JAN 25-26, 2018

PLANT SCIENCE SYMPOSIUM

AT UNIVERSITY OF FLORIDA

ADVANCING FRONTIERS IN PLANT SCIENCES

PLANT SCIENCE Council

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2nd Annual Plant Science Symposium

A DuPont Plant Sciences Symposia series

Jan 25-26, 2018

ADVANCING FRONTIERS IN PLANT SCIENCES

VENUE:

CANCER & GENETICS RESEARCH COMPLEX
University of Florida
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SYMPOSIUM SCHEDULE

Thursday, January 25th, 2017

12:00 PM	**Phenotypic Prediction Workshop Ends**
12:00 - 01:30 PM	**Check-in / On-site Registration / Set up Posters**
01:30 - 01:40 PM	**Opening Remarks - Jessica Chitwood**
01:40 - 01:50 PM	**Welcome remarks**
01:50 - 02:00 PM	**Welcome Remarks - UF/IFAS**
02:00 - 04:00 PM	**Poster viewing and judging**
06:30 - 08:30 PM	**Social at Swamphead**

Friday, January 26th, 2017

08:00 - 09:00 AM	**Check-in / Breakfast / On-site registration**
09:00 - 09:15 AM	**Welcome / Introductions: Jessica Chitwood**
09:15 - 10:05 AM	**Invited Speaker: Dr. Thomas Gradziel**
10:10 - 11:00 AM	**Invited Speaker: Dr. Thomas Burks**
11:00 - 11:10 AM	**Coffee Break**
11:10 - 12:00 PM	**Invited Speaker: Dr. Seth Murray**
12:00 - 01:30 PM	**Lunch Break and Poster Viewing Session**
01:30 - 02:20 PM	**Invited Speaker: Dr. Vivian Irish**
02:25 - 03:25 PM	**Student Talks: Travel Award Winners**
03:25 - 03:35 PM	**Coffee Break**
03:35 - 04:25 PM	**Invited Speaker: Dr. Jose Rotundo**
04:25 - 04:35 PM	**Student Travel Awards Ceremony - DuPont Pioneer**
04:35 - 04:45 PM	**Student Poster Awards - UF/IFAS**
04:45 - 05:00 PM	**Closing Remarks: Dr. Esteban Rios**

SPEAKERS

Dr. Thomas Gradziel

Professor, Department of Plant Sciences
University of California, Davis

Dr. Gradziel's research focuses on the genetic improvement of almond and peach. Strategies employed include wild germplasm characterization, preservation and introgression, intra-and inter-specific hybridization, marker assisted selection, and epigenetic manipulation. Breeding objectives include developing productive, high quality market almond varieties and rootstocks which combine the novel traits required to meet emerging grower, processor and market demands, including self-fruitfulness, improved disease/pest resistance and improved water use efficiency.

If all you have is a hammer, everything looks like a nail: Peculiar Perspectives from Fruit Breeding

Plant breeding is undergoing a revolution in our ability to efficiently identify, select, and even modify individual genes contributing to phenotype. Final phenotype, however, is determined not just by the presence of a desired gene, but also interactions within the gene locus (allelic), between genes and genetic components, between genomes, as well as epigenetic interactions. A major barrier to the fuller exploitation of these effects for crop improvement is the requirement to provide growers with uniform and true-to-type plants. The emphasis of most crop breeding strategies on producing true-to-type seed, inherently limits the types of genomic synergisms exploited. Because most fruit and nut cultivars are vegetatively propagated, a wider range of manipulations remain accessible. Examples will be presented from my peach and almond breeding program which routinely utilizes interspecific hybrids and introgression lines as well as binary plant systems and epigenetic rehabilitation.

SPEAKERS

Dr. Thomas Burks

Professor, Department of Agricultural and Biological Engineering
University of Florida

Dr. Burks grew up on a farm in central Kentucky, and has always been interested in agriculture, later becoming interested in developing robotics technology to help improve agricultural production. Dr. Burks received his PhD at the University of Kentucky, and did a Post doctorate there as well. He has worked in industry for a combined 10 years in the midwestern grain industry and in the food processing industry, prior to coming to UF. His primary research focus is in automation, robotics and machine vision applications in agriculture with an emphasis on citrus harvesting.

Digital and Smart Ag Technology Mega Trends are transforming Agriculture (Field to Fork) into a High-Tech Industry: Challenges and Opportunities

People get excited about the latest technology trends, but in the end, food, water, and shelter are the most important things we have to sustain. With a growing global population, shrinking water supplies, a shrinking farm labor pool, and concerns over climate changes, it is imperative that we as a society look for ways to increase food production in a more sustainable and efficient way, with greater global access. Plant and agricultural based science along with engineering research will be imperative to securing a future food supply for the USA and world. Dr. Burks will talk about the impact technologies can have on the future of agriculture. Precision Agriculture based production approaches and accelerating technology sectors termed, “SmartAg” and "Digital Agriculture" may pave the way towards more efficient and environmentally friendly food production, of which plant based production is the largest sector. Dr. Burks' research focuses on Precision Ag and SmartAg concepts using Robotics and Automation to improve production practices related to the Florida Citrus industry. He will also share other current activities at UF Agricultural and Biological Engineering Department relevant to plant production.

SPEAKERS

Dr. Seth Murray

Associate Professor, Department of Soil and Crop Sciences
Texas A&M University

Dr. Murray's research interests focus on improving the productivity, sustainability (economic and environmental) and quality of agricultural production through scientific research and development; mostly in maize (corn). The approaches used to conduct this research include 1) high-throughput field phenotyping (UAVs/drones, ground vehicles, NIRS), 2) molecular quantitative genetic discovery (including QTL mapping, GWAS), 3) statistical modeling and novel analysis methods (including big data and metanalysis), 4) development of new breeding and genetics approaches (including use of computer simulations), and ultimately 5) applied maize (corn) field breeding (classical and molecular). Primary traits of interest for discovering genetic variation and improving in maize for are yield, southern adaptation, stress (aflatoxin resistance, drought tolerance), plant height, composition (colored grain, high grain antioxidants, low phosphorus), and perennialism.

Transdisciplinary Frontiers in Field Based Phenomics

A major barrier to improving scientific understanding and improvement of crops has been the resources needed to characterize phenotypic traits across genetics (G) and environments (E). In the past, labor demands have necessitated choosing only one or a few phenotypic traits to be monitored and a very limited number of G, E, and time points – typically at the end of season. Technological advancements including unmanned aerial vehicles (UAVs, i.e. drones), unmanned ground vehicles (UGVs), sensors, and accompanying data processing improvements in computing and statistics open new opportunities to understand biology, make actionable decisions in agriculture, and better predict winners in plant breeding. Phenomics today is analogous to where genomics was 30 years ago; we can use the history of genomics discoveries and methodologies as a blueprint for a path forward in the area of plant phenomics. Importantly, there are currently no ready to use applications of UAVs in plant phenomics, many unanswered questions and the many steps require different areas of expertise and partnering with other disciplines to develop transdisciplinary techniques. For the last four years the Texas AgriLife Unmanned Aerial Systems (UAS) in Agriculture Project (Shi et al. 2016) has done just that, integrating expertise from over 30 faculty labs to develop new methodologies and data using UAS. In maize, our first case study was plant height; terminal plant height across different varieties is positively correlated to yield under Texas stress conditions ($R^2 = 0.61$; Farfan et al. 2013). We have been able to estimate plant height from UAS imagery throughout the growing season with comparable accuracy to manual measurements but with much more frequent revisit times, allowing divergent temporal growth patterns to be observed between genotypes in the field for the first time. We are now applying these approaches to the maize Genomes to Fields (G2F) project and developing new techniques and pipelines to estimate additional parameters from UAS. Collaborating with diverse expertise is critical for practical application of these new technologies in plant sciences.

