFUT 1) has been shown to fucosylate xyloglucan (XG). There is evidence in the literature that strongly suggests AtFUT 4 and AtFUT6 fucoslyate arabinogalactan proteins (AGPs), but do not fucosylate XGs. Obtaining the crystal structures of AtFUTs 4 and 6 will clarify the structural differences that make possible the differential fucosylation of XG and AGPs. Using the β-glucuronidase (GUS) promoter system to localize AtFUT4 and AtFUT6 in root tissue will also help to elucidate why both FUTs are expressed in the root if they make the same fucosylated structures.

Stress-Response Regulation of Septin AspE in Cell Wall Integrity and High Osmolarity/Glycerol Pathways in A. nidulans

Alex Mela
Dept. of Plant Biology, University of Georgia, Athens, GA

Septins are a small class of GTPases, which share a multitude of conserved roles, from regulating cell cycle/cytokinesis to acting as scaffolds for recruitment of molecular complexes within the cells of organisms belonging to virtually all kingdoms of life except for higher plants. Septin AspE in Aspergillus nidulans belongs to a unique, functionally unknown class of septin proteins. Here we provide evidence supporting the hypothesis that AspE may serve a role in one or more biological pathways involved in sensing the extracellular environments and regulating important developmental growth stages of the filamentous fungus A. nidulans in response to external stimuli.

Stressful situation? Find some common ground.

Rishis Masalia
Dept. of Plant Biology, University of Georgia, Athens, GA

Abiotic stress is the largest contribution to crop loss worldwide. As such, understanding how crops respond to abiotic stresses has become a primary concern for plant scientists. Unfortunately, as our climate continues to change, crops are continuously exposed to a diverse set of abiotic stresses (e.g., drought, salinity, low nutrients), which may elicit a shared or unique plant response. Here, we investigate the extent to which a single genotype of *Helianthus annuus* exhibited a shared transcriptional response across four abiotic stresses: a repeated soil dry down, salinity (100mM NaCl), osmotic stress (8.25% polyethylene glycol 6000), and finally a low nutrient stress where individuals were not given supplemental nutrients. Focusing our efforts on root and leaf tissue 10 days post-treatment, we identified 26 217 unique genes. Of this original gene set, 1 529 unique genes, 1 012 in the roots and 532 in the leaves, were differentially expressed across three water limitation stresses (dry down, salt, osmotic) in relation to a well watered control, sampled at the same time. Of these unique genes, there were fewer shared across all stresses than within individual stressors, 43 and 8 in roots and leaves. All 52 of these genes were expressed in the same direction across stresses. Expanding to include low nutrient data, 2 600 unique genes were identified, with 23 and 5 genes shared in root and leaf tissue respectively across all four stresses. Similar to the water limitation stresses, these shared genes were also in the same direction either all up or down regulated, with the exception of a single shared gene in the root tissue. Overall, this sunflower genotype has unique transcriptional responses for the four stresses, however, a shared transcriptional response was identified. This work is still ongoing.

Genotyping-by-sequencing in chile peppers from Oaxaca, Mexico yields insights into evolutionary history of different chile pepper use-types

Taitano N.1*, Bernau V.2, Mercer K.2, McHale L.2, Wallace J.1, Leckie B.3, Mazourek M.4, Jardón-Barbolla L.O.5, Kantar, Michael6, Baumler, David7, van der Knaap E.1

Studying genetic diversity among morphologically diverse named chile pepper types from near the C. annuum domestication center may elucidate fruit-trait loci, domestication, and comparisons with extensive fruit-trait and population structure research in tomato (Solanum lycopersicum). Our study objectives were 1) to determine whether various named Mexican chile pepper types, especially fresh- vs. dry-use-types, represented distinct genetic lineages 2) assess how these are related to chile peppers from around the world. 103 chile pepper seed accessions of 22 named types were collected in 2013 from 29 sites in southern Mexico. From these seedlots, 190 plants were grown and genotyped via GBS. In this population, we obtained 32,623 SNPs and built a phylogeny. We repeated SNP-calling and analysis after adding raw GBS reads from 41 C. annuum individuals from a global collection, sequenced at lower coverage. We performed in-silico genotyping using these SNPs on the published CM334, Zunla-1, and chiltepin genomes. The largest fresh- and dry-use-types clustered into separate monophyletic clades, confirming them as distinct lineages. However, some phenotypically distinct named types were polyphyletic. CM334 Mexican landrace was most related to our elite landraces. Global accessions showed close relatedness to plants from the Yucatán peninsula, indicating C. annuum spread to Eurasia via the Yucatán, as did S. lycopersicum.

