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87th Annual Meeting
Southern Section – ASPB
March 13-15th, 2026
Lafayette, Louisiana

Sponsors:

ASPB - Code of Conduct

87th Annual Meeting SS-ASPB
Participants and Contributions

Abeywickrama, H.L Thilakshi	Stress-inducible extension of tRNA fragments: formation of chimeric RNAs and their role in sequence-specific gene activation	#30 G
Acharjya, Prianka	Surviving under Stress: Potential Role of IBR5 in Plant Resilience.	Talk Room 117, 3/14 @11:15 AM
Alessi, Madaleine	Cercospora Leaf Blight infection induces cellular reactive oxygen species and organelle dysfunction	#45 G
Alonso-Cocuron, Cindy	A Code-Based Automated Pipeline for Complex Untargeted Metabolomics Data Processing	#11 U
Balem, Joseph	Keeping Cool: The role of cold response in plant wound healing	#43 G
Bangari, Mayank	Structural and biomechanical basis of stem lodging in grain sorghum under different water regimes	#31 G
Barbero Barcenilla, Borja	New Dimensions of Resilience: Telomerase and Tardigrade Protection in Space-Grown Plants	Talk Room 112, 3/13 @6:15 PM
Barbero Barcenilla, Borja	Feeding the Future: Safeguarding Nutrition and Safety in Space-Grown Crops	Talk Room 112, 3/14 @11:00 AM
Benedetto, Nicholas	Regiospecific Control and Subcellular Localization of Monoterpene Indole Alkaloid Glucosidases	#12 U
Bennetzen, Jeff	Origin, Population Genetics and Metabolomics of Yaupon Holly, an Indigenous Beverage Plant of the Southeastern US	Talk Room 112, 3/14 @9:00 AM
Bhatt, Padam	Chromatin Remodeling of Defense Gene Regulatory Elements During Plant Immune Activation	#26 G
Bommes, Anna	Investigate the Effects of Diffusible Signals from the Plant Growth-Promoting Bacterium, Azotobacter vinelandii, on Rice	Talk Room 117, 3/14 @8:45 AM
Borja, Gabriela	Unraveling the stress granule (SG) transcriptome in Arabidopsis thaliana under abiotic stress	#40 G
Bridges, Samaya	Investigating putative Arabidopsis thaliana α/β-hydrolase for potential to degrade poly(aspartic) acid	#21 G
Bryan, Thomas	Duckweed as a Bioremediator of Metal-Contaminated Waters: Efficacy and Biological Implications	#22 G
Bucio, Carlos	Designer Lipid Droplets: Redirecting Enzymatic Activity to Plant Lipid Droplets	Talk Room 112, 3/14 @5:00 PM
Burns, Sam	Assembly and Comparative Analysis of Sabal palmetto Genomes Linked to a Herbarium Specimen	#2 U
Burns, James	Genetic Analysis of Sequence Polymorphisms by Bulk Segregant Analysis	#17 U
Calhoun, Matthew	Identifying The Gene Expression Changes in Rice Roots Upon Inoculation With The Plant Growth-promoting Bacterium, Azotobacter vinelandii.	Talk Room 117, 3/14 @10:00 AM
Causey, Trenton	P.E.A.N.U.T.S: Promoting Extraterrestrial Agriculture through Novel Utilization Techniques for Sustainability	Talk Room 117, 3/14 @4:15 PM
Chitiyo, Marylou	Do plants have a role in breaking down polyaspartic acid ? The story of α/β hydrolases	Talk Room 112, 3/14 @8:30 AM
Choity, Tanzila Kamal	Overexpression of tRNA-derived small RNAs Enhances Resistance in Plants	#29 G

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Deck, Sydney	Nostoc commune and its Potential for Use in Space Agriculture	#6 U
Deeb, Brandon	Characterizing the Functional Role, Lipid Association, and Biosynthesis of Unusual Cyclopropyl Fatty Acids in Cotton	#33 G
DeScenza, Tyler	Lunar, Oxidative, Vitrified, Enhancement: Towards in situ Resource Utilization for Space Crop Production	Talk Room 117, 3/14 @5:00 PM
Doddavarapu, Bhavya	Title: Characterization of tRNA-Derived Fragments as Inducers of DIR1-Mediated Systemic Acquired Resistance in Arabidopsis thaliana	Talk Room 117, 3/14 @4:30 PM
Du, Liren	Regulation of Vegetative Phase Change by a Nucleosome Remodeling and Deacetylase-like Complex	#42 G
Egesa, Andrew	Coordination of stomatal conductance and leaf hydraulics enhances photosynthetic efficiency and safety amid environmental fluctuations in moisture and temperature in Phaseolus vulgaris L.	Talk Room 117, 3/14 @10:30 AM
Garcia, Richard	Decoding microRNA: Small Secrets with Big Impacts on Plant Survival Under Salt Stress	Talk Room 112, 3/14 @1:15 PM
Gontijo, Gabriela	Cryopreservation effects on viability, membrane integrity and biomass of Coffea canephora seeds	Talk Room 112, 3/14 @4:30 PM
Gonzalez, Jennifer	How does size affect Suppressor-mutator (Spm) transposition frequency?	#13 U
Green, Kelsey	Salinity-driven shifts in plant-animal interactions in coastal marshes	#38 G
Guedes, Isadora	SnRK1 Signaling Regulates Plant Development and Reproduction in Rice	#23 G
Guerra, Janelle	Investigating the role of RNA in drought, heat, and combined stress in Sorghum bicolor	#41 G
Hamlin, Madison	Developing mPing-based Constructs for Transposase Assisted Target Site Integration	#9 U
Hasenstein, Karl	From auxin research to space experiments – perspectives of plant biology	Talk Room 112, 3/15 @9:30 AM
Holley, Nathan	Structural Determinants of Promiscuity in 10-Hydroxycamptothecin O-Methyltransferase from Camptotheca acuminata	#36 G
Huang, Chien-Yu	RNA silencing and epigenetic regulation in plant innate immunity and crop protection	Talk Room 112, 3/14 @10:15 AM
Huang, Pei-Cheng	A Broadly Distributed Rhizobacterium, Roseateles chitinivorans P500, Promotes Growth and Systemic Resistance via Jasmonic Acid-Dependent Oxylipin Signaling in Grasses	Talk Room 117, 3/14 @1:15 PM
Huez, Grant	Characterizing the Diversity of NLR Genes in Switchgrass	Talk Room 112, 3/14 @1:00 PM
Ibrahim, Batoul	Functional expression of NanoLuc luciferase as a versatile bioluminescent reporter in plants	#34 G
Ighalo, Deborah	Coordinated Transcriptional Regulation of Oil Biosynthesis by Avocado WRINKLED1 and WRINKLED2 in Non-Seed Tissues	Talk Room 112, 3/14 @9:15 AM

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Ingole, Hrishikesh	Developing Solutions for Peanut-Allergic Individuals Through Crossbreeding and Gene Editing	#39 G
John, Susan	From Surface Architecture to Transcriptome Reprogramming: Multilevel Mechanisms of Desiccation Tolerance in Pleopeltis polypodioides	Talk Room 112, 3/14 @10:30 AM
Kasayian, Mary	Effects of N-acylethanolamine Analogs on Physcomitrium patens Growth	Talk Room 117, 3/14 @9:00 AM
Kasili, Remmy	Determining the Physiological functions of LCIC: a close homolog of LCIB	#49
Kawalski, Nathan	Use of minimal microbiomes with spaceflight history to improve plant growth in Martian Regolith Simulants	#7 U
Kesarwani, Pragya	Drought and heat stress induced genome-wide dynamics of alternative polyadenylation and 3'UTR length in Sorghum bicolor	#47
Kimbrell, Jamie	Establishing Stress Phenotypes in Cotton: A Baseline for Lipid Remodeling Studies	#20 G
Koirtyohann, Kathryn	Nanopore sequencing of circRNA from salt-stressed maize	Talk Room 117, 3/14 @4:00 PM
Kong, Feng	Degradation of Arabidopsis SQUAMOSA-Promoter-Binding-Protein-Like Transcription Factors by Bacterial Effector-Triggered-Immunity is required for full activation of ETI	Talk Room 117, 3/14 @1:00 PM
Krueger, Jaqueline	Quorum Sensing in Chlamydomonas reinhardtii Strain Variants	#4 U
Lee, Sally	Elemental and Nutrient Profiling of Cross-Bred Tomato Plant, 'Inkspot,' Using Spectroscopic Methods (LIBS)	#16 U
Libault, Marc	What We Can Learn from Plant Single-Cell -Omics?	Keynote Room 112, 3/15 @10:30 AM
Lima, Gleice	An In-frame Deletion in OsTOR Leads to Altered Vegetative Development and Biomass Distribution in Rice	#27 G
Longo, Antonella	Structural and functional studies of the high affinity nitrate transporter NRT2.1 and its partner NAR2.1 from M. truncatula.	Talk Room 117, 3/14 @1:30 PM
Lundy, Anne	Identification & characterization of Arabidopsis alpha/beta hydrolase mutants with putative role in PAA degradation	#1 U
Maurya, Chandan	An Inducible Cre–lox System for Heritable Marker Excision in Rice	Talk Room 117, 3/14 @4:45 PM
Miklave, Nicholas	Controlling the bolting of Raphanus sativus by red and far-red light	#32 G
Mirzanejad, Amir	Caught in the Act: Capturing Decisive Junctures of Regioselective Diversification Steps in Plant Metabolic Pathways	Talk Room 117, 3/14 @1:45 PM
Mohanty, Devasantosh	IIdentification of a plasma membrane complex that interacts with phyB to regulate ROS production	Talk Room 112, 3/15 @9:15 AM
Moua, Zongca	Investigating the Molecular Mechanisms via which the Plant Growth-Promoting Bacterium, Azospirillum brasilense, Improves Growth in Salt-Stressed Rice	#15 U
Muhammad Aslam, Mehtab	Small RNA-Mediated Activation: A Global Overview and Its Role in Plant Immunity	Talk Room 112, 3/15 @9:00 AM

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Murphy, Katie	From Pixels to Phenotypes: High-Throughput Image Analysis for Plant Biology	Keynote Room 112, 3/13 @6:30 PM
Nandy, Soumen	An Inducible Cre-lox System for Selectable Marker Excision in Cowpea (Vigna unguiculata)	#50
Olofintuyi, Damilola	Improving upland cotton abiotic stress resistance through the co-overexpression of vacuolar H+ pyrophosphatase, SUMO E3 ligase and vacuolar membrane NO_3^-/H^+ antiporter genes	#24 G
Opara, Ikechukwu	Elucidating the Role of Auxin in Photosynthate Allocation in Plants	Talk Room 117, 3/14 @11:00 AM
Patel, Ohm	Reconstitution of induced systemic resistance to engineer disease-resistant plants	#10 U
Peak, Gabrielle	Altering the terminal inverted repeat sequences of the soybean CACTA transposable element dTgm9 inhibits its transposition	#5 U
Qiu, Yongjian	Functional Redundancy in PIF4-Mediated Thermosensory Transcriptional Regulation	Talk Room 112, 3/14 @10:00 AM
Ramos, Javier	Investigating the roles of small RNAs in regulating drought, heat, and combined drought and heat stress in Sorghum	Talk Room 112, 3/14 @4:45 PM
Rashotte, Aaron	Different Cytokinins and their Roles in Delaying Leaf Senescence	Talk Room 112, 3/13 @6:00 PM
Redfern, Bryce	How strain-specific EPS variants shape host permissiveness and immune modulation in Medicago symbiosis	Talk Room 112, 3/14 @1:45 PM
Renken, Kaili	Investigating mPing transposition in Camelina sativa	Talk Room 112, 3/14 @11:15 AM
Ross, Sarah	Evaluation of Arabidopsis thaliana Genotype and Root Phenotype in LMS-2 and Calcium-Supplemented Soil	Talk Room 117, 3/14 @10:15 AM
Rust, Gabrielle	Viability of genetically altered cyclic fatty acids expression in cotton	#19 U
Samin, Samia Islam	Reconstruction of induced systemic tolerance to engineer drought tolerant plants	Talk Room 112, 3/14 @10:45 AM
Sathasivam, Malarvizhi	Conserved Mechanisms of Plant Lipidome Remodeling under Heat and Cold Stresses Revealed through Meta-Analysis	#44 G
Singh, Satyam Kumar	Hormone crosstalk at the interface of CRF mediated flower and root development.	Talk Room 112, 3/14 @4:15 PM
Sligar, Madeleine	ISS-Derived Bacterial Inoculates for Plant Growth Promotion	#3 U
Storm, Amanda	Characterizing Unknowns in Plants and Pathogens	#48
Sun, Maylee	Effects of plant composition (neighbor presence and maternal lineage), and inundation regime on black mangrove (Avicennia germinans) growth	#37 G
Taylor, Claire	Investigating an ethylene insensitive mutant in the model plant Arabidopsis	#18 U
Taylor, McKenna	Plant Growth Responses to International Space Station-Derived Microbes in Simulated Microgravity by Clinorotation	Talk Room 112, 3/14 @1:30 PM
Thakur, Neha	Exploring the function of plant immune receptors in regeneration	#46

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Thingujam, Doni	Integrated Physiological and Transcriptomic Analysis of Oxidative Stress Responses in Duckweed (Lemnaceae)	Talk Room 117, 3/14 @11:30 AM
Vasquez, Yanis	Rice expressing AtDREB1A transcription factor improves Nitrogen Use Efficiency	#25 G
Vinodh Kumar, Dwaraka	Unravelling the molecular mechanism of chalkiness by transcriptomic analysis of rice targeted in VPP5 gene	#28 G
Wang, Ying	Preparing for the outbreaks of viroid diseases in crops	Talk Room 112, 3/14 @8:45 AM
Weatherwax, Anna	Vermiculture: Creating Viable Regolith-Substrate Using Earthworms	#8 U
Weerakkody, Heshini N.	A Guide or an Escort? Role of IBR5 in auxin signaling pathway in Arabidopsis	Talk Room 117, 3/14 @10:45 AM
Weng, Jing-Ke	Integrated Omics for Studying Plant Metabolism in the Age of AI	Keynote Room 112, 3/14 @2:00 PM
Widmier, Audrey	Establishing simulated growth chamber conditions to bypass annual field cycles for the mechanistic dissection of seasonal growth arrest in Populus	Talk Room 112, 3/14 @4:00 PM
Williams, Jack	Assessing plant diversity across salt marsh restoration and the cascading effects on ecosystem function	#35 G
Yang, Li	Plant Wound Healing: From Biophysical Cues to Hormonal Signaling	Talk Room 117, 3/14 @9:15 AM
Yehiav, Allona	Kin Recognition in Simulated Microgravity by Clinorotation	#14 U
Yeo, Yujeong	Understanding the ecological and genetic drivers of rice microbiomes across irrigation systems, cultivars and compartments	Talk Room 112, 3/14 @11:30 AM
Zhang, Liang	A novel RG-I acetyltransferase that functions in vascular tissue and root cap	Talk Room 117, 3/14 @8:30 AM

Program

March 13	**March 13**	**March 13**	**March 13**	**March 13**
Room 112 5 pm	Andrew Palmer	Opening Remarks		
Room 112 5:15 pm	Laura Malaguerra Tessa Burch-Smith	ASPB Introduction		
Room 112 5:30 pm	ASPB Ambassadors	Introduction		
Moderator: Amanda Storm				
Room 112, March 13 6:00 PM	Rashotte, Aaron	Different Cytokinins and their Roles in Delaying Leaf Senescence		
Room 112, March 13 6:15 PM	Barbero Barcenilla, Borja	New Dimensions of Resilience: Telomerase and Tardigrade Protection in Space-Grown Plants		
Keynote Room 112, 6:30 PM	**Murphy, Katie**	**From Pixels to Phenotypes: High-Throughput Image Analysis for Plant Biology**		
March 14	**March 14**	**March 14**	**March 14**	**March 14**
Concurrent Session 1 - Moderator: Chandan Maurya				
Room 112, 8:30 AM	Chitiyo, Marylou	Do plants have a role in breaking down polyaspartic acid ? The story of α/β hydrolases		
Room 112, 8:45 AM	Wang, Ying	Preparing for the outbreaks of viroid diseases in crops		
Room 112, 9:00 AM	Bennetzen, Jeff	Origin, Population Genetics and Metabolomics of Yaupon Holly, an Indigenous Beverage Plant of the Southeastern US		
Room 112, 9:15 AM	Ighalo, Deborah	Coordinated Transcriptional Regulation of Oil Biosynthesis by Avocado WRINKLED1 and WRINKLED2 in Non-Seed Tissues		
9:30 AM – 10 AM	**Break and Poster session**			
Moderator: Neha Thakur				
Room 112, 10:00 AM	Qiu, Yongjian	Functional Redundancy in PIF4-Mediated Thermosensory Transcriptional Regulation		
Room 112, 10:15 AM	Huang, Chien-Yu	RNA silencing and epigenetic regulation in plant innate immunity and crop protection		
Room 112, 10:30 AM	John, Susan	From Surface Architecture to Transcriptome Reprogramming: Multilevel Mechanisms of Desiccation Tolerance in Pleopeltis polypodioides		
Room 112, 10:45 AM	Samin, Samia Islam	Reconstruction of induced systemic tolerance to engineer drought tolerant plants		
Room 112, 11:00 AM	Barbero Barcenilla, Borja	Feeding the Future: Safeguarding Nutrition and Safety in Space-Grown Crops		
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Room 112, 11:30 AM	Yeo, Yujeong	Understanding the ecological and genetic drivers of rice microbiomes across irrigation systems, cultivars and compartments		
11:45 AM – 1:00 PM	**Lunch**			
Moderator: Andrea Westerband				
Room 112, 1:00 PM	Huez, Grant	Characterizing the Diversity of NLR Genes in Switchgrass		
Room 112, 1:15 PM	Garcia, Richard	Decoding microRNA: Small Secrets with Big Impacts on Plant Survival Under Salt Stress		