SPEAKERS

Dr. Vivian Irish

Chair & Professor, Molecular, Cellular and Developmental Biology
Yale University

Dr. Irish obtained her Ph.D. from Harvard University, where she characterized the role of the DPP/TGFbeta signaling pathway in specifying dorsal-ventral polarity in the Drosophila embryo. After postdoctoral work investigating anterior-posterior patterning in Drosophila, she turned her attention to exploring patterning processes in the Arabidopsis flower. For a number of years, she has focused on characterizing the genes and pathways regulating organogenesis and growth in the flower. She has also explored the extent to which these pathways are conserved across different flowering plant species. Using molecular, genetic, and modeling approaches, her current research is centered on understanding how these processes are integrated in forming a petal, a simple laminar organ of few cell types, but whose form varies widely in different plant species.

A thorny question: the regulation of stem cell activity

Stem cells have remarkable capabilities; they divide essentially without limit to give rise to both differentiated derivatives and to replenish the stem cell population. Thorns represent an unusual population of plant stem cells that undergo programmed terminal differentiation. To understand the molecular mechanisms underlying stem cell proliferation and arrest in plants, we are investigating thorn development in Citrus. As part of this effort, we have developed improved CRISPR/Cas9 methodologies for work with Citrus, and have used these approaches to investigate the mechanisms underlying the control of thorn stem cell proliferation and arrest.

SPEAKERS

Dr. Jose Rotundo

Du Pont Pioneer

Dr. Rotundo received his Ph.D. from Iowa State University where he worked on Crop Physiology and Production. Upon graduation, he worked as a Postdoctoral Research Associate in Iowa State University and then joined The National Scientific and Technical Research Council as Assistant Research Scientist. His research focused on different aspects of Soybean crop physiology impacting both seed yield and quality. Dr. Rotundo currently works at Du Pont Pioneer.

Soybean Genetic Progress and Resource Use Efficiency

Recent retrospective studies showed a 1% annual soybean genetic gain. This genetic improvement was associated with reduced lodging, shortened vegetative phase duration, and a slight reduction in seed protein concentration. However, the influence of genetic gain in resource use efficiency has been less explored. In this work, we assess the impact of genetic progress on nitrogen and radiation use efficiency of cultivars released between 1980 and 2015. The hypothesis is that the year of release will be not correlated by these processes. This is because there are different physiological strategies to attain higher yields. Additionally, we will evaluate how these efficiencies change in contrasting environments associated with drought stress.

TRAVEL AWARD WINNERS

Bonny Michael Oloka

North Carolina State University

Linkage and QTL analysis in a hexaploid sweetpotato mapping population

Bonny Michael Oloka[1,2], Bode Olukolu[1], Benard Yada[2], Milton O. Anyanga[2], Doreen Chelangat[2], Paul Musana[2], Agnes Alajo[2], Guilherme da Silva Pereira[3], Marcelo Mollinari[3], Zhao-Bang Zeng[1,3], G. Craig Yencho[1]

[1]*Dept. of Horticultural Science, NC State University, Raleigh NC 27695-7609.*

[2]*National Crops Resources Research Institute, Namulonge, P.O. Box 7084, Kampala, Uganda.*

[3]*Bioinformatics Research Center, Dept. of Statistics, NC State University, Raleigh NC 27695- 7566.*

Genetic improvement of sweetpotato, *Ipomoea batatas* (L.) Lam., for important agronomic traits has been slow over the years in the global arena especially in sub-Saharan Africa where the crop is a staple. This is largely due to sweetpotato's complex hexaploid (2n = 6x = 90) genetics, its large genome size and out-crossing nature with significant self and cross incompatibilities, high heterozygosity, and a wide array of biotic and abiotic stresses. We developed a bi-parental mapping population from the sweetpotato cultivars "New Kawogo" x "Beauregard" (NKB), consisting of 287 segregating F1 progeny, and used next-generation sequencing, computing and bioinformatics technology to develop high quality SNPs, which we used for linkage mapping and QTL analysis. Using a modified genotyping by sequencing (GBS) pipeline, we were able to mine 1,409,131 SNPs from the alignment of sequence files from the NKB population to the *I. trifida* reference (version 3.0) at a rate of 74.4%. We were able to call 132,201 SNPs using SuperMASSA software and after filtering for segregation distortion and missing data we retained 5,624 high quality SNPs along with their respective dosage information. We used these SNPs to build a genetic linkage map and have identified all 15 linkage groups. QTL analysis for sweetpotato weevil, sweetpotato virus disease and storage root yield is in progress. These tools will facilitate more efficient introgression of important traits and subsequent faster genetic gain of key traits in this complex yet globally important crop.

TRAVEL AWARD WINNERS

Chathurika Wijewardana

Mississippi State University

Impact of water stress on soybean seed physiology, quality, and chemical composition

Chathurika Wijewardana[1], Nacer Bellaloui [2] and K. Raja Reddy [1]

[1]*Department of Plant and Soil Sciences, Mississippi State University, Starkville, MS, USA*

[2]*USDA-ARS, Stoneville, MS, USA*

Soybean seed quality is often determined by proteins, fatty acids, carbohydrates, isoflavones, and minerals. Thus, maintaining an improved seed quality is imperative to sustain overall human and animal nutritional aspects. The objective of this study was to investigate the effects of water stress during reproductive stage on seed yield components, composition, and minerals using two soybean cultivars grown under sunlit controlled conditions. Plants grown in pots were subjected to five levels of water stresses, 100, 80, 60, 40, and 20% of daily evapotranspiration of the control at flowering and continued until maturity. Plants were harvested 126 d after planting and seed vigor, quality, and mineral traits were examined. Results of the analysis of variance showed significant effects of cultivar, water stress, and their interactions on the studied traits. Seed weight of both cultivars was negatively impacted by soil moisture stress. Seed protein, ash, palmitic and linoleic acids, sucrose, raffinose, stachyose, N, P, K, and Ca significantly decreased whereas oil, fiber, stearic, oleic and linolenic acids, Fe, Mg, Zn, Cu, and B increased in response to soil moisture deficiency. The relationship between seed protein and oil was negatively correlated while seed dry weight exhibited strong positive correlations between seed protein, sucrose, and N content. The changes in seed constituents could be due to changes in nutrient accumulation and partitioning in soybean seeds under water stress. This information suggests the requirement of adequate soil moisture condition during flowering and seed formation stages to obtain higher nutritional value of soybean seeds.

TRAVEL AWARD WINNERS

Kyle W. Swentowsky

University of Georgia

A novel maize kinesin causes neocentromere activity and meiotic drive, altering inheritance across the genome

Kyle W. Swentowsky[1], Weihong Qui[2], Kuo-Fu Tseng[2], R. Kelly Dawe[1,3]

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[3]*Department of Genetics, University of Georgia, Athens, GA 30602*

Originally discovered 75 years ago, maize Abnormal Chromosome 10 (Ab10) lines display meiotic drive where the segregation ratios of alleles linked to chromosome knobs are significantly altered from the expected 50:50. It is estimated that meiotic drive in maize has had evolutionary consequences on a genome-wide level by affecting segregation of alleles near knobs. The cytological cause of meiotic drive is neocentromere activity during female meiosis where knobs are directed towards the poles and arrive before centromeres. During female meiosis in plants, only the single lowest of the four cells survives and neocentromere activity favors the knob-containing chromosome to migrate into what will become the functional megaspore. Knobs are composed of two distinct tandem repeat arrays termed knob180 and TR1. Ab10 itself contains genes required for meiotic drive and neocentromere activity, but prior to this work none of these genes had been described. We show that the distal tip of Ab10 contains the eight-member *Kindr* (*Kinesin driver*) gene family and that *Kindr* is necessary for meiotic drive and knob180 neocentromeres to occur. *Kindr* encodes a functional minus end-directed Kinesin-14A homolog protein that is present in meiotic anthers and ears of Ab10 but not N10 plants. Furthermore, immunolocalization studies show that KINDR colocalizes specifically with knob180 knobs during male meiosis. Despite colocalization, KINDR does not undergo a direct protein-DNA interaction with knob180 DNA sequences. In summary, our work has identified a novel Ab10 kinesin that contributes to meiotic drive by facilitating meiotic neocentromere activity of the knob180 knobs.