Surveying Chromatin Features for the Identification of Intergenic Transcriptional Regulatory Elements in Maize

Bill Ricci, Lexiang Ji, Zefu Lu, Bob Schmitz, Xiaoyu Zhang

Transcriptional regulatory elements (TREs) interact with and modulate the expression of target genes via the action of sequence-specific DNA binding factors. TREs confer specificity for when and where genes are expressed during development and in response to stimuli. The importance of characterizing and cataloging the regulatory elements of a genome is akin to the importance of cataloging the protein-coding regions. However, identifying TREs poses a challenge because (1) they may act on target genes in an orientation- and distance-independent manner, (2) sequence conservation may be limited to small transcription factor binding sites, thus limiting sequence-based identification methods. An alternative approach is to identify structural and biochemical features of chromatin that mark TREs with high fidelity. The chromatin signatures of human regulatory elements have been extensively characterized, however a set of predictive chromatin signatures has yet to be developed for regulatory elements in plants. Here, we combine datasets on DNA accessibility (ATAC-seq), cytosine methylation, transcriptional status (RNA-seq and RNA PolII ChIP) and histone N-terminal covalent modifications (ChIP) in the model crop Zea mays. Preliminary analyses reveal an abundance of potential regulatory elements in the gene-distal intergenic space, as well as an abundance of potentially unannotated genes in the new maize RefGen_V4 annotation.

Investigating SMAX1 Degradation in the Karrikin Signaling Pathway

Nick Morffy

The timing of seed germination is crucial to a plant's success. A recently identified class of signaling molecules found in smoke, karrikins (KAR), have been shown to be potent germination stimulants.[1] Genetic studies have identified some of the genes responsible for mediating KAR responses including *MAX2*, an F-box protein, *KAI2*, the putative KAR receptor, and *SMAX1*, a negative regulator of KAR responses that inhibits germination.[2-5] It is currently unknown how KARs regulate SMAX1 and induce germination.

Interestingly, strigolactones (SL), endogenous plant hormones that regulate a number of growth processes including shoot branching, share some components with KAR signaling. *MAX2* is required for both KAR and SL signaling, and the SL receptor, *D14*, is a paralog of *KAI2*. *SMXL6*, *SMXL7*, and *SMXL8*, paralogs of *SMAX1*, act as negative regulators of SL signaling. In SL signaling, the hormone stimulates the degradation of SMXL6 and SMXL7 in a MAX2 and D14-dependent manner, leading to SL responses. Recently it was also shown that SMAX1 is degraded in response to KAR when expressed under the SMXL5 promoter.[13]We hypothesize that KARs stimulate the degradation of SMAX1 in a MAX2 and KAI2-dependent manner.

In order to test the contributions of MAX2 and KAI2 to KAR induced SMAX1 degradation, we have utilized a number of complementary approaches including transient expression in *Nicotiana benthamiana* leaves and in *Arabidopsis thaliana* mesophyll protoplasts, *in vitro*degradation with recombinant SMAX1, and Arabidopsis transgenic lines expressing GFP-tagged SMAX1 in several genetic backgrounds.

Drought Resistance Not Lost in Cultivated Sunflower (*Helianthus annuus*)

Burns, Victoria A.[1], Donovan, L.A.[1]

[1]University of Georgia, Department of Plant Biology

Drought is one of the main abiotic factors limiting crop growth and yield. It is hypothesized that during the domestication of crops, high performance in ideal conditions was selected at the cost of reduced stress resistance (Mayrose et al 2011). Verifying the presence of a tradeoff between maximum performance and stress resistance is important to inform future studies looking to introgress beneficial alleles from wild plants into their cultivated relatives. To test for the loss of drought resistance in cultivated sunflower (*Helianthus annuus* L.) we compared the growth and performance of four populations of wild sunflower (*Helianthus annuus*) and four genetically diverse lines of cultivated *H. annuus* under well watered and water-limited conditions. Stress tolerance was assessed by analyzing the following four stress indices in terms of total biomass produced (as a proxy for yield): stress tolerance index, mean productivity, geometric mean productivity, and harmonic mean. Although there was a significant drought effect on all of the biomass traits, wild and cultivated plants were not found to differ significantly. Only five of the 17 measured growth and performance traits had a significant species type by water treatment effect—bud mass ratio, height relative growth rate, leaf mass area, chlorophyll content index and days to budding. For these variables, wild *H. annuus* generally had significantly steeper reaction norms than cultivated *H. annuus,* suggesting a higher phenotypic plasticity. A wild line consistently ranked most drought resistant, as measured by the four stress indices, however, most of the wild and cultivated lines overlapped in indices values. Our preliminary results suggest that although wild and cultivated *H. annuus* respond differently to drought, there is no significant difference in their resistance to drought. Our results do not support the hypothesis that cultivated *H. annuus* lost drought resistance during cultivation.