Room 112, 1:30 PM	Taylor, McKenna	Plant Growth Responses to International Space Station-Derived Microbes in Simulated Microgravity by Clinorotation
Room 112, 1:45 PM	Redfern, Bryce	How strain-specific EPS variants shape host permissiveness and immune modulation in Medicago symbiosis
Amanda Storm introduces:		
Keynote Room 112, 2:00 PM	**Jing-Ke Weng**	**Integrated Omics for Studying Plant Metabolism in the Age of AI**
3:00 PM – 4:00 PM	**Break and Poster session – Undergraduate Poster Judging**	
Moderator: Pragya Kesarwani		
Room 112, 4:00 PM	Widmier, Audrey	Establishing simulated growth chamber conditions to bypass annual field cycles for the mechanistic dissection of seasonal growth arrest in Populus
Room 112, 4:15 PM	Singh, Satyam Kumar	Hormone cross at the interface of CRF mediated flower and root development.
Room 112, 4:30 PM	Gontijo, Gabriela	Cryopreservation effects on viability, membrane integrity and biomass of Coffea canephora seeds
Room 112, 4:45 PM	Ramos, Javier	Investigating the roles of small RNAs in regulating drought, heat, and combined drought and heat stress in Sorghum
Room 112, 5:00 PM	Bucio, Carlos	Designer Lipid Droplets: Redirecting Enzymatic Activity to Plant Lipid Droplets
Lobby 5:15 – 6:30 PM	**Poster Session**	
Concurrent Session 2 - Moderator: Mehtab Muhammad Aslam		
Room 117, 8:30 AM	Zhang, Liang	A novel RG-I acetyltransferase that functions in vascular tissue and root cap
Room 117, 8:45 AM	Bommes, Anna	Investigate the Effects of Diffusible Signals from the Plant Growth-Promoting Bacterium, Azotobacter vinelandii, on Rice
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Room 117, 9:15 AM	Yang, Li	Plant Wound Healing: From Biophysical Cues to Hormonal Signaling
9:30 AM – 10 AM	**Break and Poster session**	
Moderator: Feng Kong		
Room 117, 10:00 AM	Calhoun, Matthew	Identifying The Gene Expression Changes in Rice Roots Upon Inoculation With The Plant Growth-promoting Bacterium, Azotobacter vinelandii.
Room 117, 10:15 AM	Ross, Sarah	Evaluation of Arabidopsis thaliana Genotype and Root Phenotype in LMS-2 and Calcium-Supplemented Soil
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Program

Room 117, 11:30 AM	Thingujam, Doni	Integrated Physiological and Transcriptomic Analysis of Oxidative Stress Responses in Duckweed (Lemnaceae)
11:45 AM – 1:00 PM	**Lunch**	
Moderator: Susan John		
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Room 117, 1:45 PM	Mirzanejad, Amir	Caught in the Act: Capturing Decisive Junctures of Regioselective Diversification Steps in Plant Metabolic Pathways
3:00 PM – 4:00 PM	**Break and Poster session - Undergraduate Poster Judging**	
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Room 117, 4:15 PM	Causey, Trenton	P.E.A.N.U.T.S: Promoting Extraterrestrial Agriculture through Novel Utilization Techniques for Sustainability
Room 117, 4:30 PM	Doddavarapu, Bhavya	Title: Characterization of tRNA-Derived Fragments as Inducers of DIR1-Mediated Systemic Acquired Resistance in Arabidopsis thaliana
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Room 117, 5:00 PM	DeScenza, Tyler	Lunar, Oxidative, Vitrified, Enhancement: Towards in situ Resource Utilization for Space Crop Production
Lobby 5:15 – 6:30 PM	**Poster Session**	
7:00 PM	**Banquet & Awards Atchafalaya Ballroom B - Student Union**	
March 15	**March 15**	**March 15** **March 15** **March 15**
Moderator: Borja Barbero		
Room 112, 9:00 AM	Muhammad Aslam, Mehtab	Small RNA-Mediated Activation: A Global Overview and Its Role in Plant Immunity
Room 112, 9:15 AM	Mohanty, Devasantosh	Identification of a plasma membrane complex that interacts with phyB to regulate ROS production
Room 112, 9:30 AM	Hasenstein, Karl	From auxin research to space experiments – perspectives of plant biology
9:45– 10:30 AM	**Break and Poster Session**	
Amanda Storm introduces:		
Keynote Room 112, 10:30 AM	**Libault, Marc**	**What We Can Learn from Plant Single-Cell -Omics**
Room 112, 11:30 AM	**Business meeting**	
Noon	Meeting ends	

POSTER LISTING

H.L Thilakshi Abeywickrama #30 G	Stress-inducible extension of tRNA fragments: formation of chimeric RNAs and their role in sequence-specific gene activation
Madaleine Alessi #45 G	Cercospora Leaf Blight infection induces cellular reactive oxygen species and organelle dysfunction
Cindy Alonso-Cocuron #11 U	A Code-Based Automated Pipeline for Complex Untargeted Metabolomics Data Processing
Joseph Balem #43 G	Keeping Cool: The role of cold response in plant wound healing
Mayank Bangari #31 G	Structural and biomechanical basis of stem lodging in grain sorghum under different water regimes
Nicholas Benedetto #12 U	Regiospecific Control and Subcellular Localization of Monoterpene Indole Alkaloid Glucosidases
Padam Bhatt #26 G	Chromatin Remodeling of Defense Gene Regulatory Elements During Plant Immune Activation
Gabriela Borja #40 G	Unraveling the stress granule (SG) transcriptome in Arabidopsis thaliana under abiotic stress
Samaya Bridges #21 G	Investigating putative Arabidopsis thaliana α/β-hydrolase for potential to degrade poly(aspartic) acid
Thomas Bryan #22 G	Duckweed as a Bioremediator of Metal-Contaminated Waters: Efficacy and Biological Implications
James Burns #17 U	Genetic Analysis of Sequence Polymorphisms by Bulk Segregant Analysis
Sam Burns #2 U	Assembly and Comparative Analysis of Sabal palmetto Genomes Linked to a Herbarium Specimen
Tanzila Kamal Choity #29 G	Overexpression of tRNA-derived small RNAs Enhances Resistance in Plants
Sydney Deck #6 U	Nostoc commune and its Potential for Use in Space Agriculture
Brandon Deeb #33 G	Characterizing the Functional Role, Lipid Association, and Biosynthesis of Unusual Cyclopropyl Fatty Acids in Cotton
Liren Du #42 G	Regulation of Vegetative Phase Change by a Nucleosome Remodeling and Deacetylase-like Complex
Jennifer Gonzalez #13 U	How does size affect Suppressor-mutator (Spm) transposition frequency?
Kelsey Green #38 G	Salinity-driven shifts in plant-animal interactions in coastal marshes
Isadora Guedes #23 G	SnRK1 Signaling Regulates Plant Development and Reproduction in Rice
Janelle Guerra #41 G	Investigating the role of RNA in drought, heat, and combined stress in Sorghum bicolor

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Madison Hamlin #9 U	Developing mPing-based Constructs for Transposase Assisted Target Site Integration
Nathan Holley #36 G	Structural Determinants of Promiscuity in 10-Hydroxycamptothecin O-Methyltransferase from Camptotheca acuminata
Batoul Ibrahim #34 G	Functional expression of NanoLuc luciferase as a versatile bioluminescent reporter in plants
Hrishikesh Ingole #39 G	Developing Solutions for Peanut-Allergic Individuals Through Crossbreeding and Gene Editing
Remmy Kasili #49	Determining the Physiological functions of LCIC: a close homolog of LCIB
Nathan Kawalski #7 U	Use of minimal microbiomes with spaceflight history to improve plant growth in Martian Regolith Simulants
Pragya Kesarwani #47	Drought and heat stress induced genome-wide dynamics of alternative polyadenylation and 3'UTR length in Sorghum bicolor
Jamie Kimbrell #20 G	Establishing Stress Phenotypes in Cotton: A Baseline for Lipid Remodeling Studies
Jaqueline Krueger #4 U	Quorum Sensing in Chlamydomonas reinhardtii Strain Variants
Sally Lee #16 U	Elemental and Nutrient Profiling of Cross-Bred Tomato Plant, 'Inkspot,' Using Spectroscopic Methods (LIBS)
Gleice Lima #27 G	An In-frame Deletion in OsTOR Leads to Altered Vegetative Development and Biomass Distribution in Rice
Anne Lundy #1 U	Identification & characterization of Arabidopsis alpha/beta hydrolase mutants with putative role in PAA degradation
Nicholas Miklave #32 G	Controlling the bolting of Raphanus sativus by red and far-red light
Zongca Moua #15 U	Investigating the Molecular Mechanisms via which the Plant Growth-Promoting Bacterium, Azospirillum brasilense, Improves Growth in Salt-Stressed Rice
Soumen Nandy #50	An Inducible Cre-lox System for Selectable Marker Excision in Cowpea (Vigna unguiculata)
Damilola Olofintuyi #24 G	Improving upland cotton abiotic stress resistance through the co-overexpression of vacuolar H+ pyrophosphatase, SUMO E3 ligase and vacuolar membrane NO_3^-/H^+ antiporter genes
Ohm Patel #10 U	Reconstitution of induced systemic resistance to engineer disease-resistant plants

POSTER LISTING

Gabrielle Peak #5 U	Altering the terminal inverted repeat sequences of the soybean CACTA transposable element dTgm9 inhibits its transposition
Gabrielle Rust #19 U	Viability of genetically altered cyclic fatty acids expression in cotton
Malarvizhi Sathasivam #44 G	Conserved Mechanisms of Plant Lipidome Remodeling under Heat and Cold Stresses Revealed through Meta-Analysis
Madeleine Sligar #3 U	ISS-Derived Bacterial Inoculates for Plant Growth Promotion
Amanda Storm #48	Characterizing Unknowns in Plants and Pathogens
Maylee Sun #37 G	Effects of plant composition (neighbor presence and maternal lineage), and inundation regime on black mangrove (Avicennia germinans) growth
Claire Taylor #18 U	Investigating an ethylene insensitive mutant in the model plant Arabidopsis
Neha Thakur #46	Exploring the function of plant immune receptors in regeneration
Yanis Vasquez #25 G	Rice expressing AtDREB1A transcription factor improves Nitrogen Use Efficiency
Dwaraka Vinodh Kumar #28 G	Unravelling the molecular mechanism of chalkiness by transcriptomic analysis of rice targeted in VPP5 gene
Anna Weatherwax #8 U	Vermiculture: Creating Viable Regolith-Substrate Using Earthworms
Jack Williams #35 G	Assessing plant diversity across salt marsh restoration and the cascading effects on ecosystem function
Allona Yehiav #14 U	Kin Recognition in Simulated Microgravity by Clinorotation

ABSTRACTS

Authors

ABSTRACTS

H.L Thilakshi Abeywickrama (Department of Biology, Texas State University, San Marcos, TX 78666, U.S.A); Sung-Il Kim (Department of Biology, Texas State University, San Marcos, TX 78666, U.S.A, current address - Department of Molecular Cellular and Developmental Biology, University of Michigan, Ann Arbor, MI, U.S.A); Hong Gu Kang (Department of Biology, Texas State University, San Marcos, TX 78666, U.S.A)

Stress-inducible extension of tRNA fragments: formation of chimeric RNAs and their role in sequence-specific gene activation

Our recent findings highlight the significance of small RNAs derived from tRNAs, termed tRNA fragments (tRFs), as important molecules in the transcriptional reprogramming associated with defense responses. tRF physically binds to their target location in a sequence-specific manner and is induced before biotic stress-responsive genes are activated, indicating a role in transcriptional activation. Interestingly, we have observed that some tRFs undergo extension via RNA hybrid formation, resulting in chimeric RNAs that consist of the initial tRF sequence followed by the sequence of the corresponding target gene. Our results show that these chimeras accumulate significantly in response to pathogen challenges. Furthermore, mutations in the 5' end sequence reduced chimeric RNA levels, indicating that this stress-inducible process is strictly sequence-specific. To further characterize these species, we utilized biotin-labeled tRFs for affinity purification; these isolated molecules are currently undergoing high-throughput sequencing for detailed structural analysis.

Prianka Acharjya (Biology, Texas State University), Heshini N. Weerakkody (Biology, Texas State University), Israel Arellano (Biology, Texas State University), Sunethra Dharmasiri (Biology, Texas State University), and Nihal Dharmasiri (Biology, Texas State University)

Surviving under Stress: Potential Role of IBR5 in Plant Resilience.

Plants often face many environmental stresses such as drought, salinity, and osmotic stress that disrupt their optimal growth and development, eventually affecting the productivity. As climate change intensifies these environmental stresses, improving stress tolerant crops has been a major goal for sustainable agriculture. By integrating hormonal and environmental signals, plants regulate their growth and development. Auxin, a major phytohormone, is involved in this process. We previously isolated an auxin resistant mutant, indole-3-butyric acid resistant5 (ibr5), which exhibited altered response to environmental stresses suggesting the involvement of IBR5 and auxin in plant responses to stress. Recent findings show that IBR5 interacts with catalase to regulate its enzyme activity, suggesting that IBR5 plays a role in H2O2 detoxification. Previous work from our laboratory indicates that IBR5 interacts with Ca2+/Calmodulin in calcium dependent manner. Our work, along with others, have revealed that auxin and environmental stress conditions results in a rapid and transient increase of calcium in plant cells, suggesting complex and intricate signaling mechanisms during plant stress responses. Here we discuss the potential role IBR5, auxin, and calcium signaling in orchestrating plant responses to environmental stresses.

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ABSTRACTS

Cercospora Leaf Blight infection induces cellular reactive oxygen species and organelle dysfunction

Accounting for around 90% of oilseed production, soybean (Glycine max) crops in the United States are responsible for contributing over $120 billion to the national economy each year, with the Midsouth region bringing in up to 15% of annual yield. Foliar diseases caused by Cercospora species, such as Cercospora leaf blight (CLB) and frogeye leaf spot (FLS), threaten significant economic losses in the Midsouth region of the United States. A potent virulence factor produced by several Cercospora species is the light-activated phytotoxin cercosporin, which generates reactive oxygen species (ROS) in host tissue, leading to membrane damage and cell death. The overarching impact of cercosporin-associated oxidative stress on host organelle structure and redox dynamics is not yet completely understood. To examine early cellular responses during infection, transmission electron microscopy was used to observe internal cellular structure in soybean leaf tissue following inoculation with Cercospora cf. flagellaris, the dominant species associated with CLB in the southern states. Inoculated soybean tissue revealed pronounced starch accumulation within chloroplasts, along with altered structural appearances of both chloroplasts and mitochondria relative to non-inoculated controls. These changes were observed in parallel with increased hydrogen peroxide accumulation, consistent with elevated oxidative stress during early stages of infection. To further assess the impact of cercosporin-associated ROS production, soybean leaves were chemically treated with compounds that inhibit cercosporin production prior to inoculation. Preliminary data suggests a significant difference in hydrogen peroxide accumulation between treated and untreated soybeans following pathogen inoculation. Collectively, these preliminary findings indicate that early Cercospora infection is associated with early ultrastructural changes and altered redox homeostasis in soybeans. The observed changes in chloroplast and mitochondrial structure, together with hydrogen peroxide accumulation, suggest that cercosporin-associated oxidative stress contributes to early cellular modifications during host-pathogen interaction.

