



# 2023 MEETING OF THE SOUTHERN SECTION OF THE AMERICAN SOCIETY OF PLANT BIOLOGISTS

March 25-27<sup>th</sup>  
Fayetteville, Arkansas  
at the  
HILTON GARDEN INN FAYETTEVILLE

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## PROGRAM-Schedule

<b>Saturday, Mar 25<sup>th</sup></b>		
		<b>Room</b>
2:00 – 6:00 pm	<b>Meeting Registration</b>	Lobby-Redbud
2:00 – 5:30 pm	<b>Poster Setup</b>	Redbud
5:30 – 5:45 pm	<b>Welcome Session</b> – Message from <b>Chair-Ashlee McCaskill</b> and <b>Nathan McKinney</b> <i>Associate Vice President for Agriculture and Assistant Director of the Arkansas Agricultural Experiment Station</i>	Redbud
5:45 – 7:15 pm	<b>General Session 1</b> – Faculty Presenters – <b>Moderator Colleen Doherty</b>	Redbud
5:45-6:15	<i>“Comparative Genomics as a Tool for Discovering Missing Vitamin Metabolic Genes in Plants” Hasnain Ghulam, University of North Georgia</i>	
6:15-6:45	<i>“Genome-wide Association Study and Genomic Prediction of Disease Resistance in Spinach” Ainong Shi, University of Arkansas</i>	
6:45-7:15	<i>“Using Structural Modeling and in Planta Complementation Studies to Unravel the Alternating-Access Mechanism in Plant NPFs” Antonella Longo, University of North Texas</i>	
7:15 – 8:30 pm	<b>Opening Night Mixer and Networking Event</b>	Redbud
8:30 – 9:30 pm	<b>Executive Committee Meeting</b>	
<b>Sunday, Mar 26<sup>th</sup></b>		
6:30 – 8:00 am	<b>Breakfast and Poster Setup</b>	
8:00 – 8:15 am	<b>Opening Session &amp; Welcome</b>	Redbud
8:15 – 8:25 am	<b>UADA and UARK Welcome &amp; Remarks</b>	Redbud
8:30 – 10:00 am	<b>General Session 2</b> - Faculty and Postdoctoral Presenters - <b>Moderator</b>	Redbud
8:30-9:00	<i>“Towards Understanding Heat Stress Tolerance in Rice Using a Chromosomal Segment Substitution Library” Jai Rohila, USDA-ARS</i>	
9:00-9:20	<i>“Rice Can Grow and Survive in the Martian Regolith” Abhilash Vakkada Ramachandran, University of Arkansas</i>	
9:20-9:40	<i>“In-silico analysis of rice Target of Rapamycin (TOR) mutations generated by CRISPR/Cas9 targeted mutagenesis”</i>	

	<i>Chandan Maurya, University of Arkansas, System Division of Agriculture</i>	
9:40-10:00	<i>"Arabidopsis telomerase takes off: uncoupling telomerase activity from telomere maintenance in space" Borja Barbero Barcenilla, Texas A&amp;M University</i>	
10:00 – 10:30 am	<b>Break</b> (coffee and tea)	Lobby-Redbud
10:30 –12:00 pm	<b>Concurrent Session 1A and B: Student Presenters</b>	
	<b>Concurrent Session 1A - Moderator</b>	Dogwood
10:30-10:45	<i>"Investigating the molecular mechanisms regulating growth promotion and salt tolerance during interactions between rice and plant growth-promoting bacteria, Azospirillum brasilense" Seth Dixon, University of Central Arkansas</i>	
10:45-11:00	<i>"trans-Zeatin N-Glucosides Regulate Salt-Induced Leaf Senescence in Arabidopsis thaliana" Risheek Rahul Khanna, Auburn University</i>	
11:00-11:15	<i>"Elucidating the Role of Major Transcription Factors in Regulating Drought Stress in Arabidopsis thaliana" Doni Thingujam, University of Alabama at Birmingham</i>	
11:15-11:30	<i>"Continuous Mowing Differentially Affects Floral Defenses in the Noxious and Invasive weed Solanum elaeagnifolium in its Native Range" Alejandro Vasquez Marcano, University of Arkansas</i>	
11:30-11:45	<i>"Assessing the Physiological Response of Arkansas Native Plant Species Treated with Common Roadside Herbicides" Rachel Woody-Pumford, University of Arkansas</i>	
11:45-12:00	<i>"Inspiring the Next Generation of Plant Scientists: How to Design Professional Development Workshops to Increase Plant Science in U.S. Classrooms" Regina Bedgood, University of Alabama at Birmingham</i>	
	<b>Concurrent Session 1B - Moderator</b>	Apple Blossom
10:30-10:45	<i>"IBR5-Mediated Regulation of Plant Auxin Response through the SCFTIR1 Complex" Emran Hossain Sajib, Texas State University</i>	
10:45-11:00	<i>"Characterization of a Putative GATA Element and Analysis of Its Role in Starch Biosynthesis Transcriptional and Metabolic Activities" Peter James Gann, University of Arkansas</i>	
11:00-11:15	<i>"Organophosphonate Recycling" Precious Richard, University of Arkansas at Little Rock</i>	
11:15-11:30	<i>"Enzyme Activity in Soil Growing Cereal Grain Crops" Torri Holder, University of Arkansas</i>	
11:30-11:45	<i>"Identification of Quorum Sensing Bacteria from the Plant-associated Microbiome of Plants Grown Aboard the International Space Station"</i>	

	<i>Tyler DeScenza, Florida Institute of Technology</i>	
11:45-12:00	<i>“Genome-wide Association Study and Genomic Prediction of Fusarium Wilt Resistance in Common Bean Core Collection” Kenani Chiwina, University of Arkansas</i>	
12:00 – 1:00 pm	<b>Lunch</b>	Redbud
1:00 – 2:30 pm	<b>Undergraduate Poster Session</b>	Redbud
2:30 – 3:30 pm	<b>Concurrent Session 2 A and B: Student Presenters</b>	
	<b>Concurrent Session 2A - Moderator Borja Barbero Barcenilla</b>	Dogwood
2:30-2:45	<i>“Evaluating the Use of Aquatic Plants in Martian Agriculture “ Sergio Solano, Florida Institute of Technology</i>	
2:45-3:00	<i>“Bax Inhibitor-1 Associates with AtIRE1A to Modulate Cytoprotective Signaling Pathway in Arabidopsis Immunity “ Danish Diwan, University of Alabama at Birmingham</i>	
3:00-3:15	<i>“Investigating the Importance of Sumoylation for Appressorium Morphogenesis by the Blast Fungus Magnaporthe oryzae“ Rachel Taylor, University of Arkansas</i>	
3:15-3:30	<i>“Conditioning Mars for Plant Growth: Anabaena cylindrica” Hayley Murphy, Florida Institute of Technology</i>	
	<b>Concurrent Session 2B - Moderator Andrew Palmer</b>	Apple Blossom
2:30-2:45	<i>“Function of Auxin Signaling Pathway in Thermomorphogenesis of Arabidopsis” Heshini Weerakkody, Texas State University</i>	
2:45-3:00	<i>“Exploring the Potential of N-glucoside Forms of Cytokinin in Delaying Leaf Senescence” Omar Hasannin, Auburn University</i>	
3:00-3:15	<i>“Investigating the Role of the Septin Cytoskeleton in Invasive Cell-to-Cell Movement by the Blast Fungus Maganporthe oryzae” Brooklynn Rogers, University of Arkansas</i>	
3:15-3:30	<i>“The Comprehensive Application of Multiplexing Techniques into Plant Research at Single-nucleus and Spatial Transcriptomics Level“ Jinbao Liu, University of Alabama at Birmingham</i>	
3:30 – 4:00 pm	<b>Break</b> (coffee and tea)	Redbud
4:00 – 5:40 pm	<b>General Session 3: ASPB Ambassadors &amp; Post-doctoral Presenters - Moderator Kent Chapman</b>	Redbud
4:00-4:20	<b>ASPB Ambassadors</b>	
4:20-4:40	<i>“Stay FLAT or BUCKLE? The causes and consequences of mechanical buckling in Arabidopsis sepals” Avilash Singh Yadav, Cornell University</i>	
4:40-5:00	<i>“Overexpression of the Transcription Factor HYR in Rice Improves Grain Yield and Grain Quality under Drought and High Temperature Stress Conditions”</i>	

	<i>Yheni Dwiningsih, University of Arkansas System Division of Agriculture</i>	
5:00-5:20	<i>“Role of HR4 and its Interactors in Arabidopsis Defense Towards the Green Peach Aphid, Myzus persicae” Anil Girija, University of North Texas</i>	
5:20-5:40	<i>“From Multiple-Cell to Single-Cell Genetics Models: The Arabidopsis Orphan Gene QQS Modulates Carbon and Nitrogen Allocation Across Species” Lei Wang, Mississippi State University</i>	
5:40 – 6:50 pm	<b>Graduate Student &amp; Professionals Poster Session</b>	Redbud
7:00 – 8:30 pm	<b>Banquet and Awards Presentations – Henry Daniell Award</b>	Redbud
<b>Monday, March 27th</b>		
6:30 – 8:00 am	<b>Breakfast and Poster Take-down</b>	
8:00 – 8:10 am	<b>Kriton Hatzios Symposium: Introduction</b>	Redbud
8:10 – 10:10 am	<b>Hatzios Symposium - Moderator Colleen Doherty</b>	
	<i>“Enabling extended planetary exploration with ISRU - plants grown in Apollo lunar regolith mount site-specific transcriptome responses” Dr. Anna-Lisa Paul, University of Florida</i>	
	<i>“Could Polyamines Mitigate Plant Stress Responses to Spaceflight Conditions?” Dr. Patrick Masson, University of Wisconsin-Madison</i>	
10:10 – 10:30 am	<b>Break (coffee and tea)</b>	
10:30 – 11:30 am	<b>Hatzios Symposium: continued</b>	
	<i>“Synthetic biology on the lunar surface” Dr. Mark Settles, NASA (Virtual)</i>	
11:30– 12:00 pm	<b>General Meeting &amp; Concluding Remarks</b>	

# Meeting Abstracts

## Oral Presentation Abstracts

### Session 1

#### **Comparative Genomics as a Tool for Discovering Missing Vitamin Metabolic Genes in Plants**

\*Hasnain, Ghulam, Department of Biology, University of North Georgia

Metabolic reconstruction and modeling rapidly highlight genes missing from metabolic networks or genes that lack matching networks, and so can guide function discovery using comparative genomics approaches. These approaches exploit the wealth of prokaryotic and plant genomes, gene expression datasets, and other post-genomic resources to predict candidates for missing genes and to join new genes to metabolic networks. Predicted functions can often be experimentally validated in prokaryote models, providing an efficient entry to understanding plant pathways.