TET-mediated epimutagenesis of the Arabidopsis thaliana methylome

Will Jordan

The creation of engineered strains of commercially important crops such as maize, squash, and cotton has resulted in vastly increased crop yields as well as resistance to pesticides and herbicides. While these strains are ideal for sustaining a rapidly expanding global population, the prioritization of homogeneity and productivity over reliable and diversified food production has resulted in a severe loss of genetic variation, nearly 75% per the United Nations Sustainable Development Knowledge Program. Here we describe "epimutagenesis", a novel method to rapidly generate expression and phenotypic variation through random demethylation of the Arabidopsis thaliana genome. Accomplished via transgenic expression of a human Ten-eleven translocation (TET) enzyme, epimutagenesis results in the emergence of novel phenotypes, as well as widespread losses of DNA methylation, mimicking weak mutants in the maintenance DNA methyltransferase MET1. Application of TET-mediated epimutagenesis to economically and agriculturally significant plant species will result in differential expression of alleles typically silenced by DNA methylation, uncovering previously hidden genetic variation.

Undergraduate Poster Abstracts

Comparing the incomparable: a methodological investigation of water limitation treatments

Liana Mosely
Faculty Advisor: John Burke

As climate change progresses, environmental conditions will become increasingly unpredictable, burdening Earth's fragile resource supply. Agricultural crops are no exception to this trend, specifically considering the resource of water. Agricultural drought, or water limitation stress, has been shown to negatively affect crop productivity, reducing crop yield necessary for human consumption. To mediate the effects of drought, plant scientists aim to develop methods that increase water use efficiency across crop species. While there are many valid ways to implement water limitation stress in a laboratory setting, often times, results gathered utilizing one method are compared with results using a different method. To determine the comparability of water limitation methods in cultivated sunflower, we established seedlings of three diverse genotypes for 25 days followed by a 10 day water limitation stress. Water limitation was simulated with four treatments: two osmotic stresses, polyethylene glycol (PEG-6000) and salt (NaCl; 100mM), as well as a 20% maintained dry down and a three day repeated dry down, all of which were compared to a well watered control. Phenotypic results, such as above and below ground biomass, specific leaf area, and stem height and diameter, were measured. Experimentation is ongoing, however, we do expect to find significant differences in phenotypic variation across water limitation treatments that outweigh phenotypic variation by genotype. This methodological study not only highlights the issue of equating water limitation treatments, but also provides a basis for further study into the optimal design of water limitation implementation.

Flora of Stone Mountain based on Digitized Specimens at GA Herbarium

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Stone Mountain Park, DeKalb County, Georgia, comprises 1,300 ha (3,212 ac) owned by the state of Georgia and administered by the Stone Mountain Memorial Association. Stone Mountain, located at the center of the park, is one of the world's largest exposed granite monoliths, covering 240 ha (593 ac) with an elevation of 514 m (1,670 ft) at its summit. The University of Georgia Herbarium has 1,205 vascular plant vouchers collected from Stone Mountain Park dating from 1843 to 2011, and 689 were collected for a floristic survey in the mid-1990s conducted by Michael Moore and David Giannasi. The goals of this project were to: (1) compile all specimen label data for the park, (2) georeference and plot each specimen, and (3) create a vegetation map of the park based on label data. The vouchers comprised 721 species. The four largest families were Asteraceae (96 spp.), Poaceae (71 spp.), Fabaceae (50 spp.), and Cyperaceae (33 spp.). Eighteen percent of the species in the park were exotic. Three state-ranked rare plant species (S1, critically imperiled) or S2 (imperiled) occur within the park: Anemone berlandieri, Isoetes melanospora, and Waldsteinia lobata. Specimen label data and various map resources were used to plot the locality of each specimen. GPS coordinates, assigned through GeoLocate, were combined with label habitat data and infrared imagery and were used to make a general vegetation map of Stone Mountain Park.