TRAVEL AWARD WINNERS

Suraj Sapkota

University of Georgia

Identification of a Major QTL Conferring Resistance to Leaf Rust in Wheat cultivar AGS2000

Suraj Sapkota[1], Yuanfeng Hao[2], Jerry Johnson[2], and Mohamed Mergoum[2]

[1]*Institute of Plant Breeding, Genetics, and Genomics, University of Georgia, Griffin Campus, Griffin, GA*

[2]*Department of Crop and Soil Science, University of Georgia, Griffin Campus, Griffin, GA*

Leaf rust (LR) disease, caused by the fungal pathogen *Puccinia tritcina*, is a destructive foliar disease of wheat worldwide. Gene combination of *Lr37*/*Yr17*/*Sr38* has been used in Georgia (GA) to prevent the loss from LR; however, with the emergence of new virulent races, these genes have lost their effectiveness. AGS2000 and P26R61 are the most common soft red winter wheat (SRWW) cultivars in Southeastern US, and have been used as good sources of resistance to leaf and stripe rusts, and powdery mildew. To characterize the genetic basic of LR resistance in AGS2000, a mapping population of 178 recombinant inbred lines (RILs) has been developed from a cross with P26R61. This population was genotyped using a combination of SSR, DArT, and SNP markers, and a total of 2734 markers were used for the construction of genetic map. Phenotypic evaluation of parents and RIL population was conducted at the seedling stage against a prevalent race of LR in Georgia. QTL mapping revealed a major QTL on chromosome 2BL which explained 20.32% of total phenotypic variation in AGS2000. Additionally, a minor QTL was also detected on chromosome 5B. QTL on 2BL is most likely to be a novel gene, and can be used in marker-assisted selection for LR resistance.

POSTERS

1. The role of NAD in tomato resistance against Root-knot nematode

Noor Abdelsamad[1], Homan Regmi[1, 2], Shova Mishra[1], and PM DiGennaro[1]

[1]*Department of Entomology and Nematology, College of Agriculture and Animal Science, University of Florida, Gainesville, USA*

[2]*Gulf Coast Research and Education Center, University of Florida, Wimauma, USA*

Root-knot nematodes (RKN; *Meloidogyne* spp.) are among the most damaging pests to tomato production in the US, with damage ranging from 25-100% yield loss. The current and best management option is to use cultivars carrying the nematode-resistant gene (*Mi*); however, there are virulent RKN populations known to exist that break *Mi*-mediated resistance. The goal of this project is to characterize *Mi*-mediated resistance pathways and induce them without the presence of the pathogen. Triggering innate plant immunity using chemical elicitors is a proven strategy to combat other plant pathogens and we believe this method may augment or supplement *Mi*-resistance in tomato. Nicotinamide adenine dinucleotide (NAD) is one such chemical elicitor that regulates plant responses to different biotic stresses. We investigated the role of NAD in tomato resistance against RKN, by comparing different NAD treatments along with several RKN species with varying levels of virulence, and multiple tomato cultivars with a range of nematode susceptibilities. Soil drenching with NAD for seven consecutive days, reduced infective-juvenile penetration, gall formation, and subsequently, the number of eggs produced by adults. Investigations are currently in progress to further understand how NAD induces tomato resistance against RKN.

POSTERS

2. Gene Discovery for Flavor and Disease Resistance in Strawberry

Chris Barbey[1], Kevin Folta[1,2], Vance Whitaker[2], Seeonghee Lee[2], Sujeet Verma[2]

[1]*Plant Molecular and Cellular Biology Program, University of Florida, Gainesville FL*

[2]*Department of Horticultural Sciences, University of Florida, Gainesville, FL*

Associating crop traits with their causative genetics is crucial for agricultural improvement. This deductive process is challenging in cultivated strawberry, due to an unusually complex auto-allooctoploid genome. Contemporary techniques such as whole genome sequencing typically have insufficient resolution to discriminate octoploid strawberry's numerous allelic variants. Two strawberry traits of broad importance are improved flavor and disease resistance. To identify candidate genes controlling these traits, high-resolution genomics assays were applied to detect sequence variations at the subgenomic level. For associating flavor phenotypes, fruit volatile metabolomes were rigorously derived from 263 individuals using a series of statistical alignment techniques on non-targeted GC/MS data. Over 25,000 subgenomic sequence variants were tracked through multiple generations using a specially designed octoploid strawberry SNP-array. These inherited sequence variants were successfully correlated with the production of various strawberry flavor and aroma volatile compounds. Among these, Linalool (floral-aroma), Methyl Anthranilate (grape-aroma), and Methyl 2-Hexenoate (pineapple-aroma) and others were genetically associated with high confidence and precision. Demonstrating the validity of these results, linalool was mapped precisely to the locus of its known biosynthesis allele. In a similar approach, high-variance transcripts from 65 fruit transcriptomes were successfully correlated to their genotypes, indicating segregating *cis* and *trans* genetic factors associated with differential fruit gene expression. To sequence strawberry disease resistance genes (R-genes), PacBio-SMRT sequencing (4kb reads; 98% accuracy) was performed on libraries pre-enriched on the benchtop for R-gene sequences. This method intensifies sequencing power on the relevant fraction of the strawberry genome, enabling R-gene resolution to the subgenomic level. For this purpose, a 50,000 capture-probe array was designed based on 3,307 unique strawberry R-genes mined from various genomic and transcriptomic sequence resources. Both DNA and mRNA are being sequenced from sixteen strawberry accessions, representing a diverse set of disease resistant germplasm. The discoveries made from these approaches will provide significant advances to basic understanding in strawberry, and assist in the practical improvement of cultivated varieties.

3. Boron Uptake in Tomatoes on Sandy Soils

Gurcan D Baysal[1] and Rao Mylavarapu

1Soil and Water Sciences, College of Agriculture and Animal Science, University of Florida, Gainesville, USA

Boron (B) is an essential micronutrient for plants with important metabolic functions such as glucose transportation, cell wall synthesis, etc. In order to determine a suitable analytical method for extractable B and to determine B uptake in tomatoes cultivated in sandy soils of Florida, a replicated greenhouse study was proposed, where a comparison of granular and foliar applications of B to achieve 1, 2, and 3 mg kg-1 of B was implemented. The study is on-going in the greenhouse. Data comparing analytical methods and protocols for determining extractable B is presented here. Hot water extraction of soil B with 5 min boiling time analyzed on ICP showed promising results.

POSTERS

4. Visual Detection in Controlled Growth Environments Using Single-Image Normalized Differential Vegetation Index (SI-NDVI)

Nicole Beisel[1], Jordan Callaham[2], Anna-Lisa Paul[1,2], and Robert Ferl[1,2,3].

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[2]*Department of Horticultural Sciences, University of Florida, Gainesville, Florida USA*

[3]*Interdisplinary Center for Biotechnology Research, University of Florida, Gainesville, Florida USA*

The single-image normalized differential vegetation index (SI-NDVI) imaging system was created by altering a commercially available action camera as an early stress detection method for plants growing in controlled conditions. The SI-NDVI imaging system was developed as part of the EDEN-ISS project, which aims to transform a shipping container into a completely controlled greenhouse capable of supporting plant cultivation on the International Space Station (ISS), and eventually on extraterrestrial platforms. To detect plant stress, SI-NDVI compares spectral reflectance patterns of plant leaves in both the near-infrared (NIR) and visible light spectrums. Images collected by the SI-NDVI imager can be analyzed both qualitatively and quantitatively to study trends in plant health over time. For qualitative analysis of SI-NDVI images, the open source program ImageJ is used to apply various color look-up tables (LUTs) to create false color images highlighting differences in plant health. For quantitative analysis, Excel is used to generate line graphs to examine changes in plant health over time. Salt and drought stress assays were used as model abiotic plant stressors to test the early detection capabilities of the SI-NDVI imaging system. SI-NDVI analyses done on both abiotic plant stressors were able to detect a decline in plant health before the stress was visibly apparent. Plant stress was detected as early as fifteen minutes after exposure to high salinity conditions, and as early as 1.5 hours following drought exposure using SI-NDVI analysis. Through early detection of plant stress, the implementation of SI-NDVI in controlled greenhouse conditions can support successful growth of crops in extreme environments, and may eventually be used to remotely monitor crop growth on Mars.