The concepts of metabolite damage and repair are new and at the frontier of metabolic research. Metabolite damage arises because enzymes in all organisms, although regarded as specific, in fact frequently make mistakes that lead to toxic damage products. Such products can also arise from spontaneous chemical side reactions of metabolites. Genetic and genomic evidence from prokaryotes and eukaryotes has implicated a network of conserved enzymes that repair damaged metabolites. Understanding damage and repair processes is foundational to interpreting and manipulating metabolism, and knowledge of such systems is very important for successful biotechnology applications.

#### **Genome-wide Association Study and Genomic Prediction of Disease Resistance in Spinach**

\*Ainong Shi<sup>1</sup>, Gehendra Bhattarai<sup>1</sup>, Haizheng Xiong<sup>1</sup>, Carlos A. Avila<sup>2</sup>, Bo Liu<sup>3</sup>, Vijay Joshi<sup>4</sup>, Larry Stein<sup>4</sup>, Beiquan Mou<sup>5</sup>, Lindsey J. du Toit<sup>6</sup>, James C. Correll<sup>3</sup> <sup>1</sup>Department of Horticulture, University of Arkansas, Fayetteville, AR 72701, USA; <sup>2</sup>Department of Horticultural Sciences, Texas A&M AgriLife Research and Extension Center, Weslaco, TX, USA; <sup>3</sup>Department of Plant Pathology, University of Arkansas, Fayetteville, AR 72701, USA; <sup>4</sup>Texas A&M AgriLife Research and Extension Center, Uvalde, TX 77801, USA; <sup>5</sup>Crop Improvement and Protection Research Unit, USDA-ARS, Salinas, CA 93905, USA; and <sup>6</sup>Washington State University, Mount Vernon, WA 98273, USA

Downy mildew (*Peronospora effusa*), white rust (*Albugo occidentalis*), Fusarium wilt (*Fusarium oxysporum* f. sp. *spinaciae*), Stemphylium leaf spot (*Stemphylium vesicarium* and *S. beticola*), and Pythium root-rot and dumpling off (*Pythium* species) are major yield-limiting diseases of spinach (*Spinacia oleracea*). The use of host resistance is the most economical and environment-friendly approach to manage these diseases in spinach production. The objectives of this study were to evaluate disease resistance, to conduct a genome-wide associating study (GWAS) to identify single nucleotide polymorphism (SNP) markers associated with disease resistance, and to perform genomic prediction (GP) to estimate the prediction accuracy (PA) for selecting disease resistance in spinach. Several GWAS panels with over 300 spinach genotypes each were phenotyped in greenhouse and field conditions and genotyped with millions of SNPs generated from 2nd-generation DNA sequencing technologies. GWAS was performed using

TASSEL 5 and GAPIT 3 tools and GP by BLUP and Bayesian models. So far, dozens of germplasm lines were observed; SNP markers and candidate genes were identified; and highly PA was estimated for the resistance in each of the five diseases in spinach. The SNP markers and the high PA will provide breeders with robust tools to improve selection for resistance to the five economically important diseases of spinach through marker-assisted selection and genomic selection in spinach breeding programs.

### **Using Structural Modeling and in Planta Complementation Studies to Unravel the Alternating-Access Mechanism in Plant NPFs**

Longo\*, Antonella; Yu, Yao-Chuan; Dickstein, Rebecca

Department of Biological Sciences and BioDiscovery Institute, University of North Texas, Denton, TX, United States

Symbiotic nitrogen fixation is a complex and regulated process that takes place in root nodules of legumes and allows legumes to grow in soils that lack nitrogen. The mechanism(s) by which legumes modulate nitrate uptake to regulate nodule symbiosis remain unclear. In *Medicago truncatula*, the nitrate transporter MtNPF1.7 has been shown to control nodulation, symbiosis, and root architecture. MtNPF1.7 belongs to the nitrate/peptide transporter family and is a symporter with nitrate transport driven by proton(s). The proposed mechanism of transport for NPFs is based on the alternating-access model. In the evolutionary related bacterial POTs, two sets of salt bridges were proposed to form alternatively in the outward-open (Oo) or inward-open conformations (Io). In NPFs only one set of residues is conserved for a putative Oo salt bridge. We carried out in planta complementation of the severely defective *mntip-1* mutant plants with mutants of the Oo salt bridge forming residues (1). Based on our results we question the existence of the salt bridge in the Oo conformation. Recent cryo-EM structures of the evolutionarily related mammal PepTs in the Oo (2), available after our publication, revealed that the two residues predicted to form the Oo salt bridge are not at a minimum donor-acceptor distance in the apo-proteins validating our observation for MtNPF1.7.

(1) Yu, et al., *Front. Plant Sci.*, doi:10.3389/fpls.2021.685334.

(2) Parker, et al., *Sci. Adv.*, doi:10.1126/sciadv.abh3355.

## **Session 2**

### **Towards Understanding Heat Stress Tolerance in Rice Using a Chromosomal Segment Substitution Library**

Rohila\*, Jai, Dale Bumpers National Rice Research Center, United States Department of Agriculture - Agricultural Research Services, Stuttgart, USA

Rice is an important cereal crop for world's food security. Increasing ambient temperatures during recent years have shown that it is sensitive to heat stress and as a result the rice produced has lower grain yield and quality, and eventually affect agricultural or bioeconomy of the US, and food security around the globe. To understand the complex stoichiometry of rice and ambient temperatures during cropping season we conducted some in-silico analysis and a two-year field study using a chromosomal segment substitution library (N=121) developed from

a cross between heat stress susceptible parent (cv. Lemont) and comparatively heat stress tolerant parent (cv. TeQing). The in-silico results revealed a diurnal effect of heat stress where daytime and nighttime temperatures found differentially affecting yield and quality traits. The two-year replicated field study revealed that cv. TeQing harbors multiple interesting genomic regions associated with multiple thermotolerant mechanisms and thus improving rice performance for yield and quality of cv. Lemont, a premium US rice cultivar under increased ambient temperatures. Considering a narrow genetic base of US rice varieties, identified thermotolerant genetic loci (QTL) could be useful to increase performance of the US rice varieties under changing climate. Moreover, identified QTLs are novel targets for fine mapping experiments, and towards understanding and increasing climate resiliency of rice crop under climate change.

### **Rice Can Grow and Survive in the Martian Regolith**

Gann, Peter James, Cell and Molecular Biology Program and Department of Crop, Soil and Environmental Sciences, University of Arkansas, Fayetteville, Arkansas, USA; Vakkada Ramachandran\*, Abhilash, Arkansas Center for Space and Planetary Sciences, University of Arkansas, Fayetteville, Arkansas, USA; Dwiningshi, Yheni, Department of Crop, Soil and Environmental Sciences, University of Arkansas, Fayetteville, Arkansas, USA; Dharwadker, Dominic, Department of Chemistry and Biochemistry, University of Arkansas, Fayetteville, Arkansas, USA; Srivastava, Vibha, Cell and Molecular Biology Program and Department of Crop, Soil and Environmental Sciences, University of Arkansas, Fayetteville, Arkansas, USA

As space exploration advances, the importance of tapping resources from other planets, known as In-Situ Resource Utilization (ISRU), becomes increasingly vital to reduce the cost of resupply missions. On Mars, resources such as water, regolith, light, and CO<sub>2</sub> can be used to grow food, and previous studies have demonstrated the possibility of growing plants such as *Arabidopsis thaliana* in Martian regolith simulants such as JSC-1 and MMS-1. This study focuses on the development, impact on stress related genes, and the survivability of OsSnRK1a and OsTOR mutants of rice plants grown in MMS1. Results showed that plants grown in pure MMS1 had stunted growth, poor root morphology, and lower photosynthetic activity, but the addition of any proportion of PM in MMS1 improved growth and root characteristics compared to 100% MMS1. While the rice plants showed signs of stress in MMS1, the study suggests that the physical and chemical characteristics of MMS1 can support their growth, provided the levels of Mg(ClO<sub>4</sub>)<sub>2</sub> are kept in check. Additionally, the study provides evidence that rice plant with OsSnRK1a mutation has the potential to germinate in MMS1 with low levels of Mg(ClO<sub>4</sub>)<sub>2</sub>. Overall, the results demonstrate that it is possible to grow rice plants in Martian regolith, and the growth can be improved by amending the soil with potting mix. More studies are needed to determine if rice growth on Martian soil can be improved through gene editing.

### **In-silico analysis of rice Target of Rapamycin (TOR) mutations generated by CRISPR/Cas9 targeted mutagenesis.**

Maurya\*, Chandan, and Srivastava, Vibha, Department of Crop, Soil & Environmental Sciences, University of Arkansas System Division of Agriculture, Fayetteville, AR, USA



Target of Rapamycin (TOR) is an evolutionarily conserved protein kinase that regulates metabolism in response to energy. However, only limited information is currently available on its phosphorylation targets in plants. Knockout mutations in TOR are embryo-lethal, however, we could develop two independent in-frame deletions in rice TOR (OsTOR) kinase (ostor<sup>Δ3</sup> and ostor<sup>Δ9</sup>) that impacted plant growth under energy-sufficient condition. In high sucrose environment, these mutants generated lower biomass, while no significant changes were observed in the low sucrose environment. In-silico analysis was carried out towards understanding how <sup>Δ3</sup> and <sup>Δ9</sup> in-frame deletions could affect TOR activity. The phosphoryl transfer from the ATP bound to the catalytic residue to the substrate is a core part of kinase activity, and Mg<sup>++</sup> plays an important role in making the ATP tail available for the transfer. The 3D protein analysis showed that the catalytic site was unchanged in <sup>Δ3</sup> and <sup>Δ9</sup> OsTOR but Mg<sup>++</sup> binding was altered. Specifically, Mg<sup>++</sup> binding occurred in the catalytic site of the WT but not in the catalytic sites of <sup>Δ3</sup> and <sup>Δ9</sup> models. Accordingly, RNA-Seq showed changes in the key pathways regulated by TOR, including ribosome biogenesis, primary metabolism and secondary metabolic pathways in the two mutants. Overall, these observations indicate that TOR signaling is mis-regulated in the two mutants possibly due to structural changes that affect Mg<sup>++</sup> binding with the catalytic residues.

