2017 Meeting of the Southern Section of the American Society of Plant Biologists

PROGRAM

April 8-10, 2017

DoubleTree by Hilton Hotel Orlando Downtown

Orlando, FL

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Meeting Schedule at a Glance

Saturday, April 8th

2:00 – 6:00 p.m.	Field Trip to Blue Spring State Park (*Meet at the **hotel lobby** at **1:50 pm. Bus leaves at 2:00 pm sharp***)
1:00 - 6:00 p.m.	Registration – Hilton DoubleTree Orlando Downtown **Prefunction Area** Poster Set-Up (**Summerlin-Princeton**)
5:30 - 8:00 p.m.	Networking Welcome and Mixer (**Prefunction Area)**
8:00 - 9:30 p.m.	Executive Committee Meeting (**Commerce Club**)

Sunday, April 9th

6:45 - 7:50 a.m.	Breakfast **(Prefunction Area and Orange)**
7:55 - 10:00 a.m.	Plenary Session **(Summerlin-Princeton)**
10:00 – 10:30 a.m.	Coffee Break, Posters open for viewing
10:30 a.m. – 12:00 p.m.	Concurrent general talks and Graduate Oral Competitions, Session 1A **(Summerlin-Princeton)**; 1B (**Sumter-Seminole**)
12:00 – 1:30 p.m.	Lunch (**Prefunction Area and Orange**)
1:30 - 2:45 p.m.	Concurrent general talks and Graduate Oral Competitions, Session 2A **(Summerlin-Princeton)**; 2B (**Sumter-Seminole**);
2:45 – 3:15 p.m.	Coffee Break (posters are open)
3:15 – 4:30 p.m.	Graduate Oral Competitions, Session 3A **(Summerlin-Princeton)**; 3B (**Sumter-Seminole**);
4:30 – 5:45 p.m.	Poster Session, UNDERGRADUATE poster competition **(Summerlin-Princeton)**
5:45 – 6:45 p.m.	Poster Session, GRADUATE and GENERAL posters **(Summerlin-Princeton)**
7:00 – 9:00 p.m.	Banquet and Awards Ceremony, **Manatee Ballroom**

Monday, April 10th

7:00 - 7:50 a.m.	Breakfast (**Prefunction Area and Orange)**
7:55 a.m. – 12:00 p.m.	Kriton Hatzios Symposium (**Summerlin-Princeton)**
12:00 p.m.	General business meeting (**Summerlin-Princeton)**
12:30 p.m.	Meeting adjourns

Detailed Meeting Schedule

Saturday, April 8th

2:00 p.m. - 6:00 p.m. Field Trip to Blue Spring State Park
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Sunday, April 9th

6:45 a.m. - 7:50 a.m. Breakfast (**Prefunction Area and Orange**)

7:55 a.m. – 8:15 a.m. Opening Remarks (**Summerlin-Princeton**)
7:55 a.m. Ken Korth, Chair, SS – ASPB
8:05 a.m. Introductions of Kriton Hatzios Symposium speakers

8:15 A.M. – 10:00 A.M. Plenary Session (Summerlin-Princeton)

8:15 **Rice and the pathogen *Xanthomonas*: Beyond PTI and ETI**
(001) *Frank White* *University of Florida*

8:40 **RAF-mediated signal transduction – perception and response to pathogens and environmental stress in model and crop systems**
(002) *Sorina Popescu* *Mississippi State University*

9:05 **Role of the geminivirus AL2 protein in inducing autophagy**
(003) *Garry Sunter* *University of Texas at San Antonio*

9:30 **Elongator: an epigenetic regulator of plant immune responses**
(004) *Zhonglin Mou* *University of Florida*

10:00 A.M. – 10:30 A.M. – Coffee Break – (Prefunction Area) (posters open for viewing)

10:30 A.M. – 12:00 P.M. Concurrent Session 1A (Summerlin-Princeton)

Moderator: Rebecca Dickstein

10:30 **Identification of a novel gene *LSR1* that plays a role in high light tolerance in the green micro-alga *Chlamydomonas reinhardtii*.**
(005) *Mautusi Mitra* *University of West Georgia*

10:45 A Rosetta Stone for Nodulation: Translating an Interkingdom Signal at the Interface of a Crucial Host-Microbial Symbiosis.

(006) *Andrew G. Palmer* *Florida Institute of Technology*

11:00 Evaluation of Soybean Breeding Lines for Seed Germination and Composition under High Heat and Dryland Production in the Midsouthern USA

(007) *Nacer Bellaloui* *USDA Agricultural Research Service*

****Graduate Student Oral Competition**

11:15 The maize LINC complex components

(008) *Hardeep Gumber *** *Florida State University*

11:30 Interactions of nitrogen and carbon metabolism in the submerged aquatic plant, *Hydrilla verticillata*

(009) *Molly Miller *** *University of South Alabama*

11:45 The RDN arabinosyltransferase family plays a crucial role in nodulation regulation signaling and root architecture patterning in *Medicago truncatula* and *Arabidopsis thaliana*

(010) *Stephen Nowak *** *Clemson University*

10:30 A.M. – 12:00 P.M. Concurrent Session 1B (Sumter-Seminole)

Moderator: Nihal Dharmasiri

10:30 A current model of group IIA intron excision in the chloroplast of land plants.

(011) *Michelle M. Barthet* *Coastal Carolina University*

10:45 Three Way Symbiosis: Unlocking the Potential of a Plant, Fungus, and Virus Interaction

(012) *Blake Cleckler* *University of West Alabama*

11:00 Genetic dissection of seedling stage salinity tolerance in rice using introgression lines of a salt tolerant landrace Nona Bokra

(013) *Venkata Ramana Rao Puram* *Louisiana State University Agricultural Center*

****Graduate Student Oral Competition**

11:15 Comparative transcriptomics analysis reveals similarities of key gene expression between rice and *Brachypodium* during formation of nodule-like structures

(014) *Jacklyn Thomas *** *University of Central Arkansas*

11:30 Transcriptional regulation of the plant immune transcription coactivator NPR1

(015) *Matthew Dommel *** *University of Florida*

11:45 The Arabidopsis calcium sensor protein CML38 is an essential hypoxia response protein that assembles with translating and non-translating mRNA nucleoprotein complexes

(016) *Sterling Field *** *University of Tennessee*

12:00 P.M. – 1:30 P.M Lunch (Prefunction Area and Orange)

1:30 P.M – 2:45 P.M. Concurrent Session 2A (Summerlin-Princeton)

Moderator: Jay Shockey

1:30 **Discovery and implications of a mammalian endocannabinoid ligand in moss**
(017) *Aruna Kilaru* *East Tennessee State University*

1:45 **Additional functional characterization of *Medicago truncatula* MtNPF1.7 transporter**
(018) *Rebecca Dickstein* *University of North Texas*

****Graduate Student Oral Competition**

2:00 **Generation of disease resistance in tomato using genes encoding the Elongator subunits**
(019) *Juliana Pereira *** *University of Florida*

2:15 **Characterizing a Novel Arabidopsis Gene Identified from Spaceflight Experiments that Might have a Putative Role in Regulating ROS Homeostasis.**
(020) *Natasha J Sng*** *University of Florida*

2:30 **Construction and Comparison of Large Gene Co-expression Network in Maize Using RNA-Seq Data**
(021) *Ji Huang *** *Florida State University*

1:30 P.M – 2:45 P.M. Concurrent Session 2B (Sumter-Seminole)

Moderator: Mustafa Morsy

1:30 **Spatial and Temporal Resolution of mRNA Profiles During Early Nodule Development**
(022) *Suchitra Chavan* *Clemson University*

1:45 **Agricultural land-use legacies and habitat restoration shape diversity and composition of plants and soil microbes in longleaf pine savannas**
(023) *Nash Turley* *University of Central Florida*

****Graduate Student Oral Competition**

2:00 **Characteristics of Raf-like family of Integrin-Linked Kinases: Structure, phylogeny, and role in transcriptional reprograming for abiotic and biotic stress response**
(024) *Gizem Dimlioglu *** *Mississippi State University*

2:15 **IBR5 interacts with GTP binding proteins to regulate plant auxin response**
(025) *Idrees Ahmad *** *Texas State University*

2:30 **Conserved functionality of the chloroplast RNA helicase ISE2: *Physcomitrella patens* and beyond.**
(026) *Jessica Fernandez *** *University of Tennessee*

2:45 P.M. – 3:15 P.M. Coffee Break (Prefunction Area) (posters are open)

3:15 P.M – 4:30 P.M. Concurrent Session 3A (Summerlin-Princeton)

**Graduate Student Oral Competition

Moderator: Ashlee McCaskill

3:15 **Identification of genetic suppressors of the *sunn*-1 hypernodulating phenotype**
(027) *Diptee Chaulagain *** *Clemson University*

3:30 **A Novel Receptor-Like Kinase Involved in Fungal Pathogen Defense in *Arabidopsis thaliana***
(028) *Justin Ray *** *University of Alabama*

3:45 **IBR5 may regulate auxin responses in Arabidopsis through interaction with SCF Complex**
(029) *Timothy Cioffi *** *Texas State University*

4:00 **Subtle temperature differences may well determine who wins: a story of four submerged aquatic plant species**
(030) *Molly Miller *** *University of South Alabama*

4:15 **Characterization of Nuclear Apyrases in *Arabidopsis thaliana***
(031) *Gayani Weeraratne *** *University of Texas at Austin*

3:15 P.M – 4:30 P.M. Concurrent Session 3B (Sumter-Seminole)

**Graduate Student Oral Competition

Moderator: Karen E. Koch

3:15 **Isolation and characterization of a male fertility gene (Ms4) in soybean**
(032) *Sandi Win Thu *** *Texas Tech University*

3:30 ***Chlamydomonas reinhardtii*, a unicellular Model for Quorum Sensing at the Interkingdom Interface**
(033) *Timothy Haire *** *Florida Institute of Technology*

3:45 **Overexpression of the Arabidopsis *ELP3* and *ELP4* genes enhance disease resistance in woodland strawberry**
(034) *Qi Zhao *** *University of Florida*

4:00 **Characterization of the spaceflight methylome: whole-genome bisulfite sequencing and transcription profile analysis of *Arabidopsis thaliana* grown aboard the International Space Station (ISS)**
(035) *Collin LeFrois *** *University of Florida*

4:15 **A Shift from 2D to 3D: Redefining how we study plasmodesmata structure**
(036) *Brandon Reagan *** *University of Tennessee*

4:30 P.M. – 6:45 P.M. Poster Session (Summerlin-Princeton)

4:30 – 5:45 p.m. **Undergraduate** Poster Session Competition

5:45 – 6:45 p.m. **Graduate and General** Poster Session

Undergraduate students – posters P1 – P15

(* - undergraduate poster competition entry)

Undergraduate student presenters should be at their poster from 4:30 – 5:45 p.m. for competition judging and general discussion.

P1*. **Identification of a novel gene *LSR1* that plays a role in high light tolerance in the green micro-alga *Chlamydomonas reinhardtii*.**
(037) *Kevin Nguyen & Ja'von Swint* *University of West Georgia*

P2*. **The Role of InvINH1 as an Invertase Inhibitor**
(038) *Noni Davis* *Spelman College*

P3*. **Screening *Medicago truncatula* Tnt1 insertion lines for mutants in the Autoregulation of Nodulation pathway**
(039) *Cameron Corbett* *Clemson University*

P4*. **Novel *M. truncatula* CLE peptides in nodule regulation**
(040) *Christina Chiu* *Clemson University*

P5*. **Improving Crop Productivity using Symbiotic Fungi**
(041) *Haley Turner* *University of West Alabama*

P6*. **Crop production on the rise as fungal endophytes help with the cause**
(042) *Mantricia Densmore* *University of West Alabama*

P7*. ***Littoraria irrorata* Preference for Salt Marsh Habitat**
(043) *Samantha Garcia* *Louisiana State University Shreveport*

P8*. **Effects of exogenous ß-alanine on primary root growth, potassium accumulation and polyamine biosynthesis in *Arabidopsis thaliana***
(044) *Thomas Detchemendy* *University of Tennessee at Chattanooga*

P9*. **Assessing Genetic Diversity within Natural Populations of Smooth Cordgrass to Ensure Effective Restoration Efforts**
(045) *Michelle Gaynor* *University of Central Florida*

P10*. **An *in vitro* functional splicing assay for the putative maturase MatK**
(046) *Christopher Logan Pierpont* *Coastal Carolina University*

P11*. **Protein-Protein Interactions Associated with Splicing of Chloroplast Group IIA Introns**
(047) *Alexandra Margets* *Coastal Carolina University*

P12*. ***Arabidopsis thaliana* NIP2;1 : An Aquaporin superfamily lactic acid channel induced in roots during low oxygen stress**
(048) *Clayton Nunn* *University of Tennessee Knoxville*

P13*. Comparison of growth between Bt and conventional field corn
(049) *Kelsey Smith* *Emory & Henry College*

P14*. Developing an Activation Tagging System for Wheat Mutagenesis
(050) *Amanda Askins* *University of South Carolina Aiken*

P15*. Determining the role of homologous recombination in replicative transposition of *mPing*
(051) *Lisette Payero* *University of South Carolina Aiken*

Graduate students – posters P16 – P34

Graduate student presenters should be at their poster from 5:45 – 6:45 p.m. for general discussion.

P16. The Arabidopsis calcium sensor protein CML38 is an essential hypoxia response protein that assembles with translating and non-translating mRNA nucleoprotein complexes
(016) *Sterling Field* *University of Tennessee*

P17. Characterizing a Novel Arabidopsis Gene Identified from Spaceflight Experiments that Might have a Putative Role in Regulating ROS Homeostasis.
(020) *Natasha J Sng* *University of Florida*

P18. A Novel Receptor-Like Kinase Involved in Fungal Pathogen Defense in *Arabidopsis thaliana*
(028) *Justin Ray* *University of Alabama*

P19. Isolation and characterization of a male fertility gene (Ms4) in soybean
(032) *Sandi Win Thu* *Texas Tech University*

P20. Characterization of the spaceflight methylome: whole-genome bisulfite sequencing and transcription profile analysis of *Arabidopsis thaliana* grown aboard the International Space Station (ISS)
(035) *Collin LeFrois* *University of Florida*

P21. Nucleosome Occupancy is Altered in Mutants of Maize SWI/SNF-like Chromatin Proteins
(052) *Linda Stroud* *Florida State University*

P22. Cytogenetic analysis of *Humulus lupulus* (hops)
(053) *Katherine Easterling* *Florida State University*

P23. Characterization of fatty acid amide hydrolase in *Physcomitrella patens*
(054) *Md Imdadul Haq* *East Tennessee State University*

P24. The Identification and Characterization of Kinase Orthologs in Soybean and Cotton in the Effort to Improve Plant Resistance against Environmental Stresses
(055) *Norbert Bokros* *Mississippi State University*

P25. Biochemical characterization of tomato fatty acid amide hydrolase
(056) *Sujan Shrestha* *East Tennessee State University*

P26. Potential allelopathic effects of *Eichhornia crassipes* and *Lemna gibba* on the invasive water fern *Salvinia molesta*
(057) *Jessica Mast* *Louisiana State University Shreveport*

P27. **Biological control of root-knot nematode in cotton by suppression of candidate susceptibility genes**
(058) *Najmeh Nejat* *Mississippi State University*

P28. **The identification and characterization of a mutant defective in dark to light transition**
(059) *Ananya Mukherjee* *Louisiana State University*

P29. **Alpha Carbonic Anhydrases of *Arabidopsis thaliana***
(060) *Lance Pounds* *Louisiana State University*

P30. **Regulator of Gene Silencing Calmodulin-like proteins: Potential targets of abiotic and biotic stress responses**
(061) *Craig Conner* *University of Tennessee Knoxville*

P31. **Chemical and Molecular Responses to Kin Recognition Events in a Model Angiosperm**
(062) *Thiara Bento* *Florida Institute of Technology*

P32. **Lignin nanotubes as a gene delivery system into plant and animal cells**
(063) *Michael Riley II* *University of Florida*

P33. **Evaluating Candidate Genes for Anthracnose Resistance in Sorghum with Virus-Induced Gene Silencing**
(064) *Lauren Stutts* *University of Florida*

P34. **Ethylene Responses in *Azospirillum brasilense* (Azo)**
(065) *Celeste Rodriguez* *University of Knoxville*

General Poster Session – posters P35 – P41

Presenters should be at their poster from 5:45 – 6:45 p.m. for general discussion.