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A Code-Based Automated Pipeline for Complex Untargeted Metabolomics Data Processing

Untargeted metabolomics is a powerful, discovery-driven approach that enables comprehensive characterization of metabolic profiles across diverse biological systems. By capturing thousands of molecular features, untargeted metabolomics offers substantial biological insights. However, the complexity and scale of untargeted metabolomics data processing remain major analytical bottlenecks. Existing workflows often rely on scattered and difficult software tools, extensive manual intervention, and non-standardized processing strategies, limiting reproducibility and slowing down biological interpretation of results. To address these challenges, a custom, code-based software framework was designed to simplify, standardize, and automate complex untargeted metabolomics data processing. This framework integrates essential processing steps – including identification, feature filtering, and data amalgamation – into a modular and adaptable

pipeline compatible with diverse experimental designs and analytical platforms. Emphasis was placed on transparent software architecture and reproducible execution to support consistent handling of high-dimensional metabolomics datasets. Application of this framework substantially reduces processing time and user intervention while preserving biologically meaningful data across samples. This procedure was tested on coffee from the Coffea arabica accessions IAC 2211-6 and IAC 125 RV resistant and susceptible to the causal agent of bacterial blight (Pseudomonas coronafaciens pv. garcae), respectively, to identify biomarkers of resistance. By aligning computational workflows with downstream biological and pathway-level analyses, these coding programs lower the technical barrier to untargeted metabolomics and enhance interpretability. This presented framework facilitates reproducible, scalable, and biologically informed metabolomic analyses, accelerating discovery through streamlined and automated data processing.

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Keeping Cool: The role of cold response in plant wound healing

An essential feature of an organism is the ability to maintain a barrier between its environment and its interior. Failure to do so, as is the case in wounding, usually results in extreme distress or death. Given that plants are sessile organisms, they are subject to many different types of wounding. These wounds are often the primary method by which pathogens bypass physical host defenses and initiate infection. Understanding how plants respond to wounding and complete the healing process can serve as the basis for improving resistance to pathogens that use wounds for entry. A recently observed component of plant wounding is evaporative cooling, which has been shown to be responsible for wound-induced temperature reduction and cold-responsive gene induction. This relationship allows for 1) the monitoring of healing progression in wounded tissue and 2) investigation into the role of cold response in wound healing. A machine-learning based pipeline for thermal image analysis expedites comparison of wound healing progression in plants of differing age, genotype, environment, etc. Mutant Arabidopsis plants, including cold-responsive and phytohormone signaling deficient genotypes, have been found to have reduced healing capacity relative to wild-type Arabidopsis. Functional characterization of these healing-related pathways and immune response crosstalk will be used to develop novel approaches to reducing risk of infection via wounds. This work seeks to understand the disparities in plants that have poorer healing capacity, and establish methods to improve plants' capacity to heal after wounding events.

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Structural and biomechanical basis of stem lodging in grain sorghum under different water regimes

Sorghum [Sorghum bicolor (L.) Moench] is generally grown under water-limited conditions in the tropical and subtropical regions worldwide. Drought stress during the post-anthesis phase can

lead to mechanical failure of the sorghum stalks and induce lodging. Lodging poses significant agronomic challenges and lowers grain yield and quality. In present study, a novel field-based phenotyping device; DARLING (Device for Assessing Resistance to Lodging in Grains) was used to evaluate the bending strength of 34 sorghum inbred lines grown under well-watered and limited-water conditions at the New Deal Research over two years. The tested stalks from field also tested for material and geometrical analysis in the laboratory. Among the geometric properties slenderness ratio was negatively correlated (r =-0.36), while moment of inertia (r = 0.58*) and section modulus (r=0.60*) are positively correlated with the bending strength. The integrated puncture score shows a stronger correlation with bending strength than maximum puncture force under both well-watered (r = 0.58*) and water-limited (r = 0.64*) conditions, suggesting a strong influence of geometric properties over material properties on bending strength. Furthermore, to understand the genetic control of stem strength, a bi-parental population derived from a cross between RTx430 and SC35, consisting of 181 individuals, was phenotyped using DARLING for stem strength. One major QTL was identified on Sb01 under both irrigated and water limited conditions. No colocalization with previously reported QTLs for plant height and stay-green traits was observed, indicating novel and independent genetic control of stem strength. Candidate genes, encoding WD40 repeat proteins, gibberellin-regulated proteins, and F-box domains were identified within the stable QTL region. Additionally, breeder-friendly markers will be developed to integrate the identified novel QTL into breeding lines, facilitating the development of lodging-tolerant hybrids. Overall, enhancing stalk strength offers an effective strategy for lodging resistance while addressing the trade-off between yield and stability.

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Feeding the Future: Safeguarding Nutrition and Safety in Space-Grown Crops

Space agriculture is vital for sustaining human life beyond Earth, yet crops grown under extraterrestrial conditions face serious nutritional and safety challenges. Plants cultivated aboard the International Space Station (ISS) show reduced levels of key minerals such as calcium and magnesium, while those grown on lunar regolith simulants often accumulate high concentrations of toxic metals including aluminum, copper and chromium. These findings underscore the need for strict evaluation of nutrient content and contaminant load in space-grown food. Nutrient deficiencies could intensify spaceflight-related health problems such as bone demineralization, immune dysfunction, and gastrointestinal disorders linked to increased intestinal permeability (“leaky gut”). Meanwhile, heavy metal uptake from regolith substrates introduces additional toxicity

risks that could compromise crew health over extended missions. To feed humanity beyond Earth, we must not only grow plants that survive in space, but ensure they nourish and protect those who depend on them.

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New Dimensions of Resilience: Telomerase and Tardigrade Protection in Space-Grown Plants

To grow life beyond Earth, we must engineer plants that can endure the unfiltered radiation of deep space. Outside Earth's magnetic shield, galactic cosmic rays, neutrons, and gamma radiation threaten genome stability, particularly at telomeres; regions highly vulnerable to oxidative damage. Plants engineered to express high levels of telomerase or the tardigrade-derived Dsup (damage suppressor) protein showed significantly reduced radiation-induced DNA damage under simulated GCR, neutron, and gamma exposure, and most notably aboard the International Space Station (ISS). Although the mechanism of Dsup remains unknown, its origin from extremotolerant tardigrades suggests a potent ability to protect DNA. Plants expressing either high telomerase or Dsup consistently displayed lower genomic oxidation, demonstrating enhanced resilience in harsh radiation environments. These findings identify two promising pathways to strengthen plant radiotolerance and advance the development of durable, self-sustaining crops for long-duration and interstellar missions.

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Regiospecific Control and Subcellular Localization of Monoterpene Indole Alkaloid Glucosidases

Monoterpene indole alkaloids (MIAs) are one of the most diverse classes of specialized metabolites with ~3000 members produced by medicinal plants such as Catharanthus roseus and Rauvolfia serpentina. Many of these MIAs exhibit an array of biological activities but are difficult to synthesize. Currently, the production of several clinically important MIAs is achieved via direct extraction from medicinal plants with low yields. To increase MIA production, metabolic engineering may be used by reconstituting plant metabolic pathways into microbial systems. Functional characterization of enzymes involved in these pathways is critical to accelerate metabolic engineering efforts. In many MIA-producing species, strictosidine and its aglycone serve as precursor and central intermediates of diverse alkaloids, respectively. However, Camptotheca acuminata utilizes multiple isomers of strictosidinic acids to produce chemotherapeutic

camptothecin. In this study, in silico workflow combining homology modeling, post-docking molecular dynamics refinement, followed by quantum mechanical energetic analysis was employed to investigate the substrate binding architecture of one C. acuminata strictosidinic acid glucosidase (CaAGD1) compared with high-fidelity C. roseus 3α-(S)-strictosidine (CrSGD). The behavior of CaAGD1 was assessed by determining its subcellular localization for the prospect of metabolic engineering in microbial systems. CaAGD1 was fused with yellow fluorescence protein (YFP) for expression in Nicotiana benthamiana and visualization via fluorescence microscopy. As was found previously with CrSGD, CaAGD1 was localized in the nucleus. These comparative structural analyses combined with subcellular localization studies revealed evolutionary insights into plant glucosidases and the improved yield of diverse phytochemicals.

Jeff Bennetzen (Department of Genetics and Georgia Research Alliance, University of Georgia); Ben Long (Department of Genetics, University of Georgia)

Origin, Population Genetics and Metabolomics of Yaupon Holly, an Indigenous Beverage Plant of the Southeastern US

Yaupon holly (inappropriately designated Ilex vomitoria) is endemic to the Southeastern US. Yaupon leaves were used by Indigenous peoples as a caffeinated beverage source for thousands of years. Yaupon tea's popularity with early European colonists led to a campaign of erasure by the British East India Company, causing its abandonment as a beverage for nearly two hundred years. In the last 70 years, first as a landscape plant and then as a tea, yaupon has re-emerged as an economically and culturally significant plant. I will describe our germplasm collection, nursery development, DNA genotyping, population genetic analysis and preliminary metabolomics on this robust native plant, which is unusual both in its coastal growth preferences and its close relatedness to South American hollies.

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Chromatin Remodeling of Defense Gene Regulatory Elements During Plant Immune Activation

Following pathogen attack, plants undergo rapid transcriptional reprogramming of defense genes, mediated by diverse epigenetic mechanisms. The induction of defense genes through chromatin remodeling, which facilitates the transcriptional machinery's access to chromatin, is well documented at later stages of infection; however, early defense remains largely uncharacterized. tRNA-derived fragments (tRFs) have recently been found to be early responsive genome-binding immune players known to regulate more than 500 effector-triggered immunity (ETI) genes in Arabidopsis. We scanned chromatin accessibility in multiple time points at promoter/enhancer and tRF-binding regions of PR1 (Pathogenesis-Related 1) gene to see the nature of change in accessibility in response to both pathogen and tRF over time using ATAC-PCR. We found that promoter/enhancer and tRF-binding regions in the PR1 gene become accessible in 1-hour post-infiltration, reaching accessibility levels comparable to those observed at later time points. This result identifies early chromatin remodeling as a defining feature of immune activation. Taking together, these findings support a model in which tRF-induced chromatin remodeling is among the earliest events in the initiation of defense responses.

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Investigate the Effects of Diffusible Signals from the Plant Growth-Promoting Bacterium, Azotobacter vinelandii, on Rice

Plants form associations with beneficial microbes, including arbuscular mycorrhiza (AM), rhizobia, and 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 (LRS) 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 and the host genetic pathways 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 to 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. One recent study showed that diffusible signals from Azospirillum brasilense, a PGPB, stimulated growth in Arabidopsis thaliana. We established an experimental system in which diffusible signals from PGPB Azotobacter vinelandii could promote rice growth. Our results suggest that the bioactive signals secreted by A. vinelandii are recognized by rice, leading to enhanced growth. Recently, we performed an RNA-sequencing experiment to identify the underlying transcriptomic changes regulating the effects of these microbial signals on rice. Preliminary analyses revealed 665 differentially expressed genes (DEGs) in our dataset. We are currently performing the datamining and expect plant genes encoding receptor kinases, transcription factors, and hormone pathways to be differentially expressed. Our results will identify the host genetic pathways regulated by the microbial signals. In the long term, we plan to identify the chemical nature of these microbial signals, which could have important implications for sustainably improving agriculture and addressing human health concerns.

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Unraveling the stress granule (SG) transcriptome in Arabidopsis thaliana under abiotic stress

Climate change is one of the greatest challenges facing agriculture today, as increasing heat, drought, and cold stress severely impact plant growth and yield. Plants are sessile organisms and cannot escape unfavorable environmental conditions; instead, they rely on intrinsic defense mechanisms for survival. One such response is the rapid formation of stress granules (SGs). These membrane-less condensates form when translation is stalled leading to the accumulation and condensation of specific proteins, mRNAs, including some metabolites. By reorganizing and protecting key molecules, SGs help cells survive stress and recover efficiently when conditions improve. While proteomic and metabolomic profiles of heat-induced SGs are studied, transcriptomic analyses were limited. Therefore, we analyzed the stress granule–associated transcriptome under heat, cold, and drought conditions in Arabidopsis thaliana. To achieve this, an Arabidopsis transgenic line overexpressing RBP47b-GFP was used. RBP47b is a well-established SG marker protein. Four-week-old plants of this line were exposed to heat, drought, or cold stress. Following stress treatment, stress granules were isolated by immunoprecipitation using anti-GFP

beads pulling down the GFP-tagged scaffold protein RBP47b. After which RNA was isolated and sequenced. RNA-Seq analyses revealed that most transcripts originated from exonic regions (49%) and were mRNAs (>75%). The SG-associated transcriptome varied across conditions, with minimal overlap of differentially expressed genes between heat, cold, and drought. Drought caused the largest changes (1,181 up and 527 down), followed by heat (302 up and 41 down) and cold (161 up and 527 down). Enriched biological processes for these transcripts included stress response and ER protein folding under heat, general stress and defense signaling under drought, and cold/ABA, water-related responses, primary metabolism, and photosynthesis under cold. Comparison with total RNA m6A profiles revealed that m6A-modified transcripts are present in SGs, with most corresponding to upregulated genes. Overall, these findings indicated that stress granules selectively sequester mRNAs in a condition-specific manner, reflecting the distinct cellular responses to heat, cold, and drought stress.

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Investigating putative Arabidopsis thaliana α/β-hydrolase for potential to degrade poly(aspartic) acid

Polyaspartic acid (PAA) is a biodegradable polymer and is increasingly being incorporated into agricultural systems as a biostimulant to enhance nutrient availability and crop performance. Its protein-like backbone and the abundance of negatively charged carboxyl groups make PAA well-suited for interaction with biological systems, biodegradation, and environmentally friendly applications. Although bacterial hydrolases have generally been implicated in the biodegradation process of PAA into aspartate, plants are known to release root extracellular enzymes, including α/β-hydrolases into the rhizosphere. However, it is not clear whether plant hydrolases contribute to PAA association or breakdown. Previously, we showed that some hydrolase enzymes, nitrogen assimilation, and the amino acid metabolism pathways in Arabidopsis thaliana were upregulated in response to PAA (250 ppm). The objective of the study is to begin characterizing putative A. thaliana hydrolases for their potential to break down PAA. These enzymes belong to the α/β-hydrolase superfamily, based on predicted domains and other structural features, and were shown to be highly upregulated in response to PAA. Bioinformatics analyses were conducted using AlphaFold Server and PyMOL to predict the structure. The results show that the protein possesses structural and electrostatic features that enable interaction with PAA. We have also established that the core α/β-hydrolase domains align with the structure of bacterial homologues that are known to interact with and degrade PAA. To date, we have attempted to identify expression conditions in E.coli with the aim of obtaining soluble enzyme to assay for activity. We have successfully expressed and purified the protein, establishing feasibility for downstream enzymatic characterization. Current efforts focus on identifying if enzymatic cleavage of the substrate PAA is occurring. Preliminary findings suggest enzymatic potential within plants to recognize and cleave polyaspartic acid, expanding the functional scope of plant α/β hydrolases. If confirmed these results open new avenues for understanding polymer–enzyme interactions.

ABSTRACTS

Thomas Bryan (University of Alabama in Huntsville)

Duckweed as a Bioremediator of Metal-Contaminated Waters: Efficacy and Biological Implications

A common sight in ponds and streams worldwide, duckweeds are among the simplest angiosperms in existence. Resilient, rapidly propagating, and fast growing; duckweeds serve as ideal model organisms for research of the biotic and abiotic roles of plants within aquatic systems. This research is focused on determining the viability of duckweed to serve as a bioremediator of metallic oxide particles in contaminated waters. Metallic oxide particles are regularly introduced to the environment by industrial processes, as well as the natural weathering of metallic minerals. While benign at low concentrations, these particles pose a threat of toxicity to any organisms utilizing affected waterways when present in high quantities. This research seeks to analyze the bioremediation potential of four duckweed species, Lemna minor, Lemna tenera, Spirodella polyrhiza, and Wolffia globosa, for aluminum, titanium, and iron oxides Utilizing a combination of dry mass analysis, ICP-OES, TEM analysis, RNA expression, and rootlet imaging, the degree of uptake of each metal for each species will be determined. Additionally, the biological impacts induced by the absorption of the metals will be analyzed to determine implications for the long-term viability of bioremediative populations. If duckweeds readily absorb these metal oxides, then it could serve as a cheap and reliable means of decontaminating waterways. Such information would also serve to improve our understanding of the complex physical and chemical interactions between metal oxides and plant tissues.