Predicting Taste of Wild Yeast in Craft Beer due to 4-VG Production

Rosemary Wills, John Ludwig, Douda Bensasson

Faculty Advisor: Douda Bensasson

The Southern Brewing Company wants to know if wild yeast native to Athens, GA can be used to brew local beer. To predict the suitability of wild Athens yeast for brewing, we compared the genomes of domestic yeast strains to those of wild strains from our region. Wild-type strains of S. cerevisiae produce 4-vinylguaiacol (4-VG), which causes an off-flavor in beer that most brewers want to avoid. Proteins produced by the FDC1 and PAD1 genes are involved in the production of this chemical. Past work showed that S. cerevisiae from beer often have premature stop codons in the FDC1 and PAD1 genes, but only 7 wild strains were studied. Here we analyzed 273 S. cerevisiae genome sequences, including data from 102 beer strains and 85 wild woodland strains from around the world, with a focus on yeasts from Eastern USA. None of the woodland strains contained premature stop codons or mutations likely to affect the function of FDC1 or PAD1. We predict that they are therefore likely to produce 4-VG and the off-flavor associated with it.

Testing the Repeatability of Sunflower Biomass Accumulation

Nicole Reisinger

Faculty Advisor: Lisa Donovan

With climate change, rising population levels, the rise of richer diets, and an increase in poor agricultural conditions, such as saline soils, the research and breeding of sturdier plants is essential to feed people and livestock. One of the objectives of this experiment was to see if results could be recreated from one study to the next. Genotypes used in this experiment were chosen based on previous experiments that suggested whether the genotype was resistant to salt. Of the genotypes selected, four were thought to be resistant, three were thought to be susceptible, and four were thought to be somewhere in between. To test the genotypes for repeatability, 480 sunflowers were grown in a scheme that allowed for 4 duplicates of 10 genotypes in four different treatments. The treatments gradually reached salt concentrations of 0 mM, 100 mM, 200 mM, and 300mM as the experiment went on. A third of the sunflowers were harvested every three weeks and the plant parts were divided up into separate bags containing the leaves, stem, roots, sla petioles, and sla leaves, which were then weighed after drying. As expected, the plants under higher stress accumulated the least biomass, but to varying degrees depending on the genotype's resilience. Showing that results can be duplicated in several experiments allows for a clearer picture as to which genotypes can be used to breed sturdier, more resistant plants.

Soil respiration 6 years after wind disturbance and salvage logging at Boggs Creek

Sydney H. Mai, Callie A. Oldfield

Faculty Advisor: Chris Peterson

Soil CO2 efflux, emitted by the heterotrophs and autotrophs, is an integral component of the carbon cycle. Carbon storage in the soil is an ecosystem storage which can affect the global carbon cycle and alter primary productivity. Soil CO2 efflux, can be affected by abiotic factors such as forest and soil disturbances caused by windthrow. In this study, we measure CO2 efflux in three different conditions (unsalvaged – affected by windthrow event, salvaged – affected by windthrow event and salvage logging, and control – intact forest not affected by windthrow event) using a LiCor 6400 with soil respiration attachment at Boggs Creek in the Chattahoochee-Oconee National Forest, which experienced a tornado in 2012. We found that salvaged and unsalvaged plots had greater variance in the mean soil CO2 efflux than in control plots, which may be a result of greater microtopographic and canopy variation in the disturbed plots. In addition, we found that unsalvaged and salvaged plots had significantly higher soil respiration efflux than control plots, and. salvaged plots had significantly higher soil respiration effluxes than unsalvaged plots. We speculate that the higher CO2 efflux in the salvaged and unsalvaged plots is due to the soil disturbance and increased removal of soil organic material caused by the windthrow event. These findings are important because they indicate that wind disturbances may have a lasting impact on the soil CO2 efflux. Understanding the role of soil CO2 efflux in a forest recovering from wind disturbance is important as wind disturbances increase in frequency.

Effects of Salvage Logging on Tree Biomass

Rhett N. Parr, Callie A. Oldfield, and Chris J. Peterson

Faculty Advisor: Chris Peterson

In 2012, a tornado ripped through the mountains near Boggs Creek in Cleveland, GA. To study the effects of the tornado and subsequent salvage logging on tree biomass, permanent plots were set up in wind damaged areas that experienced salvage logging, wind damaged areas without salvage logging, and areas where no damage had occurred. In 2017, the mean tree biomass was compared between plots with and without salvaging. Severity of wind damage was not significantly different between salvaged and unsalvaged plots ($p = 0.93$). Using ANOVA, we found that there was no statistically significant difference in biomass between salvaged or unsalvaged plots in 2017 ($p = 0.65$). Furthermore, salvaged and unsalvaged plots had significantly lower biomass than control plots, with p-values of 0.0017 and 0.0055 respectively. These results indicate that salvage logging did not have an effect on the mean tree biomass five years after a wind disturbance. This data indicates that salvage logging does not have an adverse effect on the biomass of a recovering forest following cases of severe wind damage.