P35. **Determining the Sequences Involved in *mPing* Transposition**
(066) *Jazmine I. Benjamin* *University of South Carolina Aiken*

P36. **Testing Strategies to Produce Targeted Insertion of *mPing***
(067) *Mary E. Roby* *University of South Carolina Aiken*

P37. **Possible Suppression of *Salvinia molesta* by Allelopathy of two Waterlilies, *Nymphaea mexicana* and *Nymphaea odorata***
(068) *Amy Anne Erickson* *Louisiana State University Shreveport*

P38. **Additional functional characterization of *Medicago truncatula* MtNPF1.7 transporter**
(018) *Rebecca Dickstein* *University of North Texas*

P39. **Naturally-occurring high oleic acid cottonseed oil: identification and functional analysis of a mutant allele of *Gossypium barbadense* fatty acid desaturase-2**
(069) *Jay Shockey* *USDA-ARS*

P40. **Arabidopsis transcriptome in the face of hypobaria, a novel abiotic stress**
(070) *Mingqi Zhou* *University of Florida*

P41. **Helping Students Understand How DNA Mutations Cause a Phenotype by Incorporating Computational Molecular Modeling into the Classroom**
(071) *Tara Phelps-Durr* *Radford University*

7:00 P.M. – 9:00 P.M. Banquet and Awards Ceremony, Manatee Ballroom

8:15 – 8:25 P.M. *Harry Klee, President of ASPB* - **"The changing face of ASPB"**

8.25 – 8.30 P.M. *Ken Korth* - **Presentation of Student Awards**

Monday, April 10th

7:00 A.M. - 7:50 A.M. Breakfast (**Prefunction Area and Orange**)

7:55 Phenotyping Solutions for Basic and Applied Research in Plant Biology and Agriculture
(072) *Todd M. DeZwaan* *LemnaTec Corporation*

2017 Kriton Hatzios Symposium (Summerlin-Princeton)

8:10 - 8:20 *Ken Korth and Jay Shockey,* **Welcome and 2018 SS-ASPB meeting**
8:20 - 8:25 *Imdadul Haq,* **SS-ASPB Student Ambassador**
8:25 - 8:30 *Nihal Dharmasiri,* **Symposium Speakers Introductions**

8:30 Establishment of Heterochromatin: How the cell recognizes and triggers transposable elements for trans-generational silencing
(073) *Keith Slotkin* *Ohio State University*

9:15 Epigenetic regulation of gene expression in maize
(074) *Karen McGinnis* *Florida State University*

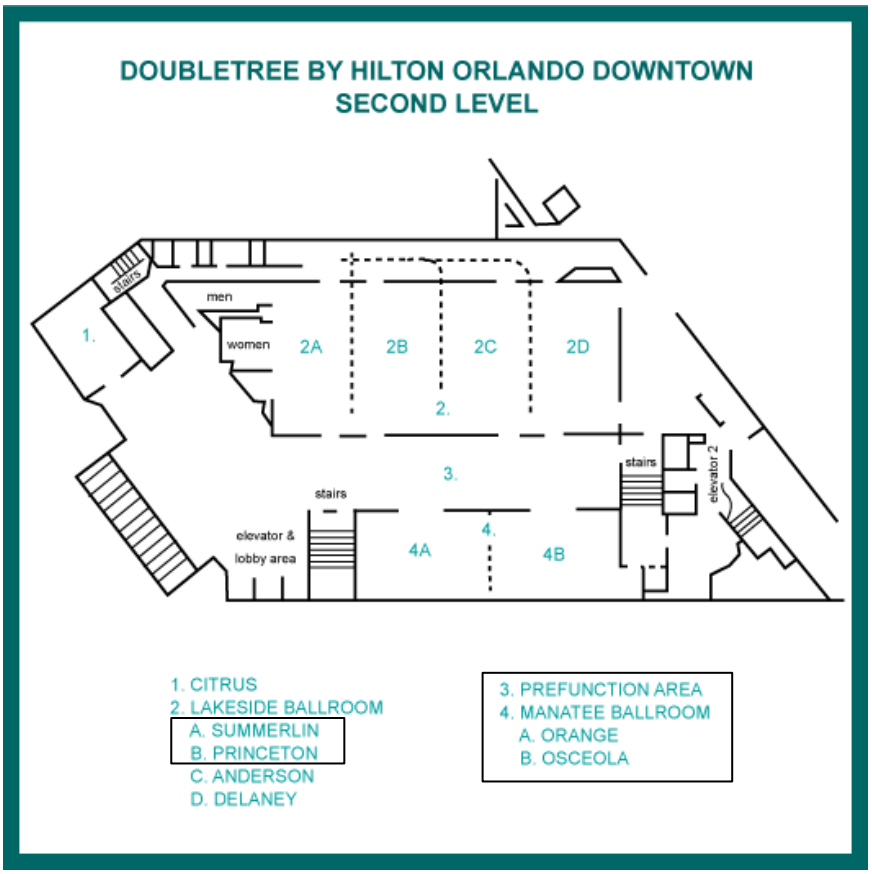
10:00 A.M. – 10:30 A.M. Coffee Break (Prefunction Area)

10:30 Molecular mechanisms of interplay between ethylene signaling and chromatin regulation in Arabidopsis
(075) *Hong Qiao* *University of Texas at Austin*

11:15 Large-Scale Heterochromatic Remodeling Facilitates DNA Repair
(076) *Scott Michaels* *Indiana University*

12:00 P.M. General Business Meeting (Summerlin-Princeton)

12:30 P.M. Meeting Adjourns


DOUBLETREE BY HILTON ORLANDO DOWNTOWN
SECOND LEVEL
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lobby area
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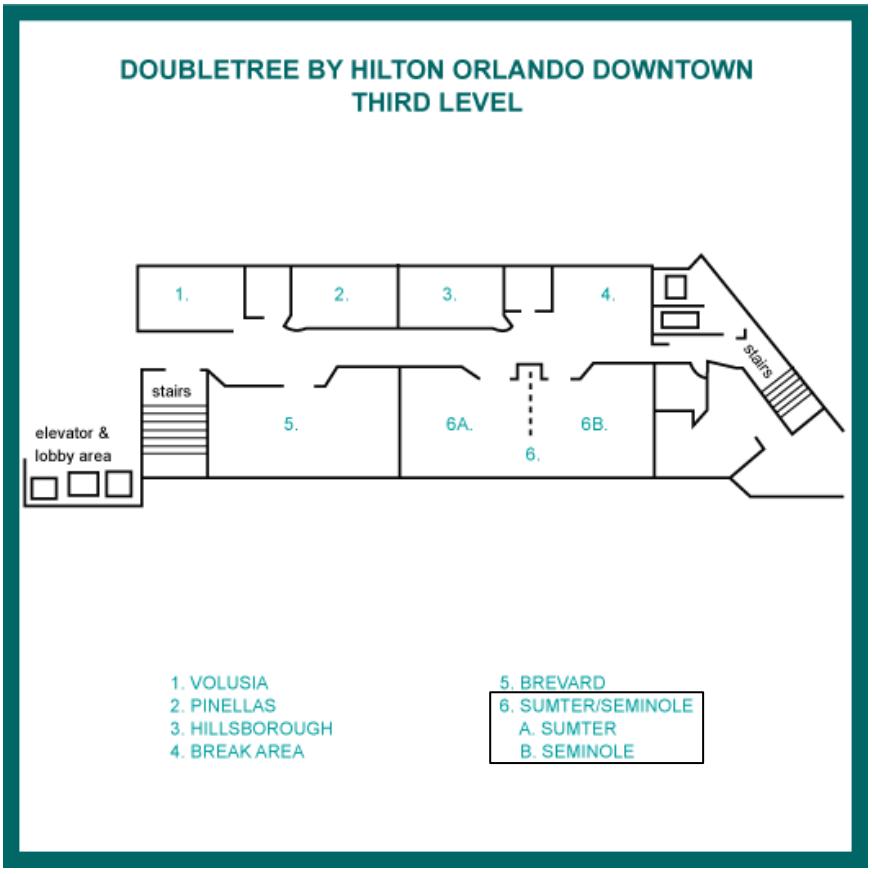
1. CITRUS
2. LAKESIDE BALLROOM
A. SUMMERLIN
B. PRINCETON
C. ANDERSON
D. DELANEY
3. PREFUNCTION AREA
4. MANATEE BALLROOM
A. ORANGE
B. OSCEOLA


DOUBLETREE BY HILTON ORLANDO DOWNTOWN
THIRD LEVEL
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6B.
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1. VOLUSIA
2. PINELLAS
3. HILLSBOROUGH
4. BREAK AREA
5. BREVARD
6. SUMTER/SEMINOLE
A. SUMTER
B. SEMINOLE

2017 SS-ASPB MEETING ABSTRACTS

7:55 - 10:00 a.m. Plenary Session

001 **Rice and the pathogen *Xanthomonas*: Beyond PTI and ETI**

Frank White

Department of Plant Pathology, University of Florida-Gainesville, 2550 Hull Rd, Gainesville, FL

The interaction of rice and the pathogen *Xanthomonas oryzae* pv. *oryzae* involves many of the same biochemical features of other bacterial/plant interactions. However, when looking at the genetic factors controlling the disease and the mechanisms of virulence, a surprising number of unique features have been discovered, some very recent. The findings indicate that the two have move on beyond the classical PTI and ETI models, and fighting has moved into other realms of plant defense. The curious dependence of Xoo on induction of a member of the host SWEET gene family will be discussed as well as host and pathogen adaptive features surrounding the relationship.

Keywords: rice, bacterial blight, *Xanthomonas*, SWEET

002 **RAF-mediated signal transduction – perception and response to pathogens and environmental stress in model and crop systems**

Sorina C. Popescu [1], Gizem Dimlioglu [1], Norbert Bokros [1], George Popescu [1,2]

[1] *Dept. of Biochemistry, Molecular Biology, Entomology and Plant Pathology, Mississippi State University, Starkville, MS*
[2] *Institute for Genomics, Biocomputing, and Biotechnology, Mississippi State University, Mississippi State, MS 39759*

Understanding plant response and adaptation to stress are fundamental problems in biology. Our research focuses on the intracellular signal processing triggered by pathogens and abiotic stress factors, and how signaling networks modulate plant phenotypes. In particular, we aim to understand the composition and structure of signal processing pathways and the principles that govern their function in experimental models and crops. One study will be presented that exemplifies our research focus. The project is centered on the calmodulin-binding protein ILK1, a component of the MAP3K-RAF family of kinases (Popescu et al., 2017). We demonstrate the importance of ILK1 at the confluence of biotic and abiotic stress pathways and highlight the importance of the nutritional status of the plant and ion-mediated processes in ILK1 function (Brauer et al., 2016). Unpublished, preliminary results on the study of ILK1-like homologs in crops will be presented as well.

Keywords: abiotic stress, immunity, Integrin-linked kinases, ion transport

003 **Role of the geminivirus AL2 protein in inducing autophagy**

Garry Sunter[1], Maria Lockwood[2], Jianhua Ruan[3]

[1] *Department of Biology, University of Texas at San Antonio*
[2] *Department of Biology, University of Texas at San Antonio*

[3] *Department of Computer Science, University of Texas at San Antonio*

Resistance to infection depends on interactions between pathogen and host, and one initial response involves recognition of microbial- or pathogen-associated molecular patterns (MAMPS/PAMPs) by pattern recognition receptors. This generally stimulates non-specific responses to molecules common to both pathogenic and non-pathogenic microbes, and results in PAMP-triggered immunity (PTI). For plant virus infections it has been proposed that RNA silencing is part of the PTI response, and as counter-defense viruses encode suppressors of silencing (VSRs). Geminiviruses encode small multifunctional proteins (AC2/C2), which act to counter plant immune responses including RNA silencing, and inactivation of SNF1-related protein kinase (SnRK1), and adenosine kinase (ADK). Inactivation of SnRK1 and ADK leads to enhanced susceptibility to infection and suppression of gene silencing respectively. AC2/C2-mediated inactivation of SnRK1 causes differential expression of autophagy-related genes, which can directly target intracellular pathogens, including viruses. A comparison of the Arabidopsis transcriptome when Spinach curly top virus C2 or antisense (as)SnRK1 was over-expressed revealed a number of genes differentially regulated by both treatments. This is interpreted to represent a response to SnRK1 inhibition. Using genes that were differentially regulated in response to both C2 and asSnRK1 a novel network-based method for identifying gene functional modules was applied. A large complex network was identified, containing a smaller sub-network consisting of up-regulated genes with functions associated with autophagy and senescence. We measured significant increases in expression of genes within this sub-network using qPCR, which is interpreted to be a consequence of the inactivation/inhibition of SnRK1. A link between geminivirus-encoded VSRs and autophagy through the conserved SnRK1 pathway has the potential to provide information on geminivirus pathogenesis.

Keywords: Geminivirus, AL2, autophagy, defense

004 **Elongator: an epigenetic regulator of plant immune responses**

Zhonglin Mou, Christopher T. DeFraia, Xudong Zhang, Chenggang Wang, Yongsheng Wang

Department of Microbiology and Cell Science, University of Florida, Gainesville, FL 32611

Plants are constantly exposed to potential microbial pathogens and solely rely on innate immunity to battle against microbial invasion. The efficacy of plant immunity is tightly correlated with the kinetics and magnitude of the transcriptional changes activated by the invading pathogen. Numerous proteins have been shown to regulate plant immunity-associated transcriptional reprogramming, among which is the multitasking protein complex named Elongator. Elongator was first purified as an interactor of hyperphosphorylated RNA polymerase II in yeast, and was later identified in animal and plant cells. The Elongator complex is composed of two copies of each of its six subunits (ELP1 to ELP6), with ELP1 and ELP2 serving as scaffolds for complex assembly, ELP3 being the catalytic subunit, and ELP4-ELP6 forming an accessory complex. It has been reported that Elongator functions in diverse cellular processes, including histone modification, exocytosis, α-tubulin acetylation, transcriptional silencing, genome stability maintenance, DNA methylation and/or demethylation, tRNA modification, and microRNA biogenesis. Interestingly, Elongator plays kingdom-specific roles in distinct organisms. For instance, yeast Elongator mutants exhibit resistance to the zymocin γ-toxin and sensitivity to salt, caffeine, and temperature, whereas human Elongator deficiency leads to defective neuron development, manifested as the familial dysautonomia disease. In plants, research on Elongator has been largely limited to the model plant Arabidopsis thaliana. Arabidopsis Elongator (AtELP) mutants display pleiotropic phenotypes, including hypersensitivity to abscisic acid, resistance to oxidative stress, severely aberrant auxin phenotypes, altered cell cycle progression, abnormal root development, and disease hypersusceptibility. Recent studies have shown that AtELP2 and AtELP3 regulate the kinetics of pathogen-induced transcriptome reprogramming. In-depth investigation further revealed that AtELP2 regulates pathogen-

induced transcriptome changes likely through maintaining histone acetylation levels, modulating the genomic DNA landscape, and influencing pathogen-induced dynamic DNA methylation changes. This presentation will discuss recent advances in understanding the critical epigenetic role of Elongator in plant immune responses.

Keywords: The Elongator complex, plant immunity, transcriptional reprogramming, histone acetylation, DNA methylation, *Arabidopsis thaliana*

10:30 A.M. – 12:00 P.M. Concurrent Session 1A

005 **Identification of a novel gene *LSR1* that plays a role in high light tolerance in the green micro-alga *Chlamydomonas reinhardtii*.**

Mautusi Mitra, Kevin Nguyen, Ja'von Swint, Joel III Page, Katherine Smith, Tai Truong, Kenneth Kim

University of West Georgia, Department of Biology, 1601 Maple Street, Carrollton, GA 30118

Photo-autotrophs employ diverse photo-acclimatory and photo-protective strategies to avoid, minimize, and repair photo-oxidative damage in stressful and fluctuating light conditions. Chlamydomonas is an elegant model system to study eukaryotic oxygenic photosynthesis. Our laboratory has generated a mutant library of Chlamydomonas by random insertional mutagenesis using the pBC1 vector. This vector contains the APHVIII gene that confers resistance to paromomycin. The mutant library was screened under heterotrophic, mixotrophic, and photo-autotrophic growth conditions under different light intensities resulting in the isolation of 20 mutants. We recently characterized the mutation locus in one of the isolated high light sensitive mutant, *lsr1a*, using the adapter ligation mediated-PCR. The sequencing of the PCR products revealed two insertion sites of pBC1 in lsr1a. One pBC1 insertion site is in the fourth exon of a novel functionally uncharacterized gene, namely *Cre11.g467757* (LSR1/Light Stress Related 1). The second insertion site of pBC1 is in *Cre02.g095095*. *Cre02.g095095* codes for a secretory cell wall protein pherophorin-C12 (PHC12) of unknown function. *lsr1a* is chlorophyll-deficient and super-sensitive to high light when screened in both photo-autotrophic and mixotrophic growth conditions and photo-bleaches under high light. *lsr1a* has an overall slower growth rate compared to wild type. The growth phenotype of lsr1a is very similar to that of another uncharacterized CLiP mutant LMJ.RY0402.051109 (*lsr1b*), which has a mutation in the fourth intron of the gene *Cre11.g467757*, indicating strongly that *Cre11.g467757* is responsible for the growth phenotype of *lsr1a* under high light. Our preliminary data indicates that LSR1 undergoes growth condition mediated-post-transcriptional regulated splicing via an intron inclusion. We will be presenting our physiological and molecular research on *lsr1*.

Keywords: Chlamydomonas, Photosynthesis, High light stress, regulated splicing

006 **A Rosetta Stone for Nodulation: Translating an Interkingdom Signal at the Interface of a Crucial Host-Microbial Symbiosis.**

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Density-dependent phenotypic switching in bacteria, the phenomenon of quorum sensing (QS), is instrumental in many pathogenic and mutualistic interactions. In many Gram-negative bacteria, QS is regulated by N-acylated-L-homoserine lactones (AHLs). AHL-dependent phenotypes are diverse, including virulence factor production, motility, biofilm formation, bioluminescence, and root nodulation. As QS bacteria and their hosts have coevolved over millions of years, it is not surprising that many eukaryotes are able to sense QS signals. However, how these hosts integrate and utilize this information is poorly understood. Synthetic AHL analogues which can be introduced both in culture and under native conditions provide a unique chemical-based approach to monitoring QS at the host-microbial interface. We hypothesized that by utilizing this approach it may be possible to distinguish between responses specific to the bacteria and AHL-induced responses in hosts which influence the outcome of a pathogenic or mutualistic interaction. Exploiting the well-established legume-rhizobia symbiosis (nodulation), specifically between *Medicago truncatula* and *Sinorhizobium meliloti* we tested this hypothesis. Our findings support AHLs as an interkingdom signal utilized not only by a prospective pathogen or mutualist but by the host as well. We discuss our findings within the broader implications to host-microbial interactions and the evolution of mutualistic symbioses.