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Designer Lipid Droplets: Redirecting Enzymatic Activity to Plant Lipid Droplets

Lipid droplets (LDs) are dynamic organelles that play central roles in lipid storage, metabolism, and stress responses in plants. While LD-associated proteins regulate droplet formation and maintenance, the ability to deliberately modify LD composition remains limited. Here, we explore a protein-targeting strategy to engineer lipid droplet composition by localizing enzymes of interest directly to the LD interface. We designed a chimeric protein consisting of GFP-tagged Lipid Droplet-Associated Protein (LDIP) fused to a protein of interest (POI) at the C-terminus. This construct leverages LDIP's native lipid droplet targeting capability to recruit enzymatic activity to LDs, with the goal of locally altering lipid composition or metabolic output. Constructs were expressed in tobacco leaf tissue, and subcellular localization was assessed using fluorescence microscopy to confirm lipid droplet association. Preliminary results indicate that the GFP-LDIP-POI fusion localizes to globular structures consistent with LDs, supporting the feasibility of LDIP-mediated targeting. Ongoing work focuses on assessing the impact of POI localization on LD morphology and lipid composition. This approach establishes a modular platform for directing metabolic enzymes to lipid droplets and provides a framework for rational engineering of lipid storage compartments in plants. Preliminary results indicate that the GFP-LDIP-POI fusion localizes punctate structures consistent with LDs, supporting the feasibility of LDIP-mediated targeting. To assess whether POIs retain enzymatic functionality in the chimeric context, lipid extracts were analyzed by gas chromatography. These analyses enable screening for specific lipid products generated by the POIs and provide a means to evaluate the efficacy of enzyme activity on LDs. Overall, this work contributes to the development of synthetic biology strategies for spatial control of metabolism in

plant cells and has potential applications in metabolic engineering, stress resilience, and the production of value-added lipids.

Sam Burns (Computer Science, Engineering & Mathematics, USC Aiken), C. Nathan Hancock (Biology and Geology, USC Aiken)

Assembly and Comparative Analysis of Sabal palmetto Genomes Linked to a Herbarium Specimen

Sabal palmetto is a palm native to the southeastern United States, Cuba, and the Bahamas, yet its genomic diversity and population structure remain largely uncharacterized. We assembled a Sabal palmetto genome during an undergraduate bioinformatics course and expanded the work to quantify local genetic diversity in the Aiken, South Carolina region. This project now aims to create a permanent, verifiable reference by linking our genomic dataset to a curated herbarium specimen at the University of South Carolina Herbarium (USCH). We collected leaf tissue from 20 trees in Aiken and generated resequencing reads to characterize genetic variation. Reads were aligned to the reference assembly, processed through a standard variant-calling workflow, and variants are annotated to estimate the amount and distribution of genetic variation across sampled trees. In parallel, we are preserving and formally depositing a representative specimen from Fort Moultrie so the sequence data are anchored to a physical specimen that can be re-examined for identity and future study. By coupling population-scale resequencing with an archived specimen, this work strengthens reproducibility and enables confident reuse of the dataset.

James Burns (Dept. of Biological, Ecological, and Earth Science); C Nathan Hancock (Dept. of Biological, Ecological, and Earth Science)

Genetic Analysis of Sequence Polymorphisms by Bulk Segregant Analysis

Glycine max, commonly known as soybean, is an important crop producing about 40% of the world's edible vegetable oil and protein meal. Soybeans require low amounts of chemically fixed nitrogen and as a result, have lower production and energy costs than most crops. One of the goals of the Hancock laboratory is to identify genes important for soybean growth. To accomplish this, mutagenized soybean populations are screened for abnormal growth. We performed genetic analysis on an F2 population segregating for a dwarf phenotype, which indicated that the phenotype was recessive. The goal of this project is to analyze the variants segregating in the F2 plants to identify which mutation is causing the dwarf trait. F2 seeds and controls were planted in the field and heights were determined throughout the growing season. DNA was extracted using the CTAB method, grinding via bead mill, chloroform for phase separation, isopropanol for precipitation, and washed with ethanol. The DNA was quantified, diluted, and analyzed using genotyping primers targeting identified mutations. This project has enabled me to learn about genetics in a way that prepares me for a career in agricultural genetics.

Matthew Calhoun (Biology, UCA); Anna Bommes (Biology, UCA); Zongca Moua (Biology, UCA); Madelynn Matchett (Biology, UCA); Karis Turner (Biology, UCA); and Arijit Mukherjee (Biology, UCA).

Identifying The Gene Expression Changes in Rice Roots Upon Inoculation With The Plant Growth-promoting Bacterium, Azotobacter vinelandii.

As global populations grow and natural resources become increasingly constrained, crop systems must transition from high-input, chemically dependent models to biologically optimized systems that leverage naturally occurring beneficial microbes. One option to improve crop production sustainably is to take advantage of existing beneficial plant-microbe associations. For instance, major crops such as rice and maize can benefit from associations with different plant growth-promoting bacteria (PGPB). Studies have shown that these PGPB (e.g., Azospirillum, Herbaspirillum, Azotobacter) promote plant growth primarily via nitrogen fixation and phytohormone secretion. However, our current understanding of the underlying molecular mechanisms involved in these associations is limited. First, we set up an experimental system where Azotobacter vinelandii could promote rice growth. Next, to identify the gene expression changes occurring in rice roots upon inoculation with A. vinelandii we performed an RNA-seq experiment recently. Preliminary analyses revealed 417 differentially expressed genes (DEGs) in our dataset. We are currently performing the datamining and expect to identify genes involved in the flavonoid biosynthesis pathway, defense, and hormone signaling to be differentially expressed as these genes have been implicated to play important roles in other plant-microbe symbioses. Similarly, we also expect to identify several genes encoding for transcription factors, protein kinases, and transporters in our dataset. Overall, our study will identify several promising targets for future genetic studies and offer key insights into the genetic pathways regulating this important plant-microbe association.

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P.E.A.N.U.T.S: Promoting Extraterrestrial Agriculture through Novel Utilization Techniques for Sustainability

Space crop production is anticipated to be mission-critical for enabling a sustainable, long-term human presence on the Lunar and Martian surface. Given the lack of in situ resources, crop cultivation will require continuous human or automated inputs, including water, atmospheric regulation, and bioavailable nutrients. Consequently, the development of efficient, closed-loop waste-recycling systems will be essential for successful bioregenerative life support systems. Regolith-based agriculture proposes an alternative to the cost and risk associated with continuous resupply. However, due to fine particle sizes, harsh chemical compounds, and a general lack of available nutrients, extraterrestrial regolith is compositionally harmful to plant growth. On Earth when a soil-like substrate exhibits dense compaction and excessive drainage similar to that of these extraterrestrial regolith simulants, inert ‘spacers’ such as perlite or vermiculite are a typical solution. However, shipping bulk quantities of inert spacer materials is not feasible due to resupply limitations, thus highly lignocellulosic plant waste may be able to function analogously. Here Arachis hypogaea (Peanut) shells have been explored for their ability to promote plant growth within a lunar regolith simulant as an in situ generatable spacing amendment. Lactuca sativa (Lettuce) has been grown in this amended regolith simulant and characterized by plant growth metrics such as above and below ground biomass, root and stem lengths, scanning electron microscopy, and quantitative pigmentation analyses. The amended regolith simulant has also been characterized for plant growth metrics such as water-holding capacity, pH, and bulk density. Peanuts have also been grown in a reclaimed Martian regolith simulant to determine growth feasibility and metrics within a similar high compaction and high drainage substrate. Further growth trials and characterization will

be conducted to determine relevance and repeatability, and further chemical analyses will be conducted as a follow-up study.

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Do plants have a role in breaking down polyaspartic acid ? The story of α/β hydrolases

Poly(aspartic acid) (PAA) is an environmentally friendly biopolymer applied as a biostimulant to enhance crop growth and yields. The mechanism by which PAA enhances yield is not established, although the general hypothesis is that the polymer functions to hold nutrients within the rhizhosphere due to the negative charges associated with the backbone structure. Like other biostimulants, PAA triggers physiological and molecular changes, but its association and dynamics with the plant roots are not understood. Hydrolase enzymes from river bacteria Pedobacter and Sphingomonas spp. are known to sequentially break down polyaspartic acid to its monomer units. Interestingly, aspartate is an essential metabolite for plant growth processes. To investigate molecular responses to PAA, a whole genome transcriptome analysis was conducted using Arabidopsis thaliana seedlings treated with 250 ppm PAA. RNA sequencing identified 462 differentially expressed genes (DEGs), with 245 upregulated and 217 downregulated. Key pathways affected included photosynthesis—highlighted by the upregulation of 11 light harvesting complex genes—as well as amino acid and nitrogen metabolism. Physiological measurements supported the transcriptomic findings. PAA treated Arabidopsis plants exhibited a 33% increase in leaf area, a 25% increase in chlorophyll content ($p \leq 0.05$), and a four fold increase in photosynthetic rate ($p \leq 0.001$). These changes suggested enhanced nutrient assimilation and raised new questions about potential plant mediated modification or utilization of PAA. Further bioinformatic analyses revealed several Arabidopsis homologues of bacterial PAA degrading hydrolases. Ongoing work is focused on characterizing candidate Arabidopsis α/β hydrolases to determine their potential to degrade or modify PAA. These findings improve our understanding of plant responses to polyaspartic acid and provide a basis for its mode of action. Further investigation into the biological degradation pathways will promote efforts to integrate PAA into sustainable crop production systems.

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Overexpression of tRNA-derived small RNAs Enhances Resistance in Plants

The significance of small RNAs derived from tRNAs, known as tRNA fragments (tRFs), is increasingly recognized in transcriptional reprogramming associated with plant defense responses. These tRNA fragments (tRFs), demonstrate sequence-specific binding to their target genes, leading

to the induction of transcription. However, functional characterization of tRFs in plants has been challenging because there are currently no well-established transgenic systems specifically designed for their stable expression. To overcome this limitation, we developed a transgenic system driven by a constitutively active U6 promoter, which is commonly used to express guide RNAs in CRISPR/Cas9 systems. We selected a set of tRFs for functional analysis, including fragments that are induced after infection with avirulent Pseudomonas syringae and others that were not. The infection-induced tRFs were collectively named pathogen-responsive tRFs (patro-tRFs). Functional analyses revealed that overexpression of patro-tRFs, achieved through transient expression in Nicotiana benthamiana and stable transformation in Arabidopsis, triggered ion leakage consistent with immunity-associated programmed cell death. Furthermore, transgenic Arabidopsis lines expressing patro-tRFs exhibited upregulation of the defense marker gene PR1. Although the upregulation of PR1 gene was moderate, these findings suggest that tRFs may play a role in immune signaling and highlight their potential utility in crop improvement strategies.

Sydney Deck (Department of Aerospace, Physics, and Space Sciences, Florida Institute of Technology) Haley Murphy (Department of Ocean Engineering and Marine Sciences, Florida Institute of Technology) Dr. Andrew Palmer (Department of Ocean Engineering and Marine Sciences, Florida Institute of Technology)

Nostoc commune and its Potential for Use in Space Agriculture

Martian and Lunar regolith are both incredibly hostile to plant life for several reasons. If humanity wants to establish long-term colonies on the Moon and Mars, a process is needed to make in-situ resources available for use. This process must be low-cost and sustainable, thus making bioweathering and biomining attractive avenues for research. Both Lunar and Martian regolith are severely lacking in bioavailable carbon and nitrogen sources. Nostoc commune is a cyanobacterium that can fix atmospheric nitrogen and make it biologically available. At the same time, it also excretes polysaccharides that can readily serve as a carbon source. We have proposed using N. commune to introduce these nutrient sources into the regolith by culturing it in Lunar and Martian regolith simulants. Culturing bacteria in regolith is a sustainable, low-maintenance process, which adds to its appeal as a practical solution. Once N. commune had grown to cover the surface of the regolith, over four weeks, the regolith was dried, and the bacteria mixed in to ensure even distribution. In the experiment, the bacteria were grown in sand, LHS-2, and JEZ-1. Once the samples had been dried and mixed, they were each transferred into pots, with seeds of Arabidopsis thaliana (Columbia-0). While preliminary, we discuss our findings in terms of their potential to the use of microorganisms like N. commune as a biofertilizer in a Lunar or Martian regolith-based agriculture system.

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Characterizing the Functional Role, Lipid Association, and Biosynthesis of Unusual Cyclopropyl Fatty Acids in Cotton

The prevalence of cotton as one of the world's most valuable non-food cash crops is largely owed to the value associated with the fibers produced. Though fiber synthesis and improvements remain a key area of cotton research, the presence of unusual fatty acids presents a unique opportunity to further increase the value of the plant. These unusual fatty acids, known as cyclopropyl fatty acids (CFA), are characterized by the presence of a 9,10-cyclopropyl group on the hydrocarbon tail that gives these molecules unique oxidative and reactive stability somewhere in between that of saturated and unsaturated fatty acids. CFA have widespread application owed to this chemical behavior, with industrial uses as biofuel/biofuel additive, cold flow improver, waterproof liner, synthetic resin, and as a chemical feedstock. Despite their discovery in cotton and other plants decades ago, little has been reported about CFA, leaving significant knowledge gaps surrounding their synthesis, how they are trafficked in the lipidome, and their potential function. To this end, my research focuses on attempting to identify enzymes involved in CFA synthesis as well as characterizing the distribution of CFA in the lipidome to inform headgroup specificity and elucidate their role in plants. Initial attempts to identify putative genes involved in CFA synthesis utilized a virus-induced gene silencing (VIGS) approach followed by subsequent fatty acid analysis via gas chromatography flame ionization detection (GC-FID). Though silencing has not revealed any new genes directly involved in CFA synthesis, two targets have shown their capability to alter CFA content transiently. Cyclopropane synthase (GhCPS) and fatty acid desaturase (GhFAD2) both compete for the same substrate, oleic acid, resulting in significant decreases/increases in CFA content when silenced and making them ideal targets to tease apart the mechanisms surrounding these unusual fatty acids. Multiple large omics analyses have been performed on these targets, including RNA-Seq, metabolomics, and lipidomics, and have revealed details about changes in fatty acid derived signaling molecules associated with CFA levels. This presentation explores the many approaches taken to understand this pathway and the unique advantages CFA might confer to cotton.

Tyler DeScenza (BES, Florida Institute of Technology) Andrew Palmer (OEMS, Florida Institute of Technology)

Lunar, Oxidative, Vitrified, Enhancement: Towards in situ Resource Utilization for Space Crop Production

Lunar, Oxidative, Vitrified, Enhancement (L.O.V.E): Presently, the Technological Readiness Level (TRL) of hydroponics for space agriculture applications surpasses that of regolith-based agriculture (RBA) on the Moon. Lunar regolith presents several challenges, making it a sub-optimal growth medium for many plants. Existing studies show lunar regolith to not be a viable substrate for space crop production 'off the shelf'. However, there is the potential for Lunar regolith to contribute both to crop production and the larger goals of Bioregenerative Life Support Systems (BLSS) even if it does not serve as a direct substrate. One relevant approach is to modify regolith components by binding them via vitrification and sintering techniques to limit chemical leeching. High temperature vitrification and sintering have long been practiced on Earth, as vitrified composites benefit from increased weathering resilience and stability under a wide range of temperature fluctuations. Here we present a viable vitrification process for the fabrication of Lunar Regolith composite ceramics. Our process is based on the composition of Lunar Highland Simulant 1 (LHS-1) which is similar in properties to classical ceramics with iron oxide glaze. Materials generated by this process were evaluated for their ability to support crop growth in hydroponic systems as an alternative to

substrates like Lightweight Expanded Clay Aggregate (LECA). We consider this hybridization of regolith-based agriculture with hydroponics in terms of its improved in situ resource utilization (ISRU) as well as its capacity to support plant growth both alone and as a component of a BLSS.

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Title: Characterization of tRNA-Derived Fragments as Inducers of DIR1-Mediated Systemic Acquired Resistance in Arabidopsis thaliana

Abstract: Systemic acquired resistance (SAR) enables plants to develop long-lasting, broad-spectrum immunity following a localized pathogen attack. The Defective in Induced Resistance 1 (DIR1) gene encodes a lipid transfer protein essential for SAR signal movement, yet its potential link to RNA-mediated defense pathways remains unclear. Here, we investigate the involvement of DIR1 in regulating small RNA (sRNA)-mediated immune signaling in Arabidopsis thaliana. Using dir1-2 mutant and wild-type plants, we analyzed the accumulation and systemic movement of defense-associated sRNAs following pathogen challenge. Conventional resistance assays revealed enhanced resistance in primed wild-type plants compared to mock-treated controls, whereas dir1-2 mutants displayed compromised systemic resistance. In addition, expression of the SAR marker PAD3 gene accumulated in distal leaves of primed wild-type plants but were markedly reduced in dir1-2. Interestingly, the systemic movement of an immunity-associated tRNA-derived fragment was compromised in dir1-2 relative to wild-type plants. These data suggest that DIR1 facilitates the transport or stabilization of sRNA-based immune signals that mediate SAR establishment. Our results uncover an unrecognized crosstalk between lipid-based and RNA-mediated signaling networks and provide new insights into the molecular mechanisms by which DIR1 coordinates systemic immunity in plants.