### **Arabidopsis telomerase takes off: uncoupling telomerase activity from telomere maintenance in space**

Barbero Barcenilla\*, Borja, Department of Biochemistry and Biophysics, Texas A&M University; Meyers, Alexander, Department of Experimental and Plant Biology, Ohio University; Castillo-Gonzalez, Claudia, Department of Biochemistry and Biophysics, Texas A&M University; Min, Ji-Hee, Department of Biochemistry and Biophysics, Texas A&M University; Padke, Chinmay, Department of Biochemistry and Biophysics, Texas A&M University; Land, Eric, Department of Plant and Microbial Biology, North Carolina State University; Perera, Imara, Department of Plant and Microbial Biology, North Carolina State University; Aquilano, Roberto, Faculty of Exact Sciences, Engineering and Surveying, National University of Rosario/CONICET; Canaday, Emma, Department of Experimental and Plant Biology, Ohio University; Wyatt, Sarah, Department of Experimental and Plant Biology, Ohio University; Shippen, Dorothy, Department of Biochemistry and Biophysics, Texas A&M University

To realize NASA's goal of human space colonization, plants will be required for food production, carbon dioxide removal and oxygen generation. Understanding plant adaptation to spaceflight is essential for space expansion. Transcriptomic data show space flown plants upregulate multiple stress response pathways, including genomic and oxidative stress. Telomeres are essential structures that safeguard genome stability and are an important biological marker of survivability. Recent studies reveal that astronauts aboard the ISS experienced an increase in telomere length, but the cause is unknown. Here we explore the impact of spaceflight on telomere dynamics and telomerase activity in Arabidopsis. We report that telomerase activity was dramatically elevated in space-flown plants. Spaceflight also led to increased 8-oxoguanine content in DNA and increased mitochondrial and chloroplast DNA, consistent with oxidative stress. Interestingly, telomere length was unaltered by spaceflight. The mechanism for telomerase induction and elevated oxidative stress during spaceflight is unclear, as neither parameter is altered by simulated microgravity. We postulate that excess telomerase accumulates during spaceflight is commandeered to mitigate the impact of oxidative damage on the genome and organelles. The inherent capacity of plants to maintain telomere

homeostasis under the stress of space flight conditions may enhance their generational survival for space exploration and colonization.

## **Concurrent Session 1A**

### **Investigating the molecular mechanisms regulating growth promotion and salt tolerance during interactions between rice and plant growth-promoting bacteria, *Azospirillum brasilense***

Dixon\*, Seth, Department of Biology, University of Central Arkansas; Degon, Zachariah, Department of Biology, University of Central Arkansas; Hoggard, Samuel, Department of Biology, University of Central Arkansas; Price, Hunter, Department of Biology, University of Central Arkansas; Mukherjee, Arijit, Department of Biology, University of Central Arkansas

Major food crops, such as rice and maize, display severe yield losses (50-80%) under moderate to extreme salinity. Problems associated with soil salinity are anticipated to worsen because of adverse climatic conditions. For improving crop performance under saline conditions, it is necessary to implement sustainable agricultural strategies. One option is to take advantage of beneficial plant-microbe associations. Plants can form associations with different beneficial microbes including, arbuscular mycorrhiza, rhizobia bacteria, plant growth-promoting bacteria (PGPB). Several studies have suggested that PGPB improve plant growth via multiple mechanisms, including nitrogen fixation, hormone synthesis, protection against biotic and abiotic stresses, etc. *Azospirillum brasilense* is one of the most studied PGPB to mitigate salinity stress in different crops such as maize and wheat. However, not much is known about the molecular mechanisms by which *A. brasilense* mitigates salt stress. Recently, we optimized an experimental system where rice growth was improved in *A. brasilense*-inoculated plants compared to the uninoculated plants grown under high salt concentrations. Furthermore, we performed an RNA-seq experiment to identify the transcriptomic responses in rice plants during *A. brasilense*-mediated salt stress tolerance. Our results suggest that *A. brasilense* modulates the expression of key genes to improve rice growth under salt stress.

### **trans-Zeatin N-Glucosides Regulate Salt-Induced Leaf Senescence in *Arabidopsis thaliana***

Khanna\*, Rishiek Rahul, Department of Biological Sciences, Auburn University, Auburn, AL, USA; Hasannin, Omar, Department of Biological Sciences, Auburn University, Auburn, AL, USA; Rashotte, Aaron M., Department of Biological Sciences, Auburn University, Auburn, AL, USA

Abiotic stresses including salinity are a major constraint to plant productivity. Under salt stress conditions leaf tissue undergoes accelerated senescence that is characterized by lowered efficiency of photosynthetic machinery. Cytokinin (CK); N<sup>6</sup>-adenine derivative phytohormones, are known to delay natural leaf senescence, wherein exogenous CK treatment results in chlorophyll levels being retained for longer duration. However, there are a number of different forms of CK and there is limited information on how individual CK forms function in this response and whether they alter physiological and molecular responses under salt-induced leaf senescence. Here, we tested trans-Zeatin (tZ) and its N-glucoside (tZNGs) forms; tZ7G and tZ9G, for their ability to delay leaf senescence in *Arabidopsis thaliana*. Using a modified dark-induced

leaf senescence CK bioassay, detached leaves were treated with different CK forms and analyzed for photosynthesis performance and mRNA transcript level changes using photosystem II (PSII) efficiency and RNA-sequencing respectively, under different phases of salt-induced leaf senescence. Our study showed that tZ and tZ7G improved PSII efficiency in late phases of salt-induction. At the transcript level, tZ, tZ7G, and tZ9G produced differential gene expression across both developmental and salt-stressed senescence. Additionally, we found that tZNGs trigger gene expression at different phases compared to tZ.

### **Elucidating the Role of Major Transcription Factors in Regulating Drought Stress in *Arabidopsis thaliana***

\*Doni Thingujam, Nilesh Kumar, Bharat K. Mishra, Jinbao Liu, Binoop Mohan, Karolina M. Pajerowska-Mukhtar and M. Shahid Mukhtar Department of Biology, The University of Alabama at Birmingham, USA

Drought is one of the prominent abiotic stresses encountered by plants resulting in serious problems in plants performance. Transcription factors (TFs) play an exceedingly important role in regulating drought resilience to withstand this complex phenomenon. Although, many of the TFs and their functions pertinent to drought are still unknown. Therefore, exploring the regulatory mechanisms of such novel TFs in drought stress is significant. Here, in our study, a high-resolution drought-mediated transcriptome of *Arabidopsis* was deciphered via a system biology-based approach to identify potential TFs. To validate the predictions of network analysis data, four important TFs; FBH3, ABI5, LCL5, and DAG2, which strongly exhibited association with the drought were further selected for downstream functional analyses. Firstly, the expression of these four TFs and their regulated target genes were studied through the qRT-PCR under drought stresses. Moreover, oxidative stress was induced via the use of diverse chemicals and phenotypic analyses were performed. Specifically, we observed a significant difference in the chlorophyll contents and anthocyanin levels in the mutant lines of selected TFs under these oxidative stress conditions in comparison to the wild-type *Arabidopsis* plants. Overall, we discovered four major TFs in our systems biology analyses and provided experimental evidence for their roles in drought stress.

### **Continuous Mowing Differentially Affects Floral Defenses in the Noxious and Invasive weed *Solanum elaeagnifolium* in its Native Range**

\*Vasquez Marcano, Alejandro, Department of Entomology and Plant Pathology, University of Arkansas, Fayetteville, USA; Dearth, Robert, Department of Biology, University of Texas Rio Grande Valley, Edinburg, USA; Kariyat, Rupesh, Department of Entomology and Plant Pathology, University of Arkansas, Fayetteville, USA

In weeds, disturbance has been found to affect life history traits and mediate trophic interactions. In urban landscapes, mowing is an important disturbance, and we previously showed that continuous mowing leads to enhanced fitness and defense traits in *Solanum elaeagnifolium*, Silverleaf Nightshade (SLN). However, most studies have been focused on foliar defenses, ignoring floral defenses. In this study we examined whether continuous mowing affected floral defenses in SLN using mowed and unmowed populations in South Texas in their native range. We found flowers of mowed SLN plants larger than unmowed flowers while unmowed flowers were heavier than mowed flowers. Additionally, flowers on plants that were

mowed frequently were both heavier and larger. Mowed plants had higher spine density and consequently unmowed flowers had higher herbivore damage. Additionally, early instar *Manduca sexta* fed on mowed flowers-based artificial diets had significantly less mass than the control, and unmowed, although in later instars mowing had no effect. Looking at frequency of mowing affecting these traits, we found caterpillars fed on high mowing frequency diets were heavier than those on low mowing frequency diets. Collectively, we show that mowing compromises floral traits and enhances plant defenses against herbivores and should be accounted for management.

### **Assessing the Physiological Response of Arkansas Native Plant Species Treated with Common Roadside Herbicides**

Woody-Pumford\*, Rachel C, Horticulture Department, University of Arkansas, Fayetteville, USA; Bertucci, Matthew B, Horticulture Department, University of Arkansas, Fayetteville, USA

Herbicides are not currently recommended for the initial establishment of prairies with native plant species. However, native plantings commonly occur on roadsides and areas where herbicides are typically used to prevent encroachment by invasive and weedy plant species. This study assesses the physiological response of a selection of native plant species when exposed to common roadside herbicides. Using a spray chamber, labeled rates of clopyralid, florpyrauxifen-benzyl, metsulfuron, and quinclorac were sprayed on container-grown plants of black-eyed Susan (*Rudbeckia hirta*), butterfly milkweed (*Asclepias tuberosa*), purple coneflower (*Echinacea purpurea*), buffalograss (*Buchloe dactyloides*), and switchgrass (*Panicum virgatum*). Following application, plants were maintained in a greenhouse and the heights and number of leaves were measured. Regardless of treatment, butterfly milkweed, black-eyed Susan, buffalograss, and switchgrass did not have any significant differences in leaf number 27 DAT. Butterfly milkweed and purple coneflower did not have significantly different heights than their untreated counterparts 27 DAT. However, by 27 DAT black-eyed Susan plants treated with metsulfuron and clopyralid had significantly more leaves than the plants treated with florpyrauxifen-benzyl. Untreated purple coneflower plants had significantly more leaves 27 DAT than the herbicide treated plants. Buffalograss and switchgrass exhibited reduced heights when treated with florpyrauxifen-benzyl.