Keywords: Quorum sensing, nodulation, chemical biology, interkingdom signaling, AHLs, symbiosis, host-microbial interactions

007 Evaluation of Soybean Breeding Lines for Seed Germination and Composition under High Heat and Dryland Production in the Midsouthern USA

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Although the Early Soybean Production System (ESPS) in the Midsouthern USA increased seed yield under irrigated and non-irrigated conditions, heat stress and drought still lead to poor seed quality in heat sensitive soybean cultivars. The objective of this research was to identify breeding lines that possess high germination, nutritional quality, and yield potential under high heat and dryland production conditions. We hypothesized that breeding lines derived from exotic germplasm may possess physiological and genetic traits that could result in higher seed germinability under high heat conditions. A two-year non-irrigated field experiment was conducted using maturity groups (MG) III and IV breeding lines derived from exotic soybean accessions previously selected for adaptability to the ESPS. Results showed that three exotic breeding lines had consistently higher germination across the 2 years, with a mean germination percentage of ≥80%. Two out of the three lines with ≥80% germination had high seed protein, oleic acid, N, P, K, B, Cu, and Mo in both years. Significant ($P \leq 0.05$) positive correlations were found between germination and oleic acid and between germination and K and Cu in both years. However, significant negative correlations were observed between germination and linoleic acid, Ca, and hard seed in both years. The high germinability genotypes had a lower content of Ca in the seed, which may explain the lower rates of hard seed in those lines. Differences in yield, germination, diseases, and seed composition between years could be due to heat and rainfall differences between years, as well as to genotypic differences among lines. The use of the high germinability lines identified in this research will help breeders to develop improved soybeans with high seed nutritional qualities and high germinability under dryland production conditions.

Keywords: soybean nutrition, seed composition, mineral nutrition, seed protein, seed oil, germination, seed diseases

Graduate Student Oral Competition

008 **The maize LINC complex components**

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The nuclear envelope (NE) is a double-membraned structure physically separating the nucleoplasm from the cytoplasm in eukaryotes. The Linker of Nucleoplasm to Cytoplasm (LINC) protein complexes act as signal-transducing and dynamic bridges across this envelope. The LINC complex is comprised of proteins from four major cellular areas: (a) Lamins or CRWNs at the chromatin periphery in the nucleus, (b) SUN domain proteins in the INM, (c) KASH domain proteins in the ONM, and (d) cytoskeleton and other proteins in the cytoplasm. Plant LINC complexes are not fully defined, but components range from highly conserved (SUN, tubulin, actin) to fast evolving (KASH and nuclear proteins). During meiotic mid-prophase, the LINC complex tethers telomeres to the nuclear envelope, where homologous chromosomes synapse and recombine with each other. We recently discovered a novel meiotic structure, the meiotic SUN belt, which encircles the meiotic prophase nucleus, transiently forming a half-belt with telomeres cluster at zygotene stage. To better understand meiotic and other LINC functions, we have begun a candidate gene screen, starting with KASH domain protein gene family (at least 14 members) of maize. Bioinformatic, biochemical (coIP), microscopic (3D cytology), and genetic analyses are underway to test candidates. Progress will be discussed, including proteomic coIP detection of LINC candidates - CRWN, KASH, cytoskeleton and motor proteins. Fluorescent fusion proteins are being produced for localization and interaction assays. These multiple and complementary approaches are advancing our knowledge of the structure and function of the maize LINC complexes, while revealing new candidates for coordination of nuclear processes.

Keywords: SUN, KASH, LINC, Meiosis

009 **Interactions of nitrogen and carbon metabolism in the submerged aquatic plant, *Hydrilla verticillata***

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Hydrilla verticillata is an invasive, submerged aquatic plant that has been dubbed the "perfect aquatic weed" (Langeland, 1996). This nickname is appropriate for many reasons, not least of which is the incredible phenotypic plasticity exhibited by this plant. *H. verticillata* is a facultative C3-C4 intermediate with both mechanisms operating in the same cell (i.e. in the absence of Kranz anatomy). Although carbon metabolism has been well-characterized in the species, we know very little about nitrogen metabolism and its tight coupling to carbon status in this plant. Thus, the objective of this work was to determine how photosynthetic state affects nitrogen uptake and assimilation in *H. verticillata*. C4 photosynthesis was induced over 14 days; C4 status was confirmed via enzyme assay for phosphenolpyruvate carboxylase (PEPC). Plants maintained in the C3 state served as experimental controls. Upon confirmation of C4 induction, plants were placed in N-free Hoagland's medium for 24 h to deplete nitrogen stores, after which plants were exposed to 100 µM KNO_3- for 24 h. Subsequent assays for nitrate reductase (NR) activity and nitrate uptake were conducted. Within the first 3 h of induction, C3 plants had significantly higher uptake rates than C4 plants (0.49 + 0.02 µmol NO3- g FW-1 h-1 cf. 0.28 + 0.04 µmol NO_3- g FW-1 h-1). After 8 h nitrate exposure, NR activity in C3 plants was 14-fold

higher than in plants undergoing C4 photosynthesis (1651.3 + 295.6 nmol NO_2- g FW-1 h-1 cf. 115.5 + 9.3 nmol NO_2- g FW-1 h-1). These data suggest that nitrogen uptake and assimilation in *H. verticillata* is influenced by photosynthetic state, and that this metabolic coupling influences resource use and competitive outcomes in nature.

Keywords: carbon metabolism, nitrogen metabolism, C4 photosynthesis, nitrate reductase, nitrate uptake

010 The RDN arabinosyltransferase family plays a crucial role in nodulation regulation signaling and root architecture patterning in *Medicago truncatula* and *Arabidopsis thaliana*

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Legumes can create specialized root organs known as nodules to establish a symbiotic relationship with nitrogen fixing bacteria. Autoregulation of Nodulation (AON) is an important signaling pathway in legumes that limits nodule number in relation to the nitrogen (N) need of the plant. After colonization by rhizobia, two signal peptides in the CLAVATA3/ENDOSPERM SURROUNDING REGON (CLE) gene family, MtCLE12 and MtCLE13, are expressed in the nodule meristem, truncated by proteases and predicted to be modified with a tri-arabinose moiety on each hydroxyproline, then translocated to the shoot where they signal through a receptor-like kinase. Root determined nodulation1 (MtRDN1), homologous to the HYDROXYPROLINE ARABINOSYL TRANSFERASE (AtHPAT) gene family in Arabidopsis, is implicated by genetics as the enzyme responsible for modifying MtCLE12, and mutation of MtRDN1 causes supernodulation. The observation that constitutively expressed RDN2 can rescue to rdn1-2 mutant, led to the use of RNAi toward MtRDN2 and MtRDN3 in roots. We found that knockdown of MtRDN2 increases nodule density while knockdown of MtRDN3does not significantly increase nodule density, and GUS expression analysis reveals different expression patterns of MtRDNs within the root, suggesting a divergent role of MtRDN1 from other family members. Arabidopsis with multiple Athpat mutations display changes in root architecture on media with both high and low N concentrations, but with increased effect in high N, suggesting AtHPATs play a role in N sensing. To learn how nitrate or inoculation by rhizobia influences nodule specific CLE expression we tested transcript levels by qPCR. To determine if root length and lateral root density phenotypes are a result of changes in arabinosylation of cell wall proteins versus modification of small peptides, glycome profiles and total sugar estimations of cell walls are being resolved. Further, mass spectrometry of the arabinosyl states of nodule specific CLE peptides is being employed. Also, a glycosyltransferase assay is being developed to characterize the enzymatic activity of MtRDN1 produced in vitro. This work is supported by NSF IOS#1146014, the Clemson Creative Inquiry Program and a Clemson Wade Stackhouse Fellowship to SN.

Keywords: RDN, CLE, Nodulation, Legume, arabinosyltransferase

10:30 A.M. – 12:00 P.M. Concurrent Session 1B

011 A current model of group IIA intron excision in the chloroplast of land plants.

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The removal of introns from precursor RNAs is an essential step in gene expression. In the chloroplast of land plants, the majority of group IIA introns are believed to be excised by the chloroplast-encoded maturase Maturase K (MatK). Maturases are enzymes of prokaryotic ancestry that tend to bind an excise a single-intron target. MatK, however, has been shown to bind to seven group IIA introns of the chloroplast. These introns reside within precursor RNAs for essential chloroplast proteins and tRNAs. At present, biochemical confirmation of MatK splicing activity is lacking, leaving questions regarding the role of MatK in chloroplast group IIA intron excision. Further, several nuclear-encoded proteins have been shown to have an essential function in intron excision of some of the same seven group IIA intron targets as MatK. Based on overlapping targets, it is possible that the implicated nuclear-encoded splicing factors form a splicing complex with MatK to facilitate group IIA intron excision in the chloroplast. We have expressed and purified MatK protein as well as four of the seven postulated MatK-intron targets in an effort to determine the role of MatK in chloroplast group IIA intron excision. Further, we have initiated co-immunoprecipitation experiments to assess protein interactions between MatK and nuclear-encoded or other protein cofactors that may be relevant to chloroplast intron excision. Recent updates regarding splicing mechanisms in the chloroplast and the role of MatK in chloroplast intron excision will be presented.

Keywords: chloroplast, spliceosome, MatK, maturase

012 Three Way Symbiosis: Unlocking the Potential of a Plant, Fungus, and Virus Interaction

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In Yellowstone National Park, panic grass (*Dichanthelium lanuginosum*) is able to grow in geothermal soils that reach temperatures >50°C. This plant is capable of growing under extreme temperature due to a symbiotic relationship with a fungus (*Curvularia protuberata*), harboring a double-stranded RNA virus known as Curvularia Thermo-Tolerance Virus (CThTV). Neither one of these partners could survive temperatures above 38°C alone. The mechanism behind this plant-fungus-virus association is unknown. Our lab has discovered that fungal trehalose plays a crucial role in adaptation to heat stress mediated by the three-way symbiosis. Fungal melanin has also been found to play a key role in stress tolerance. Furthermore, the interaction of a fungal translationally controlled tumor protein (TCTP) and catalase/peroxidase (KatG) with CThTV proteins may alter cell cycle and cellular redox. Knock out of genes controlling the trehalose, melanin, TCTP, and KatG pathways in the *C. protuberata* carrying CThTV abolished thermotolerance . On the other hand, over-expression of the same genes in non-thermotolerant *C. protuberata* without CThTV provided tomato plants with improved thermotolerance, but not to the same effectiveness as the original fungal isolate carrying the virus. We propose a model in which *C. protuberata*, containing the CThTV, is able to confer thermotolerance in

plants by utilizing the production of large quantities of trehalose that function as a stress-signaling molecule or as an osmoprotectant. This signal would go on to regulate processes such as carbon utilization and cell division during stress. Melanin possibly alters fungal cell walls to control trehalose movement into plant tissues during heat stress.

Keywords: Symbiotic Interaction; Thermotolerance; Trehalose; Melanin; Tranlationally Controlled Tumor Protein (TCTP); Catalase/Peroxidase (CAT)

013 **Genetic dissection of seedling stage salinity tolerance in rice using introgression lines of a salt tolerant landrace Nona Bokra**

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Salinity is the second most important abiotic stress affecting rice production worldwide. Molecular breeding for salt tolerance is the most feasible approach for improving the productivity of rice in salt affected soils. Rice is sensitive to salt stress at seedling and reproductive stages; however, the seedling stage salinity tolerance is crucial for better crop establishment. Identified QTLs for salt tolerance in rice from previous studies were rarely exploited for rice improvement through marker-assisted breeding. QTL mapping using introgression lines is an important strategy for identification and simultaneous transfer of desirable alleles contributing to salinity tolerance into elite genetic background. In the present study, 138 introgression lines (ILs) of BC3F4 generation derived from the cross between a elite salt susceptible japonica rice cultivar Jupiter and a salt tolerant indica landrace Nona Bokra were phenotyped for salt tolerance at seedling stage under hydroponics and were genotyped using 126 simple sequence repeat (SSR) markers. A total of 40 additive QTLs were detected by interval mapping for all the eight morpho-physiological traits studied, whereas 33 novel additive QTLs were detected by ICIM. The phenotypic responses and genomic composition and novel QTLs identified from the study elucidate that apart from the Na+ and K+ concentration in shoots, the Na/K ratio is the key factor for determining salinity tolerance. The mechanisms of tolerance might be due to homeostasis between Na+ and K+ or Na+ compartmentalization or synthesis of compatible solutes. The tolerant ILs identified in the study may be used as genetic stocks to improve salinity tolerance in rice breeding program. Fine mapping, map based cloning, and identification and transfer of candidate genes can be undertaken using these selected tolerant lines to provide molecular insights into salt tolerance mechanisms in Nona Bokra.

Keywords: Quantitative trait loci, Rice, Seedling Stage, Salinity tolerance, Microsatellite markers

Graduate Student Oral Competition

014 **Comparative transcriptomics analysis reveals similarities of key gene expression between rice and *Brachypodium* during formation of nodule-like structures**

Jacklyn Thomas[1], Ryan Hiltenbrand[1], Hannah McCarthy[1], Karl Dykema[2], Megan Bowman[2], Ashley Spurr[1], Andres Vega[1], Ha Ram Kim[1], Mary Winn[2], Arijit Mukherjee[1]

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Several studies have shown that plant hormones play an important role in root nodulation during legume-rhizobia symbiosis. For example, auxins can induce nodule-like structures (NLS) on legume roots even in the absence of rhizobia. Our lab established an efficient and high-throughput experimental system to induce the formation of NLS on roots of land plants including rice and the model legume, *Medicago truncatula*. We used synthetic auxin, 2,4-D in these experiments and were able to induce NLS at a very high frequency (>90%). Our results suggested that NLS formation followed a similar developmental program in rice and *M. truncatula*. Recently, we extended our study to *Brachypodium distachyon*, a model plant used for comparative and functional grass genomics. Our results show that like rice, in response to auxin, *B. distachyon* roots form NLS at a high frequency and their numbers increase over time. Our goal is to genetically characterize the pathway leading to NLS formation in grasses. Towards that goal, we performed RNA-seq experiments in rice and *B. distachyon* to identify differentially expressed genes (DEGs) during NLS formation. We identified 1991 DEGs in rice and 618 DEGs in *B. distachyon* roots containing NLS. We validated the RNA seq data in both rice and *B. distachyon* by checking the expression of a few genes using reverse transcriptase polymerase chain reaction. We identified 76 orthologous genes in rice and *Brachypodium* differentially expressed during NLS formation. Several of these genes have been shown to be involved in auxin response and transport, and root development. This is quite promising for our long-term goal of characterizing the genetic pathway controlling the formation of NLS in grasses. We believe these findings will have important implications towards improving nitrogen fixation in non-legumes, especially cereals.

Keywords: Nodule-Like Structures, Rice, Brachypodium, RNA-Sequencing

015 **Transcriptional regulation of the plant immune transcription coactivator NPR1**

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Crop loss due to disease is a large problem facing agriculture today. However, plants possess a robust immune system able to fight potential pathogens and disease is the exception rather than the rule. The plant immune system is composed of different layers that work to eliminate invading pathogens before pathogen colonization has begun. The first layer of the plant immune system is called pathogen-associated molecular pattern (PAMP)-triggered immunity (PTI). Once PAMPs are recognized by pathogen recognition receptors, the plant initiates PTI. PTI involves the accumulation of cytoplasmic calcium, initiation of mitogen-activated protein kinase signaling cascades, defense-gene associated transcriptional reprogramming, and the production of reactive oxygen species in order to attack and kill the invading pathogen. Plant pathogens have evolved a variety of methods to circumvent plant recognition and establish themselves to obtain nutrients and cause disease. Successful pathogens can deploy avirulence factors or effectors that disrupt or delay PTI signaling, enabling effector-triggered susceptibility and plant tissue colonization. Plants in turn have developed specialized genes that can recognize, directly or indirectly, pathogen effectors, and are called resistance genes. Once a pathogen's effector has been recognized, the plant will activate effector-triggered immunity (ETI). ETI often involves local cell death, termed the hypersensitive response. Local infection also triggers systemic acquired resistance (SAR) throughout the plant. While local defense responses serve to reduce the spread of pathogens that subsist on living tissues, SAR is a broad-spectrum resistance, serving to protect the plant from future infections. The immune transcription coactivator NPR1 is vital to both local resistance and SAR. It is well known that NPR1 is regulated heavily at both the transcriptional and post-translational levels, yet how the transcription of the NPR1 gene is regulated has not been fully understood. This presentation will discuss our recent discoveries on the mechanisms regulating the NPR1 gene transcription.

Keywords: Systemic acquired resistance, transcription coactivator, NPR1, transcriptional reprogramming, plant immunity

016 **The Arabidopsis calcium sensor protein CML38 is an essential hypoxia response protein that assembles with translating and non-translating mRNA nucleoprotein complexes**

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Plants encounter a severe low oxygen (hypoxia) stress state under conditions of submergence or poor soil aeration due to decreased respiration and accompanying energy crisis. Plants adapt to hypoxia by conserving energy through suppression of the translation of non-essential mRNA transcripts. These non-essential transcripts are routed to cytosolic messenger ribonucleoprotein (mRNP) structures, including stress granules (where mRNA is sequestered) or to processing bodies (where mRNA is degraded). Arabidopsis thaliana CALMODULIN-LIKE 38 (CML38) is a calcium sensor protein, and is among the 49 core hypoxia genes induced during prolonged hypoxia stress. Null alleles of CML38 show a decreased survival under conditions of argon-induced hypoxia, suggesting a critical role for CML38 as a target for calcium signals during the adaptive response. CML38 is a member of a specialized group of calcium sensor proteins, referred to as the 'regulator of gene silencing' calmodulins (rgsCaM) which are proposed to be regulators of post transcriptional gene silencing. CML38 localizes to hypoxia-induced mRNA protein particles (mRNPs) that co-localize with stress granule and processing body protein and mRNA markers. Reoxygenation, which leads to release of transcripts from stress granules, results in loss of CML38 from granules. CML38 also shows localization to hypoxia induced polysomes in a calcium-dependent manner. The current hypothesis is CML38 is a specialized, hypoxia-stress specific calcium sensor that is necessary for optimal survival to hypoxia stress, and may be involved in posttranscriptional regulation of mRNA translation, storage and stability during the anaerobic response. Ongoing experiments are aimed at identifying CML38 binding and regulatory targets, as well as investigating the effects of CML38 knockout mutation on RNA homeostasis during hypoxia.