Liren Du (Biological Science department, University of South Carolina), Tieqiang Hu (Biological Science department, University of South Carolina), Mingli Xu(Biological Science department, University of South Carolina)*

Regulation of Vegetative Phase Change by a Nucleosome Remodeling and Deacetylase-like Complex

Flowering plants undergo a juvenile-to-adult vegetative phase transition before entering the reproductive stage, and the precise timing of this transition is critical for plant fitness. Previous studies have shown that the chromatin remodeler PICKLE (PKL) and the histone deacetylase HDA9 act together to regulate vegetative phase change. In animals, orthologs of PKL and HDA9 are components of the Nucleosome Remodeling and Deacetylase (NuRD) complex. However, whether a comparable NuRD-like complex exists in plants has remained unclear. Our studies of vegetative phase change revealed that mutations in PKL, HDA9, MSI4, and POWERDRESS (PWR)—genes whose animal orthologs are NuRD components—result in delayed vegetative phase transitions. Although mutations in METHYL-CPG-BINDING DOMAIN 7 (MBD7)—whose animal ortholog MBD2 is also a component of NuRD—do not affect the timing of phase change, MBD7, PKL, HDA9, PWR,

and MSI4 physically interact and bind regulatory regions of MIR156A and MIR156C, including CG-methylated regions. During vegetative development, H3K27ac levels at these loci decrease at early stages, followed by increased deposition of the repressive histone mark H3K27me3 at later stages. Our findings suggest the existence of a functional NuRD-like complex in plants that integrates DNA methylation with Polycomb-mediated gene silencing to regulate vegetative phase change.

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Coordination of stomatal conductance and leaf hydraulics enhances photosynthetic efficiency and safety amid environmental fluctuations in moisture and temperature in Phaseolus vulgaris L.

Higher photosynthetic efficiency in plants is challenged by fluctuating environmental conditions that affect water availability and CO2 conductance. However, through adaptation, some crops have acquired anatomical traits that support enhanced photosynthetic efficiency under such limiting conditions. Knowledge of the extent and impact of these adaptations in important crop plants, such as common beans, remains limited. Using common beans from the Andean and Mesoamerican gene pools, we have explored leaf anatomical traits in relation to photosynthetic performance under variable light and CO2 conditions. We evaluated photosynthetic responses to varying light levels and found a higher maximum photosynthetic rate under light-saturated conditions in a genotype with higher stomatal conductance and reduced vulnerability to cavitation, compared to a genotype that exhibited a lower light-saturated photosynthesis, higher intrinsic water use efficiency, but greater vulnerability to cavitation. Our results indicate greater coordination of leaf organs, tissues, and cellular characteristics that affect stomatal conductance, leaf hydraulics, and photosynthetic gas exchange in common beans from the Andean and Mesoamerican gene pools. These results provide insights into existing natural variation in photosynthetic adaptation traits, which can be leveraged in breeding for photosynthetic efficiency in common beans and other closely related species.

Richard Garcia; Kieu Tran; Maheshi Dassanayake

Decoding microRNA: Small Secrets with Big Impacts on Plant Survival Under Salt Stress

MicroRNAs are small regulatory non-coding RNAs that understudied especially in extremophytes, plants that are naturally adapted to harsh environments. Extremophytes serve as exemplars for evolutionary innovations to survive high salinities lost in the process of crop domestication. Genetic insight derived from extremophytes allows new crop designs that can expand current agriculture to saline marginal lands. In this study, we aimed to identify known and novel miRNA orthologs in the Brassicacea extremophyte models Schrenkiella parvula and Eutrema salsugineum that may regulate transcriptional responses under salt stress. We first annotated genomic loci of miRNA genes expressed in roots and shoots on the recently resequenced genomes of the extremophyte models. Our goal was to investigate how miRNA driven regulation of salt stress responses had divergently evolved in extremophytes compared to Arabidopsis thaliana, a more

sensitive to salt stress. We assessed the expression networks of pri-miRNA, miRNA, and their predicted target mRNAs at different salt intensities in roots and shoots at different durations of salt treatments of the extremophyte models compared to those networks observed for Arabidopsis thaliana. We found salt-responsive miRNA-mRNA target pairs and their associated gene networks that were functionally distinct among the three model species. Our data shows that program cell death and root suberization were among the key biological processes associated with differential gene copy number variation of miRNA loci in the target genomes. The same processes were associated with the loss of differential expression for both miRNA and mRNA targets under high salinity in the extremophytes compared to Arabidopsis. Our initial results suggest that the loss of miRNA regulation promoting continuous growth under salt is a key trait in the extremophytes that facilitates their resilient growth in saline habitats.

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Cryopreservation effects on viability, membrane integrity and biomass of Coffea canephora seeds

Coffea canephora is one of the most widely cultivated species within the genus Coffea. Seeds of this species exhibit low tolerance to desiccation and storage at low temperatures, which limits ex situ conservation. Cryopreservation, defined as storage in liquid nitrogen at −196 °C, represents a viable strategy for long-term conservation; however, its effectiveness depends on the maintenance of seed viability and biomass. This study aimed to evaluate the viability of C. canephora seeds with different moisture contents and subjected to cryostorage, as well as to assess the effects on seed biomass. The experiment was conducted in a completely randomized design arranged in a factorial scheme, being wet basis moisture contents (15%, 16%,17% and 18%) X 4 treatments: PLN (control, without cryopreservation), AL (cryopreserved in aluminum foil), FT (cryopreserved in 15 mL Falcon tubes), and MB (cryopreserved in mesh bags). Four replicates were used for tetrazolium and electrical conductivity tests, and three replicates were used for biomass assessments. Analysis of variance, and mean comparisons were performed using the Scott–Knott test ($p > 0.05$). Viability of cryopreserved seeds was significantly affected by moisture content and packaging. Prior to cryostorage (PLN), seeds exhibited the highest viability, particularly at 17% and 18% moisture. After cryopreservation, AL stored maintained high viability at 18% and 17% moisture. In contrast, FT stored seed showed intermediate performance, while MB stored seeds resulted in pronounced viability reductions at 16% and 15% moisture. Electrical conductivity values were lower in PLN and AL treatments, especially at 17% and 18% moisture, indicating greater membrane integrity. Higher conductivity values were observed in MB and FT, particularly at lower moisture contents. Fatty acid content remained stable across all treatments. Protein content was highest in the control (PLN) at 17% and 18% moisture, showed intermediate values in AL and FT after cryopreservation, and was lowest in MB. Starch content was low in all treatments (<1%). Total biomass was highest in PLN at 17% and 18% moisture. Among cryopreserved treatments, aluminum foil resulted in the highest

biomass values at 17% and 18% moisture, followed by FT at 17% and 18%, whereas MB exhibited the greatest biomass reductions at 17% and 18% moisture. In conclusion, the use of aluminum foil packaging at 17–18% seed moisture content was the most effective condition for cryopreserving C. canephora, ensuring higher viability, biomass preservation, and cellular integrity.

Jennifer Gonzalez (University of South Carolina-Aiken); Dr. C. Nathan Hancock (University of South Carolina-Aiken)

How does size affect Suppressor-mutator (Spm) transposition frequency?

Transposable elements (TEs) are sequences that can jump from one location to another within the genome. The Class II TE Suppressor-mutator (Spm) element was the first discovered in maize. Spm is 8.3 kb in size and encodes the transposase proteins needed to facilitate transposition. Other smaller versions called defective Spm (dSpm) lack transposase sequences due to internal deletions but can still transpose when transposase protein is provided. Previous studies have shown that some TEs form miniature inverted repeat transposable elements (MITEs) with higher transposition frequency compared to larger ones. However, MITE versions of Spm have not been observed. The goal is to test the transposition frequency of Spm and dSpm elements of different sizes to see how size affects their mobility. To test our hypothesis, we assembled Spm elements of various sizes and performed yeast transformation to move them into yeast expressing Spm TNPA and Spm TNP2 proteins. We are currently performing yeast transposition assays to determine the transposition frequencies. We anticipate that element size affects the ability of the Spm elements to transpose. Understanding this mechanism will allow us to develop Spm derived elements with high transposition frequency that can be developed into genome editing tools.

Kelsey Green (School of Biological Sciences, University of Louisiana at Lafayette); Robyn Zerebecki (School of Biological Sciences, University of Louisiana at Lafayette);

Salinity-driven shifts in plant-animal interactions in coastal marshes

Coastal marshes are experiencing increasing salinity stress as sea level rise, drought, and altered freshwater inflows reshape Gulf Coast estuaries. Spartina alterniflora, the foundation salt marsh grass, tolerates a wide salinity range; however, elevated salinity can reduce sediment oxygen availability, thereby influencing root development and plant performance. Through burrowing, ecosystem engineering fiddler crabs alter sediment conditions, enhancing aeration and facilitating Spartina growth. Facilitative interactions tend to be more important under high abiotic stress (i.e., stress gradient hypothesis; SGH) but can also collapse at the extreme ends of a stress gradient. While the SGH has been widely tested in plant–plant interactions, we know far less about how plant stress responses interact with animals that modify physical conditions along stress gradients. Our study will test whether the Spartina–crab interaction changes direction and strength across a salinity gradient. I predict that burrowing improves sediment conditions in ways that support Spartina growth at moderate salinity, but that these benefits weaken, collapse, or reverse as salinity approaches levels that constrain either partner. A key unknown is which component of the interaction becomes limited first: the plant's ability to respond to improved sediment conditions or the crab's ability to maintain burrowing under stress. To identify where these thresholds occur, we will conduct field surveys across a natural salinity gradient from Texas to Louisiana to document patterns in porewater salinity, burrow activity, and Spartina performance. These observations will guide a greenhouse experiment that manipulates fiddler crab presence and tidal water salinity to examine their impacts on plant performance. Specifically, we will grow Spartina under two salinity

regimes: moderate salinity representing typical marsh conditions and a higher salinity treatment simulating saltwater intrusion. Plant responses (e.g., shoot production and biomass) will be compared across salinity regimes in the presence and absence of crab burrowing. By determining when facilitation persists, weakens, or reverses, this work advances our understanding of plant stress interactions and provides a basis for predicting when sediment-modifying animals are likely to support or hinder Spartina establishment. These insights are essential for selecting restoration sites and anticipating how coastal plantings will perform under future salinity conditions.

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SnRK1 Signaling Regulates Plant Development and Reproduction in Rice

Sucrose Non-Fermenting Related Kinase 1 (SnRK1) is an evolutionarily conserved protein kinase of the SNF1/AMPK family that functions as a central regulator of plant energy signaling, integrating metabolic homeostasis with growth and developmental processes. However, the functional roles SnRK1 signaling in plants is mostly limited to Arabidopsis. Here, the role of SnRK1 signaling in plant development was investigated in rice (Oryza sativa L.), that contains three functional paralogs, SnRK1a, SnRK1b, and SnRK1c, with SnRK1b and SnRK1c sharing high sequence similarity, using the snrk1a single and snrk1bc double mutants generated by CRISPR/Cas9 in the japonica cultivar Kitaake. Disruption of SnRK1 signaling resulted in pronounced defects in growth, development, and reproductive performance. During germination, both mutants showed reduced shoot and root elongation compared with the wild-type plants, with greater growth retardation in snrk1bc. Impaired seedling growth was evident under both energy-sufficient and starvation conditions, with starvation markedly exacerbating the phenotype. Under energy-sufficient conditions, mutants displayed reduced seedling length and biomass accumulation relative to wild-type plants and under starvation, seedlings of both mutants appeared thinner and showed reduced shoot elongation, whereas root length remained largely unaffected. Notably, reduction in shoot and root biomass was most pronounced in snrk1bc seedlings. Consistent with these observations, snrk1bc seedlings developed severe starvation-induced morphological abnormalities, including reduced culm thickness, chlorosis, and leaf rolling. At later developmental stages, both mutants showed significant reductions in total biomass, seed weight per plant, and seed number per panicle. Reproductive defects differed between the two mutants, with snrk1a plants exhibiting an increased incidence of empty spikelets, indicative of reduced fertility; whereas snrk1bc plants produced a higher proportion of shrunken/defective seeds, reflecting post-fertilization defects. Overall, this study demonstrates that SnRK1 signaling plays a dual role, promoting growth under favorable conditions while acting as a key regulator of adaptive responses during stress.

Manohar Chakrabarti (School of Integrative Biology & Chemical Sciences)

Investigating the role of RNA in drought, heat, and combined stress in Sorghum bicolor

We explore the cereal crop Sorghum bicolor (RTx430) and its molecular responses to drought, heat, and combined drought and heat stresses at the transcriptional level over the course of 1 and 6hrs of stress treatments. The study was conducted on sorghum seedlings subjected to stress treatments, specifically heat treatment was imposed by exposing seedlings to 45℃, drought was induced by polyethylene glycol treatment (PEG), and a combination of both drought and heat treatment. The focus of the study was to conduct differential transcript expression analysis in responses to individual and combined stress treatments, and to elucidate uniqueness and commonalities among responses to individual and combined stresses. A set of 2487 transcripts displayed differential expression in responses to all stress treatments. Groups of 3100, 2416, and 3352 transcripts exhibited differential expression specifically in response to drought, and heat, and combined drought and heat treatment. Gene Ontology and pathway analyses were conducted to decipher biological and molecular pathways that were impacted significantly in response to individual and combined drought and heat treatment. We aimed to provide deeper insights into the molecular mechanisms that enable a plant's abiotic stress adaptability and help in the efforts to develop more stress-resilient crops. In understanding the fundamental molecular functions of such a drought and heat resilient crop, we can develop climate-resilience by over and under regulating similar transcripts in other crop species that do not hold the same resiliency.

Madison Hamlin (Biological, Environmental and Earth Sciences. University of South Carolina Aiken)
C. Nathan Hancock. (Biological, Environmental and Earth Sciences. University of South Carolina Aiken)

Developing mPing-based Constructs for Transposase Assisted Target Site Integration

CRISPR has been developed into an effective genome editing technology for modifying or knocking out genes. However, CRISPR alone has its limitations and lacks the ability to target transgenes to specific locations within the genome. The transposase assisted target site integration (TATSI) system has been developed to target the mPing transposable element to a specific location in the genome using the Pong transposases proteins (ORF1 and TPase) along with Cas9 and a guide RNA. This technology uses mPing as a vehicle to carry genetic cargoes, such as promoter sequences or an entire gene, to specific locations which can modify plant gene expression and function. Binary plasmids suitable for testing targeted insertion into the Arabidopsis GL1 gene were made containing Cas9 and the AtGL1 gRNA. Arabidopsis plants were transformed using the floral dip method, and the resulting seeds were screened for Red Florescence Protein (RFP) expression before planting. We observed the absence of trichomes indicating that the CRISPR components were functioning, but there was no evidence of excision or insertion of the mPing element. This suggested that the Pong ORF1 and TPase proteins were not being expressed properly. We are now testing constructs with ORF1 and TPase linked together using a T2A peptide sequence to see if this induces mPing transposition better than the independent genes tested previously. If successful, these plasmids will allow us to test if the use of the hyperactive version of mPing and will improve the efficiency of targeted insertion.

Karl H. Hasenstein (University of Louisiana at Lafayette)

From auxin research to space experiments – perspectives of plant biology

My talk will recount research ranging from studies of auxin transport to gravitropism, changes in gene expression and plant responses to space. The now retired use of radioisotopes as instrument of biological research characterized auxin transport and a quantification of binding sites

that eventually became identified as PIN proteins. Modelling of auxin transport in roots resulted in the 'inverted fountain' model that gave rise to the functional analyses of auxin transport and growth regulation during gravitropism. The still unresolved problem of how mechanical signals are translated to biochemical signals led to studies of amyloplasts as mechano-transducers, when they begin to function as gravity sensors and thus the onset of gravisensitivity in seedlings. The goal to displace amyloplasts by biophysical means resulted in the application of high-gradient magnetic fields (HGMF). Amyloplast movement by HGMF resulted in space experiments that demonstrated not only their ability of inducing curvature but also the acclimation of plants to weightlessness and response to hyperstimulation by instruments (clinostats) that were originally believed and designed to simulate microgravity. The need to assess gene expression on small scales led to the development of solid phase gene extraction (SPGE) which showed that altered elongation growth affects gene transcription and is therefore part of its feedback loop. Comparisons of repeated, supposedly identical, space experiments showed that the variability of gene expression in space is as large as on Earth, but also that plants acclimate to the complex space environment. This research also offers grounds for optimism that plants grown in space or on the Moon will be as nutritious as those grown on Earth. The research was supported by many NASA, NSF, DOE, and LA grants.

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Structural Determinants of Promiscuity in 10-Hydroxycamptothecin O-Methyltransferase from Camptotheca acuminata

Medicinal plant Chinese Happy Tree (Camptotheca acuminata) synthesizes the chemotherapeutic monoterpene indole alkaloid camptothecin through a biosynthetic pathway involving a series of specialized enzymes. 10-Hydroxycamptothecin O-methyltransferase (Ca10OMT) is a fascinating plant enzyme that exhibits unusual substrate promiscuity. Notably, it accepts a broad range of compounds, including nonalkaloids such as flavonoids and phenolics. Structural features of the enzymatic active site that enables this promiscuity are not completely understood. To investigate the substrate binding architecture of Ca10OMT, the study employs an in silico workflow that combines homology modeling, refinement of post-docking molecular dynamics, and quantum mechanical energetic analysis. Results unveiled a bifunctional substrate pocket: one face is populated with polar residues whereas the opposite face exposes hydrophobic groups that interact with nonpolar regions of diverse substrates. Combined chromatographic separation and biochemical assays provided evidence for the preferential methylation of non-neighboring hydroxyl groups in a family of dihydroxybenzaldehyde positional isomers. Precise rotation and orientation of the substrate within the active site were identified as key structural determinants for regiospecificity of the methyl transfer from S-adenosyl-L-methionine. These findings highlight the impact of synergistic empirical-computational strategies in studying enzymatic transformations of plant natural products.