### **Inspiring the Next Generation of Plant Scientists: How to Design Professional Development Workshops to Increase Plant Science in U.S. Classrooms**

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Within the world of scientific research, plants fill a relatively small niche. Likewise, in high school science courses, plants are briefly covered, if at all. However, plant science is an incredibly important facet of biology, often disregarded. Additionally, plants can serve as models for the central dogma of molecular biology, climate change, environmental responses

of organisms, biotechnology, and more. There is a push for science teachers to provide updated topics to their students and more hands-on learning opportunities via implementation of the Next Generation Science Standards. As such, teachers are required to attend professional development workshops and use what they learn to implement new lessons into their classrooms. This opens an opportunity to formulate professional development workshops about general plant biology and using plants as models for ubiquitous biology concepts. Additionally, plants are affordable and accessible thus increasing opportunities for kids at underfunded schools to perform hands on science experiments. Here, I will outline strategies used to create a plant centered professional development workshop called Plant GIFT (Plant Genomics Internship for Teachers) including the experiments conducted with teachers, potential changes to be implemented moving forward, and preliminary results from year one of this workshop. Over 4 years these workshops will train 60 teachers and potentially impact 10,000 students per year for a generation

## **Concurrent Session 1B**

### **IBR5-Mediated Regulation of Plant Auxin Response through the SCFTIR1 Complex**

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The plant hormone auxin controls plant growth and development by primarily regulating cell division, cell elongation, and cell differentiation. These processes are regulated by the expression of auxin-related genes, which is achieved through the degradation of AUX/IAA repressors by the ubiquitin proteasome pathway involving the SCFTIR1/AFBs complex. This complex comprises the F-box protein TIR1/AFBs, along with ASK1, CUL1, and RBX1. Prior research found the involvement of IBR5 in the auxin response pathway since the primary root growth of *ibr5* mutant lines showed resistance to auxin. The IBR5 gene encodes a dual specificity phosphatase, which has an essential yet unknown function in the auxin signaling pathway. Intriguingly, the degradation of Aux/IAs is much faster in *ibr5* mutants compared to wild type, which contradicts other known auxin signaling mutants. The purpose of this research was to establish the role of IBR5 in the auxin response pathway by investigating its effects on several proteins associated with the SCFTIR1/AFBs complex. Results show that IBR5 regulates the abundance and the localization of some components of the SCFTIR1 complex and thereby regulates AUX/IAA protein turnover, thus playing a vital role in plant auxin signaling.

### **Characterization of a Putative GATA Element and Analysis of Its Role in Starch Biosynthesis Transcriptional and Metabolic Activities**

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Exploring upstream regulatory elements of rice genes that control transcriptional activities is essential in developing strategies to accelerate biochemical processes such as starch biosynthesis. Cis-elements in genes associated with the starch biosynthesis can be mutagenized to improve starch accumulation. Here, we describe a cis-element in the vacuolar H<sup>+</sup> translocating pyrophosphatase gene (V-PPase) and present evidences of its role in modulating starch biosynthesis. A putative GATA element is found in the upstream region of V-PPase, encoding the enzyme that hydrolyzes inorganic pyrophosphate (PPi). The GATA element is conserved in japonica rice accessions and predicted to bind nine GATA transcription factors (OsGATA). Disruption of this GATA element by CRISPR/Cas9 suppressed V-PPase, thereby increasing the pool of PPi. Moreover, the expression of starch biosynthesis and PPi-dependent genes, pathways on starch metabolism, and utilization of sucrose to form starch are upregulated. The improved efficiency of starch formation upon GATA element disruption is possibly due to the increased PPi that serves as the alternative source of energy in starch biosynthesis. Altogether, our findings provide evidence on the role of a GATA element in regulating V-PPase expression that in turn influences PPi concentration and the starch biosynthesis rate in the developing endosperms. Targeted mutagenesis of this element can be used as an approach to increase starch biosynthesis rate in rice.

### **Organophosphonate Recycling**

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Phosphorus plays vital role in cell. It is found in various forms, like carbon-oxygen-phosphorus (C-O-P) linkage & the chemically inert, lysis resistant carbon-phosphorus (C-P) bond. Organophosphorus compounds containing the C-P bond are referred to as (organo)phosphonates. phosphonate occur both naturally & synthetically, & they are often used as agrochemicals, coolants, & industrial additives. In US, more than 20K tons of phosphonate are released yearly into the environment in the form of herbicides & detergent wastes where it becomes toxic. There is a growing interest to understand the mechanisms by which phosphonate are degraded by bacterial species. This will help to resolve phosphonate pollution. There are 3 known classes of enzymatic systems that have been mechanistically characterized which can lyse the C-P bonds of phosphonate compounds. These include phosphonate hydrolases, the C-P lyase complex, & an oxidative pathway. Unfortunately, those enzymatic systems of C-P degradation are insufficient to break down those C-P released into the environment. The goal of my project is to engineer & mechanistically characterize novel enzymes/microorganisms that will degrade C-P more efficiently in order to minimize the environmental impacts of these compounds. The approach is to clone & express the promising C-P degradation genes from different wild type bacteria, select highly efficient ones for further enhancement by various genetic methods including mutagenesis & evolution.

## **Enzyme Activity in Soil Growing Cereal Grain Crops**

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Enzyme activity is an indicator of microbial activity and nutrient cycling in soil. Soil microorganisms are the primary source of soil enzymes; however, plants also contribute to enzyme activity through rhizodeposits that consist of enzymes and carbohydrates that stimulate microorganisms. Enzyme activity under different crop species is thought to result from varying plant nutrient acquisition strategies. A greenhouse trial was established to confirm differences in soil phosphatase and sulfatase activities observed in a field study growing winter wheat and barley compared to perennial systems. Soil enzyme activities were measured at early emergence and again after harvest in the field study. Phosphatase activity under wheat varied greatly over the season, while phosphatase activity under barley remained unchanged. Sulfatase activity increased under barley over the season, while activity under wheat remained unchanged. Using the soil collected from the field study, wheat and barley were grown in the greenhouse, with unplanted soil serving as the control. Soil phosphatase activity was lower in the wheat rhizosphere compared to barley and control soils; however, sulfatase activity was greatest in the wheat rhizosphere compared to barley and control soils. These results indicate that the interaction between soil microbes and the plant rhizosphere varies by crop species and further investigation of the functional ecology may optimize management for soil nutrient cycling capability.

## **Identification of Quorum Sensing Bacteria from the Plant-associated Microbiome of Plants Grown Aboard the International Space Station.**

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Long-term settlements on the moon, Mars, or elsewhere are critically dependent on the development of sustainable food production systems in part or completely. Microbe-free agriculture in these environments is not only impossible, it is also impractical given the beneficial roles they play. Examples include solubilization of nutrients, nitrogen fixation, antibiotic production, and more. Despite efforts to maintain sterility, microbes abound on the International Space Station (ISS) including in association with plants. We have been screening the population of plant-associated microorganisms for beneficial phenotypes many of which are regulated by cell density, a phenomenon known as quorum sensing (QS). However, it remains unclear if quorum sensing even occurs under microgravity conditions or would be retained in the spaceflight environment. Here we explore whether the plant-associated microbiome aboard the ISS retains the potential for QS.

## **Genome-wide Association Study and Genomic Prediction of Fusarium Wilt Resistance in Common Bean Core Collection**

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Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *phaseoli* (Fop), is one of the important diseases that cause substantial production loss in common bean (*Phaseolus vulgaris* L.) production. The objective of this study were to conduct genome-wide association study (GWAS) to identify single nucleotide polymorphism (SNP) markers associated with resistance to Fop pathogen and to perform genomic prediction (GP) to estimate selection accuracy (PA). GWAS was performed in 157 USDA common bean accessions using TASSEL 5 and GAPIT 3, phenotyped with Fop race 1 and race 4, and genotyped with 4,740 SNPs of BARCBean6K\_3 Infinium BeadChips. The GWAS identified 16 SNP markers on chromosomes Pv04, Pv05, Pv07, Pv8, and Pv09 to be associated with Fop race 1 resistance; 23 SNP markers on chromosome Pv03, Pv04, Pv05, Pv07, Pv09, Pv10, and Pv11 with Fop race 4 resistance; and 7 SNP markers on chromosomes Pv04 and Pv09 associated with both Fop race 1 and race 4 resistances. Seventeen genes were recognized as candidates for Fop resistance situated on chromosomes Pv03, Pv04, Pv05, Pv07, Pv08, Pv09, and Pv10. GP was performed for Fop race 1 and race 4 resistances and the PA fluctuated from 0.26 to 0.55 for both Fop race resistances. This investigation provides useful information for common bean genetic improvement programs to select Fop resistance through maker-assisted selection (MAS) and genomic selection (GS).

## **Concurrent Session 2A**

### **Evaluating the Use of Aquatic Plants in Martian Agriculture**

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Sustainable approaches to agriculture on Mars are required to realize long-term settlement of the Red Planet. Ideally, crops grown on Mars should be highly nutritious, easy to grow, produce high yields, and be used for more purposes than nutrition. Macrophytes offer many of these qualities. In this ongoing project, *Lemna minor* was grown over a period of two months in various Martian regolith simulants to assess its potential for Martian agriculture. Growth was assessed using image analysis of *L. minor* surface coverage. Surface area data was also used to build a model used to predict biomass in *L. minor*. Early data shows that *L. minor* grows best in JSC Mars-1 regolith simulant which exists in a largely amorphous phase “ $\hat{\epsilon}$ ” whereas it performs poorly in MMS-1 which is almost completely crystalline and less soluble. Moderate growth was



seen in MGS-1, which contains a mixture of amorphous and crystalline material. JSC Mars-1 was observed to dissolve quicker than MMS-1. It should be noted that amorphous solids are more soluble in water than highly organized crystalline solids. This indicates that the geological characteristics of the regolith simulants influence L. minor growth. Further analysis is needed by looking at the nutrients in the water and at the geological properties of washed regolith.

### **Bax Inhibitor-1 Associates with AtIRE1A to Modulate Cytoprotective Signaling Pathway in Arabidopsis Immunity**

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Unfolded Protein Response (UPR) is a universal, integrated signaling network governed by an evolutionarily conserved stress sensor IRE1 that responds to endoplasmic reticulum (ER) stress and orchestrates cellular survival or death decisions. Here, we elucidated the intricate relationship between Arabidopsis Bax Inhibitor-1 (AtBI-1) and AtIRE1A during pathogen-induced acute ER stress. Our comprehensive biochemical study revealed that the C-terminal domain of AtBI-1 associates with kinase domain of AtIRE1A, and two phosphoacceptor residues are essential to maintain this interaction. Furthermore, we showed direct contribution of AtBI-1 in AtIRE1A-mediated AtbZIP60 splicing. Using higher order mutants, bacterial infections and biochemical analyses, we determined that AtBI-1 and AtIRE1A act in concert to positively contribute towards disease resistance and suppression of cell death. In summary, our study provided insights into a novel molecular, genetic and biochemical interplay between two evolutionarily conserved ER-associated proteins in the AtIRE1-AtbZIP60 arm of cytoprotective UPR signaling pathway upon bacterial pathogen infection.