POSTERS

5. Characterization of the molecular and cellular role of EVE1 in plant vascular development

Johnathon Blahut1, Kelly Balmant2, Daniel Conde2,3, Christopher Dervinis2, David Oppenheimer1,4, Matias Kirst1,2

1 Plant Molecular and Cellular Biology Graduate Program, University of Florida, Gainesville, Florida 32611, USA. 2 School of Forest Resources and Conservation, University of Florida, Gainesville, Florida 32611, USA. 3 Centre for Biotechnology and Genomics, Technical University of Madrid, Madrid 28223, Spain. 4 Department of Biology, University of Florida, Gainesville, Florida 32611, USA.

A remaining hallmark of land colonization is the variation in complexity of the water-conducting tissues across the plant kingdom. The vascular cells of mosses and liverworts can be surprisingly complex with thickened cell walls and plasmodesma-derived perforations. These features mimic the water-conducting tissues observed among the angiosperm clade which has adopted vessels for improved conductive efficiency. In most cases, vessels show greater hydraulic conductivity owing to intervessel pits and perforation plates. To better understand this complexity, we mapped quantitative trait loci associated with vessel-related traits and discovered the Enlarged Vessel Elements 1 (EVE1) gene in poplar. Stems of hybrid poplar trees overexpressing EVE1 display higher hydraulic conductivity, vessel number per sapwood area and vessel diameter without a concomitant increase in cavitation. Further analysis of relative transcript abundance among unrelated individuals suggests a role of EVE1 in determining vessel size. Recent protein electrophoresis studies have revealed that the EVE1 locus produces a small molecular weight membrane protein in Populus deltoides stems. Immunolocalization using sapling stem sections suggest that the EVE1 protein localizes specifically to developing vessel elements but is largely absent of mature vessels. The discovery and characterization of EVE1 represents a starting point towards identifying other genes involved in plant vascular transport.

6. The gall midge *Orseolia javanica* (Diptera: Cecidomyiidae), a candidate biological control agent of cogongrass (*Imperata cylindrica*)

James P. Cuda[1], William A. Overholt[2] and Purnama Hidayat[3]

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[3]*Department of Plant Protection, Bogor Agricultural University, Bogor, West Java, Indonesia*

Cogongrass (*Imperata cylindrica* (L.) P. Beauv.; Poaceae) is a federal listed noxious weed that occurs in Florida and other southeastern states. This invasive grass infests cattle pastures, golf courses, lawns, and also thrives in poor soil conditions such as ditch banks, roadside and railroad rights-of-way as well as reclaimed phosphate-mining areas. Control of cogongrass relies primarily on mowing and the application of chemical herbicides. For example, in 2009 the state of Alabama dedicated $6.3 million of federal stimulus funds exclusively for chemical control of this invasive weed. Biological control using natural enemies from the native range of cogongrass has received little attention and no biological control agents have been introduced anywhere in the world. A review of the literature on natural enemies of cogongrass identified several insect herbivores from the native range. One of these is an Indonesian gall midge *Orseolia javanica* Kieffer and van Leeuwen-Reijinvaan (Diptera: Cecidomyiidae). From 2015 to 2016, surveys were conducted at several locations in Central and West Java, Indonesia where *O. javanica* galls were discovered. Midge galls were abundant along levees separating rice paddies in the Cianjur District. Larval feeding induces the formation of linear galls in which one larva develops. Published results of limited host range testing with cultivated and wild rice, corn, sorghum and two other non-cultivated grasses showed midges survived only in cogongrass. Performance of the midge on two Florida cogongrass clones is being evaluated in Indonesia. The goal of this research is to introduce *O. javanica* and perhaps other host-specific natural enemies into Florida to selectively stress/weaken cogongrass, and make it less competitive. Biological control can be integrated with other control methods to provide a sustainable IPM solution to the cogongrass problem.

7. Rhizotron Chambers: An alternative to evaluate early root traits in peanut.

M.D. GOYZUETA1, K.A. RACETTE2, B.L. TILLMAN1, D.L. ROWLAND2

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Early root characteristics are of great importance to the successful establishment and development of field grown plants. Nevertheless, early assessment of root architecture traits is not common due to the lack of a nondestructive protocol. The objective of this study was to develop a nondestructive protocol for the assessment of peanut root traits and evaluate its potential for use as a screening tool in peanut breeding programs. Six peanut cultivars (FloRun '107', Georgia-06G, Georgia-13M, TUFRunner '297', TUFRunner '511', and TUFRunner '727') were used in the experiments. One seed of each variety was sown in a transparent rectangular plastic tube with Turface Athletics® QuickDry® as media. Tubes were placed in three different environments: laboratory conditions with a mean temperature of 24° C, a growth chamber with a mean temperature of 19.5° C, and a growth chamber with a mean temperature of 28° C. Tubes were placed at a 74° angle to force roots to follow the tube wall for in situ root evaluation at 7, 12, and 14 DAP with an Epson Scanner. After scanning the tubes, roots were harvested, cleaned and scanned again for analysis with the WinRhizo® software. Pearson Correlation between the tubes scans and the harvested roots was assessed using SAS® 9.4, at an alpha level of 0.05. The correlation diminished at 12 and 14 DAP as compared to 7 DAP due to root exploration of non-visible portions of the tube. Therefore, the harvested roots tended to be greater in size and number compared to the root traits observed in situ. Additionally, some cultivars showed a greater reduction of the correlation leading to the hypothesis that cultivars have different strategies for soil exploration.Detecting Plant Stress before

8. Using copper sulfate media to screen for copper resistance in plant pathogenic bacteria

Steven Herd-Bond

University of Florida, Plant Diagnostic Center

Various species of Xanthomonas bacteria cause disease in many agriculturally important crops. Copper sulfate bactericidal sprays are widely used to control bacterial pathogens in many of these crops. As with any chemical control method, development of resistance is a concern when one method of control is repeatedly used. The purpose of this research is to determine an efficient and reliable method of testing for copper resistance in diagnosed pathogenic bacteria. The method for screening has two parts. The first part uses differential media to determine if there is copper resistance. Before using the differential media, any copper resistance genes must be induced. The induction broth is an MGY broth amended with 1 mg/L of copper sulfate ($CuSO_4$ x $5H_2O$). Incubation of the sample in the induction broth for 2 hours at room temperature is sufficient to induce resistance genes. The differential media is an MGY media amended with 200 mg/L of $CuSO_4$ x $5H_2O$. Once the bacteria have been incubated in the induction broth, the cultures are then streaked on the differential media and incubated at 37 degrees Celsius for 48 hours. If the bacteria are resistant to copper there will be plentiful colonies; if the bacteria is sensitive there will be no growth. The second part of identifying copper resistant strains of bacteria involves molecular identification of the plasmid responsible for conferring resistance. This is done with a polymerase chain reaction (PCR) and Sanger Sequencing. The PCR reaction uses specific primers that only amplify the plasmid that confers resistance to copper.

POSTERS

9. Metabolite Profiling of *Candidatus* Liberibacter Infection in Hamlin Sweet Oranges

Wei-Lun Hung,[1] Yu Wang,[1]

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Huanglongbing (HLB), also known as Citrus Greening Disease, caused by *Candidatus* Liberibacter asiaticus (CLas) is considered the most serious citrus disease in the world. CLas infection has been shown to greatly affect metabolite profiles in citrus fruits. However, due to uneven distribution of CLas throughout the tree and minimum bacterial titer requirement for polymerase chain reaction (PCR) detection, the healthy trees may test false negative. To prevent this, metabolites of healthy Hamlin oranges (CLas-) obtained from the citrus undercover protection systems (CUPS) were investigated. Comparison of the juice obtained from Las- and Las+ (asymptomatic and symptomatic) trees revealed significant differences in both volatile and non-volatile metabolites. However, no consistent pattern could be observed in alcohols, esters, sesquiterpenes, sugars, flavanones and limonoids as compared to previous studies. These results suggest that CLas may affect metabolite profiles of citrus fruits earlier than detecting infection by PCR. Citric acid, nobiletin, malic acid and phenylalanine were identified as the metabolic biomarkers associated with the progress of HLB. Thus, the differential metabolites found in this study may serve as the biomarkers of HLB in its early stage, and the metabolite signature of CLas infection may provide useful information for developing a potential treatment strategy.