Chien-Yu Huang (Department of Plant Pathology and Crop Physiology, Louisiana State University AgCenter)

RNA silencing and epigenetic regulation in plant innate immunity and crop protection

Epigenetic regulation and RNA silencing are pivotal regulatory mechanisms to program gene expression in stress responses and many biological processes. The key components of these regulatory mechanisms are important players that fine-tune plant immunity and defense responses. To identify new RNA silencing components, including proteins and small RNA species, that responded during the plant immune response, we used comparative small RNA profiling and interactors associated with Arabidopsis AGO2, the major Arabidopsis Argonaute protein that promotes plant antibacterial resistance, as approaches. We identified new interactors of AGO2 and regulators of RNA silencing in response to pathogen infection, including a clade of DEAD-box RNA helicases. Using comparative small RNA profiling, we have identified regulators and molecules that contribute to defense responses in the model plant Arabidopsis and in other crops. For example, the core subunit of chromatin remodeler was found as a negative regulator at the epigenetic level in the innate immune system; multifunctional antimicrobial peptides were identified and used to manage crop diseases. Here, we highlight the importance of epigenetic regulation and RNA silencing in plant innate immunity, and their use as powerful approaches for developing strategies to manage crop diseases.

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A Broadly Distributed Rhizobacterium, Roseateles chitinivorans P500, Promotes Growth and Systemic Resistance via Jasmonic Acid-Dependent Oxylipin Signaling in Grasses

Harnessing root-associated microbiomes to promote beneficial microbial compositions could offer a sustainable strategy to increase crop resilience. Major challenges impeding this strategy are the lack of understanding of which native members of the microbiome benefit the host and the molecular signaling events underlying these benefits. In this study, we isolated a strain of Roseateles chitinivorans, RcP500, corresponding to the most abundant bacterial taxon in the switchgrass root microbiome. Inoculation of roots with RcP500 promoted growth and induced systemic resistance (ISR) to Bipolaris leaf spot of switchgrass and closely related Panicum hallii. R. chitinivorans is also highly abundant in the rhizosphere and root microbiomes of maize and rice and enhanced the growth of these two plant species. Furthermore, RcP500 elicited ISR in maize against anthracnose leaf blight and southern corn leaf blight. Bioassays and root metabolite profiling in maize wild-type and jasmonic acid (JA)-deficient opr7opr8 mutant plants revealed the requirement of JA-dependent processes in RcP500-elicited synthesis of the JA precursor, 12-OPDA (cis-(+)-12-oxo-phytodienoic acid), and an α-ketol, 9,10-KODA (9-hydroxy-10-oxo-12(Z)-octadecadienoic acid), two oxylipins previously implicated in ISR signaling. Xylem sap transfusion of RcP500-colonized plants to naïve receiver plants corroborated the role of JA in promoting these signaling intermediates. Whereas root JA synthesis was downregulated upon RcP500 colonization, gibberellic acid was induced, suggesting a potential mechanism behind the simultaneous growth promotion and ISR triggered by this bacterium. Overall, this study identified a novel rhizobacterium

with a broad host range that promotes growth and systemic resistance across multiple plant species in a JA-dependent, ketol-driven manner.

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Characterizing the Diversity of NLR Genes in Switchgrass

Most cloned plant resistance (R) genes belong to one gene family, the nucleotide binding leucine rich repeat (NLR) genes. NLR genes code for intracellular receptors that detect pathogen infection by binding to pathogen produced effector proteins. NLR genes present in domesticated crops and model plants have been well studied. However, NLR genes in wild and recently cultivated crops are less understood and may contain untapped genetic diversity. Observing NLR genes in undomesticated plants may further reveal evolutionary patterns for how plant populations adapt to their local biotic environment. Switchgrass (Panicum virgatum) is a biofuel feedstock native to North America that is also grown for ornament and rangeland purposes. Although switchgrass breeding only began recently, genomic resources are plentiful, including telomere to telomere haplotype resolved genomes from phylogenetically diverse switchgrass accessions and from other related Panicum grasses. Genomics assisted breeding of switchgrass for disease resistance is hampered without the identification and annotation of switchgrass R genes. Here, we surveyed the NLR gene content of five geographically distinct switchgrass accessions for genomic distribution, genetic architecture, relation to NLR genes of economically significant crops, and other features. We found over 1000 putative NLR genes per switchgrass genome with an enrichment on chromosome 8. We examined NLR gene architecture and identified 181 distinct integrated domains, some possibly novel. By comparing NLR groups across various monocot crop species and wild relatives, we identified groups of conserved and variable genes, many of which are uniquely present in switchgrass. These results build towards a pangenomic understanding of NLR gene diversity in switchgrass and NLR gene evolution in a natural system.

Batoul Ibrahim (Biology, Texas Tech University); Atinder Singh (Biology, Texas Tech University); Gengxiang Jia (Biology, Texas Tech University); Zhixin Xie (Biology, Texas Tech University)

Functional expression of NanoLuc luciferase as a versatile bioluminescent reporter in plants

Reporter genes are indispensable tools for quantifying gene expression and regulatory dynamics in living cells. Among bioluminescent reporter systems, firefly luciferase (Fluc) represents a well-established and widely used standard for both imaging- and lysate-based assays. However, the relatively large size of the Fluc protein (~66 kDa) can pose challenges when fused to proteins of interest, potentially interfering with native protein function. This work explores the potential of NanoLuc luciferase (Nluc), a novel bioluminescent reporter derived from the deep-sea shrimp Oplophorus gracilirostris, for applications in plant biology. Nluc offers key advantages over conventional luciferase reporters, including its substantially smaller size (19.1 kDa) and markedly higher sensitivity. Here we demonstrate that fully functional Nluc is readily expressed in plants through both transient expression in Nicotiana benthamiana leaves and stable transformation in Arabidopsis thaliana. Nluc activity was validated in transgenic plants in three distinct contexts: (1)

as a standalone reporter driven by the strong constitutive cauliflower mosaic virus (CaMV) 35S promoter; (2) as a standalone reporter under the control of a well-characterized Arabidopsis promoter responsive to phosphate starvation; and (3) as a chimeric fusion protein with ARGONAUTE1 (AGO1), a multidomain small RNA (sRNA)-binding protein with ribonucleolytic activity central to sRNA-mediated gene silencing, expressed from the native AGO1 promoter. Together, these results establish Nluc as a robust and versatile bioluminescent reporter for plant biology research, offering high sensitivity with minimal functional interference.

Deborah Ighalo (Biological Sciences, East Tennessee State University) Jyoti Behera (Biological Sciences, East Tennessee State University) Aruna Kilaru (Biological Sciences, East Tennessee State University)

Coordinated Transcriptional Regulation of Oil Biosynthesis by Avocado WRINKLED1 and WRINKLED2 in Non-Seed Tissues

WRINKLED1 (WRI1) is a key transcription factor regulating oil biosynthesis in plant seeds, yet the mechanisms underlying high oil accumulation in non-seed tissues and the functional roles of WRI paralogs remain poorly understood. Avocado (Persea americana), a basal angiosperm, provides a unique system to address these questions, as its mesocarp accumulates exceptionally high levels of oil (60–70% of dry weight), predominantly composed of oleic acid. Here, we show that both PaWRI1 and PaWRI2 are functionally active regulators of lipid metabolism. Transient expression in Nicotiana benthamiana leaves demonstrated that PaWRI1 and PaWRI2 enhance lipid droplet formation and triacylglycerol (TAG) accumulation, with the strongest effects observed when both factors were co-expressed. qRT-PCR analysis revealed selective upregulation of plastidial glycolytic and fatty acid biosynthetic genes, with co-expression leading to greater induction of several key genes than either factor alone. Yeast one-hybrid assays further demonstrated that PaWRI1 and PaWRI2 directly bind AW-box and AW-like promoter elements of lipid metabolic genes. PaWRI2 was found to be both self-activated and activated by PaWRI1, indicating an interdependent regulatory relationship in non-seed tissues. Building on these findings, microscale thermophoresis (MST) assays will be used to quantitatively determine the DNA-binding affinities of recombinant PaWRI1 and PaWRI2 for AW-box elements, providing mechanistic insight into WRI-mediated transcriptional control of lipid biosynthesis. This work establishes PaWRI2 as a functional transcriptional regulator of oil biosynthesis and advances our understanding of WRI-mediated control of lipid metabolism in non-seed tissues.

Hrishikesh Ingole (Plant and Environmental Sciences, Clemson University) Zachary Jones (Plant and Environmental Sciences, Clemson University) Gautam Saripalli (Plant and Environmental Sciences, Clemson University)

Developing Solutions for Peanut-Allergic Individuals Through Crossbreeding and Gene Editing

Peanuts are an important food and oilseed crop cultivated in the South and Southeast United States. However, ~2% of children and adults in the US are affected by peanut allergies caused by four major allergen proteins (Arah1, Arah2, Arah3, and Arah6) and, therefore, are unable to consume them. Current solutions are limited to preventive medication and oral immunotherapy (Palforzia), and each of these therapies has limitations. Therefore, this study was focused on developing an affordable solution to this problem. A diversity panel of 93 lines was screened for

reduced allergen protein. The resulting interesting lines were then used to develop two bi-parental populations. These lines were further screened for Biochemical (LC/MS) and Immunological (ELISA) assays. Genetic crosses were made between the identified reduced immunogenic lines to stack the deficiency of different allergenic proteins in a single genotype. Genetic mapping using these protein traits allowed the identification of QTLs (regulators of protein accumulation in seeds) for major allergens. The results revealed will perhaps allow us to develop reduced immunogenic lines and a genetic marker for screening the germplasm for peanut allergens. Simultaneously, a CRISPR-mediated multi-gene editing approach is also being used to induce mutations in the genes encoding for the above allergens. Two constructs were bombarded, which targeted four genes. The generated T0 and T1 plants were screened for cpf1 and GFP. Protein profiling of the lines revealed a reduction in the four major allergens. Lines with reduced content of immunogenic proteins identified based on protein profiles are being tested for allergenicity using sera derived from sensitive individuals. Overall, this research will help in releasing a peanut cultivar that will be a healthier and safer option for sensitive people.

Susan P. John (University of Louisiana at Lafayette); Karl H. Hasenstein (University of Louisiana at Lafayette)

From Surface Architecture to Transcriptome Reprogramming: Multilevel Mechanisms of Desiccation Tolerance in Pleopeltis polypodioides

Pleopeltis polypodioides, an epiphytic resurrection fern, survives prolonged desiccation and rapidly recovers upon rehydration. To elucidate its tolerance mechanisms, we investigated morphological, physiological, biochemical, and molecular responses to drought and heat stress. Unlike most vascular plants that rely exclusively on internal vascular tissues for water transport, Pleopeltis supplements water uptake through hydrophilic dorsal peltate scales. Time-lapse imaging demonstrated that rehydration depends on surface water spreading via film diffusion between overlapping scales. Removal of scales significantly reduced water retention, rehydration efficiency, and metabolic recovery, indicating that external surface properties are critical for water management. Biochemical analyses revealed increased reactive oxygen species (ROS), lipid hydroperoxides, glutathione oxidation activity, and unsaturated fatty acids during dehydration, whereas catalase activity declined. Although abscisic acid (ABA) levels peaked during moderate dehydration, ABA had limited influence on stomatal movement. Instead, stomatal regulation was more strongly affected by light, nitric oxide, and calcium signaling. Dried fronds also exhibited greater thermotolerance than hydrated fronds, accompanied by distinct lipid remodeling responses to heat stress. RNA-Seq transcriptomic analysis showed that approximately 42% of transcripts were differentially expressed across hydration stages. Dehydration upregulated genes associated with fatty acid biosynthesis, oxidative stress responses, cytoskeletal organization, and primary metabolism, while transcripts related to photosynthesis, ABA signaling, and cell wall processes were downregulated. Overall, desiccation tolerance in Pleopeltis polypodioides depends on external water transport via peltate scales, coordinated metabolic reprogramming, oxidative stress regulation, and stress-specific lipid remodeling—insights that may inform strategies to engineer drought-tolerant crops.

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New York, NY 10031, USA); Aruna Kilaru (Department of Biological Sciences, East Tennessee State University, Johnson City, TN 37614, USA)

Effects of N-acylethanolamine Analogs on Physcomitrium patens Growth

N-acylethanolamines (NAEs) are bioactive lipid signaling molecules that regulate plant growth and development, with their cellular levels largely controlled by fatty acid amide hydrolase (FAAH). In Arabidopsis thaliana, synthetic NAE analogs such as pentadecylphenol ethanolamide (Pdp EA) and cardanol ethanolamide (Cardanol EA) enhance FAAH activity and alleviate NAE-induced growth inhibition, highlighting how subtle structural modifications can influence NAE metabolism and developmental outcomes. We examined the effects of FAAH-enhancing NAE analogs on gametophyte development in the moss Physcomitrium patens to assess the evolutionary conservation and mechanistic basis of NAE-mediated growth regulation. Gametophytes were treated with increasing concentrations (1–100 µM) of Pdp EA or Cardanol EA, and growth was monitored over a 29-day period and analyzed using Image J. Preliminary results show clear dose-dependent responses to both analogs. While low concentrations produced growth comparable to untreated controls, higher concentrations altered growth trajectories, with compound-specific enhancement emerging at later developmental stages. These trends mirror observations in Arabidopsis and support the hypothesis that FAAH-enhancing NAE analogs promote growth by increasing NAE turnover. Ongoing analyses combine morphological and molecular approaches to resolve underlying mechanisms. Microscopy-based assessment of actin organization and chloroplast structure will evaluate effects on cellular architecture and photosynthetic capacity, while biochemical assays and qPCR analysis of FAAH and growth-associated genes will test whether growth enhancement reflects direct enzymatic activation, receptor-mediated signaling, or transcriptional regulation. Together, this work aims to define how NAE metabolism contributes to growth control across plant evolutionary lineages.

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Determining the Physiological functions of LCIC: a close homolog of LCIB

Photosynthesis supports about 90% of life in the biosphere and is the foundation of almost every food chain. Photosynthetic aquatic organisms account for over 50% of all carbon fixed in the biosphere hence function as a carbon sink. Green algae –Chlamydomonas reinhardtii plays a key role in global photosynthesis and has an efficient photosynthetic process because it has a biophysical carbon dioxide concentrating mechanism (CCM). CCM components are Carbonic Anhydrases (CAs), Bicarbonate Transporters and Pyrenoid where the enzyme Rubisco is sequestered. CAs are metalloenzymes that interconvert CO2 and bicarbonate. CAs avail CO2 for photosynthesis and bicarbonate for fatty acid/nucleotide synthesis. The Low CO2 Inducible B (LCIB) is an active CA and is needed for acclimation to Low CO2 (LC). The absence of LCIB causes cells to die in LC but grow in HC and VLC. LCIB interacts with a close homolog LCIC- in vivo and invitro. In Chlamydomonas- LCIB/C recaptures leaking CO2 from the Pyrenoid and hydrates it to bicarbonate (HCO3-). LCIB/LCIC prevents leakage of CO2 from the pyrenoid and therefore plays a critical role in making photosynthesis efficient Chlamydomonas. Chlamydomonas and other plants have LCIB-like proteins, but their functions are not yet known. This poster addresses the physiological functions of Chlamydomonas LCIC, a close homolog of LCIB.

Nathan Kawalski (APSS Florida Tech) , McKenna Taylor (OEMS Florida Tech), John Z. Kiss (BMES Florida Tech), Andrew Palmer (OEMS Florida Tech)

Use of minimal microbiomes with spaceflight history to improve plant growth in Martian Regolith Simulants

As we get closer to establishing a settlement on Mars, certain challenges associated with mission success are receiving increasing scrutiny, one of the most relevant of these is the issue of in situ (on-site) food production. The high costs and logistical concerns associated with transporting food and agricultural materials to space make planet cultivation essential to ensure food security. While hydroponic cultivation of crops will be a major source of food, mid-range of long-term settlements will likely employ the surface regolith for crop production as well. However, this material is high in salts, while low in organic and nitrogen content, making germination and growth a significant obstacle in mission planning. This project explores the use of plant growth-promoting bacteria (PGPB) to enhance plant development in Martian regolith, thereby reducing the number of fertilizers which need to be transported from Earth. Here we consider three bacterial species-Paenibacillus pabuli, Pseudomonas fulva, and Bacillus subtilis-all derived from ISS cultures and with previously established PGP properties. All three species are evaluated individually as well as collectively for their potential to improve plant growth in commercial Martian Regolith Simulants. These bacteria are known to assist in nutrient uptake, growth promotion, stress resistance, and more. This research aims to test how well these PGPBs can assist in plant growth under ideal growth conditions. By studying their effects in sterile environments, we hope to determine which bacterial strains are most effective in assisting plant growth. The findings could contribute significantly to developing sustainable agricultural systems for future space missions and aid in the human habitation of Mars.