### **Investigating the Importance of Sumoylation for Appressorium Morphogenesis by the Blast Fungus *Magnaporthe oryzae***

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The plant pathogenic fungus *Magnaporthe oryzae* forms a specialized pressure-generating infection cell called an appressorium on the leaf surface, which it uses to mechanically rupture the otherwise impenetrable cuticle, enabling colonization of the underlying tissue and the establishment of blast disease. Appressorium differentiation by *M. oryzae* is cell cycle-regulated and requires programmed cell death of a three-celled propagative spore, as well as extensive remodeling of the microtubule, actin, and septin cytoskeletons. Recent studies have proposed the importance of sumoylation – the enzymatic conjugation of a small ubiquitin-like modifier to target proteins, for various aspects of infection-related development by *M. oryzae*, including the formation of septin ring-like structures within the base of appressoria, through direct sumoylation of four core septin proteins. Here, using fluorescence microscopy-based live-cell imaging of sumoylation-deficient *M. oryzae* mutants, *ira2*, *uba2* and *ira2*, *smt3*, we determine the importance of global sumoylation for key stages of appressorium morphogenesis in vitro, including nuclear division and the formation and remodeling of higher-order septin structures.

Together, our data provides new perspective on the importance of sumoylation for infection-related development by the blast fungus.

### **Conditioning Mars for Plant Growth: *Anabaena cylindrica***

Haley Murphy\*, Indigo Boggs\*, Lea Adepoju, Andrew Palmer

As crewed space operations increase in frequency and duration, new challenges emerge for potential settlements on extraterrestrial bodies. It will be crucial to establish a sustainable food supply for inhabitants of Mars to create successful self-reliant settlements given its six-month journey is twice the travel time to the moon. An in-situ resource utilization (ISRU) approach leverages the available resources on site to facilitate renewable crop production. The most consistently available resource, Martian regolith, is a promising candidate as a substrate for plant growth as it contains many inorganic nutrients required for the task, though it lacks the necessary carbon and nitrogen deposits. On Earth, autotrophic pioneering species of cyanobacteria can simultaneously fix carbon and nitrogen as well as survive microgravity. We hypothesize that these activities could be performed on Mars to achieve the same effect and improve local regolith as a substrate for plant growth. In the present study we introduce the quick-growing cyanobacteria *Anabaena cylindrica* to Martian regolith simulant (MRS) and monitor development and characterize changes in carbon and nitrogen content in the substrate to determine the species overall potential to improve viability of plant growth in Martian regolith. Our findings impact understanding of how terrestrial ecology and farming methods may be employed to support off-world settlements.

## **Concurrent Session 2B**

### **Function of Auxin Signaling Pathway in Thermomorphogenesis of *Arabidopsis*.**

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Anthropogenic activities like industrialization, deforestation have largely contributed to global warming affecting almost every aspect of the earth, including agricultural production. Limited crop yield, which is directly related to food scarcity, is a frequently discussed topic today due to the rapidly increasing global population. Impact on crop yield being one of the major consequences of global warming, prompt and effective growth and development responses to increasing temperature is crucial for the survival of crop plants. Although we have expanded our knowledge on how plants respond to the high ambient temperature, our knowledge on molecular mechanisms involved in this process is far from complete. Increase in temperature induces hypocotyl elongation of *Arabidopsis* through the enhanced biosynthesis of auxin. This process requires the Phytochrome Interacting Factor 4 (PIF4), which integrates multiple environmental hormonal signaling pathways to control the growth and development of plants. Here we discuss the regulation of the levels of PIF4 protein by several alleles of auxin related

mutants in response to high temperature and light, indicating a mechanistic connection among environmental factors, auxin and plant growth and development.

### **Exploring the Potential of N-glucoside Forms of Cytokinin in Delaying Leaf Senescence**

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Leaf senescence is a complex process regulated by hundreds of senescence-associated genes (SAGs) and influenced by various phytohormones, including ethylene, jasmonic acid, salicylic acid, gibberellic acid, auxins, and cytokinin (CK). Among these, CK has been shown to have significant anti-senescence activity in leaf senescence bioassays. However, the mechanism underlying this activity remains unclear. Moreover, while more than 30 naturally occurring CKs are known to exist in plants, only a few base forms (tZ, iP, DZ, and cZ) have been studied for their anti-senescence activity. Recent research has focused on using genetic approaches to elucidate the network of genes and proteins responsible for CK's anti-senescence activity. Our physiological data suggest that N7- and N9-conjugates of CK may also delay leaf senescence significantly in 16-, 18-, 20-, and 30-day-old *Arabidopsis* leaves, indicating that other compounds besides base forms may also have anti-senescence activity and potentially other functions. CK plays a crucial role in delaying leaf senescence, but its mechanism of action and the full range of CK compounds with anti-senescence activity require further investigation. The insights gained from this research may have implications for the development of new strategies for delaying senescence in plants.

### **Investigating the Role of the Septin Cytoskeleton in Invasive Cell-to-Cell Movement by the Blast Fungus *Magnaporthe oryzae***

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The blast fungus, *Magnaporthe oryzae*, uses a specialized pressure-generating infection cell called an appressorium to break into host cells, in a process mediated by a class of membrane-associated GTP-binding proteins called septins. These filament-forming cytoskeletal proteins assemble into a ring-like structure at the base of the appressorium during its maturation, which is essential for its form and functionality. Septins are absent in plants, making them compelling targets for fungicide design. Having entered the first host cell, invasive *M. oryzae* hyphae move between adjacent epidermal cells via plasmodesmata, allowing the rapid colonization of host tissue. Emerging cell biological data supports a role for septins in this invasive cell-to-cell movement. Given that septins are essential for appressorium-mediated plant infection, here we describe our efforts to generate conditional septin mutants to directly test the requirement of higher order septin structures for invasive colonization by *M. oryzae*. We describe the generation and in vitro characterization of *M. oryzae* mutants harboring putative temperature-sensitive mutations within the GTP-binding domain of Sep5 (Sep5G29V/R35E), as well as the creation of a tetracycline-repressible Sep5 mutant. Outcomes of this research will provide new

insight into the importance of higher order septin structures for the biotrophic colonization of host tissue and the progression of blast disease.

### **The Comprehensive Application of Multiplexing Techniques into Plant Research at Single-nucleus and Spatial Transcriptomics Level**

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Single-cell and spatial transcriptomic assay have emerged as powerful tools to interrogating the heterogeneous epigenomic and transcriptomic profiling of complex biological tissues or systems. The well-developed single-cell platforms by 10X genomics now enables an increased cell/nucleus throughput for RNA and chromatin accessibility profiling. However, the tremendous cost of reagents and the limited sample loading are impeding the run of samples at large collections. Towards this issue, we integrate the newly-developed RNA and ATAC co-assay workflow by 10X genomics and Tn5 transpososome-based barcoding technique to achieve the multiplexing of multiple samples into per run and simultaneous profiling of open chromatin and gene expression at same-cell resolution. In addition to single-nucleus multi-ome multiplexing, we also set up to increase the scalability of sample processing at spatial transcriptomic level on 10X visium platform by applying multiple-samples embedding approaches, which makes the utmost of chip spaces and greatly reduce the cost.

## **Session 3**

### **Stay FLAT or BUCKLE? The causes and consequences of mechanical buckling in Arabidopsis sepals**

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To address how organ shape reproducibility is achieved, we screened for variable organ size and shape (vos) mutants in Arabidopsis sepals. The vos3 mutant exhibits ectopic lumps and outgrowths on the sepal abaxial epidermis. A point mutation in the upstream region of ASYMMETRIC LEAVES 2 (AS2), a key transcription factor involved in adaxial identity specification results in ectopic expression of AS2 on the sepal abaxial surface in vos3. We show that in initial stages, cell growth patterning on vos3 abaxial surface is disrupted, causing mechanical stress mediated buckling. Our mathematical model predicts that overgrowth and reduced stiffness of the abaxial vs adaxial surface can in theory, cause buckling. Outer surface cells of vos3 grow sideways, leading to the initial buckle. Using osmotic treatments, we found that outer epidermis of vos3 is significantly softer compared to the inner surface, whereas both epidermal layers exhibit similar stiffness in WT. Thus, both conditions for buckling are met in vos3 and not in wild type sepals. Also, overexpression of KRP1 in vos3 both limits the sideways growth and

severely reduces buckling, supporting the model. We also find PIN forms ectopic convergence sites in *vos3* located to the buckles, where outgrowths start forming. Live imaging *vos3* in the presence of NPA showed no difference in buckling although the outgrowth formation is largely reduced suggesting buckling as a mechanism driving plant development.

### **Overexpression of the Transcription Factor HYR in Rice Improves Grain Yield and Grain Quality under Drought and High Temperature Stress Conditions**

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Climate change triggers environmental stresses, including drought and high temperature stress which negatively affect photosynthesis and limit grain yield. The HYR (Higher Yield Rice) transcription factor gene regulates photosynthetic carbon metabolism (PCM) in rice. Overexpression of HYR (Os03g02650) in rice lines enhances photosynthetic capacity and contributes to higher grain yield under normal conditions as well as under drought and high temperature stress conditions. Since HYR is involved in regulation of PCM and response to environmental stress signals we were interested in studying the genetic basis of this response. The results show that expression of HYR was strongly affected by circadian rhythm. The circadian system may be an important target for optimizing PCM and yield under stress. HYR lines of IR-64 HYR and Vandana HYR showed higher filled grain per panicle number under normal and environmental stress conditions compared to WT. Most of the HYR lines produced higher filled grain per panicle number under control and environmental stress conditions with longer, wider, heavier, and less chalkiness compared to WT. Alteration of the root anatomy components of the HYR lines, increasing in metaxylem number and aerenchyma area, and also decreasing in metaxylem size and cortical cell file number under normal and environmental stress conditions showed a significant positive correlation with grain yield and grain quality characteristics.

### **Role of HR4 and its Interactors in Arabidopsis Defense Towards the Green Peach Aphid, *Myzus persicae*.**

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Green peach aphid (GPA; *Myzus persicae* S lzer), a phloem sap-consuming hemipteran insect, is a major pest of multiple crop species in the Brassicaceae, Solanaceae and Rosaceae family. However, how plants control GPA infestation is poorly understood. We have utilized the interaction between the model plant *Arabidopsis thaliana* and GPA to identify plant genes and mechanisms involved in defense against GPA. The HOMOLOG OF RPW8 4 (HR4) in *Arabidopsis*

encodes a transmembrane and coiled-coil domain-containing protein, which is required for limiting GPA infestation. HR4 is a close homologue of the atypical R gene, RESISTANCE TO POWDERY MILDEW 8 (RPW8), which is involved in defense against powdery mildew disease. Subcellular localization studies using a HR4-GFP fusion indicated that HR4 localizes to the plasmodesmata and as punctate spots at the plasma membrane, reminiscent of microdomain-localized membrane proteins. In order to identify other components of HR4-conferred resistance to the GPA, we have initiated a yeast 2-hybrid protein-interaction screen to identify Arabidopsis proteins that interact with HR4. The outcome of these experiments will be presented.