10. Crop canopy and soil environmental response to complex maize-legume intercropping systems in semi-arid Southern Africa

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A major challenge to the adoption of maize (*Zea mays* L.)-legume rotations among small landholders in Southern Africa is a strong reliance on maize as a staple grain. Intercropping dual purpose legumes with maize may be a viable alternative to rotations for small landholders in the region. The objective of this study was to determine the optimal time to plant lablab (*Lablab purpureus* L.) into a maize monoculture and maize-cowpea (*Vigna unguiculata* L.) mixture to maximize maize and cowpea grain yields and legume aboveground biomass production. A two-year field study was conducted in Limpopo Province, South Africa during the 2013-14 and 2014-15 rainy seasons. Results from the 2013-14 season are presented. A split-plot design was used with maize monocultures and maize-cowpea mixtures as whole plots, while subplots consisted of lablab planted 0, 2, 4, and 8 weeks after planting whole plots. Maize was planted in basins supplemented with cow manure (236 g basin-1) and sidedressed with 12-9-12 (5.4 g basin-1). Maize and cowpea grain yields were not affected by lablab planting time and averaged 1630 kg ha-1 and 687 kg ha-1 across treatments, respectively. Cowpea intercropped with maize and lablab produced 2.23-3.23 Mg ha-1 of biomass (dry matter) by 4 months after planting (MAP). Lablab planted simultaneously with maize, either with or without cowpea, accumulated little biomass while maize and cowpea were actively growing; however, between 4 and 6 MAP, lablab biomass increased by 225% (maize-lablab) and 300% (maize-cowpea-lablab). Lablab growth during this period led to soil temperatures that were up to 4°C lower than maize monocultures. Preliminary results suggest that maize grain yield is not affected by legume intercropping, while cowpea intercropped with maize can provide a supplemental food source. Lablab showed potential for substantial biomass accumulation after maize and cowpea senescence, providing ground cover into the dry season.

11. Dissecting the involvement of root hair in peanut root rhizobial invasion

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Peanut, (*Arachis hypogaea* L.) undergo a different type of infection process entirely different from the intracellular infection thread infection process, this alternative infection process in peanut exhibit crack entry or intercellular invasion and has gotten less attention. Further understanding of the peanut infection mechanisms and its nodulation would promote improvement of biological nitrogen fixation and subsequently the yield of peanut. The objective of this work was to confirm whether in peanut, root hair is required for rhizobial invasion as reported for legumes invaded through intracellular invasion via infection thread and to investigate the relationship between root growth hormone (auxin) and nodulation. Our results showed that root hair is not required for peanut root rhizobial invasion, although nodulating peanut lines always have root hairs in their lateral root as oppose to the non-nodulating line, we assume a pleiotropic effect or linkage gene effect in play. We also gathered that the non-nodulating peanut lines has dysfunctional auxin pathway hence their inability to grow lateral root under auxin treatment.

POSTERS

12. Dry Matter Yield in Paspalum Interspecific Hybrids Subjected to Nitrogen Fertilization or in Mixture with Legumes

Eder A. Minski da Motta[1], Miguel Dall'Agnol[1], Cleber H. Lopes de Souza[1], Mariana M. Valli[1], Douglas Neto[1], Leonardo Duarte Felix[1] and Esteban F. Rios[2]

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Paspalum species have been improved through artificial hybridization technique, which has made available novel genetic resources for livestock production systems; however, it is unknown the productive potential of these new hybrids when subjected to nitrogen (N) fertilizer or in mixture with legumes. The goal of this study was to evaluate dry matter yield (DMY) in hybrids of P. plicatulum x P. guenoarum in response to different N rates and legume mixtures. The experiment was a randomized complete block design in split-plot arrangement with three replications. Treatments were five N rates (0, 60, 120, 240, and 480 kg ha−1 N), and one grass legume mixture (Trifolium repens L. + Lotus corniculatus L.) as whole plots, and six genotypes (4 hybrids: 1020133, 102069, 103084, 103061, P. guenoarum ecotype "Azulão" and Megathyrsus maximus cv. "Aruana" used as a control) as subplots. Data were analyzed using R statistical software. There was a significant ($P<0.001$) three-way interaction among genotype, nitrogen rate and harvest for DMY. In general, greater DMY was harvested with rates of 240 and 480 kg N ha−1. Significant differences were observed for DMY among genotypes depending on harvest date and N rates. There was variability for DMY among the genotypes in the mixture with legumes. In general, the grass-legume mixture showed higher DMY than the control (0 kg N ha−1) and similar to 60 kg N ha−1. Hybrids 1020133 and 102069 produced similar DMY compared to the controls across harvest dates and N rates. DMY harvested in Paspalum interspecific hybrids responded to increasing N fertilization rates; however, that response varied across harvests dates. In this experimental condition, grass-legume mixture yield can be an alternative practice to replace to the application of 60 kg N ha−1.

13. The role of phytohormones in citrus response to the Huanglongbing pathogen, Candidatus Liberibacter asiaticus and its vector, Diaphorina citri

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Upon phytopathogen infection or vector herbivory, plants process several defensive responses. These defenses are mainly regulated by phytohormones. In citrus, Huanglongbing (HLB) is a destructive disease causing great losses in citrus industries worldwide. HLB is caused by Candidatus Liberibacter asiaticus (CLas) and transmitted by the Asian citrus psyllid (ACP), Diaphorina citri. To explore the role of phytohormones in citrus response to HLB, we studied the effect of CLas-infection and/or D. citri-infestation on the phytohormonal profile of Valencia sweet orange (Citrus sinensis) leaves using GC-MS running in the selective ion monitoring mode (SIM-mode). In addition, the gene expression for 52 genes involved in phytohormones biosynthetic pathways were investigated. Overall, we were able to quantify 13 different phytohormones belonging to six groups (auxins, salicylates, gibberellins, cytokinins, jasmonic acid [tJA], abscisic acid [ABA]). Generally, CLas-infection and/or D. citri-infestation altered the levels of total auxins, salicylates, tJA, and ABA as groups, but did not affect the levels of gibberellins and cytokinins. All auxins and their precursor (tryptophan) were increased to higher levels in all treatments compared to control. CLas-infection induced the accumulation of all salicylates, ABA, and their precursors (phenylalanine and zeaxanthin, respectively), while D. citri-infestation increased the tJA levels and its precursor (linolenic acid). The expression levels of genes involved in the biosynthesis of auxins, salicylates, and ABA were upregulated after the CLas-infection, while the tJA- biosynthetic genes were upregulated in D. citri-infested plants. In addition, gibberellins-, and cytokinins-biosynthetic genes were remained the same. we hypothesize that both ABA and auxins play key roles in mediating the plant response directly or indirectly by activation of SA- and/or JA-mediated pathways. This leads to complex cross talk among different phytohormone groups, which interact positively or negatively together. The crosstalk between these groups is the subject of ongoing research.