Pragya Kesarwani (SIBCS and University of Texas Rio Grande Valley, Edinburg); Manohar Chakrabarti (SIBCS and University of Texas Rio Grande Valley, Edinburg)

Drought and heat stress induced genome-wide dynamics of alternative polyadenylation and 3'UTR length in Sorghum bicolor

Abiotic stresses like drought and heat severely affect plant growth and physiology. It is crucial to understand stress responsive gene regulation. Alternative polyadenylation (APA) can regulate gene expression at the post-transcriptional level and can result in variable 3'-untranslated regions (3' UTRs). However, the dynamics and functional roles of alternative 3' UTRs under drought and heat stress remain largely unexplored in many crops. This study has analysed differential APA, and 3' UTR changes in Sorghum bicolor seedlings under control, drought and heat treatment. The widespread APA dynamics were identified with drought and heat stress inducing 507 and 2214 differentially utilized poly(A) clusters (PACs) respectively and among those 158 were shared across heat and drought stresses. Sets of differentially utilized PACs were represented by 241 drought-responsive and 1193 heat-responsive APA genes, respectively. A set of 140 genes displayed differential APA in responses to both stresses. Gene Ontology analysis was conducted to elucidate biological and molecular processes that displayed significant stress-responsive alternation in APA. Read-weighted 3' UTR length analysis further revealed stress-specific lengthening or shortening events. These findings indicate that APA and the resultant alternative 3' UTR usage constitute a key post-transcriptional mechanism by which S. bicolor adapts to drought and heat stress. Our study also identified sets of genes displaying both stress dependent differential expression and APA or 3’UTR length. Altogether, this study reveals the dynamics of stress-dependent APA and 3' UTR

remodelling in Sorghum bicolor and highlights alternative polyadenylation as a central mechanism coordinating transcript stability and adaptive gene expression under abiotic stress.

Jamie Kimbrell (BioDiscovery Institute, Department of Biological Sciences, UNT); Patrick Horn (BioDiscovery Institute, Department of Biological Sciences, UNT)

Establishing Stress Phenotypes in Cotton: A Baseline for Lipid Remodeling Studies

Cotton (Gossypium hirsutum) is a major global fiber and oilseed crop, yet its early developmental stages are highly vulnerable to temperature stress. Episodes of cold (<15 °C) and heat (>35 °C) are increasingly common with climate change, leading to poor germination, growth retardation, and membrane damage. Membrane lipids are central to stress defense, maintaining fluidity, compartmental stability, and enabling recovery through remodeling of saturated and unsaturated fatty acids. Although lipid remodeling is recognized as a key process in plant stress tolerance, its temporal dynamics and relationship to physiological recovery remain poorly defined in cotton. My work addresses this gap by establishing preliminary stress phenotypes as a baseline for future studies. Using time-resolved fatty acid profiling alongside photosynthetic and growth measurements, I tracked how cotton seedlings respond to short-term cold and heat stress. These data capture coordinated lipid, photosynthetic, and growth adjustments across stress and recovery phases, setting the stage for investigations into lipid memory and adaptive remodeling. This research provides a first step toward linking stress-induced fatty acid changes with photosynthetic performance and growth outcomes in cotton seedlings. Defining these lipid-based stress phenotypes establishes a foundation for future work on lipid memory and supports efforts to improve cotton resilience under a changing climate.

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Nanopore sequencing of circRNA from salt-stressed maize

High soil salinity is a source of abiotic stress in plants that causes crop yield loss annually. Highly saline soil prevents plants from effectively taking up water even in the presence of adequate soil moisture, causing osmotic stress. The effects of salt stress on plants include leaf curling and wilting, stunted growth, and accumulation of reactive oxygen species (ROS) in various tissues. Expression of genes involved in salt stress response is regulated both transcriptionally and post-transcriptionally through a variety of mechanisms. Noncoding RNAs (ncRNA) are often regulators of such processes, through mechanisms such as epigenetic regulation and RNA interference. Some ncRNA bind to and regulate the functions of other ncRNA, as is the case with RNA molecules known as microRNA (miRNA) sponges, which sequester miRNA from their functions. Many circular RNA (circRNA) have been identified as miRNA sponges and as regulators of biological processes in a variety of animal and plant species. However, they remain understudied and poorly characterized in most plants. Characterizing circRNA via short read RNA-seq methods is difficult because circRNA reads must be distinguished from those of the parent gene mRNA, typically by identifying back splice junction sequences. Long read methods such as nanopore sequencing allow for complete sequencing of the entire length of the circRNA, providing higher confidence in identification and characterization of circRNA from sequence data. However, long read circRNA-seq methods were developed in the context of human cells and have had very minimal use in plants. The adaptation of long read circRNA-seq methods could prove very useful for the identification and characterization of plant circRNA. To evaluate the potential functions of circRNA

as regulators of salt stress response, nanopore circRNA-seq was completed using RNA from salt-treated maize. Preparation of circRNA-enriched sequencing libraries from leaf tissue was performed using a modified version of a protocol known as CIRI-long, which has never before been utilized in maize. Methodology for plant circRNA enrichment, library preparation, and nanopore sequencing will be outlined, and proposed uses of this sequencing data to characterize salt stress responsive and miRNA sponging circRNA will be discussed.

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Degradation of Arabidopsis SQUAMOSA-Promoter-Binding-Protein-Like Transcription Factors by Bacterial Effector-Triggered-Immunity is required for full activation of ETI

Plant immunity is highly dynamic and tightly regulated, enabling plants to defend against diverse pathogens while minimizing growth and development costs associated with prolonged defense activation. MicroRNA 156 (miR156) regulated squamosa promoter binding protein like transcription factors (SPLs), is a conserved pathway that controls developmental timing across plant species, yet its detailed role in age-dependent immunity remains unclear. In our current work, we found that miR156 and its target SPL10, contributes to age-related immunity against the bacterial pathogen Pseudomonas syringae pv. tomato DC3000, demonstrating the dual roles of miR156/SPL10 in plants' development and immunity. Genetic analyses revealed that spl10 mutants supported higher bacterial growth than wild type when infected with virulent bacteria, indicating enhanced susceptibility under basal defense conditions. In contrast, when challenged with bacteria carrying avirulence effectors, spl10 mutants exhibited reduced bacterial growth relative to wild type, suggesting that SPL negatively regulates effector-triggered immunity (ETI). Transcriptomic profiling under ETI conditions showed enhanced induction of defense-associated genes, including PAD4 and EDS1, in spl10 mutants. Chromatin immunoprecipitation followed by qPCR demonstrated that SPL10 directly binds to the PAD4 promoter and regulates its basal expression. Histochemical staining assays revealed distinct immune phase–dependent regulation: SPL10 protein remained stable during pattern-triggered immunity (PTI) but was specifically degraded during ETI. This ETI-associated SPL degradation was blocked by $LaCl_3$ treatment and required EDS1 signaling, indicating that calcium signaling and immune regulators coordinate SPL10 turnover. Additionally, trypan blue staining and ion leakage assay indicated that SPL10 promotes ETI-induced cell death, suggesting that SPL decouples ETI-associated cell death from pathogen resistance. Together, our findings uncover a dual function of the miR156/SPL10 module in integrating developmental timing with immune responses. We propose that SPL10 acts as a developmental brake on ETI by directly repressing PAD4, and that ETI signals relieves this repression through EDS1-dependent SPL10 degradation. This study provides mechanistic insight into how plants couple age-dependent development with immune competence.

Jaqueline Krueger (Department of Ocean Engineering and Marine Sciences, Florida Institute of Technology) Andrew Palmer (Department of Ocean Engineering and Marine Sciences, Florida Institute of Technology)

Quorum Sensing in Chlamydomonas reinhardtii Strain Variants

The world of microorganisms is complex, being built of much more than the living cells that define it. One of the most important complexities of the microbial world is quorum sensing. Quorum sensing relies on cell density to mediate phenotypic switching in a population, allowing them to coordinate efforts that, when either performed or restricted in conjunction, increase survival, such as in biofilm formation, virulence, and motility. This process occurs due to the production of signaling molecules, which increase as the population increases, resulting in the detection of the molecule and triggering a switch in phenotype. This mechanism has been observed across a myriad of bacteria clades. Its presence in eukaryotic organisms is far less common yet could indicate that this complex communication is more ubiquitous in microorganisms than previously thought. Chlamydomonas reinhardtii, a model species of unicellular algae, is one of the only eukaryotes to exhibit quorum sensing (alongside some yeasts); however, the extent of this signaling across species and even subspecies remains unknown. The phenotypic switch observed in C. reinhardtii is a significant increase in swim speed during high cell density. Therefore, to characterize the extent of quorum sensing in C. reinhardtii, their swim speeds at both high and low cell density must be collected and compared. Videos of their swimming behavior are collected and analyzed using computer-assisted tracking. They are then compared using graphical and statistical analysis. By using this method to contrast multiple strains' behaviors, more about the nature and pervasiveness of quorum sensing in C. reinhardtii is able to be revealed. In addition, by extracting the media from a high cell density culture (and thus with it the quorum signaling molecules) and combining it with low cell density cells, which have likewise been extracted from their media, a phenotypic switch may also be observed. This can be used to confirm that it is a signal molecule present in the media that is causing the change and not another variable.

Sally Lee, University of North Carolina at Chapel Hill (Primary Presenter); Rafael R Loureiro, Department of Biology, Winston-Salem State University/ United States Air Force Academy; Beatriz Fontoura, Department of Chemistry University of Scranton; Gabrielle Erwin, Winston-Salem State University; Kelsey Howey, Department of Chemistry, University of Scranton

Elemental and Nutrient Profiling of Cross-Bred Tomato Plant, 'Inkspot,' Using Spectroscopic Methods (LIBS)

Laser-induced breakdown spectroscopy (LIBS) enables rapid, multi-element analysis of plant macronutrients and micronutrients with minimal sample preparation and without acid digestion. In this study, Solanum lycopersicum 'Inkspot', an anthocyanin-rich, compact-growth tomato cultivar derived from 'Tiny Tim' and selected for stress tolerance, was cultivated in lunar and Martian regolith simulants. Prior work on this cultivar quantified antioxidant responses (superoxide dismutase [SOD] and catalase [CAT]) and lipid peroxidation (malondialdehyde [MDA]). Here, we shift from physiological endpoints to elemental profiling using LIBS. Two samples, GE and GNE, leaves, stems, and roots, were analyzed by LIBS in wavelengths ranging 265 nm to 810 nm. Leaves, stems, and roots were previously homogenized and pressed into pellets for the LIBS analysis. Analysis showed that GE has higher intensity levels of sodium (Na) and potassium (K) across its tissues, and GNE had higher intensities of calcium (Ca) in its tissue. Sodium provides an ion osmotic balance and supports photosynthesis when there are potassium deficiency in the plant.

Potassium is crucial for macronutrients and drives photosynthesis and enzyme activity. Calcium indicates the plant's stability, specifically the cell wall structure and cell division. Iron (Fe) was another prominent element in this study, with high intensities in both samples. Fe is an essential micronutrient related to chlorophyll biosynthesis and redox metabolism. The samples showed identical peaks in the analysis, indicating the same elemental contributors. Some notable peaks can be Mg I (280.98 nm), Mg II (279.08 nm, 280.27 nm), Ca II (393.37 nm, 396.85 nm), Fe I (373 nm), Na I (589.00 nm, 589.59 nm), K I (769.8, 766.48 nm), and P (800.27 - 809.01 nm). Different results may suggest differences in genetics, although the cross-breeding method was identical. Genetic variation may indicate the contrast of the elemental intensity variation among the plant samples. Further analysis may be needed to confirm that the different results are from the genetic variation.

Marc Libault

What We Can Learn from Plant Single-Cell -Omics?

Each plant cell is different based on its biological function, developmental stage, interaction with its environment, and, consequently, its use of genomic information. Enhancing crop performance in the field through genetic engineering would require personalizing strategies to each cell/cell type composing the plant. The implementation of such a strategy requires a deep and high-resolution understanding of the role and activity of crop genes. To precisely characterize the activity of each gene in each cell type composing a plant, we and others reported the use of single nucleus RNA sequencing (sNucRNA-seq) and single nucleus Assay for Transposase Accessible Chromatin sequencing (sNucATAC-seq) technologies. To date, most of these studies were conducted on the model plant Arabidopsis thaliana. In this presentation, we will discuss the broad application of these technologies on various crop species and plant organs to gain a more detailed picture of the differential use of the genomic information between cell types and the evolution of gene activity between plant species. Focusing on the biology of the soybean root and nodule, we provide a perspective regarding the challenges and strategies to analyze crop single-cell biological datasets, the strong potential in using spatially resolved transcriptome to support the analysis of single nucleus transcriptomic datasets, and the emergence of single-cell multi-omic approaches to better decipher the mechanisms controlling plant gene activity. We expect that single-cell/nucleus technologies associated with spatial information will provide a new understanding of plant gene activity and function. Such knowledge will be essential to establishing meaningful genomic engineering strategies to improve crop performance.

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An In-frame Deletion in OsTOR Leads to Altered Vegetative Development and Biomass Distribution in Rice

Target of Rapamycin (TOR) is a highly conserved protein kinase in eukaryotes. In rice, this gene exists as a single copy, designated as OsTOR (Oryza sativa TOR), and is responsible for coordinating

both vegetative and reproductive growth under energy-rich conditions. Knockout mutations in TOR are lethal; however, small independent in-frame deletions in the kinase domain of OsTOR (Δ3 and Δ9) produced viable mutants with altered activity as indicated by transcriptomic and phosphoproteomic analysis. This study evaluated the effects of Δ3 and Δ9 in-frame deletions on growth and vegetative development during the first 50 days after emergence (DAE). Two independent experiments were conducted in a greenhouse. Three independent plants per genotype were sampled at each time point. Plant height, fresh and dry biomass of shoots and roots, as well as chlorophyll content, were measured at 10, 20, 30, 40, and 50 DAE, enabling the assessment of the temporal dynamics of OsTOR mutations. Initial growth (10–20 DAE) was similar among wild-type (WT), Δ3, and Δ9 plants, indicating that OsTOR mutations do not impair seedling establishment. From 30 DAE onwards, the Δ9 mutant exhibited greater height and higher shoot and root biomass compared to Δ3 and WT, with Δ3 being intermediate and WT displaying the lowest accumulation of fresh and dry biomass. These results suggest that OsTOR deletions modulate vegetative growth, potentially boosting growth under normal energy conditions. Chlorophyll content increased throughout development in all genotypes, reaching the highest levels in Δ3, suggesting greater photosynthetic potential, followed by Δ9, while WT consistently exhibited the lowest values. In summary, this study demonstrates that the Δ3 and Δ9 deletions distinctly modulate vegetative growth and metabolism. The Δ9 mutant tended to favor resource allocation toward structural growth, whereas Δ3 appeared to favor the maintenance and production of photosynthetic pigments. These results suggest that in-frame deletions in OsTOR alter the way the plant allocates resources between structural growth and photosynthetic pigment production.

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Structural and functional studies of the high affinity nitrate transporter NRT2.1 and its partner NAR2.1 from M. truncatula.

The application of nitrogen-based fertilizers is necessary to achieve high yields in agriculture as low nitrogen availability is one of the main limiting factors for plant growth and development. However, applied fertilizers are not fully utilized by plants resulting in excessive accumulation of nitrogen in water and in the air causing a range of challenging environmental problems including excessive algal growth and acid rains. Therefore, understanding how plants uptake and assimilate nitrogen from the soil can potentially help in improving the use of fertilizers. In our current research, we are carrying out functional and structural studies to answer outstanding questions regarding the molecular mechanisms at the basis of nitrate acquisition by the NRT2 family of high-affinity nitrate transporters and their partner protein, the Nitrogen Assimilation Related or NAR2, focusing on NRT2.1 and NAR2.1 from Medicago truncatula. We plan to explore the MtNRT2.1-MtNAR2.1 interaction by bimolecular fluorescent complementation (BiFC) experiments and split-ubiquitin assays; to identify potential proton binding residues in NRT2s by structural modeling and site directed mutagenesis; and to structurally characterize the MtNRT2.1 and MtNAR2.1 complex by small angle scattering and cryo-electron microscopy. So far, we performed BiFC experiments in tobacco leaves and were able to show that MtNRT2.1 and MtNAR2.1 interact on the plasma membrane where they restore the fluorescent signal for YFP. Mating-based split-ubiquitin experiments confirmed their interaction in yeast. We also obtained structural models of MtNRT2.1 based on the crystal structures of bacterial Nitrate Nitrite Porters (NNPs). While bacterial NNPs

lack protonatable residues in the substrate-translocation pathway, potential proton binding sites were identified in the MtNRT2.1 model. Therefore, we hypothesize that NRT2s are nitrate-proton symporters in contrast to NNPs that are nitrate/nitrite antiporters. An AlphaFold model of the putative tetramer formed by MtNRT2.1 and MtNAR2.1 is guiding mutagenesis studies that will be tested with the split-ubiquitin assay. Understanding nitrate assimilation and exploring the molecular mechanisms of nitrate transport may result in the improvement of nitrogen acquisition and nitrogen-use efficiency in crop plants. As an example, field experiments showed that co-overexpression of OsNAR2.1 and OsNRT2.3a increases rice biomass and total nitrogen accumulation, improving rice yield.