### **From Multiple-Cell to Single-Cell Genetics Models: The Arabidopsis Orphan Gene QQS Modulates Carbon and Nitrogen Allocation Across Species**

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The Arabidopsis orphan gene, Qua-Quine Starch (QQS) was previously identified as a regulator of carbon (C) and nitrogen (N) partitioning across multiple plant species, such as Arabidopsis, rice, corn, soybean, potato. As to QQS functional mechanism, our prior findings from multiple-cell genetic models showed that QQS modulates this important biotechnological trait by replacing NF-YB (Nuclear Factor Y, subunit B) in its interaction with NF-YC. Recently, we expanded these prior findings by developing single-cell genetic models, *Chlamydomonas reinhardtii* and *Saccharomyces cerevisiae*, to refactor the functional interactions between QQS and NF-Y subunits to affect modulations in C and N allocation and we updated QQS functional model. Such synthetic biology strategies provided experimental evidence to support the *œmimicry*-mode for orphan gene function, and a mechanistic understanding of QQS function, which impacts C and N allocation across species.

## **Poster Presentation Abstracts**

### **Poster 01**

#### **Drought Stress Response in Diverse Rice Genotypes for Physiological and Grain Yield traits**

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Rice (*Oryza sativa* L.) is an important cereal crop that uses 30% of the global freshwater resources during its life cycle. Drought stress is a major constraint, affecting various physiological processes such as photosynthesis and water use efficiency (WUE) that are crucial processes for plant growth and production of assimilates reducing rice grain yield. However, the abundant diversity of rice has naturally evolved phenotypic variation for photosynthesis and

WUE associated with grain yield, from which tolerant rice genotypes can be identified for improvement of rice productivity traits for superior biomass, economic yield, and WUE. For this study, a sub set of 14 diverse rice accessions from the USDA Rice Mini-Core Collection (URMC) consisting two major subspecies Indica and Japonica rice accessions was studied for photosynthesis, WUE, grain yield under varying semi drip irrigation (SDI) drought stress volumetric treatments (40%, 60%, 80% and control). These genotypes with different drought resistant ability were further studied, for effect of varying exogenous ABA and PEG osmotic stress on radicle and plumule growth and compared to compared with normal condition. The response to ABA was similar to PEG and water stress in the field indicated the genotypes variation and ranking for the treatments was based on the reduction rate of radicle and plumule growth parameters and yield reduction rate.

## **Poster 02**

### **Understanding the Mechanism of Resistance to Soil-Applied Fomesafen in *Amaranthus palmeri***

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Palmer amaranth is one of the most competitive and aggressive weed species that has become a devastating problem in several crops in USA. *A. palmeri* has a high tendency to evolve multiple herbicide resistance due to genetic variability and its dioecious nature, resulting in obligate cross-pollination. The recent evolution of resistance to protoporphyrinogen oxidase (PPO) inhibitors in *A. palmeri* is a major concern. PPO inhibitors applied as pre-emergence are effective in controlling populations that are resistant to foliar-applied PPO herbicides. We found six populations that were resistant to recommended field dose of soil-applied fomesafen in a preliminary screen. The survivors from these populations were genotyped for all known resistance-conferring target site (PPO2) mutation (TSM). A total of 64% and 36% survivors had single and double TSMs, respectively, with 69% of plants carrying functional TSM in both alleles of PPO2. Expression analysis of PPO2 showed 3- to 6-fold upregulation in all survivors from resistant populations tested. Female -biased sex ratio was observed in these survivors. Computational search of genes around the PPO2 locus was conducted with the hypothesis that the alteration in regulation of PPO2 is linked with low or none pollen production, resulting in a biased sex ratio or reduced fecundity. Analysis of survivors of soil-applied fomesafen with known sex-specific markers is ongoing.

## **Poster 03**

### **Evaluation of *Echinochloa colona* Exposed to Sublethal Doses of Auxin Herbicides and Abiotic Stress (Drought and Heat) Across Generations**

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Quinclorac is a major auxinic herbicide used in rice production. About 1/3 of quinclorac-

resistant *Echinochloa colona* (junglerice) populations are cross-resistant to the new auxinic rice herbicide, florpyrauxifen-benzyl (FPB). This study aims to evaluate the effect of recurrent selection with a sublethal dose of auxinic-herbicides (SLAH) and abiotic stress (AS) on junglerice control. Two experiments were conducted in the greenhouse, Fayetteville, Arkansas, USA. Each experiment was a two-factor completely randomized design. Study-1 involved (1) heat stress (30C and 45C at 7 d before and after herbicide application) and (2) herbicide (quinclorac, FPB, nontreated-check). Study-2 involved (1) drought stress (well-watered and drought-stress at 50% of soil capacity) and (2) herbicide (as in Study 1). The plant material had been subjected to three generations (G3) of SLAH and AS, starting with the susceptible G0. G3 seedlings were established and sprayed with 0.125X doses of quinclorac. The dose was increased to 0.25X for G4 and G5. The FPB dose was 0.125X for all generations. Plant injury was evaluated at 7 and 21 d after treatment. Plants treated with either quinclorac or FPB at 45C tended to be more tolerant in G5. Drought stress did not increase the tolerance of junglerice to FPB across generations. The joint effect of heat stress and SLAH on the efficacy across generations suggests a rapid selection of junglerice-resistant populations to FPB.

#### **Poster 04**

##### **Effect of Cytokinin in tomato stress response and delay in leaf senescence**

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Tomato is a high-valued vegetable crop that is often subjected to salt and oxidative stress. CK plays a major role in responding to these stresses and delaying leaf senescence. Recent studies claim that out of the 4 different base forms of CK, cis Zeatin (cZ), trans zeatin (tZ), Isopentyl adenine (iP) and Dihydrozeatin (DHZ), cZ which was thought to be inactive for many years seems to show active function towards these stresses. Evidence strongly supports that cZ levels are increased in both salt and oxidative stress while other base forms are increased and decreased in salt and oxidative treatments respectively. However, the studies conducted on cZ are limited. Therefore, the main objective of this study is to determine the cZ activity in salt and oxidative stress using modified CK bioassays and to compare the cZ activity compared to other CK base forms in two different time points of tomato life cycle. Microtome (MT) leaf discs were exposed to 150 mM NaCl and 20 mM H<sub>2</sub>O<sub>2</sub> for 4 days and Fv/Fm analysis was conducted. The results suggest that the cZ delays the senescence in tomato. These preliminary data should be aimed at selecting the time points to conduct the transcriptomic analysis to identify novel genes involving in cZ regulation and their effect towards the oxidative and salt stress in tomato by experimenting them in transiently altered transgenic lines of tomatoes for potentially improved response to salt and oxidative stress.



## **Poster 05 - Undergraduate**

### **Two Iron Limitation Methods Are Associated with Different Cellular Responses in *Synechocystis* sp. PCC 6803**

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Iron limitation is a serious abiotic stress for photosynthetic organisms. In this study, two methods of inducing iron limitation were compared in *Synechocystis* sp. PCC 6803. The two methods compared were dilution with iron-free media and treatment with iron chelator 2,2'-bipyridyl. The cellular responses to iron limitation stress were analyzed using cell growth, protein expression, heme levels, and the relative expression of iron homeostasis regulatory genes: *isiA*, *furA*, *perR*, and *pfsR*. Both methods were associated with a decreased growth rate. The growth rate was more severely limited in 2,2'-bipyridyl cultures. Additionally, 2,2'-bipyridyl treatment was associated with lower expression of *IsiA* and some photosystem subunits. Heme levels were higher in dilution treated cultures than in 2,2'-bipyridyl treated cultures. Variations in gene expression were also observed. These results suggest that there are differences in how iron limitation is initiated between the two methods. These observations contribute to our overall knowledge of how abiotic stress affects photosynthetic systems.

## **Poster 06 – Undergraduate**

### **The impact of selenium nanoparticles on cyanobacterial cells**

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The impact of selenium nanoparticles on cyanobacterial cells

In order to understand the impacts of selenium nanoparticles on the health of the aquatic ecosystem. Here, we propose to investigate in depth the cytotoxic effects of selenium nanoparticles on cyanobacterial strains such as *Synechocystis*, *Synechococcus* and *Anabaena* using various concentrations of selenium nanoparticles (up to 35 ppm) for up to 7 days to determine the dose- and time-dependent effects. We will assess the cytotoxic or beneficial effects through quantification of cell viability, biomass and photosynthetic pigments such as chlorophyll-a, carotenoids and phycocyanin. The interactions of selenium nanoparticles with the algal cells will be examined using scanning electron microscopy (SEM) to determine the morphological alterations or injuries caused by the nanoparticles. I will also study the intracellular alterations of algal cells resulted from the exposure using transmission electron microscopy (TEM). Furthermore, I will use Fourier transformed infrared (FTIR) spectrum to determine the biomolecules in algal cell surface involving in binding to selenium nanoparticles. Understanding the interaction mechanisms of nanoparticle with algal cells can inspire redesign

strategies to reduce nanoparticle toxicity while augmenting their beneficial effects or maintaining the novel functionalities they convey.

### **Poster 07**

#### **Expression Levels of Select Genes in 3D-Clinorotated Dwarf *Triticum aestivum* L.**

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A 3D clinostat was built with independently-controlled perpendicular frames to allow the sum of the perceived gravity vectors to net to near zero with a minimum amount of disturbance due to centrifugal force. To better characterize the abiotic stress response of *Triticum aestivum* L. cv. USU-Apogee under this simulated microgravity condition, several genes with altered expression reported in gravitropism and microgravity studies of the model plants *Arabidopsis thaliana* L. and *Zea mays* L. were initially selected and compared to sequences in *T. aestivum* to identify preliminary candidate genes for analysis. Primers for both these genes of interest and housekeeping genes were designed, and a subset of the initial gene/primer candidates was selected for further study based on the slopes of the primer efficiency standard curves and dissociation curve profiles. Finally, relative quantification of the target genes in response to 24 h of continuous clinorotation was analyzed via qPCR. It was found that mRNA corresponding to a cytoplasmic aconitase (cACO) was downregulated 35%, and RNA from a J-domain protein was downregulated 30% compared to the upright stationary control plants.