14. Transgenerational Stress Memory Impacts Seed Quality and Early Development of Peanut (*Arachis hypogaea* L.)

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Increases in the duration and severity of drought events are threatening water resources across the U.S. and, consequently, the use of water within agricultural systems is being challenged more than ever before. Primed acclimation (PA) is a water-saving irrigation management strategy that can enhance the ability of the crop to respond to drought through exposure to mild or moderate water deficits during early development. Peanut generally responds positively to PA within a single season and yield maintenance under drought conditions has been achieved through this strategy. However, preliminary studies suggest that peanuts may develop a 'memory' of water deficits that can persist in subsequent generations, potentially through epigenetic mechanisms. Therefore, the objective of this study was to better characterize the impacts of this transgenerational stress memory (TSM) on seed quality and vigor. Field-grown plants of five peanut varieties were subjected to two irrigation treatments: fully irrigated (FI) (receiving 1.9 cm per irrigation event) and PA (receiving 60% FI until the time of midbloom and 100% of FI, thereafter). Fully mature seeds were collected from these parent sources representing two treatments: 1) offspring from non-stressed (FI) plants (ONP) and 2) offspring from stressed (PA) plants (OSP). Seeds were grown in rhizotron tubes in a growth chamber for 12 days and parameters of early root development were measured. Additionally, germination and seed vigor were tested using traditional methods. Results indicate that impacts of TSM vary by cultivar; in some cultivars OSP had greater root growth as measured by total root length at 12 days than ONP, while in other cultivars the opposite was true or there was no difference in root growth between offspring types. The implication of these results is that irrigation management strategies may need to be customized to individual varieties for seed production to maximize seed quality and vigor.

15. Endophytic fungi of tea (*Camellia sinensis*) and their interactions with the pathogen *Colletotrichum camelliae*

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Endophytic fungi and their roles in phytobiomes are emerging topics in the study of plant pathology, with many potential uses still not well understood. Certain endophytes have been shown to inhibit the growth of plant pathogens by the production of compounds or volatiles, by means of competition, or some combination of these. Anthracnose, a disease caused by *Colletotrichum camelliae*, is currently a disease of concern for tea growers in Florida. We isolated endophytes from tea plants (*Camellia sinensis*) grown in a research plot in Citra, FL, maintained them in pure culture, and identified them by morphology and DNA sequences. We performed dual culture assays on Potato Dextrose Agar to determine if any of these isolated endophytes displayed inhibitory properties against the pathogen *Colletotrichum camelliae*. Measurements of the overall areas of colony growth (mm^2) as well as the zones of inhibition (mm) were taken after eight days. This experiment was replicated twice. *Epicoccum nigrum* and two *Penicillium* species appeared to inhibit the growth of *C. camelliae*, but only one of the *Penicillium* species and *E. nigrum* showed statistically significant differences in the size of the inhibitory zones from those endophytes which showed zero inhibition. The inhibitory zones of the *Penicillium* and *E. nigrum* were 3.14 mm and 3.07 mm, respectively. Our results show that locally occurring endophytes can serve an inhibitory role against a common pathogen of tea. Further research will be conducted to understand the nature of the inhibitory properties of these endophytes.

16. Identification of a Major QTL Conferring Resistance to Leaf Rust in Wheat cultivar AGS2000

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Leaf rust (LR) disease, caused by the fungal pathogen *Puccinia tritcina,* is a destructive foliar disease of wheat worldwide. Gene combination of *Lr37*/*Yr17*/*Sr38* has been used in Georgia (GA) to prevent the loss from LR; however, with the emergence of new virulent races, these genes have lost their effectiveness. AGS2000 and P26R61 are the most common soft red winter wheat (SRWW) cultivars in Southeastern US, and have been used as good sources of resistance to leaf and stripe rusts, and powdery mildew. To characterize the genetic basic of LR resistance in AGS2000, a mapping population of 178 recombinant inbred lines (RILs) has been developed from a cross with P26R61. This population was genotyped using a combination of SSR, DArT, and SNP markers, and a total of 2734 markers were used for the construction of genetic map. Phenotypic evaluation of parents and RIL population was conducted at the seedling stage against a prevalent race of LR in Georgia. QTL mapping revealed a major QTL on chromosome 2BL which explained 20.32% of total phenotypic variation in AGS2000. Additionally, a minor QTL was also detected on chromosome 5B. QTL on 2BL is most likely to be a novel gene, and can be used in marker-assisted selection for LR resistance.

17. Advancing Harvest Index in Wheat through Genome Wide Association Analysis of Stem and Spike partitioning traits

Dipendra Shahi[1], Jahangir Khan[1], Muhsin Ibrahim Avci[1], Sumit Pradhan Shrestha[1], Atik Rahman[1], Jia Guo[1], Zhiyu Kang[1] Md Ali Babar[1]

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Wheat (*Triticum aestivum* L.) is one of the widely grown crop in the world and supplies about 20 percent of the total calories of the world population. In the last decades, there has been no significant progress in maximum expression of harvest index (HI) from post Green Revolution values of 45% in spring wheat and 50% in winter though HI has a hypothetical limit of 65% in wheat. Novel traits need to be identified and utilized to maximize partitioning of biomass to grain yield to reduce competition from alternative sinks such as leaves, stems and infertile tillers without compromising physiological function and structural integrity. The main objective of this study is to identify molecular markers associated with spike and stem partitioning traits that permit photosynthesis products to be consistently translated to grain yield through genome-wide association study (GWAS). We characterized 248 US soft wheat genotypes in in two locations in Florida (Quincy and Citra) for different dry matter partitioning indices, fruiting efficiency, harvest index and yield. Our preliminary data showed significant variation among genotypes for stem partitioning index, spikes/m^2, spikelets/spike, fruiting efficiency, harvest index and yield.

18. Effect of narrow band width light emitting diodes on vegetative cuttings of *Petunia* X *hybrida* cv 'Mitchell Diploid'

Sadikshya Sharma, Thomas Colquhoun

Department of Environmental Horticulture, University of Florida

Plant growth and physiology are regulated by light quality. Production of plants indoor requires artificial light to fulfill light requirements. In this study, we used different narrow band width light emitting diodes (LEDs) to determine specific wavelength of light required by the petunia which could be applied by commercial propagators. We grew vegetative cuttings of *Petunia* X *hybrida* cv 'Mitchell Diploid' under narrow band lights; red (660 nm), yellow (600 nm), green (525 nm), blue (450 nm) and white (control) which delivered a photosynthetic photon flux (PPF) of 100μmol m^{-2} s^{-1} for 16 hours per day. Plant height, days to flowering, number of flowers were maximum under blue light. Shoot dry weight was maximum under blue light whereas root dry weight was maximum under red light. Leaf area was maximum under green and white while root length maximum under white LED light, maximum internode length under green light and chlorophyll content under white and red light was greater compared to other light treatments. There were no significant differences for leaf number, fresh shoot weight and fresh root weight. This research highlighted the effects of light quality on morphology and physiology of petunia and the application of narrow wavelength LEDs for commercial ornamental plant production.

19. Preharvest vine desiccation timing for spring fresh-market potato in Florida

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Potato skinning is the removal of the outer layer of epidermal cells on the tuber. Potato skinning increases water loss, provides entry points for disease, and decreases consumer preference. Preharvest vine desiccation artificially promotes tuber maturation and reduces skinning injuries during harvest and handling operation. The study objective was evaluate the effect of desiccation application timing on yield, internal quality, degree of skinning, peel resistance, and post-harvest quality maintenance of potato cultivars. A field experiment was conducted during spring of 2017 in Hastings, FL, with a split-plot randomized complete block design. Main plot was potato cultivar: 'Soraya', 'Red LaSoda', and 'Peter Wilcox'. Subplots were diquat application timing: single application at 7, 14, or 21 days before harvest (DBH), and split applications at 7 + 14, 7 + 21, and 14 + 21 DBH. Vine desiccation practice has no negative effect on tuber yield. Diquat single application at 7 DBH leads to plant stress stimuli and development of vascular discoloration. There was significant interaction between cultivar and application timing on degree of skinning. Skinning severity was greatly reduced in treated tubers. Red LaSoda and Peter Wilcox tubers treated with a single application at 7 DBH were classified as badly skinned. Peter Wilcox had higher skinning severity than Soraya and Red LaSoda. There was no significant application timing effect on peel resistance, firmness and fresh weight loss. There was a significant increase in peel resistance from 21 DBH to harvest day. The cumulative fresh weight loss of Peter Wilcox after 21 days of storage was significantly higher than Soraya and Red LaSoda. Desiccate vines gradually, 14 and 14 + 7 DBH, for the complete kill can potentially reduce skinning injuries at harvest while decrease weight loss during storage.