Keywords: Hypoxia, stress, translation, mRNP, Calmodulin-like protein, calcium

1:30 P.M – 2:45 P.M. Concurrent Session 2A

017 **Discovery and implications of a mammalian endocannabinoid ligand in moss**

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Recently, the occurrence of a mammalian endocannabinoid ligand N-arachidonoylethanolamide (anandamide, AEA, NAE20:4), was reported in early land plants. Unlike seed plants, bryophytes such as *Physcomitrella patens* possess unique fatty acid composition that includes long-chain fatty acids such as arachidonic acid (AA, 20:4) and eicosapentaenoic acid (EPA, 20:5). We performed targeted lipid profiling to discovere long-chain N-acylethanolamines (NAEs) and their corresponding N-acyl-phosphatidylethanolamine (NAPE) precursors in *Physcomitrella* and *Selaginella*. In protonemal tissues, N-arachidonyl-PE and N-20:5-PE contributed to about 49 % and 30 %, respectively. Matured gametophytes on the other hand showed a 12 % increase in N-20:4-PE and 20 % decline in N-20:5-PE, relative to NAPE content in protonemata. In all haploid developmental stages analyzed, NAE20:4 levels

contributed to ~ 23 % of the total NAE while NAE 20:5 remained as a minor component (5 %). Interestingly, in *Selaginella moellendorffi*, an early vascular plant, N-18:2-PE species was most abundant and 20C-NAEs were present in trace amounts. To understand biological implications of anadamide, we examined the effects of exogenously applied AEA and its corresponding fatty acid (AA) on moss protonemata growth. Both AEA and AA inhibit growth of gametophytes and protonemata in a dose dependent manner, while AEA exclusively affected actin-mediated tip growth. Additionally, we identified moss ortholog for NAPE-hydrolyzing phospholipase D (NAPE-PLD) enzyme that likely generates AEA and a fatty acid amide hydrolase (FAAH) that catabolizes AEA. Both putative PpNAPE-PLD and PpFAAH are expressed in E. coli for further characterization. Our data demonstrates the occurrence of evolutionarily conserved NAE metabolic pathway in the moss, with unique composition. Functional and evolutionary implications of this mammalian endocannabinoid in early land plants, however, remains elusive.

Keywords: *Physcomitrella patens*, moss, anandamide, N-acylethanolamines

018 **Additional functional characterization of *Medicago truncatula* MtNPF1.7 transporter**

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The *Medicago truncatula NPF1.7* gene is essential for the development of symbiotic nitrogen-fixing root nodules as well as normal lateral and primary root elongation. It encodes a member of the NRT1/PTR transporter family, now called the NPF family. MtNPF1.7 has been shown to transport nitrate at high-affinity, different from other characterized members of the NPF family that transport nitrate with low affinity. Expression of Arabidopsis NPF6.3, a well-characterized dual-affinity nitrate transporter, in one of the mutants with *MtNPF1.7* defects partially rescued its root architecture defects but failed to complement the nodule defects. This and other data suggest that nitrate transport might not be the only biochemical activity of MtNPF1.7. NPF1.7 proteins have been shown to transport several different compounds including phytohormones. Studies in our lab indicate that MtNPF1.7 may transport the phytohormone indole acetic acid (IAA) in addition to nitrate, in the *Xenopus laevis* oocyte system. In addition, *MtNPF1.7* was cloned and expressed in yeast (*Saccharomyces cerevisiae*). Yeast strains expressing *MtNPF1.7* showed an increased flux of radiolabeled IAA and differential susceptibility to 5-fluoroindole-3-acetic acid, a toxic IAA analog compound. These results suggest that MtNPF1.7 functions as an IAA transporter in heterologous systems and may function as an IAA transporter in *M. truncatula*. Supported by NSF IOS-0923756.

Graduate Student Oral Competition

019 **Generation of disease resistance in tomato using genes encoding the Elongator subunits**

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Tomatoes are cultivated and consumed worldwide. The United States is the second largest of tomato producer. Florida is the top state in fresh market tomato production. Production of this crop is

threatened by a number of diseases, for which control is primarily based on chemicals and sanitary measures. The pathogens causing these diseases have evolved resistance to pesticides, overcoming host resistance. As a result, it has been difficult to identify effective and durable measures for disease management. Currently, one strategy is to utilize defense-related genes from *Arabidopsis thaliana* and their orthologs in other plants. Arabidopsis is a well-established model plant with its full genome sequenced. Thus far, many defense-related genes have been cloned and characterized in Arabidopsis, making it a suitable source of genes for engineering disease resistance in tomato. The Arabidopsis Elongator complex plays an important role in plant immunity, likely by contributing to transcription activation of defense genes. As Elongator is not specifically involved in pathogen recognition and subsequent signal transduction, it may provide durable resistance. Our results show that overexpressing Arabidopsis Elongator genes in tomato improves resistance to *Pseudomonas*. The predicted tomato Elongator genes are highly homologous to those of Arabidopsis. Importantly, the tomato Elongator gene orthologs are able to complement the morphological and defense phenotypes of the corresponding Arabidopsis Elongator mutants, indicating that they are functional. There is a necessity for long-lasting resistance in order to simultaneously control diseases caused by multiple pathogens. Generating transgenic plants with increased disease resistance would be a promising alternative to conventional methods. However, recently there has been a strong anti-GMO propaganda aiming to reach the public. Since the tomato Elongator gene orthologs are functional, they could be utilized to generate tomato plants with increase disease resistance using alternative technologies that are not considered transgenic, such as cisgenesis and intragenesis.

Keywords: The Elongator complex, tomato, disease resistance, *Arabidopsis thaliana*, transgenics

020 **Characterizing a Novel Arabidopsis Gene Identified from Spaceflight Experiments that Might have a Putative Role in Regulating ROS Homeostasis.**

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Humankind's next frontier lies in the colonization and exploration of space. One of the many challenges faced in pursuing this endeavor is creating an extraterrestrial environment capable of sustaining human life for extended periods. Utilizing plants for advance life support requires thorough understanding of basic physiological and molecular responses of plants to the spaceflight environment. The spaceflight experiment APEX01 conducted on the International Space Station revealed that 480 genes were significantly ($P<0.01$), differentially expressed in an organ-specific manner between plants grown in orbit compared to their ground controls. The majority of these genes are of known terrestrial function; representing categories such as cell wall remodeling, cell polarity and reactive oxygen species (ROS). However, 43% of these 480 genes only have putative functions or are functionally uncharacterized.

At1g05290 (OMG1) is one of these previously uncharacterized genes that were significantly induced in spaceflight roots. Analysis with bioinformatics tools showed that OMG1 belongs to the CONSTANS – like family of zinc finger proteins. Transgenic plants expressing OMG1 promoter-driven GUS reporter shows activity in the pollen, pollen tubes, root hairs, and upon wounding. Additionally, wounding experiments showed that At1g05290 expression is virtually immediate, but diminishes quickly. Rapid wounding of an omg1 knockout leaf reduces the expression levels of two genes involved in the ROS pathway, GRX480 and PUMP5. Moreover, a fluorescent ROS assay, which measures ROS production, showed that the omg1 knockout lines produced less ROS immediately after wounding.

ROS signaling is used as a signal transducer when dealing with various stimuli from abiotic stress to growth and development, yet the removal of ROS in plant cells is necessary in order to avoid oxidative damage. Therefore, this novel gene could be an adaptive strategy plants use to balance the ROS homeostasis in the unique environment of spaceflight.

Keywords: Spaceflight, Unchacterized genes, ROS, CONSTANS-like

021 **Construction and Comparison of Large Gene Co-expression Network in Maize Using RNA-Seq Data**

Ji Huang, Stefania, Vendramin Alegre, Karen McGinnis

Florida State University, Biological Science Department

With the emergence of RNA sequencing, genome-wide expression data production has reached an unprecedented level. This abundance of data has greatly facilitated maize research, but may not be amenable to traditional analysis techniques that were optimized for other data types. Using publicly available data, a Gene Co-expression Network (GCN) can be constructed and used for gene function prediction, candidate gene selection and improving understanding of regulatory pathways. Several GCN studies have been done in maize, mostly using microarray datasets. Realizing the advantage of RNA-seq and quantity of samples available, it is critical to create a RNA-seq data-based maize GCN. To build an optimal GCN from plant materials RNA-seq data, parameters for expression data normalization and network inference needed to be evaluated. A comprehensive evaluation of these two parameters on network performance using 1266 maize samples was conducted. Three normalization methods (VST, CPM, RPKM) and nine inference methods, including five correlation and four mutual information (MI) methods, were evaluated. We found that the three normalization methods had very similar performance. Correlation methods performed better than MI methods in a gene-specific manner. We also noticed that increasing sample size had a positive effect on GCN. By aggregating single networks together, the resulting aggregated network showed the best performance of all. These results allowed for an optimized gene network construction that will serve as a valuable resource for the plant science research community.

Keywords: maize; Gene Co-expression Network; RNA-Seq

1:30 P.M – 2:45 P.M. Concurrent Session 2B

022 **Spatial and Temporal Resolution of mRNA Profiles During Early Nodule Development**

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The symbiotic association between *Medicago truncatula* and *Sinrhizobium medicae* leads to formation of root nodules, which enable nitrogen fixation by bacteria to benefit the host plant and in return provides a low oxygen environment suitable for the bacterial growth. This mutually beneficial process involves communication between cells layers in tissues between the organs in the plant. The communication between cells changes across time, from the induction of the first chemical response to Nod factor to the establishment of nitrogen fixation in the nodules. Transcriptome profiling of whole roots during nodule development has identified genes involved in initiating symbiosis, but such experiments are unable to resolve the progression of events at the tissue/cellular level. To understand the signaling occurring between these cells in space and time in a coherent manner it is necessary to analyze

the transcriptome of the individual cells at specific points in time, as neighboring cells may have very different transcriptomes. The goal of this NSF funded project (IOS#1444461) is to measure the transcriptome for each cell type involved in nodule formation at 0, 12, 24, 48 and 72 hours post inoculation, using Laser Capture Microdissection (LCM) on individual cell types at defined points in nodulation. RNAseq libraries are generated for the cell types and gene co-expression networks are constructed. We report the results of protocol development and initial experiments with wild type plants.

Keywords: transcriptome , Laser Capture Microdissection, RNAseq

023 **Agricultural land-use legacies and habitat restoration shape diversity and composition of plants and soil microbes in longleaf pine savannas**

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Intensive land use activities, such as agriculture, are a leading cause of biodiversity loss and can have lasting impacts on ecological systems. Yet, few studies have investigated how land-use legacies impact multiple taxa across levels of biodiversity, including richness, composition, and phylogenetic diversity (the total amount of evolutionary history in a community). We also know little about if, and how, restoration activities might mitigate legacy effects on biodiversity. We studied ground-layer plant and soil bacteria communities in 27 pairs of Remnant (no agricultural history) and Post-agricultural (agriculture abandoned >60 years ago) longleaf pine savannas in South Carolina, USA. Half of our plots were restored by thinning trees to reinstate open canopy conditions. We found that agricultural history had no impact on plant species richness, but did alter community composition and reduce phylogenetic diversity by 566 million years per 0.1 ha. Habitat restoration increased plant species richness by 27% and phylogenetic diversity by 914 million years. Land-use history and restoration also had distinct impacts on soil bacterial communities composition, similar to what we found with plants. In both plants and soil microbes restoration altered communities but did not overcome the effects of agricultural land use on community composition. These results demonstrate the persistence of agricultural legacies, even in the face of intensive restoration efforts, and the importance of considering biodiversity broadly when evaluating human impacts on ecosystems.

Keywords: restoration, community ecology, longleaf pine savanna, soil microbes, land-use legacies

Graduate Student Oral Competition

024 **Characteristics of Raf-like family of Integrin-Linked Kinases: Structure, Phylogeny, and role in transcriptional reprograming for abiotic and biotic stress response**

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Plants have integrated signaling networks that modulate the perception of signal and responses to environmental stresses including abiotic and biotic stress factors that affect crop productivity in many

agricultural areas around the world. The signaling pathway related to cellular ion homeostasis in abiotic stress response and plant immunity are essential to explore and largely unknown. The Integrin-Linked Kinases (ILKs), a subfamily of Raf-like kinases (RAFs), are multivalent proteins that interact with multiple proteins in signaling cascades activated by both abiotic and biotic stressors. To explore the connection between plant ILKs protein structural features, interaction partners and their functions, we recently analyzed the kinase domains and the ankyrin repeat motifs of ILKs in Arabidopsis and land plant lineage. Plant ILKs drive domain-specific interactions due to their modular domain organization. The analyses also reveal that plant-specific ILK functions in multiple signal transduction pathways to regulate cellular homeostasis (Popescu et al., 2017). Our aim is now to characterize changes mediated by the Raf-like kinase ILK1 in the transcriptional program of hyperosmotic stress and innate immunity. *ilk1* mutants were subjected to RNAseq analysis to identify differentially expressed genes/pathways that relay on ILK1 activity during hyperosmotic stress or PAMP challenge. The results of this work will bring into view new information on a plant Raf-like kinases family. It would also give insight to improve pathogen resistance and stress tolerance in plants.

Keywords: Integrin-linked kinases, Plant immune response, Plant abiotic response

025 **IBR5 interacts with GTP binding proteins to regulate plant auxin response**

Idrees Ahmad, Praveen Kathare, Prabesh Ghimire, Elia Lopez, Sunethra Dharmasiri, Nihal Dharmasiri

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Auxin is a crucial plant hormone necessary for the regulation of growth and development in plants. Auxin controls the expression of auxin responsive genes, by regulating the degradation of a group of transcriptional repressor proteins known as Aux/IAA via nuclear localized signaling pathway. It has been shown that Indole Butyric acid Resistant5 (IBR5), which encodes a dual specificity phosphatase is also involved in the auxin signaling, however its exact function is not well understood. Yeast two hybrid screen, in-vitro pull-down assays and co-immunoprecipitation studies indicate that IBR5 physically interacts with small GTP binding proteins. Previous studies have also shown that these GTP binding proteins are involved in auxin related responses. Our studies further indicate possible genetic interactions between IBR5 and small GTP binding proteins suggesting that IBR5 may regulate plant auxin response through the activity of small GTP binding proteins.

Keywords: Auxin, GTP binding proteins, plant growth and development.

026 **Conserved functionality of the chloroplast RNA helicase ISE2: *Physcomitrella patens* and beyond.**

Jessica Fernandez, Tessa Burch-Smith

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The regulation of plasmodesmata-mediated trafficking is complex and not completely understood. The absence of a chloroplast RNA helicase, INCREASED SIZE EXCLUSION LIMIT2 (ISE2), results in increased plasmodesmata mediated trafficking in both *Arabidopsis thaliana* and *Nicotiana benthamiana*. ISE2 was previously identified to belong to the SKI2-LIKE subfamily of RNA helicases. However, recent phylogenetic analysis identified ISE2 as an independent protein in clade distinct from the plant SKI2 proteins. Additionally, ISE2 is present in all green photosynthesizing plants, from cyanobacteria to angiosperms. In this study, we investigate ISE2 in one of the first land plants, *Physcomitrella patens*, to

potentially gain insight into its ancestral roles in plasmodesmata-mediated intercellular trafficking. P. patens differs from *A. thaliana* by encoding two paralogs of ISE2, compared to the single copy found in *A. thaliana*. The loss of the single copy of ISE2 in *A. thaliana* results in lethality. We investigate ISE2's role in P. patens and ask whether it can rescue the lethality of *A. thaliana ise2* mutants. This study will provide insight on the functional conservation of ISE2 from moss to land plants as well as illuminate the conservation of mechanisms to regulate plasmodesmata and intercellular trafficking over the approximately 450 million years separating *P. patens* from *A. thaliana*.

Keywords: Plasmodesmata, RNA helicase, Chloroplast, P. patens

3:15 P.M – 4:30 P.M. Concurrent Session 3A
Graduate Student Oral Competition

027 **Identification of genetic suppressors of the *sunn-1* hypernodulating phenotype**

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[2] *University of North Carolina, Chapel Hill*

Autoregulation of nodulation (AON) is a long-distance signaling pathway in legumes which limits the number of nodules formed in the rhizobial-legume symbiosis. In *Medicago truncatula*, this systemic regulation includes local signaling events resulting in MtCLE12 and MtCLE13 induction in the nodule meristem to regulate nodule number, most likely by translocation of the CLE peptides to the shoot. CLEs bind a receptor complex containing the leucine-rich repeat receptor-like kinase SUNN in the shoot, followed by subsequent signal transduction to roots resulting in termination of new nodule formation. Mutation of SUNN results in a 5-10 fold increase in nodule number. We present the results of a forward genetic screen for suppressors of the *sunn-1* phenotype undertaken to identify interacting partners of the kinase. By screening an EMS mutagenized population of the weakest allele of SUNN (*sunn-1*), we identified five verified suppressor of *sunn-1* (SOS) lines. In addition to suppression of hypernodulation, some of the suppression lines have additional root phenotypes and one, SOS3, suppresses multiple hypernodulation mutants, suggesting a general suppression mechanism. To date mapping populations for two suppressor lines, SOS3 and SOS204, have been screened, and the location of the SOS204 lesion has been narrowed to a 65Kb region on Chromosome 2. We will present the effort to identify underlying mutations in these suppressor lines and ongoing characterization of the phenotypes. This work is supported by NSF IOS#1146014 and IOS#1444461, a Wade Stackhouse Fellowship to Ashley Crook, and a China Scholarship Council fellowship to Li Wen.