### **Poster 08 - Undergraduate**

#### **Biochemical and Gene Expression Analyses Reveal the Importance of UDP-Glucose Pyrophosphorylase in the Utilization of Storage Starch for Seedling Growth in Rice**

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During germination, a rice seedling growth is energized by starch stored in the endosperm. This starch must be converted to sucrose, through a series of degradation steps, to become metabolically available. The starch utilization process is inhibited by inorganic pyrophosphate (PPi) as one of the steps involves UDP-Glucose Pyrophosphorylase (UGPase) which is sensitive to PPi concentrations. Vacuolar H<sup>+</sup> pyrophosphatase (V-PPase) regulates the cellular concentration of PPi by hydrolyzing it to inorganic phosphate (Pi). Earlier, the rice V-PPase gene (Vpp5) was mutated to slow down the process of PPi hydrolysis in rice endosperm. We examined the effect of Vpp5 mutation on starch degradation and sucrose content in germinating seeds. The vpp5 mutants showed lower starch reduction and lower sucrose content in comparison to the wild-type. A strong positive correlation was found between

sucrose concentration and the expression of two starch degradation enzyme genes, UGPase and Sucrose Synthase (SuS). The  $\alpha$ -amylase (Amy) genes, on the other hand, correlated with starch reduction endosperm but not with the sucrose content. Therefore, Amy is involved in reducing starch to maltose but subsequent steps involving UGPase and SuS are possibly inhibited in vpp5 mutants, impacting the production of sucrose during germination/ seedling growth. Overall, V-PPase activity in rice endosperm directly influences starch utilization, possibly by modulating the activity of PPI-sensitive UGPase.

#### **Poster 09**

### **Assessing the Biotechnological Potential of Cotton Type-1 and Type-2 Diacylglycerol Acyltransferases in Transgenic Systems**

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The chemical properties of vegetable oils are largely dictated by the ratios of 4-6 common fatty acids contained within each oil. However, examples of plant species that accumulate from trace amounts to >90% of certain unusual fatty acids in seed triacylglycerols have been reported. Many of the general enzymatic reactions that drive fatty acid biosynthesis and accumulation in stored lipids are known, but which isozymes have evolved to specifically fill this role and how they coordinate in vivo is still poorly understood. Cotton is a rare example of a commodity oilseed that produces relevant amounts of unusual fatty acids in its seeds and other organs. In this case, unusual cyclopropyl fatty acids are found in membrane lipids and seed oils. Such fatty acids are useful in the synthesis of lubricants, coatings, and other types of valuable industrial feedstocks. To characterize the role of cotton acyltransferases in cyclopropyl fatty acid accumulation for bioengineering applications, we cloned and characterized type-1 and type-2 diacylglycerol acyltransferases from cotton and compared their biochemical properties to that of litchi, another cyclopropyl fatty acid-producing plant. The results presented from transgenic microbes and plants indicate both cotton DGAT1 and DGAT2 isozymes efficiently utilize cyclopropyl fatty acid-containing substrates, which helps to alleviate biosynthetic bottlenecks and enhances total cyclopropyl fatty acid accumulation in the seed oil.

#### **Poster 10 - Undergraduate**

### **Characterization of the TH2/At5g32470 Fusion Protein and its Role in Thiamin Metabolism in Plants**

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Thiamin is essential for the proper functioning of many central metabolic enzymes and is synthesized by plants and most bacteria. In bacteria, thiamin is phosphorylated by thiamin kinase (ThiK) and monophosphate kinase (ThiL). In plants, thiamin monophosphate is

dephosphorylated (TH2) and then pyrophosphorylated by a pyrophosphate kinase (ThDPK). The enzyme responsible for thiamin pyrophosphorylation can also phosphorylate damaged forms of thiamin, such as oxothiamin and oxythiamin. In plants, a preemptive Nudix gene can selectively dephosphorylate the damaged forms, but a salvage enzyme to repair the damaged forms is missing. Evidence suggested that the TenA domain of TH2 gene could salvage oxothiamin and oxythiamin. The TenA domain belongs to the TenA\_C subfamily, which other members have amino-HMP aminohydrolase activity. To test our prediction, we have mutated the putative catalytically important residues of TenA domain of TenA-HAD and tested the ThMP activity in the bacterial complementation assay. Currently, we are testing the oxo/oxythiamin toxicity tolerance of a bacterial strain complemented with Arabidopsis TenA-HAD. To test the invitro TenA activity we are expressing the Arabidopsis His-tagged TenA-HAD gene in E. coli and will attempt to purify the protein. An attempt will be made to complement the Arabidopsis TH2 mutant with truncated TenA-HAD protein in which the TenA domain is truncated or mutated, hoping that the substrate of the TenA domain may build up.

### **Poster 11 - Undergraduate**

#### **Tracing the Evolution of Riboflavin Biosynthesis through Comparative Analysis of Deaminase and Reductase Genes**

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Riboflavin is the precursor to produce flavin cofactors, including flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The biosynthesis of riboflavin involves a deaminase and reductase steps which are catalyzed by a bifunctional enzyme in most eubacteria. However, these two enzymes are separate in fungi, plants, and most archaea. Interestingly, the deaminase and reductase steps in plants are catalyzed by individual mono-functional enzymes, each with an inactive domain. Our research aimed to construct a phylogenetic tree to trace the evolutionary divergence of the deaminase and reductase genes in different domains of life. The results showed that plants deaminase and reductase genes are paralogs that diverged at the base of the plant lineage. We also reconstructed a bifunctional plant enzyme by fusing the functional deaminase and reductase domains. The cloned fusion gene was then introduced into an E. coli strain deficient in riboflavin production ( $\Delta$ ribD::Kan), which resulted in complementing its auxotrophy. Currently, we are characterizing the monofunctional deaminase and reductase genes from fungi and algae with the goal of constructing a comprehensive phylogenetic tree using degenerate sequences of the riboflavin deaminase and reductase genes. The findings from this study will provide new insights into the evolution of the riboflavin biosynthesis pathway in different domains of life.

### **Poster 12 - Undergraduate**

#### **Floristic Survey of the Granite Outcrops at Clinton Nature Preserve, Douglas County, Georgia**

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Granite outcrops provide an unusual habitat; where only certain species that have evolved to its conditions can survive. The Clinton Nature Preserve (CNP) is composed of a variety of habitats and is home to many granite outcrop endemic species. The site is exposed to heavy foot and bicycle traffic which has impacts on *Diamorpha smallii*, a granite outcrop endemic present at this sight. Cataloging and identifying species helps gauge species composition at this granite outcrop and is fundamental to our understanding of plant conservation at this unique habitat. A floristic survey of the CNP would help assess the diversity of plant species, as well as determine their spatial occurrence in regard to *Diamorpha smallii*. For this, we have collected many different species from the fall and spring seasons in order to identify them and understand their importance in this unique environment. Since a floristic survey has not been conducted at this site yet, we can use this assessment of the unique plant communities within the park in order to develop a conservation plan to protect the vulnerable species at the granite outcrop.

### **Poster 13**

#### **Characterization of Arabidopsis Activation Tagged genes maintaining Photosynthesis in response to Salinity and Fluctuating Light conditions**

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Salinity and fluctuating light intensity affect agricultural area. Salt and light stress affects plant growth, photosynthetic activity, and crop yield. *Arabidopsis thaliana* is plant model that provides a comprehensive knowledge of plant development, genetics, and response to abiotic stresses.

Transposon-mediated activation tagging is an efficient genetic tool that can randomly generate gain-of-function mutants for a large number of genes. Transposable element Enhancer-Inhibitor system of maize was modified to develop an activation tag (AT) mutant library in *Arabidopsis*. I-AT library was used to screen for salt tolerance and fluctuating light intensity, identified by enhanced growth and photosynthetic activity of the tagged mutants compared to the wild-type grown in saline and fluctuating light intensity conditions. The genomic DNA flanking sequences of I-ATag insertions of the activating I-element (AIE) were isolated using TAIL PCR then sequenced, and candidate flanking genes characterized. Two tolerant lines, AIE7 and AIE70 showed over-expression of adjacent genes which could be candidates for salt stress tolerance,

caused by the CaMV 35S enhancer present in the AIE enhancing expression of the candidate adjacent genes. The AIE7 mutant line with the activation tagged AT2G41430 genes, annotated as Early Response to Dehydration (ERD) protein family, and AT2G41410 as EF-hand calcium binding protein, are candidate genes for salt and fluctuating light intensity tolerance.

#### **Poster 14 - Undergraduate**

##### **Phenotypic Variation in the Quorum Sensing Responses of Wild Type Strains of *Chlamydomonas reinhardtii***

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The phenomenon of quorum sensing (QS) allows unicellular organisms to coordinate phenotypic switching based on cell density, optimizing specific behaviors to high or low cell densities as appropriate. Initially thought to be limited to prokaryotes, QS has been observed in a small number of eukaryotes, including *Chlamydomonas reinhardtii*. In the well-defined wild-type lab strain cc124, swimming speeds are positively correlated with cell density. Within this species, there is significant phenotypic variation and evidence suggests that these variances may extend to QS. Understanding how QS responses vary across one species could provide tools for identifying relevant signal molecules and the molecular mechanisms associated with QS in *C. reinhardtii*. We will investigate the QS responses of *C. reinhardtii* wild-type cc1010 by acquiring videos of cultures at distinct cell densities and tracking their movement. The behavioral changes of cc1010 low cell density cultures exposed to cc1010 high cell density media will also be observed. Identifying the QS phenotype of cc1010 will provide a better understanding of the distribution of QS within *C. reinhardtii*, as well as providing molecular and biochemical tools for understanding this novel QS system.

#### **Poster 15**

##### **Phenotypic assessment of SnRK1 mutants in rice (*Oryza sativa* var. japonica) cv. Kitaake**

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For normal growth and development, plants rely on signaling mechanisms controlled by regulators such as sucrose non-fermenting related protein kinase 1 (SnRK1). SnRK1 regulates gene networks but its precise role in plant development and stress response is not well understood. Rice contains three functional paralogs of SnRK1: SnRK1a, SnRK1b, and SnRK1c. The study focused on the function of these SnRK1 paralogs by evaluating the morphological characteristics of their mutants developed by CRISPR/Cas9 mediated targeted mutagenesis. Earlier, SnRK1c mutants were found to contain homozygous -1 to -11 bp deletions leading to early stop codon in the reading frame. SnRK1a and SnRK1b were targeted simultaneously that resulted in double-mutant lines harboring monoallelic and biallelic mutations leading to frameshift and early stop codon. Double-homozygous lines were subjected to phenotypic assessment along with the WT. Plants were grown in randomized block design in a controlled

environment in the greenhouse. Moreover, the mutant lines were grown along with the WT in germination media to measure the shoot length of the seedlings. Our results show that *snrk1a+b* double-mutants had lower shoot length compared with the WT. The *snrk1c* mutants showed phenotypic differences in the late stages, such as number of seeds per panicle and total weight of seeds per plant. These results indicate specialized functions of SnRK1 paralogs in the early vegetative and reproductive phases of the rice plant.