20. Targeted metabolomics reveals altered fatty acid metabolism in the host by Huanglongbing disease

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Candidatus Liberibacter asiaticus (*C*Las) is the presumed causal agent of Huanglongbing, one of the most destructive diseases in citrus. However, the lipid metabolism component of host response to this pathogen has not been investigated well. Here, targeted metabolic profiling of a variety of long-chain fatty acids and their oxidation products was firstly performed to elucidate altered host metabolic responses of disease. Fatty acid signals were found to decrease obviously in response to disease regardless of cultivar. Several lipid oxidation products strongly correlated with those fatty acids were also consistently reduced in the diseased group. Using a series of statistical methods and metabolic pathway mapping, we found significant markers contributing to the pathological symptoms, and identified their internal relationships and metabolic network. Our findings suggest that the infection of *C*Las may cause the altered metabolism of long-chain fatty acids, possibly leading to manipulation of the host's defense derived from fatty acids.

21. Identification of Metabolites Influencing Consumers' Hedonics and Sensory Perception of Navel Oranges Using a Targeted Metabolomics Approach

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Fruit metabolites induce the sensory responses, contributing to consumers' preferences and acceptance of Navel oranges. This study aimed to identify sensory attributes influencing hedonics and sensory perception of Navel oranges, as well as map these sensory attributes with chemicals using a targeted metabolomics approach. For this, descriptive analysis and consumer studies were performed to analyze sensory profile of Navel oranges, and find primary drivers of liking included sweetness, overall flavor and sourness. Then, metabolomic analyses were conducted to (purpose). With help of various statistics, the combined metabolomics/sensory results revealed that besides certain taste-active compounds, 6-Methyl-5-Hepten-2-One, Octanal and (-)-□-Pinene were correlated with perceived sweetness in Navel fruits; perception of 1-Penten-3-one, (-)-□-Pinene, Octanal and p-Cymene as well as taste-active molecules contributed to the overall aroma of Navel oranges. Our findings suggest that combined both consumer-oriented sensory studies and analytical methods mapped metabolomics profiling to the sensory attributes influencing hedonic and sensory perception of Navel oranges.

22. Impact of water stress on soybean seed physiology, quality, and chemical composition

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Soybean seed quality is often determined by proteins, fatty acids, carbohydrates, isoflavones, and minerals. Thus, maintaining an improved seed quality is imperative to sustain overall human and animal nutritional aspects. The objective of this study was to investigate the effects of water stress during reproductive stage on seed yield components, composition, and minerals using two soybean cultivars grown under sunlit controlled conditions. Plants grown in pots were subjected to five levels of water stresses, 100, 80, 60, 40, and 20% of daily evapotranspiration of the control at flowering and continued until maturity. Plants were harvested 126 d after planting and seed vigor, quality, and mineral traits were examined. Results of the analysis of variance showed significant effects of cultivar, water stress, and their interactions on the studied traits. Seed weight of both cultivars was negatively impacted by soil moisture stress. Seed protein, ash, palmitic and linoleic acids, sucrose, raffinose, stachyose, N, P, K, and Ca significantly decreased whereas oil, fiber, stearic, oleic and linolenic acids, Fe, Mg, Zn, Cu, and B increased in response to soil moisture deficiency. The relationship between seed protein and oil was negatively correlated while seed dry weight exhibited strong positive correlations between seed protein, sucrose, and N content. The changes in seed constituents could be due to changes in nutrient accumulation and partitioning in soybean seeds under water stress. This information suggests the requirement of adequate soil moisture condition during flowering and seed formation stages to obtain higher nutritional value of soybean seeds.

23. Rhizobium-Legume nitrogen-fixing symbiosis in alfalfa and *Medicago truncatula*

Tai-Jung Wu[1], Omani McLish[1], and Mengsheng Gao[1]

[1]*Department of Soil and Water Science, College of Agriculture and Life Science, University of Florida, Gainesville, FL, USA*

Sinorhizobium meliloti is a gram-negative bacterium that can be found in the soil or on the root of certain legumes genera and it forms a nitrogen-fixing symbiosis with legumes such as Medicago (alfalfa and annual medics), Melilotus (sweet clover), and Trigonella (fenugreek) species. This is displayed by the presence of root nodules on the roots of the subsequent plants. The nitrogen-fixing symbiosis between *S. meliloti and legumes* converts nitrogen into ammonium which then can be used for host plants' nutrition and growth. Hfq is a RNA-binding protein that controls gene expression and has been demonstrated to play a role in symbiosis. Some small RNA has been proposed to be involved in Hfq mediated gene regulation in rhizobium nitrogen fixing symbiosis. This research presents us the information of gene expression of 6 RNAs in Hfq mutant related to wild type and we discuss the potential role of small RNAs involvement in Hfq mediated gene expression that controls rhizobium nitrogen fixation symbiosis. We hope to identify a genetic pattern for RNA gene expression that acts as a genetic marker to predict the genes that will be expressed in other plants inoculated with the *S. meliloti.* Quantitative PCR techniques used to identify the small RNA sequences that are present in the mediation of Hfq in the plant strain will be utilized in the qPCR of alfalfa sprouts. We hope to identify similarities in the RNA presented to identify markers that can be used to inoculate other plants later down the road.

POSTERS

24. Veg-a-Sketch: The Plant as a Canvas, Light as a Brush, Pigments as Paint

Lauren Plotnik and Dr. Kevin M. Folta

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Light controls the accumulation of various pigments in plants. Anthocyanins provide red-purple pigments to leaves, and their accumulation in response to environmental cues has been well understood. Anthocyanin accumulation is induced by blue light acting through the cryptochrome photoreceptors. Cryptochrome receptors are influenced by green light, which at least can partially reverse the blue light response. We have surveyed a large number of red lettuces for their color plasticity in light. Several varieties, including 'Annapolis', can be grown under constant green light to produce healthy, expanded green leaves with little anthocyanin pigment. A narrow-bandwidth blue light treatment (430 nm) leads to a robust anthocyanin accumulation. When laser-cut stencils are applied to the green light-treated leaves, blue light can be applied to induce cell-autonomous accumulation of anthocyanins in this variety. Leaves are essentially painted with light, decorated with logos or other graphic elements under the stencil. We call this approach the Veg-a-Sketch, and have used the approach to demonstrate concepts in phenotypic plasticity, photoreceptor function, and light-mediated plant physiology. Seeds, lights and stencils are provided to schools free of charge through the contact of our laboratory or website (veg-a-sketch. com).

PLANT SCIENCE COUNCIL ACTIVITIES

Coming Up

TO PHD OR NOT TO PHD (PANEL DISCUSSION)

Feb. 9, 2018

This lunchtime workshop is part of a series of discussions called **"So you want to Work in Industry?"** These discussions will be geared toward students studying plant sciences. Students from off campus will also be able to join the meeting via video conferencing. A link to join from off-campus will be emailed to registered participants once available!

DATA CARPENTRY WORKSHOP

Feb. 22-23, 2018

The Plant Science Council will host a Data Carpentry Workshop on Feb 22-23, 2018. The workshop is geared towards developing fundamental data skills needed to conduct research. Check our website for details.

PLANT SCIENCE COUNCIL ACTIVITIES

Past Events

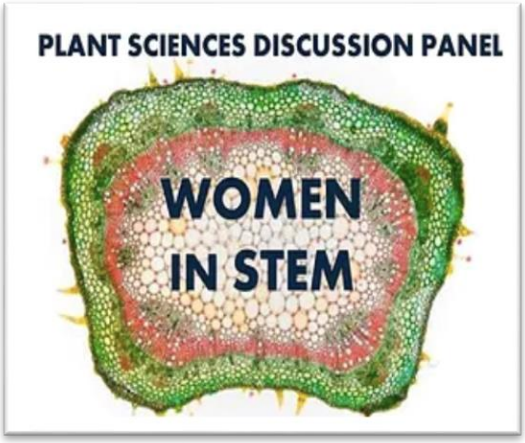
TIPS AND TRICKS FOR MASTERING THE INTERVIEW

January 12, 2018

This lunchtime workshop is part of a series of discussions called **"So you want to Work in Industry?"** These discussions will be geared toward students studying plant sciences. Students from off campus will also be able to join the meeting via video conferencing. A link to join from off-campus will be emailed to registered participants once available!