Keywords: autoregulation of nodulation, suppressor screening, EMS, SUNN, genetic mapping

028 **A Novel Receptor-Like Kinase Involved in Fungal Pathogen Defense in *Arabidopsis thaliana***

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Plants are under constant attack from a variety of disease causing organisms. Lacking an adaptive immune system, plans are naturally prepared for pathogen attack by possessing a vast array of pathogen recognition machinery. Receptor-like kinases (RLKs) are involved in the recognition of pathogen-associated molecular patterns (PAMPs) and activate resistance pathways against broad classes of pathogens. We have identified Powdery Mildew Resistant Kinase 1, an Arabidopsis gene encoding an

RLK that is highly induced by chitin at early time points and localizes to the plasma membrane. Knock-out mutants in pmrk1 are more susceptible to both *Golovinomyces cichoracearum* and *Plectosphaerella cucumerina*. PMRK1's expression is down-regulated similarly by salicylic acid, jasmonic acid and ethylene treatment. Our data show that PMRK1 is essential in early stages of defense against fungi, and provide evidence that PMRK1 may be unique to chitin-induced signaling pathways. We conclude here that PMRK1 is a critical component of plant innate immunity against fungal pathogens.

Keywords: *Arabidopsis thaliana*; Receptor-like kinases; chitin; *Golovinomyces cichoracearum*; Pathogen-associated molecular patterns

029 **IBR5 may regulate auxin responses in Arabidopsis through interaction with SCF Complex**

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Plant growth and development is a highly regulated process which involves cellular transport and reception of the growth hormone indole-3-acetic acid (IAA), or auxin. Cellular response to auxin causes the degradation of the Aux/IAA family of repressors, subsequently modulating the expression of auxin-related genes to control growth. IBR5 was initially identified as a gene involved in the auxin response pathway, as primary root growth of *ibr5-1* mutant exhibited insensitivity to indole-3-butyric acid (IBA), a precursor to IAA in plants. Additionally, *ibr5* was found to be defective in several hormone response pathways. Interestingly, Aux/IAA degradation is increased in *ibr5* mutants, which is contrary to other genes identified in the auxin signaling pathway. Our studies indicate that IBR5 interacts with the SCF complex that is required for the degradation of Aux/IAA repressors. We further characterized this interaction to understand how IBR5 may regulate Aux/IAA degradation. Using immunoblotting techniques, we have shown that IBR5 may regulate the abundance of the SCF subunits suggesting a role for IBR5 in regulation of the stability of the SCF complex.

Keywords: Plant growth and development, SCF, Aux/IAAs, Auxin

030 **Subtle temperature differences may well determine who wins: a story of four submerged aquatic plant species**

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As temperatures increases globally, shifts in the distribution of plant species are expected, with unknown effects on invasive species abundance. It is then of value to understand the role increased temperature may have on invasive species. Although nonhomeothermic organisms are the mercy of environmental temperatures, their physiology is still temperature dependent, with species dependent thermal optima. By identifying the thermal optimum of a species and determining the amount of time spent annually in that optimal temperature zone, success can be predicted under different temperature regimes. Here we identify species-specific differences in the thermal optima of four submerged plants, *Ceratophyllum demersum*, *Hydrilla verticillata*, *Myriophyllum spicatum*, and *Vallisneria neotropicalis*.

Utilizing a biochemical approach, activity of a key metabolic enzyme NADH malate dehydrogenase (MDH) was used to assess the thermal dependencies of Km and Vmax in each species. A Michaelis-Menten model was then employed to predict reaction velocity across a range of temperatures (10 - 40˚C). The predicted reaction velocities were compared to multiyear in situ temperature data. At low temperatures (10 - 20˚C), all three species had similar thermal behavior. However, at temperature > 20˚C, enzyme activity in *H. verticillata* exhibited a sharp increase to a level 2-3 times higher than M. spicatum and V. *neotropicalis*. H. *verticillata* is metabolically more competent at lower temperatures (earlier in season) allowing rapid growth earlier than other coexisting species. This data suggests that as water temperatures increase, the highly invasive *H. verticillata* will be favored over concurring species. Additionally, a northward expansion of the dioecious, southern biotype of this species is likely.

Keywords: invasive species, thermal optima, Michaelis-Menten Kinetics

031 **Characterization of Nuclear Apyrases in *Arabidopsis thaliana***

Gayani Weeraratne, Katherine A. Brown, Greg Clark, and Stanley J. Roux

University of Texas at Austin

Apyrases (nucleoside triphosphate-diphosphohydrolases) are enzymes that regulate the concentration of nucleotides by removing the terminal phosphate from NTPs and NDPs. Two of the 7 apyrases in Arabidopsis, AtAPY1 and AtAPY2, play a crucial role in regulating auxin transport and plant growth. To better understand how these apyrases exert their control over plant growth it will be important to identify the site(s) where they function and their stability in cells. The localization of AtAPY1 and AtAPY2 inside the cell is not very well defined at present, and, regarding the question of their stability/turnover in cells, it is clear that this is dependent on developmental stage and on environmental stimuli such as light, touch, and wounding. Our results indicate there is a significant level of cellular AtAPY1 and AtAPY2 in highly purified nuclei isolated from etiolated seedlings, and that level rapidly declines when the seedlings are exposed to light. To discover the biochemical properties of these enzymes we have partially purified and characterized native nuclear AtAPY1 and AtAPY2, localized them in nuclei both immunocytochemically and by GFP-tagging, and have characterized the kinetics of their rapid degradation in tissues of etiolated seedlings when these seedlings are stimulated by light. We also have initial evidence that one of their nuclear functions is to control the [ATP] in nuclei, and that their suppression results in altered splicing patterns of nuclear transcripts. Supported by NSF grant to SJR and GC.

Keywords: Arabidopsis, Apyrase, ATP, Nucleus

3:15 P.M – 4:30 P.M. Concurrent Session 3B
Graduate Student Oral Competition

032 **Isolation and characterization of a male fertility gene (Ms4) in soybean**

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Identifying a stable male-sterility system is crucial for the development of hybrid soybean. In soybean, eleven male-sterile, female-fertile mutants (ms1, ms2, ms3, ms4, ms5, ms6, ms7, ms8, ms9, msMOS, and msp) have been identified and some of which have been mapped to soybean chromosomes. The objective of this study was to isolate and characterize the ms4 gene. The ms4 gene was located on chromosome 2 using genetic linkage mapping. The comparison of the genetic linkage map with the sequence based physical map helped in localizing ms4 to a 216 Kb region that contains 23 predicted genes. One of the genes in the region Glyma.02G243200, is of particular interest as it codes for male meiocyte death 1 (mmd1) protein in Arabidopsis that triggers cell death in male meiocytes. Isolation and sequencing of the Glyma.02G243200 from the male-sterile and male-fertile lines showed that there is a single base insertion in exon 3 resulting in premature stop codon in ms4. Over-expression of soybean Ms4 functionally complemented the Arabidopsis mmd1 mutant. However, reduced number and size of pods in the complemented plant suggested some functional differences between soybean and Arabidopsis proteins. Ms4 displayed lower expression in the floral buds of mutants compared to wild type. The phylogenetic analysis showed high conservation of the Ms4 protein in the plant lineage. Characterization of the gene involved in male fertility may help to better understand the molecular mechanism of male mediated by soybean Ms4 protein and may lead a path towards development of hybrid soybean.

Keywords: sterility, ms4, mmd1, hybrid soybean, mapping

033 *Chlamydomonas reinhardtii*, a unicellular Model for Quorum Sensing at the Interkingdom Interface

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Niche communities of microorganisms, or microbiomes, have substantial influence on larger eukaryotes. Many of the phenotypes associated with bacteria comprising the microbiota are regulated through a population density based mechanism called quorum sensing (QS). Typically autoinducers with relatively short half-lives are produced and cause gene regulation changes at threshold concentrations. Gram negative bacteria utilize AHL (Acyl homoserine lactone) autoinducers, which perturb a wide array of eukaryotic systems in addition to coordinating phenotypes.

The effects of AHLs on multi-cellular eukaryotes have been extensively studied, most notably plants, in perception and remodeling of the 'quorum' signals. Plants have been shown to exhibit changes in growth, development, defense activation, production of mimic compounds, development of symbiotic tissue, and/or production of factors which degrade AHLs. Yet, little is known about how unicellular eukaryotes are influenced by AHLs. QS may also have a considerable impact on the eukaryotes that also comprise the microbiome, which in turn could influence the QS process itself.
The unicellular model organism and alga *Chlamydomonas reinhardtii* (Cr) is a natural cohabitant with numerous species of QS bacteria under diverse conditions. This well characterized single celled photoautotroph allows for direct comparison against abundant plant literature. Like plants, Cr has previously been shown to exude compounds capable of regulating AHL-mediated QS. Unicellular eukaryotes are more reliant on their environmental conditions both biotic as well as abiotic, potentially making them more immediately susceptible to the results of QS, such as being trapped inside of a biofilm or benefiting from the products of virulence factors.

AHL activity as a general modulator of plant responses is positively correlated with acyl chain length and concentration. I hypothesized AHLs will both alter Cr growth similarly, in a concentration dependent manner, and exhibit degradation of these quorum signals.

Keywords: Interkingdom signaling, quorum sensing, unicellular model, plant microbiome

034 **Overexpression of the Arabidopsis ELP3 and ELP4 genes enhance disease resistance in woodland strawberry**

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Plant immune response is associated with a large-scale transcriptional reprogramming, which is regulated by numerous transcription regulators such as the Elongator complex. Elongator is a multitasking protein complex involved in diverse cellular processes, including histone modification, DNA methylation, and tRNA modification. In recent years, Elongator is emerging as a key regulator of plant immune responses. However, characterization of Elongator's function in plant immunity has been conducted only in the model plant *Arabidopsis thaliana*. It is thus unclear whether Elongtor's role in plant immunity is conserved in higher plants. The objective of this study is to characterize transgenic woodland strawberry (*Fragaria vesca* L.) overexpressing the Arabidopsis Elongator (AtELP) genes, AtELP3 and AtELP4, and to test if F. vesca carries a functional Elongator complex. Overexpression of AtELP3 and AtELP4 in F. vesca impacts plant growth and development and confers enhanced resistance to anthracnose crown rot, powdery mildew, and angular leaf spot, which are caused by the hemibiotrophic fungal pathogen *Colletotrichum gloeosporioides*, the obligate biotrophic fungal pathogen *Podosphaera aphanis*, and the hemibiotrophic bacterial pathogen *Xanthomonas fragariae*, respectively. Moreover, the *F. vesca* genome encodes all six Elongator subunits by single-copy genes with the exception of FvELP4, which is encoded by two homologous genes, FvELP4-1 and FvELP4-2. We show that FvELP4-1 complemented the Arabidopsis Atelp4/elongata1-1 mutant, indicating that FvELP4 is biologically functional. This is the first report on overexpression of Elongator genes in plants. Our results indicate that the function of Elongator in plant immunity is most likely conserved in *F. vesca* and suggest that Elongator genes may hold the potential for helping mitigate disease symptoms and reduce the use of fungicides in strawberry industry.

Keywords: *Fragaria vesca* L., disease resistance, the Elongator complex, AtELP3, AtELP4, FvELP4, transgenic plants

035 **Characterization of the spaceflight methylome: whole-genome bisulfite sequencing and transcription profile analysis of *Arabidopsis thaliana* grown aboard the International Space Station (ISS)**

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Plants have adapted to a diversity of conditions present on Earth throughout their evolutionary history, and have developed remarkable mechanisms that enable them to thrive in a great variety of terrestrial habitats. When plants are subjected to the novel environment of spaceflight aboard the International Space Station (ISS), an environment that is outside of their evolutionary history, they respond by making unique genome-wide alterations to their gene expression profile. Despite extensive studies into this phenomenon, the underlying regulatory mechanisms that may orchestrate alterations to the gene expression profile in response to spaceflight are just beginning to be fully explored.
Epigenetic modifications, or heritable chemical alterations to DNA or its associated proteins, can play a key role in regulating gene expression by altering the availability of DNA to transcriptional machinery. In order to better understand the molecular responses that contribute to the physiological adaptation of plants to the spaceflight environment, genome-wide changes in DNA methylation for Arabidopsis thaliana (Arabidopsis) grown on the ISS were defined by whole-genome bisulfite sequencing. In addition to describing the spaceflight Arabidopsis methylome, RNA-seq transcriptomes were generated and used to compare DNA methylation maps to patterns of gene expression in plants grown on the ISS and in a comparable ground control environment.
Delving into the underlying molecular mechanisms that orchestrate genome-wide transcriptional changes revealed a remarkable ability of plants to remodel the methylation of their genome in response to a novel environment. Examinations of root and shoot organs revealed distinct, organ-specific differences in the spaceflight methylome compared to the ground controls. Through RNA-seq, 65 genes were found to be significantly differentially expressed in roots and 608 genes in leaves. This study will also have an important implication for analyzing the epigenetic state of organisms preserved in RNAlater such as practiced in a spaceflight experiment.

Keywords: Epigenetics, spaceflight, methyl-seq, RNA-seq, Arabidopsis

036 **A Shift from 2D to 3D: Redefining how we study plasmodesmata structure**

Brandon Reagan, Tessa Burch-Smith

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Intercellular communication is a critical process for all forms of multicellular life. In plants, the cell wall impedes communication via direct cell membrane-membrane contacts. In order to circumvent this obstacle, plants have evolved cell-wall-spanning pores called plasmodesmata that form direct connections with neighboring cells and allow for the trafficking of molecules ranging from single ions to large macromolecules. These pores may also contain a tightly furled tubule of endoplasmic reticulum (ER) that spans the pore and connects the ER networks of neighboring cells. Plasmodesmal structure has been studied for many years and several classifications can be made about the pores. Plasmodesmata can be classified based on their origin. Primary plasmodesmata are formed during cell division and new cell wall formation, while secondary plasmodesmata are directly inserted into an existing cell wall. How the latter occurs and what triggers the formation of new PD is unknown. Plasmodesmata may also be classified into three structural classes: simple, twinned, and branched. How the different structural features of each class relate to function remains to be determined. Traditional studies of PD structure have relied on the use of thin section transmission electron microscopy (TEM), and while these studies have elucidated many features of the pores, they have the critical drawback of taking a 2D snapshot of a 3D structure. Here, we have used the advanced serial electron microscopy imaging techniques of TEM tomography and focused ion beam-scanning electron microscopy (FIB-SEM) to investigate the 3D

structure of plasmodesmata. This has allowed us to better understand how structural features of these remarkable pores relate to their functions.

Keywords: Plasmodesmata, Structure, Tomography

Undergraduate students – posters

037 **Molecular Characterization of Two High Light-Sensitive Mutants of *Chlamydomonas reinhardtii,* defective in a novel uncharacterized gene, LSR1.**

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Photo-autotrophic growth under different light intensities is regulated by a complex interplay of several physiological processes. *Chlamydomonas reinhardtii* is a green micro-alga. It has a haploid genome, short replication time, autotrophic and heterotrophic growth ability, amenability to nuclear and chloroplast transformation, and a fully sequenced genome. All of these traits make it an elegant model system to study eukaryotic oxygenic photosynthesis. Our lab generated a mutant library of Chlamydomonas by random insertional mutagenesis using the pBC1 vector. The mutant library was screened under heterotrophic, mixotrophic, and photo-autotrophic growth conditions under different light intensities to isolate high light-sensitive mutants. One of the isolated high light-sensitive mutant is *lsr1a*. *lsr1a* is chlorophyll-deficient, hyper-sensitive to high light in photo-autotrophic and in mixotrophic growth conditions and photo-bleaches on exposure to high light. There are two insertion sites of pBC1 in lsr1a. One pBC1 insertion site is in the fourth exon of a novel functionally uncharacterized gene, Cre11.g467757 (LSR1/Light Stress Related 1). The second insertion site of pBC1 is in Cre02.g095095. Cre02.g095095 codes for a secretory cell wall protein pherophorin-C12 (PHC12) whose specific function is unknown, to date. A strong indication that LSR1 is responsible for the lsr1a growth phenotype is that lsr1a growth phenotype is like another uncharacterized Chlamydomonas CLiP [Chlamydomonas Library Project] mutant LMJ.RY0402.051109 (*lsr1b*), which has a mutation in the fourth intron of LSR1. Our preliminary data indicates that LSR1 undergoes growth condition mediated-post-transcriptional regulated splicing via an intron inclusion. We will be presenting our physiological and molecular research on *lsr1* mutants.

Keywords: lsr1a mutant

038 **The Role of InvINH1 as an Invertase Inhibitor**

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During seed development in Arabidopsis plants, the endosperm undergoes two phases, the syncytial phase and the cellularized phase. After endosperm cellularization, there is an increase in embryo growth rate, which suggests that more carbohydrates are provided to the embryo to support its growth. We discovered that two invertase inhibitors (InvINH1 and InvINH2) are expressed in the embryo-surrounding region of the endosperm during the syncytial phase, but not expressed during the cellularized phase. Since invertase hydrolyzes sucrose into glucose and fructose to support growth and development, we hypothesized that InvINH1 is down-regulated after endosperm cellularization to

increase invertase activity, which promotes embryo growth. In this project, we investigated whether InvINH1 can act as an invertase inhibitor during seed development. A region of InvINH1 gene that encodes the mature protein was cloned into an expression vector, pGEX-4T1. The construct was then transformed into E. coli expression host cells. In order to determine the function of InvINH1, we will induce InvINH1 protein expression, purify the protein, and use the protein for in vitro invertase activity assay. Understanding the role of InvINH1 as an invertase inhibitor will allow for a better comprehension of seed development in plants. This will provide a way to optimize crop growth and yield.