### **Poster 16**

#### **Investigate the effects of diffusible signals from plant growth-promoting bacterium, *Azospirillum brasilense*, on rice.**

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Plants form associations with different beneficial microbes, including arbuscular mycorrhiza (AM), rhizobia bacteria, plant growth-promoting bacteria (PGPB). In these associations, the host plants benefit from improved growth in exchange for carbohydrates for the microbe. Studies in legume-rhizobia symbiosis and AM symbiosis have shown that a molecular dialogue between the symbiotic partners is required to initiate these interactions. Furthermore, genetic and biochemical studies identified the plant and microbial signals involved in these symbioses. For instance, Nod factors are secreted by rhizobia bacteria during LRS, and Myc factors are secreted by AM fungi during mycorrhizal symbiosis. Interestingly, the direct application of these microbial signals on plants can promote their growth, and naturally, these are already commercialized. The same level of understanding doesn't exist for interactions between plants and PGPB. Recent studies have suggested that a similar signal exchange might be involved during plant-PGPB interactions. For instance, one recent study showed that diffusible signals from *Azospirillum brasilense*, a PGPB, stimulated growth in *Arabidopsis thaliana*. Our preliminary data suggest that diffusible signals from *A. brasilense* could also promote growth in rice. In the future, we intend to identify the chemical nature of the diffusible signals from *A. brasilense* and identify the plant genetic pathway involved in this interaction.

### **Poster 17 - Undergraduate**

#### **Evaluating *Chlamydomonas*-derived riboflavin as a Mechanism for Gram-negative Quorum Quenching**

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Quorum sensing (QS) is a cell density-based interorganismal signaling strategy used to activate a phenotype based on population density. In bacteria, this can be used to promote biofilm formation, virulence factor production, motility, and more. Since this is based on intermolecular signaling, it is susceptible to interference from other microorganisms in the environment.

Inhibition or quorum quenching (QQ) of Gram-negative bacteria has previously been documented in the photosynthetic unicellular eukaryote *Chlamydomonas reinhardtii*. There are two current mechanisms proposed for this QQ effect. The first is that *C. reinhardtii* metabolizes the Gram-negative quorum sensing signals, N-acyl-L-homoserine lactones raising the threshold for QS activation. The second is that *C. reinhardtii* releases an inhibitor to the QS molecules used by the bacteria. In the present study, I am focusing on riboflavin, a molecule previously shown to inhibit AHL-mediated QS at higher concentrations. Here I have evaluated whether or not *C. reinhardtii* exudes enough riboflavin for this QQ effect to occur. This will help contribute to our overall understanding of the interactions between *C. reinhardtii* and prokaryotes in the surrounding environment.

### **Poster 18 - Undergraduate**

#### **Evaluating the Efficacy of Sterilization Techniques on Martian and Lunar Regolith Simulants**

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Martian and lunar regolith simulants are used in various biological research and are critical elements in understanding the future of terrestrial life on other celestial bodies. Given the lack of available source material, researchers are forced to develop and rely on regolith simulants to replicate the surfaces of Mars and the Moon. However, microorganisms are ubiquitously distributed across our planet and could significantly impact the use of these simulants for research into space agriculture and planetary protection. Various methods could be used to sterilize regolith, including steam sterilization (autoclaving), dry heat (hot-air oven), chemical and others, each with varying degrees of efficacy. This study will evaluate preparation and sterilization methods for Martian and lunar simulants and how this may impact plant growth research. Our efforts contribute to an emerging toolbox for improved research methods using regolith simulants in biological research.

### **Poster 19 - Undergraduate**

#### **Incorporating Edible Decomposers into Sustainable Bioregenerative Life Support Systems for a Martian Settlement**

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Establishing a bioregenerative life support (BRLS) system with supplemental food production is key to sustainable space colonization efforts at sites too remote for easy resupply from Earth.



In-situ Resource Utilization (ISRU) practices leverage existing resources such as regolith to support BRLS systems, further reducing a future settlements dependency on Earth for vital goods. Decomposers are organisms capable of breaking down organic material making nutrients available for reuse by other organisms. We propose that involving edible decomposers into BRLS systems is an efficient method of recycling valuable organic and inorganic wastes for a settlements ecosystem, while also introducing a supplemental nutrient source for settlers. As decomposers with edible species, fungi are prime candidates for this study as they are resilient and are adaptable in growth whereas vegetative feedstock requires extensive care. *Pleurotus ostreatus* (Oyster mushroom), will be our model fungi due to its simplicity in growth and abundance in nature. Our previous research examining the growth and limitations of *P. ostreatus* in Mars Global Simulant (MGS-1) supports the feasibility of incorporating fungi into BRLS systems. We hypothesize that regolith will aid in the decomposition process and that using an edible fungus will reduce the steps in the sustainability chain. In the present investigation, we will optimize the ratio of inorganic to organic material that will support viable fungi growth.

## **Poster 20 - Undergraduate**

### **Comparison of Pool Characteristics of Granite Outcrops at Clinton Nature Preserve, Douglas County, Georgia**

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Southeastern granite outcrops are a distinctive habitat that support many unique plant species. These outcrops are popular for outdoor recreation which can degrade the habitat and threaten the various endemic flora. During the winter months, rainwater regularly collects in depression pits of granite outcrops. These seasonal pools can serve as habitat for a variety of organisms, including endemic plant species that are found nowhere else. In an effort to understand the species variation between granite outcrop pools, a range of characteristics are being measured. These include water and soil analyses, as well as physical descriptions. We hope these comparisons further our understanding of why endemic plant species such as *Gratiola amphiantha* and *Diamorpha smallii* are present in only some of the pools. *G. amphiantha* is rare, and its populations are extremely isolated. If a population becomes locally extinct, there is little chance of natural reintroduction. *G. amphiantha* is only present in a single pool at the outcrop and analyzing the differences between its pool and others may aid in our understanding of how to conserve this and other at risk endemic species.

## **Poster 21 - Undergraduate**

### **Clover-Rhizobia Symbiosis to Condition Martian Regolith for Plant Growth**

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Bio-regenerative life support (BRLS), the use of plants and other photosynthetic organisms to supplement life support and provide energy, is a mission critical system for future off-world expeditions and colonies. Martian regolith lacks many of the macro- and micro- nutrients essential for plants, cultivating in these conditions limits healthy plant growth and development. Considering that nitrogen and carbon compounds that are necessary for plants are not available in sufficient quantities on Mars, we must find sustainable methods to introduce them into the regolith composition and improve its physical characteristics using minimal resources. The Fabaceae plant family forms mutualistic symbiotic associations with nitrogen-fixing bacteria of the paraphyletic group, known as Rhizobia. *Trifolium repens* (clover), is a species of Fabaceae that requires minimal resources and performs nitrogen fixation via nodulation. Growing clover and tilling it into Mars regolith simulat over the course of multiple growth periods could act as a BRLS system, and sustainably alter its composition. Inoculating the clover with its symbiotic counterpart may increase root nodulation and nitrogen fixation. This BRLS system could be a minimalistic method for improving the conditions of Mars regolith to be used as a substrate for plant growth.

## **Poster 22**

### **Morphological, Physiological, and Genomics Responses of Recombinant Inbred Lines Rice Population under Drought Stress Condition**

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Rice is the main staple food for global population and drought is one of the constraints in rice production. Progeny of a cross between an adapted U.S. rice cultivars with a tropical japonica and an indica rice genotype, were screened for drought resistant (DR) traits to identify DR loci, that would be useful for breeding U.S. rice cultivars for a water saving agricultural system. A recombinant inbred line (RIL) population, generated from the cross between drought resistant tropical japonica U.S. cultivar Kaybonnet and an indica drought sensitive cultivar ZHE733, was chosen for quantitative trait locus (QTLs) analysis of drought-resistance related traits. The DR traits were quantified by measuring morphological traits, grain yield components and root

architectural traits. K/Z RIL population of 198 lines were screened in the field by giving controlled drought stress (DS) and well-watered (WW) treatment at the reproductive stage. The effect of abscisic acid (ABA) sensitivity screen on parents and 198 lines at the V3 stage in culture media was quantified by measuring root architectural traits. QTL analysis was performed with a set of 4133 SNP markers by using QTL IciMapping software. We detected 41 QTLs and 184 candidate genes and most of the candidate genes were up regulated in Kaybonnet as the drought resistant parent. The research provides important information to develop drought-resistant rice varieties with greater productivity under DS conditions.

### **Poster 23**

#### **GWAS and Genomic Selection for Genomic-Assisted Development of Sucrose Enriched Soybean Cultivars**

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Sucrose concentration in soy-derived foods is becoming a seminal trait to produce food-grade soybeans. However, limited scientific knowledge is reported on this increasingly important breeding objective. In this study, 473 genetically diverse soybean accessions and 8,477 high-quality single nucleotide polymorphisms (SNPs) markers were utilized to pinpoint genomic regions associated with seed sucrose contents through a genome-wide association study (GWAS). A total of 75 significant SNPs (LOD 6.0) were identified across GLM, FarmCPU and BLINK models, including four stable and novel SNPs (Gm03\_45385087\_ss715586641, Gm06\_10919443\_ss715592728, Gm09\_45335932\_ss715604570 and Gm14\_10470463\_ss715617454). Gene mining near 20 kb flanking genomic regions of four stable SNPs identified 23 candidate genes with most of them expressed in soybean seed and pod shell. A sugar transporter encoding major facilitator superfamily gene (Glyma.06G132500) showing the highest expression in pod shells was also identified. Selection accuracy, efficiency, and favorable alleles of 75 significantly associated SNPs were estimated for their utilization in soybean breeding programs. Furthermore, genomic predictions with three different scenarios revealed better feasibility of GWAS-derived SNPs for selection and improvement of seed sucrose concentration. These results could help in genomic-assisted breeding of sucrose-enriched soybean cultivars development for the global soy-food industry.

### **Poster 24 - Undergraduate**

#### **Anabaena cylindrica as a Biofertilizer in Bioregenerative Life Support Systems (BLSS) for Martian Settlements**

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As crewed space operations increase in frequency and duration, new challenges emerge for potential settlements on extraterrestrial bodies. It will be crucial to establish a sustainable food

supply for inhabitants of Mars to create successful self-reliant settlements given its six-month journey is twice the travel time to the moon. An in-situ resource utilization (ISRU) approach leverages the available resources on site to facilitate renewable crop production. The most consistently available resource, Martian regolith, is a promising candidate as a substrate for plant growth as it contains many inorganic nutrients required for the task, though it lacks the necessary carbon and nitrogen deposits. On Earth, autotrophic pioneering species of cyanobacteria can simultaneously fix carbon and nitrogen as well as survive microgravity. We hypothesize that these activities could be performed on Mars to achieve the same effect and improve local regolith as a substrate for plant growth. In the present study we introduce the quick-growing cyanobacteria *Anabaena cylindrica* to Martian regolith simulant (MRS) and monitor development and characterize changes in carbon and nitrogen content in the substrate to determine the species overall potential to improve viability of plant growth in Martian regolith. Our findings impact understanding of how terrestrial ecology and farming methods may be employed to support off-world settlements.