PLANT SCIENCES DISCUSSION PANEL: WOMEN IN STEM

November 16, 2017

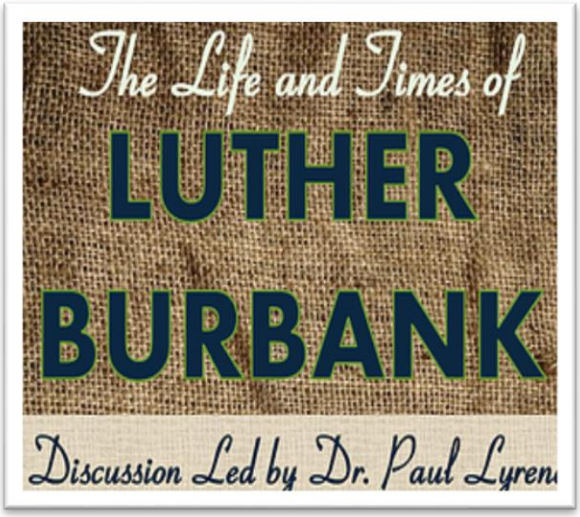


The Plant Pathology Graduate Student Organization and the Plant Science Council organized a discussion panel to talk about what it is like to be a woman working in plant sciences. Faculty members from Plant Pathology, Horticultural Sciences, Agronomy, and Environmental Horticultural Sciences served on the panel to discuss their experiences working in Plant Sciences.

PLANT SCIENCE COUNCIL ACTIVITIES

THE LIFE AND TIMES OF LUTHER BURBANK

November 07, 2017



Discussion led by Dr. Paul Lyrene

The Plant Science Council hosted its first discussion in our **Historical Perspectives** Series. The topic of discussion was Luther Burbank, American botanist, horticulturist and pioneer in plant breeding. During his career Burbank created hundreds of new varieties of fruits (plum, pear, prune, peach, blackberry, raspberry); potato, tomato; ornamental flowers and other plants. One of his most famous releases was the Russet Burbank Potato.

CAREER BUILDING, NETWORKING, & COMMUNICATING

August 17, 2017

Led by Dr. Mary Williams

The Plant Science Council organized a workshop on "Career building, networking, & communicating" for Professional Development for Plant Scientists. The workshop was led by Dr. Mary Williams, features editor of journal *Plant Cell*.

PLANT SCIENCE COUNCIL ACTIVITIES

PLANT IMPROVEMENT RETREAT

August 3 & 4, 2017

The Plant Science Council organized a Plant Improvement Retreat for students at Tampa Marriott Waterside Hotel & Marina, Tampa, FL in conjunction with the UF/IFAS Plant Breeders Workgroup. The retreat featured speakers from industry who shared their experiences of working in the industry. A Grant Writing Workshop led by Dr. Karen Koch was also conducted.

PLANT BREEDING FOR THE HOME GARDENER

March 26, 2017

The Plant Science Student Council in coordination with The Edible Plant Project, Gainesville, FL led a seminar and demonstration to equip home gardeners with the skills needed to make crosses and start to explore the world of genetic diversity!

PLANT SCIENCE COUNCIL ACTIVITIES

1ST ANNUAL PLANT SCIENCE SYMPOSIUM
Harnessing Plant Diversity to Cope with a Changing Climate
April 13-14, 2017

The Plant Science Council organized the first annual Plant Science Symposium at the University of Florida. The symposium was part of the DuPont Pioneer Plant Science Symposia Series and was entirely led by students.

SPEAKERS:

Dr. Senthold Asseng, University of Florida
Food security and climate change.

Dr. Stephanie L Greene, USDA-ARS
Wading deeper into the gene pool: using crop wild relatives to breed climate resilient crops.

Dr. P.V. Vara Prasad, Kansas State University
Impact of Climate Change and Climate Variability on Productivity of Food Grain Crops.

Dr. Jim Hancock, Michigan State University
Breeding strawberries and blueberries in a changing global environment.

Dr. Charlie Messina, DuPont Pioneer
Improving phenotypic prediction through crop model-whole genome prediction integration.

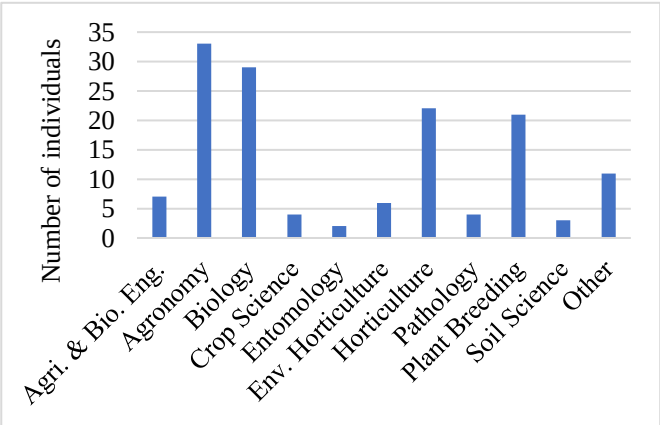
Travel Award Winners:

Regina Enninful, Kansas State University
Craig Beil, Colorado State University
Waltram Ravelombola, University of Arkansas
Uttam Bhattarai, Louisiana State University

Poster Winners:

Nichole Barber, Plant Science / Plant Health
Cecile Pereira, Microbiology & Cell Science
Pritika Pandey, Entomology & Nematology
Jack Nielsen, Agronomy Department

Distribution of participants



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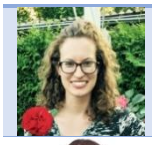
President
PhD Student, Horticulture



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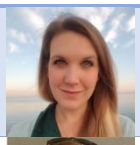
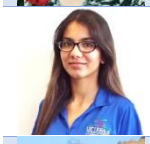
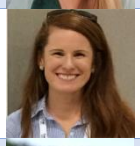


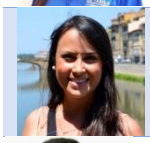
Rebecca Lauren Wente
Secretary
MS Student, Horticulture



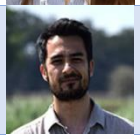
Gurleen Kaur
Treasurer
PhD Student, Horticulture



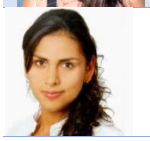
Kelsey Andersen
Professional Development Chair
PhD Student, Plant Pathology



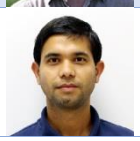
Kelly Balmant
Outreach Chair
Post-doc, SFRC



Muhsin Ibrahim Avci
Graphic Design & Social Media Chair
MS Student, Agronomy



Natalia Salinas
Off-campus coordinator
PhD Student, Horticulture



Krishna Bhattarai
Poster Chair
PhD Student, Env. Horticulture

Faculty Advisors

Dr. Esteban Fernando Rios
Faculty Advisor
Agronomy Department

Dr. Marcio Resende Jr.
Faculty Advisor
Horticultural Sciences Department

Volunteers

Chris Barbey	Juan Gonzalez
Daniel Mancero	Lauren Scott
Dev Paudel	Marco Goyzveta
Dipendra Shahi	Melinda Yin
Dorothea Hopkins	Michael Sthreshley
Edgar Sierra	Sarah Brewer
Francesco Cappai	Sienna Turner
Haley Sater	Zi-fan Zhao
James Orrock	

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Plant Science Symposium
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PLANT SCIENCE Council

The Plant Science Council at the University of Florida is formed by graduate and undergraduate students studying or interested in plant science research and extension. The Plant Science Council helps to develop leadership skills of UF students by encouraging participation in professional activities such as organizing multiple student-led seminar and workshop series. Furthermore, it promotes academic and career exploration to help students gain managerial and out-of-classroom experience.

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