Keywords: Developmental Biology, Arabidopsis

039 **Screening *Medicago truncatula* Tnt1 insertion lines for mutants in the Autoregulation of Nodulation pathway**

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Legumes have unique ability to form nitrogen fixing nodules via symbiotic association with rhizobia. Once the nitrogen requirement is fulfilled, a root-to shoot-to root signaling pathway called Autoregulation of Nodulation (AON) is activated to inhibit new nodule formation. In our lab working on *Medicago truncatula* we found the receptor kinase SUNN, a key component of AON pathway acting from the shoot, interacts with *M. truncatula* RopGEFs 1, 2, 5 and 7b in a bimolecular fluorescence complementation assay. We also identified other genes (TML-like, KLV, ACR4-like) potentially involved in the pathway based on orthologous genes identified by mutation in other legumes such as L. japonicus and soybean. In order to investigate the molecular genetics of the signal transduction pathway, we require plants with mutations in these genes to identify phenotypes and establish gene function in our model organism. We utilized the Tnt1 insertion lines created and maintained by The Samuel Roberts Noble Foundation (https://medicago-mutant.noble.org/mutant/) with NSF support as a resource to identify plants with mutations in our genes of interest. We searched the database for presence of Flanking Sequence Tags (FSTs) for all our target genes and ordered pools of lines with a possible insertion. Here, we present our strategy to find and verify mutants identified in database search as being present in the pool, and discuss future plans for mutants identified thus far. This research is supported by Clemson University Creative Inquiry.

Keywords: Nodulation, Tnt insertions, genetic screening

040 **Novel *M. truncatula* CLE peptides in nodule regulation**

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Nodules are specialized root organs that form to allow for a symbiotic relationship between legumes and rhizobia, nitrogen (N)-fixing bacteria. After formation of the nodule meristem, two small signaling peptides, MtCLE12 and MtCLE13, from the CLAVATA3/ENDOSPERM SURROUNDING REGION (CLE) family are expressed in the nodule meristem, modified into mature signaling peptides and translocated to the shoot, where they presumably interact with receptors such as SUNN to regulate further nodule formation. This Autoregulation of Nodulation (AON) pathway limits the number of nodules produced and the nitrogen fixed by the plant. A recent phylogeny paper identified several CLEs in same clade as MtCLE12 and 13, suggesting they have a similar function. Based on having a higher expression in nodules versus root in tissue-specific RNASeq datasets, we suspect these CLEs have the

potential to be involved in nodule regulation. We designed primers for qRT-PCR to five previously unnamed CLE genes and CLE4 (known not to be involved in nodule regulation), all expressed in the nodules of *Medicago truncatula*. We are testing induction by nitrate and by rhizobial inoculation using *M. truncatula* grown in an aeroponic system. The plants are treated with either 5mM nitrate or inoculated with rhizobia and samples were collected at 0, 24, 48, and 72 hours post inoculation or treatment. We are currently measuring the transcript levels of these genes with qRT-PCR and creating overexpression constructs for each CLE with the intent to observe nodulation effects in roots overexpressing each CLE. This research is supported by Clemson University Creative Inquiry and the Calhoun Honors College at Clemson University.

Keywords: Nodulation, peptides, signaling

041 **Improving Crop Productivity using Symbiotic Fungi**

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Climate change negatively affects agricultural production, which is a challenge especially with the expected increase of human population. Climate change includes heat and drought waves and increased soil salinity, which affects many agricultural industries world-wide, with the last two years being the hottest years on record. Current crop growing practices have seen success, but more sustainable methods are needed to feed the steadily increasing population. The use of microbial symbionts to increase crop production and stress tolerance is a promising approach. Our research is focused on incorporating fungal endophytes isolated from plants living in stressed environments into crop plants to identify their role in production and stress tolerance. A total of 94 fungal isolates were identified based on their phenotypic characteristics and ITS DNA sequencing. From this collection, 30 were identified as endophytic fungi. We selected 8 isolates for initial testing in tomato. Under greenhouse conditions, 2 isolates were able to improve salt and drought stress, independently, while both increased biomass growth under normal growing conditions. These 2 endophytes (name coded as H and J for IP protection) were then tested in tomato plants under field conditions. The endophyte colonized tomatoes were able to produce more tomatoes (H: 20% and J: 25%) and higher consumer taste ratings than that of the non-symbiotic control treatment. Continuing research is needed to discover more about these potentially helpful organisms and their use in aiding the agricultural industry in its continuing efforts to produce sufficient food for the growing population.

Keywords: Plant-Fungal Interaction; Symbiosis; Agriculture; Abiotic Stress Tolerance

042 **Crop production on the rise as fungal endophytes help with the cause**

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Climate change is a serious problem that affects not only the environment, but also human's food security. Drought, heat waves and increased soil salinity associated with climate change is having an impact on the United States crop production. For example, the last three years were recorded as the driest weather ever recorded in California, where significant agriculture products are made. Another example, the rise of sea levels along the coast of Florida has increased soil salinity, where a 10% increase in salinity resulted in rapid and dramatic changes in the microbial activity in plants. Fungal endophytes are

present in almost every plant growing on Earth. Those fungal endophytes obtain carbon from plants and in return they provide plants with some metabolites that can improve plants' environmental stress tolerance. We hypothesized that endophytes associated with wild plants growing in high stressed areas can improve crop production and stress tolerance. To test our hypothesis, growth rate and yield of tomato plants colonized with twelve fungal endophytes isolated from wild plants growing in saline soils were compared to non-symbiotic plants. The use of fungal endophyte is very promising and can help other crops flourish under harsh conditions like drought and salinity. While stressing the tomato plants under drought and salinity conditions, we have found that potentially five of our fungal endophytes are promising. We have some plants that can withstand the salt stress or the drought stress, but we have some such as *Fusarium oxysporum*, *Purpureocillium lilacinum*, and *Ophiocordyceps heteropoda*, that are able to withstand both stress methods.

Keywords: Plant Fungal Interactions

043 *Littoraria irrorata* Preference for Salt Marsh Habitat

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Littoraria irrorata is a common marine gastropod that is found in the salt marsh of the southern United States. *L. irrorata* consumes microalgae on the highly abundant cordgrass *Spartina*; the snails are considered grazers. The goal of this study was to determine if *Littoraria irrorata* has a preference for different salt marsh plant species, including *Phragmites*, *Juncus*, *Spartina*, and *Avicennia*. It was hypothesized that *L. irrorata* habitat preference would be *Spartina* because of the snails feeding behavior. Plants and *L. irrorata* were collected in the salt marsh behind Louisiana Universities Marine Consortium's DeFelice Marine Center in June, 2016. Mesocosms were setup with *Spartina* which was paired with each of the other plants, and ten snails were added in the center of each mesocosm. After an hour, the number of individuals on each plant species was recorded. No significant difference was found in habitat preference. The number of snails was not different on *Spartina* vs. each of the other plant species. The results did not support the hypothesis. Feeding behavior does not seem to be coupled with habitat preference. The other plant species may potentially confer other benefits which the support the snail.

Keywords: Habitat preference, *Littoraria, Spartina*

044 Effects of exogenous ß-alanine on primary root growth, potassium accumulation and polyamine biosynthesis in *Arabidopsis thaliana*

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Arabidopsis thaliana seedlings (Cape Verde Island Ecotype) were grown on two different concentrations of Murashige and Skoog Salts (MS) in the presence or absence of 5 mM ß-alanine. Primary Root elongation was severely inhibited in the presence of ß-alanine. The inhibitory effect of ß-alanine was more accentuated at 1/8X MS than on 1X MS salts. Root elongation of plants germinated in 1/8X MS salts experienced the same inhibitory effect when transferred to medium containing 5 mM ß-alanine. This suggests that growth inhibition due to the presence of ß-alanine occurs at any stage of plant development. Leaves of plants grown in the presence of ß-alanine showed reduced growth and high level

of chlorosis. Similarly to root elongation, the effect of ß-alanine on leaf growth was more accentuated on plants grown in 1/8X MS as compared to those grown in 1X MS salts. Additional studies demonstrate that the higher level of potassium in 1X MS salt medium is responsible for the attenuation in root growth inhibition in the presence of ß-alanine. Potassium uptake and accumulation in the plant tissues may be affected by the presence of ß-alanine in the medium. Furthermore, ß-alanine may be linked to the accumulation of polyamines in the tissue and ultimately affect seedling development. Therefore, further studies are being conducted to determine the potassium concentration and polyamines in the plant tissue.

Keywords: Arabidopsis, Beta-alanine, Polyamines, Putrescine, Spermidine, Spermine

045 **Assessing Genetic Diversity within Natural Populations of Smooth Cordgrass to Ensure Effective Restoration Efforts**

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The Indian River Lagoon (IRL) is one of the most biodiverse estuary systems in North America making it a conservation priority and the focus of many restoration efforts. Smooth cordgrass (*Spartina alterniflora*) is a keystone species and indicator for ecosystem health that naturally occurs along the shorelines of the IRL. *Spartina alterniflora* is often used in shoreline restoration due to its extensive rooting capacity and ability to halt shoreline loss. Clonal species, such as *S. alterniflora*, are easy to raise with regard to the number of clones reared, but using clonal species for restoration may lead to a lack of genetic diversity and adaptability that could lead to ecosystem collapse. If the genetic makeup of the transplanted samples is not taken into account then the founded population is likely to be genetically depauperate. To understand whether restored populations exhibit natural levels of genetic variation, we quantified the genetic diversity present within natural and restored *S. alterniflora* populations within the Mosquito Lagoon using microsatellite genetic markers. We found that multiple loci exhibit heterozygote excess and heterozygote deficiency in restored populations, which may be due to the use of clonal propagates in restored populations. Overall, this study allowed us to identify that our current method for selection of transplant individuals has decreased diversity in restored populations compared to natural populations, however the long-term impact of this loss of diversity is yet to be determined.

Keywords: Genetic Diversity, Restoration, Population Genetics, Conservation

046 **An *in vitro* functional splicing assay for the putative maturase MatK**

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Maturases are a group of enzymes which catalyze the removal of introns from pre-mRNA transcripts during post-transcriptional processing. Maturase K, or MatK, is proposed to be the only plastid-encoded maturase in land plants. The ORF of its gene was initially infamous for its use in plant systematics as a robust DNA barcode. Because of its unique mutational rate across lineages, it was thought to be a pseudogene, however a large body of research has since demonstrated that MatK is essential for plastid function and is conserved in most species of land plants. Recently, RNA binding assays have shown that MatK associates with several intron substrates within the plastid genome, but as of yet there has not been a direct demonstration of its proposed enzymatic function. Using molecular cloning techniques, we have designed the first in vitro functional splicing assay for MatK. Future use of this assay will better characterize MatK's role within the plastid as a group IIA intron processing enzyme.

Keywords: MatK, maturase, plastid, post-transcriptional splicing

047 Protein-Protein Interactions Associated with Splicing of Chloroplast Group IIA Introns

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Many relate the spliceosome, a multi-protein and RNA complex required for splicing of introns, to the nucleus of eukaryotic cells, but evidence suggests that the chloroplast of land plants may also contain their own specialized spliceosome. Group IIA introns of the chloroplast have been postulated to be excised by both nuclear-encoded factors such as What's This Factor 1 (WTF1) and the ribonuclease III domain protein (RNC1), as well as plastid-encoded factors, specifically Maturase K (MatK). We have initiated a series of co-immunoprecipiation studies to assess the protein-protein interactions among various hypothesized splicing factors of chloroplast group IIA introns with a specific focus on protein interaction with the MatK maturase. Collected data will be used to devise a model of group IIA intron splicing processes in the chloroplast of land plants.

Keywords: Chloroplast, spliceosome, Maturase K

048 *Arabidopsis thaliana* NIP2;1 : An Aquaporin superfamily lactic acid channel induced in roots during low oxygen stress

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Oxygen is vital for aerobic metabolism in eukaryotic cells. In Arabidopsis thaliana, oxygen deprivation resulting from flooding stress, waterlogging, or poor soil aeration results in an adaptive response that results in a coordinated genetic response that redirects resources to the expression of 49 "core hypoxia genes" that encode fermentation and glycolytic enzymes, and other proteins associated with an adaptive response. Among these core hypoxia genes is AtNIP2;1 which encodes a channel protein of the aquaporin superfamily of membrane channels. AtNIP2;1 is a root specific transcript that accumulates over 500-fold within roots within hours of the onset of hypoxia. Analysis of its transport selectivity shows that instead of water, NIP2;1 is a channel for protonated lactic acid (a toxic fermentation end product), and is the only plant NIP to show this selectivity. Analysis of Arabidopsis plants expressing AtNIP2;1-YFP translational fusions show that upon hypoxia challenge the protein accumulates on the plasma membrane of inner cortical cells and the vascular tissue of the mature root. It is proposed that its induction and localization to these cells may be related to a where it may play a role in the transport, compartmentation and homeostasis of the lactic acid which accumulates during hypoxia induced fermentation. (Supported in part by NSF MCB 1121465).

Keywords: abiotic stress, membrane protein channels, metabolism, hypoxia

049 Comparison of growth between Bt and conventional field corn

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Genetically modified organisms (GMOs) have been a topic of controversy in society with concerns of environmental impacts as well as consumer health. Bacillus thuringiensis (Bt) corn is proposed to increase yield by decreasing insect damage. This project sought to compare growth between Bt and conventional field corn. This research took place during the summer of 2016 in Sheldon, ND. Data was collected every 3 days (May -Nov, 2016). The results from this experiment, surprisingly, found there was little difference between conventional and Bt field corn growth. The next step in the research is to run PCR to detect if cross pollination with Bt affected the conventional corn.

Keywords: GMO, Bt, maize

050 **Developing an Activation Tagging System for Wheat Mutagenesis**

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Transposable elements are sequences of DNA that can jump from one location to another in the genome. A transposable element named *mPing*, first discovered in rice, requires two proteins, ORF1 and Transposase (TPase), to move in the genome. This element can be used for mutagenesis, changing an organism's genome, which is useful for gene discovery. An activation tagging version of *mPing*, called mmPing20F, was created by inserting an enhancer sequence from the promoter region of the figwort mosaic virus into a hyperactive version of *mPing*. An activation tag can show gene function by causing overexpression of nearby coding regions in the genome. Wheat is a good organism for applying activation tagging because it is a polyploid and one of the most widely grown crops in the world. Plant transformation was used to get mmPing20F:GUS and an ORF1/TPase expression construct into the wheat genome. Cross-pollination between plants with mmPing20F and plants with ORF1 and Transposase were performed. The F1 generation is being analyzed by PCR to determine if mmPing20F shows evidence of transposition. The expectation is that mmPing20F will be able to transpose if both ORF1 and TPase proteins are expressed. We are also using GUS staining to determine if mmPing20F has been removed from its original position in the GUS reporter.

Keywords: transposable elements

051 **Determining the role of homologous recombination in replicative transposition of *mPing***

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Transposable elements are mobile segments of DNA that make up a large portion of plant genomes. Class II transposable elements use a "cut and paste" mechanism in which the element is excised and reinserted elsewhere in the genome, making them powerful agents in genome evolution. One of these elements, *mPing*, has high transposition activity, and despite the fact that *mPing* utilizes a "cut and paste" mechanism, its copy number has been shown to increase over generations, suggesting the presence of a replicative transposition mechanism. This experiment will test if homologous recombination (HR) repair, a mechanism in which homologous sequences from elsewhere are used to repair double strand breaks, repairs *mPing* excision sites with an *mPing* containing homologous sequence. We measured repair of *mPing* excision sites in yeast using a reporter system in which *mPing* disrupts the *ADE2* gene, preventing cell growth until excision of *mPing* and subsequent repair of the

ADE2 gene. Previous results showed that *ADE2* restoration was higher in haploid cells than in diploid cells, suggesting that HR repair may be occurring in the diploids. To confirm the role of HR repair, we are performing transposition assays in HR deficient strains created by knocking out the *rad51* gene. We predict that in the absence of HR repair we will see equal restoration of *ADE2* function in the haploid and diploid strains. If we can confirm that HR repair is occurring, we will attempt to directly identify cases of replicative transposition by analyzing *mPing* copy number in our strains.

Graduate students – posters

052 **Nucleosome Occupancy is Altered in Mutants of Maize SWI/SNF-like Chromatin Proteins.**

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Chromatin remodelers alter DNA-histone interactions in order to regulate accessibility to transcription machinery. Such proteins have been identified and confirmed in many organisms including yeast and Arabidopsis. While there are maize proteins with similar predicted functions to these remodelers, the ability of the maize proteins to affect nucleosomes have not been investigated. This study hypothesized that a misregulation of proteins with similar domains to the know yeast and Arabidopsis chromatin remodelers would lead to altered DNA-histone interactions. Several maize proteins (CHR101, CHR106, CHR127, and CHR156) with similar functional domains to known chromatin remodelers were selected. Mutant alleles were identified for all of these proteins and altered expression of *Chr101*, *Chr106*, *Chr127*, and *Chr156* was demonstrated in homozygous mutants. Nucleosome protection assay of homozygous *chr101*, *chr106*, *chr127*, and *chr156* mutants demonstrated changes in nucleosome occupancy which implicates these putative maize chromatin proteins in altering DNA-histone interactions. Further experiments also demonstrated similar nucleosome alteration in *chr127* and *mop2*, and the absence of these changes in *mop1*, suggesting that while *Chr127* function is associated with *Mop2* and Polymerase V, it is independent of Polymerase IV. This paper is the first to demonstrate a change in DNA-histone interactions due to altered expression of maize proteins that possess known chromatin remodeler domains and therefore implicating those proteins as putative maize chromatin remodelers.

Keywords: Maize, chromatin remodeling, nucleosome

053 **Cytogenetic analysis of Humulus lupulus (hops)**

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Humulus lupulus, commonly known as hops, is an important crop around the world historically known as a main flavoring ingredient in beer. It is also revered for its particularly powerful phytoestrogens that are currently studied for HRT and breast cancer therapeutics. However, hops breeders have been limited in their ability to create strains with desirable traits due to its unusual and unpredictable inheritance patterns. This observed phenomenon has recently been shown to be associated with non-Mendelian segregation patterns in gene markers. These studies, combined with classical cytogenetic studies strongly implicate meiotic chromosome behavior as a possible mechanism for the production of unpredictable phenotypes. The role of meiosis is to decrease diploid genomes to haploid in preparation for bi-parental fertilization to initiate the progeny of the next generation. In addition, the homologous chromosome pairing and recombination required to achieve this disomic inheritance and reductive division produces a large amount of genetic variation in subsequent generations. In flowering

plants, the haploid nuclei are found in the male (pollen) and female (egg sac) gametophytes. Given the abundance and experimentally accessible male meiotic cells within anthers (pollen mother cells), a detailed descriptive analysis of the chromosome behavior in meiotic prophase nuclei from pollen mother cells of hops was carried out using 3D epifluorescence microscopy. It was observed that indeed, meiotic chromosome associations often occur as atypical multiple chromosome complexes, perhaps leading to the segregation distortion that has been previously reported.

Keywords: hops meiotic chromosome behavior

054 **Characterization of fatty acid amide hydrolase in *Physcomitrella patens***

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In plants, saturated and unsaturated N-acylethanolamines (NAEs) with acyl chains 12C to 18C are reported for their differential levels in various tissues and species. While NAEs were shown to play a vital role in mammalian neurological and physiological functions, its metabolism and functional implications in plants however, remains incomplete. Fatty acid amide hydrolase (FAAH) is one of the metabolic enzymes that breaks the amide bond in NAEs to release free fatty acid and ethanolamine. We identified FAAH in *Physcomitrella patens* and expressed heterologously in *E. coli* using Gateway cloning system. Radiolabeled NAE 16:0 and 20:4 were used as substrates to test amide hydrolase activity in vitro. In order to understand the role of PpFAAH in vivo, knock out (KO) and overexpressors (OE) were generated by homologous recombination. PpFAAH KO construct was generated by inserting 5'- and 3'-flanking regions into pMP1159 plasmid. Full length PpFAAH with stop codon was cloned into pTHUBlGATE vector in order to make OE construct. KO and OE constructs were then transformed into protoplasts of P. patens by using PEG-mediated transformation to generate mutant lines. To identify potential interacting proteins of PpFAAH, it was cloned into pDEST15 plasmid with N-terminus GST tag. Interaction between GST-tagged PpFAAH and proteins from 14-day old protonema will be visualized by SDS-PAGE and then subjected to LC-MS/MS analysis for identification. Our long-term goal is to conduct comprehensive analyses of NAE metabolite mutants to determine their role in growth and development, and mediating stress responses in *P. patens*.

Keywords: NAEs, FAAH, *P. patens*

055 **The Identification and Characterization of Kinase Orthologs in Soybean and Cotton in the Effort to Improve Plant Resistance against Environmental Stresses**

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American upland cotton (*Gossypium hirsutum*) and soybeans (*Glycine max*) are two of the most produced crops worldwide whose production needs to continue increasing in order to feed and clothe future generations. Biotic and abiotic stresses, however, are an ever-present plague on the ultimate yield production of these and every other crop we produce. In an effort to minimize reduced yields as a result of plant stress, we need to identify, characterize and ultimately promote the incorporation of entire stress

response systems into these commercial crops. Integrin-Linked Kinase 1 (ILK1) has been identified by our lab as a multi-stress regulator of immune response in Arabidopsis. A novel, reporter-based luminescence assay, produced by our lab, has also recently led to the identification of 135 kinase-effector interactors (KEIs) shown to positively and sometimes negatively regulate innate immune responses to multiple effectors from the bacterial pathogen *Pseudomonas syringae* in tomato (*Solanum lycopersicum*). The aim of this project is to identify and characterize orthologs of multi-effector kinases in the globally important commercial crops soybean and cotton. Knockdown mutants will be generated using viral induced gene silencing (VIGS) to characterize newly identified orthologous kinases involved in enhanced pathogen resistance. Potential orthologs for six KEIS and ILK1 in soybean and cotton have been identified and VIGS constructs are currently being developed. Future work will hopefully reveal new insights into how kinases work to promote enhanced plant resistance.

Keywords: Kinase, soybean, cotton, VIGS

056 **Biochemical characterization of tomato fatty acid amide hydrolase**

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N-acylethanolamines (NAEs) are present in wide range of organisms and belong to family of functionally diverse signaling lipids. They consist of a fatty acid with varying chain lengths and ethanolamine linked via an amide bond. The level of NAEs is modulated by their hydrolysis to ethanolamine and fatty acid by an enzyme fatty acid amide hydrolase (FAAH). FAAH is an integral membrane protein that belongs to "amidase signature" superfamily of proteins, which is characterized by highly conserved region rich in serine, glycine and alanine. FAAH directly or indirectly plays a role in modulation of various physiological processes by regulating NAE levels. Although the role of NAEs and its key modulator FAAH has been studied in other plants, their role in tomato model is limited and unknown. More recently, SlFAAH1, an ortholog of AtFAAH1, was identified in tomato and cloned into bacterial expression system. However, putative SlFAAH1 function and distinct features are yet to be determined. It is hypothesized that the putative SlFAAH1 catalyzes the hydrolysis of NAEs and modulates the level of NAEs during the seedling development in tomato. To this extent, a putative SlFAAH1 (previously identified and cloned in pET-23a vector) will be biochemically characterized and also effect of NAEs on seedling development will be studied. Thus far, SlFAAH1 cloned in pET-23a vector was expressed in RIL cell line (prokaryotic expression system) followed by conformation of positive transformant by colony PCR. Currently, protein expression and confirmation of SlFAAH in the positive transformant is being done. The expressed protein will be characterized for its hydrolytic activity using radiolabelled substrate. The effect of exogenous NAEs during seedling development will be studied with regards to expression level of SlFAAH1 by qPCR and composition of NAE during the seedling development to determine the role of NAE during seedling development. Thus, this study is expected to not only characterize a protein in tomato but also determine its role in mediating NAE metabolism and seedling development. Long-term studies will identify the significance of highly conserved NAE pathway in eukaryotes.

Keywords: FAAH, NAE metabolism

057 **Potential allelopathic effects of *Eichhornia crassipes* and *Lemna gibba* on the invasive water fern *Salvinia molesta***

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Experiments were conducted to assess whether two common, floating plant species, including the invasive water hyacinth, *Eichhornia crassipes*, and the native duckweed, *Lemna gibba*, influence growth and the health of the invasive water fern *Salvinia molesta*. Originally from Brazil, *S. molesta* has spread throughout the Southeast United States, dramatically changing aquatic ecosystems and causing significant ecological and economic damage. Various control methods (mechanical, chemical, and biological) have been tried, and while successful in some geographic areas, widespread control has not been accomplished. To assess whether *E. crassipes* and *L. gibba* can control *S. molesta*, assays with live plants and chemical extracts were performed. For the live-plant assay, *S. molesta* was grown in the presence and absence of the other species. The change in weight of *S. molesta* was determined and compared between treatments and controls. For the extract assay, *S. molesta* was grown in varying concentrations of *E. crassipes* and *L. gibba* extracts. The change in weight of *S. molesta* was determined and compared across treatments and controls with no extracts. The health of *S. molesta* leaves was assessed qualitatively. For the live-plant assay, both *E. crassipes* and *L. gibba* did not suppress *S. molesta* growth over controls. In contrast, in the extract assay, growth was significantly reduced by *L. gibba* at a 100M concentration over controls. *Lemna gibba* extracts generally reduced growth more than *E. crassipes* extracts. Surprisingly, the highest concentration of *E. crassipes* shoot extracts negatively affected S. molesta health over controls and other extracts. This study demonstrated that *E. crassipes* and *L. gibba* may have the potential to negatively affect *S. molesta* through allelopathy. More research needs to be conducted to determine whether *E. crassipes* and *L. gibba* extracts could be used to control field populations of *S. molesta*.

Keywords: allelopathy, *Salvinia*, *Eichhornia*, *Lemna*, invasive species

058 **Biological control of root-knot nematode in cotton by suppression of candidate susceptibility genes**

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Current studies on plant immunity indicate that pathogens suppress plant defense in order to establish infection in hosts that they would otherwise be unable to infect. For this intention, pathogens use effector molecules that interfere with different layers of the plant defense response. In this study, we will explore susceptibility gene candidates that are activated by pathogen effectors to suppress plant immunity. We selected a set of susceptibility gene (S-gene) candidates based on their homology to tomato bacterial susceptibility genes from the protein kinase family identified in our laboratory. We will generate plasmid vectors for gene silencing to obtain transgenic lines of *Gossypium hirsutum* with silenced S-gene expression. The kinase-silenced plants will be tested for their response to infection with the root-knot nematode. Through the suppression of S-genes we will be able to identify transgenic phenotypes and gain insights into the mechanisms of plant disease resistance.

Keywords: Susceptibility gene, *Gossypium hirsutum*, virus-induced gene silence (VIGS)

059 **The identification and characterization of a mutant defective in dark to light transition.**

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The unicellular eukaryotic green alga *Chlamydomonas reinhardtii* is a eukaryotic model system to study oxygenic photosynthesis. All three genomes (chloroplast, nucleus and mitochondria) of the organism have been published, and are amenable to genetic manipulations. A large scale insertional mutagenesis of C.reinhardtii was screened for cells that grew poorly on low CO2. One of the isolated colonies of interest is A144. Using adapter ligation- mediated PCR we have shown that the gene disrupted in A144 is annotated as a soluble ABC subfamily F protein with two ATP-binding cassettes (ABC). A chromodomain insertion is located within the C-terminal ABC cassette. The chromodomain insertion is unique to eukaryotic translational elongation factor 3 (eEF3). A144 grows slower than wild type (WT) strain under both mixotrophic and photo-autotrophic growth conditions. Dim-light adapted A144 is able to grow slowly in the dark. However A144, subjected to prolonged darkness (dark adapted for 4 weeks), fails to grow on fresh media in the dark and in the light under heterotrophic, mixotrophic and photo-autotrophic growth conditions. In yeast, ABC subfamily F members, including eEF3 ortholog yef3 ,are known to play a role in cell growth and viability. The 3 day-dark adapted mutant has a marked difference in the respiration rate compared to WT. We will be presenting our preliminary molecular and physiological data on the A144 mutant.

Keywords: Chlamydomonas, dark adaptation, light, ABC protein, respiration

060 **Alpha Carbonic Anhydrases of *Arabidopsis thaliana***

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Carbonic anhydrases (CAs) are zinc metalloenzymes which catalyze the interconversion of carbon dioxide and bicarbonate. It is hypothesized that CA activity facilitates CO2 flux in leaf mesophyll cells to maintain optimal rates of photosynthesis. We are studying CAs to see if they participate in the delivery of CO2 for photosynthesis in leaf cells. There are three classes of CAs (α, β and γ) in the model plant Arabidopsis thaliana. The βCAs and γCAs have been well studied, but the αCAs have received relatively little attention. There are eight αCA genes in Arabidopsis thaliana. This study investigates which αCAs are expressed in leaves and which ones might play a role in photosynthesis.
RNAseq data show that only three of the eight αCAs (αCA1, αCA2 and αCA3) are expressed in significant amounts in shoot and root tissue. Therefore, our subsequent studies focused on αCA1, αCA2 and αCA3. First, the GUS reporter system was used to determine in which specific leaf tissues each gene was expressed. In addition, knockout lines for αCA1 and αCA2 were obtained. These knockout lines of αCAs have been grown under low and high CO2 to assess the role of αCAs on dry weight and projected rosette leaf area. The intracellular localization of these CAs was examined. In a preliminary study, intracellular localization of αCA1, αCA2 and αCA3 have been determined using eGFP constructs.

Keywords: carbonic anhydrase, CO2, leaf, intracellular localization

061 **Regulator of Gene Silencing Calmodulin-like proteins: Potential targets of abiotic and biotic stress responses**

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Plants respond to stresses with both general and stress-specific responses, and frequently utilize calcium sensing proteins as intermediates to decode cytosolic calcium signals. A wide array of calcium sensor proteins, including bona fide calmodulin (CaM) as well as calmodulin-like proteins (CML) have evolved as decoders of the calcium signal. Among these are a subclade of phylogenetically and structural related "regulator of gene silencing" CaM-like proteins. Two members of this subfamily, the Arabidopsis thaliana calmodulin-like protein 38 (CML38) and the *Nicotiana tabacum* regulator of gene silencing calmodulin-like protein (RgsCaM), have been implicated in two stress responses: hypoxia and potyvirus infection. With respect to CML38, it has been found to be among the 49 core hypoxia genes induced during oxygen deprivation in Arabidopsis, and is important for plant survivability in response to hypoxia. CML38 localizes to cytosolic particles during low oxygen stress. MS analysis of CML38 pull downs, as well as co-localization analysis with mRNA particle markers, show that these particles likely represent stress granule mRNPs as well as processing bodies, supporting a role for this protein in mRNA homestasis during this response. Subsequent analysis with RgsCaM also shows co-localization with processing body markers under hypoxia, suggesting a potential role in mRNA degradation. This finding is of particular significance given the role that RgsCaM is known to play as a target for potyviruses, which are proposed to use RgsCaM to suppress virus-induced gene silencing. Interestingly, unlike CML38, rgsCaM shows no apparent localization to stress granule particles, but does associate with additional structures besides P-bodies of unknown identity. Collectively, the data suggest that these calcium sensors may be recruited to distinct mRNA particle structures to help regulate mRNA homeostasis in response to calcium signaling cues.

Keywords: Calmodulin-like 38, Regulator of gene silencing calmodulin-like protein, potyvirus, suppression of gene silencing, processing bodies

062 **Chemical and Molecular Responses to Kin Recognition Events in a Model Angiosperm**

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Competition for the limited resources available in soil plays an important role in deciding community composition and robustness in plants. The ability to identify relatedness in neighboring community members and adjust growth and development accordingly is known as kin recognition (KR). The most common phenotype associated with KR is a redistribution of the root system architecture (RSA). More specifically, the less genetically related two plants of the same species are, the more lateral roots they are likely to arrange in competition. The primary factors driving KR appear to be low molecular weight components contained in the root exudates of plants. Such signals are routinely capable of distinguishing between members of the same or different accessions, and in some cases even 'sibling' plants. The discovery that the model angiosperm *Arabidopsis thaliana* is capable of KR, offers a new opportunity to identify and map the metabolomic, proteomic, and genomic elements which control this complex example of social behaviors in plants. We recently established that the extent of KR in A. thaliana could be modulated by nutrient availability. The ability to effectively induce KR in a step-wise

fashion should allow us to effectively 'dial-in' this response facilitating analysis. In the present study we exploited this inducibility to identify the biochemical and molecular elements associated with different levels of KR responses. In this work we have coupled: (i) Liquid Chromatography-Mass Spectrometry (LC-MS) studies of root exudates, (ii) Reactive oxygen species studies, (iii) phytohormone assays, and (iv) 2D protein gels to evaluate the effects of KR on these less obvious phenotypic and proteomic responses. Refining our understanding of the elements which drive KR helps us to construct better models of ecosystem maintenance and robustness, provide insight into how plants organize 'social' architectures, and may ultimately help us identify compounds of agricultural benefit.

Keywords: Arabidopsis, kin recognition, metabolomics, proteomics

063 Lignin nanotubes as a gene delivery system into plant and animal cells

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Lignin is an aromatic cell wall polymer that is generated as a waste product by biorefineries that process plant biomass to fermentable sugars for the production of biofuels and chemicals. Lignin nanotubes (LNTs), synthesized in sacrificial membrane templates, are an attractive gene delivery system because of their flexibility, ease of functionalization and low cytotoxicity, and have been used to deliver DNA into human HeLa cells in tissue culture. The mechanism of cellular uptake of LNTs – via penetration or endocytosis – was unknown. In this study two different types of LNTs were utilized: LNTs synthesized from lignin isolated with NaOH and LNTs synthesized from thioglycolic acid lignin. These two types of lignin differ in their molecular weight and physic-chemical properties. The uptake mechanism was investigated in in HeLa cells and red onion epidermal protoplasts. This study demonstrated that LNTs can be internalized in HeLa cells and proptoplasts via the endocytic pathway. In HeLa cells this was shown based on the temperature dependence of the uptake and the ability of endocytosis inhibitors to prevent uptake. In plant protoplasts there is a size-dependent uptake of LNTs. Confocal microscopy revealed the cellular localization of the LNTs, and that the location is dependent on the source of the lignin used to generate the LNTs.

Keywords: nanomaterials, lignin, protoplasts, endocytosis

064 Evaluating Candidate Genes for Anthracnose Resistance in Sorghum with Virus-Induced Gene Silencing

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Sorghum bicolor is a member of the Poaceae family that is grown globally as a forage and grain crop. High stress tolerance relative to other crops makes it a good candidate for cultivation in hot climates and/or on nutrient-poor soil that are not suitable for the production of food crops. There is a growing interest in sweet sorghums for biofuel production, due to high sugar content and the fact that sorghum uses less water and nitrogen than some other common biofuel crops. Florida is amenable to sorghum production for biofuel, but a constraint to growth in the southeastern United States is the prevalence of the pathogen *Colletrichum sublineolum*, which causes the disease anthracnose in sorghum. *C. sublineolum* is a hemibiotrophic fungal pathogen that disperses through water and wind. Sorghum growers have reported large yield losses (up to 70%) due to infection with *C. sublineolum*. If sorghum is to be grown in Florida or other regions as a biofuel crop, it is important that we identify the mechanism for anthracnose resistance. A previous mapping study identified a quantitative trait locus (QTL) on chromosome 9 that contains 12 candidate anthracnose resistance genes. Virus-induced gene silencing (VIGS) will be used to evaluate the role of these genes in anthracnose resistance. Brome Mosaic Virus (BMV) will be modified to contain short fragments from each of the candidate resistance genes. After inoculating leaves of a resistant sorghum plant with the modified BMV, susceptibility to *C. sublineolum* will subsequently be monitored. The resistance mechanism will be elucidated by determining the exact function of the resistance gene(s) combined with histochemical analyses of resistant and susceptible plants.

Keywords: plant pathology, genetics, sorghum

065 **Ethylene Responses in *Azospirillum brasilense* (Azo)**

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Ethylene is a clear gas that is involved in many complicated processes in plants such as: root elongation, senescence, abscission, and fruit ripening. Ethylene also has a role in plant defense pathways in which the effects in plants are well-known. The ethylene receptors and ethylene signaling in plants has been extensively studied. However, the role of ethylene in bacteria is largely unexplored. A recent study from our lab demonstrated at least one bacterium, *Synechocystis*, contains a functional ethylene receptor. This raises the possibility that other bacteria also have ethylene receptors. The genome of one soil bacterium, *Azospirillum brasilense*, contains a putative ethylene receptor (AzoEtr1). *A. brasilense* is a nitrogen fixing proteobacterium that produces auxin and is used agriculturally to improve crop yield. In this study, we show that this putative receptor can bind ethylene and disruption of this gene affects various bacterial response such as biofilm formation and carotenoid levels. *A. brasilense* causes root remodeling in Arabidopsis thaliana as evidenced by shorter roots and increased root hair number. Disruption of AzoEtr1 changes the efficacy of *A. brasilense* to cause such remodeling. These data suggest that *A. brasilense* senses ethylene and this may affect plant-microbe interactions.

Keywords: Bacteria, ethylene, plant communication

General Poster Session

066 **Determining the Sequences Involved in *mPing* Transposition**

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University of South Carolina Aiken

Transposable elements (TEs) are segments of DNA that are mobilized from one location to another within a genome, often creating mutations. The TE we study is a 430 base pair element called *mPing*, which requires three components to be mobilized: transposase proteins (TPase and ORF1), terminal inverted repeats (TIRs) located at its extreme ends, and target site duplications (TSDs) flanking the element. The transposase proteins bind to the TIRs and TSDs of the transposable element to form the transposition complex. A mutant version of *mPing*, called *mmPing20*, was discovered from a mutagenesis strategy and has a nearly 1.5x higher transposition rate than that of *mPing*, suggesting that some or all of the seven base pair changes to the middle of the element function to promote transposition. The goal of this project is to identify the TIR sequences required for *mPing* transposition as well as determine which of *mmPing20*'s base changes are responsible for its increased transposition. ADE2 reporter constructs containing mutant and control elements were assayed in yeast to determine the transposition rates. We found that for *mPing*, all TIR bases are not equally necessary for transposition to occur. Highly conserved bases are more critical to the formation of the transposition complex. We expect that *mmPing20* transposition rates will be adversely affected after mutation of any of its transposition promoting base pairs. Combined, these results assist in providing a clearer picture of the role of the TIR and internal sequences in formation of the active transposition complex necessary for *mPing* transposition.

Keywords: transposable elements, *mPing*, mutagenesis, DNA, transposition

067 **Testing Strategies to Produce Targeted Insertion of *mPing***

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My project focuses on *mPing*, a 430bp miniature inverted repeat transposable element from rice that can move from one place to another within the genome. The goal of my research is to produce targeted insertion of the transposable element *mPing* in yeast by connecting the TPase protein to a DNA binding domain that recognizes a specific target sequence. Our strategy is to use the dCas9 DNA binding domain because of its high specificity for the target site, which is regulated by a guide RNA. In previous research, a dCas9/TPase fusion protein did not produce targeted insertion, possibly due to protein miss-folding or steric hindrance. To test this hypothesis, we plan to use a dCas9-Gal 11P fusion protein, which will bind with a Gal4(58-97)-TPase fusion protein. Thus, targeted mutagenesis will be achieved through a guide RNA (gRNA) directing dCas9 to the target site, resulting in the dCas9/TPase complex being recruited to the desired DNA site, encouraging *mPing* to insert near the target site. A yeast intron was added between the dCas9 and the Gal 11P domains in order to allow propagation of the construct in bacteria. We propose that if dCas9-Gal 11P and Gal4(58-97)-TPase fold correctly and interact, they will function together to produce targeted insertion. We will insert the fusion protein constructs into yeast to test the transposition rate of mPing using a yeast transposition assay. We predict that although transposition will be lower than controls, we will see an increase of insertions of *mPing* into the target site.

Keywords: *mPing*, transposable elements, transposition

068 **Possible Suppression of *Salvinia molesta* by Allelopathy of two Waterlilies, *Nymphaea mexicana* and *Nymphaea odorata***

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The allelopathic potential of two waterlily species, *Nymphaea odorata* and *Nymphaea mexicana*, was tested as a possible growth suppressant for the invasive species *Salvinia molesta*. *Salvinia molesta*, originally from Brazil, has spread throughout the Southeast United States. Aquatic plants and animals below *Salvinia* mats suffer reduced light and oxygen availability. *Salvinia* replaces native plants and reduces biodiversity. Its presence leads to significant financial losses associated with commercial and recreational fishing, hunting, and boating. To assess whether waterlilies native to the United States influence *Salvinia* growth, assays with live plants and chemical extracts were performed. For the live-plant assay, *Salvinia* and the waterlily species were grown together in buckets for a week, and the change in weight was assessed and compared between *Salvinia* that was grown in the presence of the waterlilies and in their absence. For the extract assay, *Salvinia* was exposed to varying concentrations of waterlily extracts for one week, and the change in weight was determined and compared across treatments and controls with no extracts. Qualitative assessment of the health also was made based on the condition of the leaves. In the live-plant and extract assays, the waterlilies did not suppress *Salvinia* growth; however, in the extract assays, the highest concentration of *N. odorata* pads and stems led to a reduction in *Salvinia* health, indicated by the onset of leaf death. While growth was not impacted, this study provided evidence that *N. odorata* extracts may be able to suppress *Salvinia* via allelopathy. Future experimentation is needed to assess whether longer exposure times to extracts can reduce *Salvinia* growth, how natural concentrations of *N. odorata* released in the field compare to those used in the lab, and whether the dose used here can negatively impact field populations of *Salvinia* without causing negative consequences for the rest of the ecosystem.

Keywords: allelopathy, *Salvinia*, *Nymphaea*, invasive species

069 **Naturally-occurring high oleic acid cottonseed oil: identification and functional analysis of a mutant allele of *Gossypium barbadense* fatty acid desaturase-2**

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Vegetable oils are broadly used in the manufacture of many industrial and nutritional products. Cottonseed oil is a valuable co-product derived from the processing of cottonseed fiber. In the past, it was used in a variety of food applications. In recent years, cottonseed oil has lost market share due to poor monounsaturate/polyunsaturate ratios in either native or partially hydrogenated oil. Consumer resistance towards genetically modified foods or products containing trans-fats has created strong demand for a naturally-occurring oil with high oleate levels along with reduced polyunsaturated fatty acids. We discovered multiple exotic accessions of pima cotton that contain elevated seed oil oleate content. The genome of one accession was sequenced, and a candidate mutant fatty acid desaturase-2 (fad2-1d) gene was identified. The mutant protein produced significantly less linoleic acid in infiltrated Arabidopsis leaf assays, compared to a repaired version of the same enzyme. Markers associated with this gene locus will

be useful in efforts to breed agronomic fiber accessions of pima and upland cotton that also contain the elevated oleic acid trait.

Keywords: oleic acid, linoleic acid, cotton, desaturase, trans-fats

070 **Arabidopsis transcriptome in the face of hypobaria, a novel abiotic stress**

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Extreme hypobaria (low atmospheric pressure) is a novel abiotic stress that is outside the evolutionary experience of most organisms. Plants adjust to hypobaric stress by inducing and suppressing suites of genes in unique combinations that are not equal to hypoxia. Although these initial strategies appear to enable plants to survive even severe hypobaric conditions, how plants deal with individual components of hypobaria at the genomic level is largely unknown.
A severe reduction in atmospheric pressure from a near-sea level pressure of 97 kPa to 5 kPa is accompanied by the differential expression of hundreds of genes. However, the transcriptome reaction to hypobaric conditions lying between these two extremes reveals subtle and complex responses. Excursions into even mild reductions in atmospheric pressure elicit a wide range of responses in gene expression profiles, yet a linear reduction of atmospheric pressure does not elicit a response characteristic of a simple gradient of severity. It is also clear that plants adjust over time; the complex differential gene expression patterns that were initially engaged to cope with hypobaria were mediated as plants renormalize their metabolism to this new environment. Further, comparisons between plants of different ages in response to atmospheres of varying pressure and oxygen composition indicated that plant hypobaric responses can be both tissue-specific and age-dependent.
The patterns of genome-wide gene expression changes across a gradient of atmospheric pressures, over a time course of several days and upon varying oxygen composition in plants of different ages allowed for the development of theories of how plant metabolism may be adapting to changes in atmospheric pressures in these plants. But perhaps more importantly, it provided insight into how adaptations to novel environments in general proceed – how plants may dissect new stresses and how they cope on the genetic level with a stimulus that does not have a fully developed receptor.

Keywords: hypobaria, hypoxia, low atmospheric pressure, Mars greenhouse, transcriptome

071 **Helping Students Understand How DNA Mutations Cause a Phenotype by Incorporating Computational Molecular Modeling into the Classroom**

Tara Phelps-Durr

Radford University

As a 2014 recipient of ASPB's Master Educator Program award I attended the National Center for Case Study Teaching in Science Summer Workshop and developed teaching laboratory activities that use computational molecular modeling software to help students visualize the three-dimensional (3D)

structure of proteins. The series of laboratory activities specifically helps students understand how mutations in DNA causes changes in the 3D structure of a protein and how these changes in protein structure result in a mutant phenotype. The activities begin with students comparing the phenotypes of ASYMMETRIC LEAVES 1 and 2 (AS1 and 2) mutants to normal Arabidopsis plants. Students then analyze the sequences of the AS1 and AS2 genes from the normal, as1 and as2 mutant plants to discover the DNA sequence changes that cause the mutant phenotypes. The sequence of the mutant proteins are generated by examining the DNA sequence of the mutant genes. The 3D structure of the normal and mutant proteins are generated by submitting the amino acid sequence to a free online protein modeling program. Students then visualize, manipulate and compare the 3D protein models using freely available molecular modeling software. Within the software the normal and mutant proteins can be superimposed to help students visualize the structural differences between the proteins. The protein models can be 3D printed to further help the students visualize the structural differences between normal and mutant proteins. At the end of these activities, students write a laboratory report and are assessed on their ability to describe how mutations in DNA cause changes in the corresponding RNA and protein and how these changes lead to the mutant phenotype.

Keywords: Molecular Modeling, Pedagogy

Sponsor Presentation

072 **Phenotyping Solutions for Basic and Applied Research in Plant Biology and Agriculture**

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Humans have been phenotyping plants for over 10,000 years. Beginning with the domestication of agricultural crops, plant phenotyping is the cornerstone for improving agronomic traits that increase yield. The demand for phenotyping has increased dramatically in recent decades as the exponential accumulation of genome data has accelerated our ability to breed and modify crop species. However, the ability to rapidly and reliably phenotype plants continues to be a bottleneck in the development of next generation products. This is a challenge that cuts across research areas, including breeding, ag chemistry, biotechnology, and biologicals. LemnaTec's Scanalyzer suite of products provide researchers and breeders with a variety of high-resolution imaging sensors that enable them to reliably phenotype plants for the discovery and development of new agriculture products. Our Scanalyzer products range in terms of scale and throughput to meet the needs of individual researchers, but all are capable of accurately measuring plant features that are crucial for yield in the field such as leaf area, chlorophyll content, plant height, growth rate, stress response, tip burn, biomass, drought tolerance, and many more. This presentation will describe LemnaTec phenotyping applications in laboratory, greenhouse, and field settings, and will discuss how the results are being used for basic and applied research programs.

Keywords: Phenotyping; Imaging; Agriculture; Basic Research; Phenomics; High Throughput; Agronomic Traits

073 **Establishment of Heterochromatin: How the cell recognizes and triggers transposable elements for trans-generational silencing**

R. Keith Slotkin

Department of Molecular Genetics and the Center for RNA Biology, The Ohio State University

The Slotkin laboratory investigates the epigenetic regulation of transposable elements (TEs) in the reference plant Arabidopsis. Our emphasis is on determining how the cell recognizes a new or active TE, how it deciphers the TE from an active gene, and how epigenetic TE silencing is initiated and established. Research has focused on two core projects: the small RNA-directed chromatin modification mechanisms responsible for the initiation of epigenetic silencing (the 'non-canonical' RNA-directed DNA methylation pathways), and second how germ cells and their neighboring nurse cells communicate to ensure that TEs are epigenetically marked and silenced from the very first cell of the next generation. In this presentation, recent unpublished data will be presented demonstrating the mechanisms responsible for the initiation of TE silencing and the establishment of heterochromatin.

074 **Epigenetic regulation of gene expression in maize.**

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In maize, a genetic approach has revealed *cis* and *trans* factors involved in epigenetic gene silencing, leading to the characterization of several proteins that appear to function in RNA-directed DNA methylation and gene silencing. In Arabidopsis and maize, it is clear that one major function of this pathway is transcriptional regulation of transposable elements. There are also many protein coding genes that are mis-regulated in maize mutants, contributing to complex gene expression phenotypes that could be caused by direct and indirect effects of defective silencing pathways. Ongoing work in the McGinnis Lab focuses on the mechanistic relationships between RNA-directed silencing and regulation of gene expression; recent progress from various approaches will be described.

075 **Molecular mechanisms of interplay between ethylene signaling and chromatin regulation in Arabidopsis**

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My research is focus on how plant hormones affect plant growth and plant abiotic stress response. Ethylene is one of the most important plant hormones. It plays pleotropic roles in many aspects of plant life. A model for hormone signaling has emerged in which the perception of ethylene by the receptors alters the activity of CTR1, which in turn, by an unknown mechanism, functions to relieve repression of EIN2, resulting in activation of EIN3/EIL1-dependent transcription and the activation of an ethylene response. Our recent studies have revealed that EIN2 mediates transmission of ethylene signaling that originates at the endoplasmic reticulum membrane to the nucleus and that the EIN2 C-terminus is cleaved and translocated to the nucleus to initiate the ethylene response. However, the molecular mechanism that nuclear translocation of EIN2, the function of EIN2 C-terminal end in the nucleus and how EIN2 C-terminal end communicate with EIN3 are not understood. We recently found

that ethylene specifically elevated acetylation of histone H3K14 and the non-canonical acetylation of H3K23. The up-regulation is positively associated with a set of ethylene regulated transcription activation, and the elevation requires EIN2 and partially EIN3/EIL1. Both EIN2 and EIN3 interact with a SANT domain protein EIN2 Nuclear Associate Protein ENAP1 (ENAP1), of which over expression result in elevation of Histone acetylation. These findings reveal that in the presence of ethylene, EIN2 C-terminus is involved in the regulation of the elevation of acetylation at H3K14 and H3K23. In addition, our study reveals that the plant hormone ethylene induces combinatorial effects of H3K9Ac, K14Ac and K23Ac histone acetylation in gene expression genome widely. Further, for a group of ethylene regulated genes, in the absence of ethylene the levels and the covered breadth of H3K9Ac are the preexist markers for distinguishing up- and down- regulated genes, the change in the levels of H3K14Ac and H3K23Ac are required for the alteration of gene expression in the presence of ethylene.

076 **Large-Scale Heterochromatic Remodeling Facilitates DNA Repair**

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Arabidopsis pericentromeric heterochromatin is condensed into structures called chromocenters that are enriched in histone H3 lysine 27 monomethylation (H3K27me1). Previously, we have shown that this mark is deposited by the homologous proteins ARABIDOPSIS TRITHORAX RELATED 5 (ATXR5) and ATXR6. We have used loss of function and gain of function mutants in these two proteins to investigate the role of H3K27 methylation in chromatin structure and gene regulation. *atxr5,6* double mutants show a loss in H3K27me1 that results in the over replication of heterochromatin. This over replication results in DNA damage and extensive chromocenter remodeling into unique structures we have named Over Replication-Associated Centers (RACs). Super-resolution microscopy shows that RACs have a highly ordered structure, with an outer layer of condensed heterochromatin, an inner layer enriched in the histone variant H2Ax, and a low-density core containing foci of phosphorylated H2Ax (a marker of double-strand breaks) and the DNA-repair enzyme RAD51. These results suggest a novel mechanism for heterochromatic DNA-damage repair that involves large-scale chromatin remodeling. Using gain-of-function mutants in ATXR5/6, we are able to replace heterochromatic H3K27me1 with H3K27me2 or H3K27me3. In this way, we have been begun to investigate the functional significance of H3K27 methylation level on chromatin structure, DNA replication, and gene regulation.