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Identification & characterization of Arabidopsis alpha/beta hydrolase mutants with putative role in PAA degradation

Polyaspartic acid (PAA) is a biodegradable polymer with many industrial applications, and is thermally synthesized from the naturally occurring aspartic acid. PAA is widely used in crop production to enhance plant growth and yield. Bacterial enzymes PahZ1KT-1, PahZ2KT-1 from Sphingomonas and PahZ1KP-2 from Pedobacter belonging to the α/β hydrolase superfamily are implicated in the sequential degradation of PAA to aspartate, a key metabolite for plant growth. It is known that plants release root extracellular enzymes, including hydrolases. However, it is not established whether in the absence of bacteria, plants can degrade PAA. The objective of this study is to characterize Arabidopsis mutants impaired in selected hydrolase genes to identify those with potential to degrade PAA. We conducted bioinformatics analyses and identified enzymes in Arabidopsis thaliana that are homologous to PahZ1 and PahZ2. Bioinformatics analyses of Arabidopsis and bacterial hydrolases revealed sequence identities ranging from 11-61% (PahZ1) and 18-20% (PahZ2). We obtained Arabidopsis mutant seeds and grew plants in agar-based media. Results show mutant specific differences in root length and root hair development in response to PAA. We observed delayed germination in one mutant. We have identified mutants with impaired or interesting responses to PAA and are conducting protein expression analyses in E. coli.

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An Inducible Cre–lox System for Heritable Marker Excision in Rice

A heat-inducible Cre–lox recombination system was developed for rice to enable inducible excision of selectable marker genes from transgenic plants. Two independent Cre recombinase expression constructs, each driven by a distinct soybean heat-shock promoters, HSP17.3B (B7) or HSP17.5E (D1) were introduced into rice via Agrobacterium mediated transformation. Each promoter was evaluated separately to compare inducible excision efficiency. In each construct, DsRED was used as the transformation marker and GFP as the indicator of successful recombination, leading to marker-excision. A total of 70 independent transgenic lines were generated that were heat treated to induce Cre-lox recombination and then analyzed by droplet digital PCR to determine transgene copy number. The T1 progeny of these lines were screened for the presence of excision locus (GFP+), absence of unexcised locus (DsRED-), and subsequently

verified by PCR-based diagnostics designed to distinguish excised from unexcised genomic configurations. This analysis showed that 35.14% of B7 lines and 23.3% of D1 lines derived T1 plants harbored fully excised locus. These excision-positive T1 lines were advanced to the T2 generation and analyzed for the heritability of the excision locus. The T2 data will be presented at conference. Overall, this work supports the use of a heat-inducible Cre–lox system as a practical approach for marker removal in rice and provides a practical framework for generating marker-free transgenic cereal crops such as rice.

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Controlling the bolting of Raphanus sativus by red and far-red light

Although light is the primary source of energy for carbon fixation and growth, spectral quality/color is key stimuli for photomorphogenesis and -tropism, elongation growth, and gene expression. Phytochromes are photoreceptors and temperature sensors that affect the transition from vegetative to reproductive growth, as well as controlling germination, de-etiolation, shade avoidance, and circadian clocks. Phytochrome exists in active (Pfr) or inactive (Pr) states that are interconvertible depending on the absorption of far-red and red light. Pr has a sharp absorption peak at 650-670 nm, whereas Pfr maximally absorbs at 705-740 nm. To examine the influence of phytochrome on bolting, Raphanus sativus plants were grown under LEDs providing light deficient in either red (600-700 nm; phytochrome inactive) or far-red (700-780 nm; phytochrome active) bands. In the absence of far-red light, radishes began bolting significantly earlier than when grown under red-deficient light. 50% of individuals from the "-FR" (minus far-red) treatment began bolting by the 22nd day after planting (DAP), increasing to 83% bolting by the end of a 28-day grow out. At the same time, no plants from the "-R" (minus red) light treatment had initiated bolting by DAP 28. The bulb weight at harvest of bolting radishes was significantly lower than that of non-bolting radishes. However, the bulb weight of non-bolting individuals was not affected by light, which suggests that the transition to bolting occurs during early development. Additionally, leaf biomass, total biomass (i.e., sum of bulb, leaf, and bolt), and photosystem II quantum yield were unaffected by light quality or bolting status. RNA was extracted from new-growth leaf tissue on DAP 22, 25, and 28 for quantification of genes known to affect bolting, namely GIGANTEA (LOC108806054); DELLA RGA2 (LOC108827889) and TF3 (LOC108814121). qPCR analysis will show the extent of gene transcription because of light manipulation. The ability to control bolting and therefore flower development is relevant for optimizing the production of seeds vs. (edible) biomass. This work is supported by NASA grant 80NSSC23K1204.

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Caught in the Act: Capturing Decisive Junctures of Regioselective Diversification Steps in Plant Metabolic Pathways

The biosynthesis of plant natural products represents one of the most chemically diverse and pharmacologically valuable branches of specialized metabolism. Functional characterization of participating enzymes and the precise mapping of metabolic bottlenecks continue to rely on labor-

intensive enzyme assays that hold back pathway elucidation. We present a computational framework to identify the chemical determinants of enzyme specificity in plant metabolic pathways using well-studied alkaloid-producing species as model systems. The workflow consists of (i) systematic screening of native substrate scaffold and key active-site residues with tight-binding quantum method; (ii) refinement of promising routes at the density functional theory level to obtain accurate free-energy profiles and transition-state structures; (iii) benchmarking simulated temporal snapshots of regioselective diversification steps and computed energetic parameters against empirically derived constants and product ratios reported for well-characterized enzymes. Convergence between theory and experiment validates the proposed workflow. Once validated, the same computational pipeline will be applied to two test systems: (i) substrate analogs generated by systematic modification of the precursor scaffold and (ii) enzyme variants carrying targeted amino-acid substitutions at active-site positions. These screens yield chemically interpretable descriptors (e.g., electrostatic potentials and frontier-orbitals) that govern enzymatic activity and selectivity. Iterative cycles of in silico active-site redesign and substrate modification generate a training set for machine-learning models. These models will ultimately predict how changes in substrate structure and enzymatic active-site composition can influence product distribution.

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IIdentification of a plasma membrane complex that interacts with phyB to regulate ROS production

Reactive oxygen species (ROS) regulate plant growth, development, and responses to the environment. ROS production by the RESPIRATORY BURST OXIDASE PROTEIN D (RBOHD) protein was recently shown to be regulated by PHYTOCHROME B (phyB), and phyB was found to be phosphorylated by FERONIA, highlighting the possibility that these three proteins interact to regulate ROS levels during stress. Immunoprecipitation and proximity labelling, followed by split-luciferase and functional validation assays, were used to study the interactions between FERONIA, phyB, and RBOHD during excess light (EL) stress in Arabidopsis thaliana. We reveal that phyB, RBOHD and FERONIA interact, that phosphorylation of phyB by FERONIA, as well as the kinase activity of FERONIA, are required for RBOHD-driven ROS production in response to EL stress, and that CYSTEINE-RICH RECEPTOR LIKE KINASE 10 (CRK10) and PLASMA MEMBRANE INTRINSIC PROTEIN 2;6 (PIP2;6) interact with RBOHD and phyB and are also required for EL-driven RBOHD ROS production. Our findings uncover the existence of a putative plasma membrane complex between FERONIA, RBOHD, CRK10, and PIP2;6 that interacts with phyB to regulate ROS production in Arabidopsis in response to stress. This complex could play a canonical role in the integration and regulation of multiple signaling pathways in plants.

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Investigating the Molecular Mechanisms via which the Plant Growth-Promoting Bacterium, Azospirillum brasilense, Improves Growth in Salt-Stressed Rice

Major food crops, such as rice and maize, display severe yield losses (30-50%) under salt stress. Furthermore, problems associated with soil salinity are anticipated to worsen due to changing environmental conditions. Therefore, it is necessary to implement sustainable agricultural strategies, such as exploiting beneficial plant-microbe associations, for increased crop yields. Plants can develop associations with beneficial microbes [e.g., mycorrhiza, plant growth-promoting bacteria (PGPB)]. PGPB improve plant growth via multiple mechanisms, including protection against biotic and abiotic stresses. Azospirillum brasilense, one of the most-studied PGPB, can mitigate salt stress in various crops. However, little is known about the molecular mechanisms by which A. brasilense mitigates salt stress. Previously, we established an experimental system in which A. brasilense inoculation increased plant mass in rice grown under high salt concentrations (100 mM and 200 mM NaCl) at 7 days post-inoculation (dpi). Using RNA sequencing, we identified transcriptomic changes in rice during A. brasilense-mediated salt stress tolerance at two stages: one (early) and seven (late) dpi. We identified differentially expressed genes associated with abscisic acid signaling, antioxidant defense, ion transport, calcium signaling, plant defense, and nutrient transport. Our findings revealed a dynamic, phased response in which A. brasilense promotes early stress buffering and ionic control, followed by later enhancement of nutrient acquisition pathways. Understanding these molecular events will support the development of bioinoculant-based strategies to enhance stress resilience and improve crop yields.

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Small RNA-Mediated Activation: A Global Overview and Its Role in Plant Immunity

Small RNA-mediated activation (sRNAa), also known as RNA activation (RNAa), represents a non-canonical regulatory mechanism in which small RNAs enhance, rather than repress, gene expression. First described in mammalian systems, sRNAa involves promoter- or chromatin-targeting small RNAs that associate with Argonaute proteins and induce transcriptional upregulation through epigenetic remodeling. Reported mechanisms include recruitment of transcriptional activators, modulation of histone modifications such as increased H3K4me3 and H3 acetylation, and enhanced chromatin accessibility. Unlike canonical RNA interference pathways that direct mRNA degradation or transcriptional silencing, sRNAa functions through sequence-specific chromatin engagement to stimulate transcription. Although sRNAa has been demonstrated in multiple biological contexts, including development and stress responses, its endogenous molecular framework and physiological relevance in plants remain poorly defined. In particular, the identity of activating small RNAs, their biogenesis pathways, and their roles in plant immunity are still emerging. Our recent findings identify a 31-nt 5' tRNA-derived fragment, tRF31Asp2, as an endogenous activator in plants. We show that tRF31Asp2 accumulates in the nucleus during effector-triggered immunity, associates with AGO2-clade proteins, and engages defense-related chromatin loci to promote transcriptional activation of previously silent genes. Finally, we evaluate these sRNA-mediated activation mechanisms across plant and animal regulatory systems to delineate conserved and divergent mechanistic features.

Katie Murphy

From Pixels to Phenotypes: High-Throughput Image Analysis for Plant Biology

Rising global temperatures threaten food security and crop productivity as plants struggle to grow in environmental stress conditions. Improving crop resilience therefore depends on fast, accurate, and affordable methods to quantify plant traits at scale. We apply high-throughput phenotyping and image analysis to evaluate plant growth and stress responses, with a particular focus on maize. Using the open-source image analysis platform PlantCV, we leverage computer vision approaches to extract quantitative traits from plant images. We applied these tools to identify stress-tolerant maize varieties and provide functional insight into the mechanisms underlying stress tolerance and susceptibility.

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An Inducible Cre-lox System for Selectable Marker Excision in Cowpea (Vigna unguiculata)

The objective of this study is to develop streamlined methods for generating marker-free transgenic lines by incorporating Cre-lox recombination system into cowpea transformation protocol. This approach allows marker excision in primary transgenic lines (T0) and recovery of the

marker-free progeny (T1). A T-DNA vector for Agrobacterium mediated transformation was developed that contained heat-inducible Cre and a loxPflanked selection marker gene. The vector also included RFP as the transformation marker and GFP as the reporter of marker excision. This vector design with two different heatshock promoters generated 1.4 and 0.4% transformation efficiency based on infections of ~2500 embryonic axes. The lower transformation efficiency is possibly based on leaky activity of the heat-shock promoter. The T0 plants subjected to heat treatment showed GFP fluorescence and excision footprint in PCR, indicating marker excision. In a subset of analysis, 5 out of 13 of the heat-treated T0 lines transmitted the marker-free locus to the T1 progeny. More analysis is needed to confirm the inheritance of marker-free locus; however, the data so far indicates that inducible Cre-lox system is a viable approach for generating stable marker-free cowpea lines.

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Improving upland cotton abiotic stress resistance through the co-overexpression of vacuolar H+ pyrophosphatase, SUMO E3 ligase and vacuolar membrane NO_3^-/H^+ antiporter genes

Plant development, growth, and productivity are adversely impacted by abiotic stresses like drought, salt, and extreme temperatures, thereby affecting the world's food production capacity. These stresses continue to limit cotton productivity, particularly in regions like the Texas High Plains, where rising temperatures, reduced water availability, and increased soil salinity due to excessive use of fertilizer have caused substantial yield losses. To address this challenge, this study is aimed at enhancing cotton tolerance to abiotic stresses through the co-overexpression of three stress-responsive genes: the Arabidopsis vacuolar H+ pyrophosphatase gene (AVP1) which confers drought and salt tolerance; the rice SUMO E3 ligase gene (OsSIZ1) which regulates plant growth and development, conferring increased tolerance to cold, phosphate starvation, salt, water deficit, and extreme temperature; and the Arabidopsis thaliana chlorine channel (AtCLCa), a NO3-/H+ antiporter that drives nitrate into the vacuole and could potentially confer increased salt and drought tolerance in plants. A binary vector carrying all three genes under constitutive promoters was constructed and introduced into cotton cultivars using Agrobacterium-mediated transformation. Putative transgenic plants were screened through selective marker assays and PCR confirmation. Transgenic plants exhibited significantly higher survival rates, improved water-use efficiency, increased chlorophyll content, greater retention of biomass, and improved photosynthetic efficiency compared to wild-type control. These findings demonstrated that co-overexpression of AVP1, OsSIZ1, and AtCLCa provides a synergistic strategy for enhancing cotton resilience to multiple abiotic stresses. This result also provides support for triple-gene stacking as a promising approach for the development of next-generation stress-tolerant cotton cultivars suited for the increasingly different environmental conditions

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Elucidating the Role of Auxin in Photosynthate Allocation in Plants

Plants orchestrate a sophisticated carbon economy to thrive under fluctuating environmental conditions, relying on the diurnal synthesis, storage, conversion and remobilization of starch, between leaves and other growing/storage tissues including roots. On the other hand, plant growth, development, and responses to the environment rely on many hormones, which have distinct as well as overlapping signaling pathways. Auxin, a major phytohormone, is one of such hormones with a canonical signaling pathway where auxin acts as a molecular glue for its co-receptors, SCF^TIR1/AFB protein complex and transcriptional repressor proteins, Aux/IAAs. In Arabidopsis, a gain-of-function mutation in one of the Aux/IAA proteins (AXR3/IAA17) genes (axr3) results in pleiotropic effects such as dwarfism, curled smaller leaves, late flowering and severe agravitropic roots. Studies reveal that axr3 mutant lacks gravisensing statoliths in the columella region at the root tip. Nevertheless, a closer look at the axr3 mutant indicates that it is accumulating more starch in leaves compared to the wild-type leaves. This observation led us to hypothesize that axr3 mutation may be affecting the conversion of starch into sucrose, transport of sucrose from source to sink, or reformation of starch in the root. The goal of this research is to investigate how axr3 mutation affects the starch-sucrose cycle. Understanding the mechanism by which this process is controlled by the AXR3/IAA17 gene may help us engineer improved crop plants that produce higher levels of starch with efficient resource allocation.

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Reconstitution of induced systemic resistance to engineer disease-resistant plants

A major problem faced in global agriculture and food production is plant microbial pathogens and pests. A large number of studies have thus identified resistance (R) genes for crop improvement. However, this approach is at an impasse as their ectopic expressions tend to confer protection against just one or a few pathogens, while suppressing critical aspects of plant growth. A potential solution to this pitfall is plant growth-promoting rhizobacteria (PGPR)-mediated Induced Systemic Resistance (ISR), which is a heightened state of defense against a broad spectrum of pathogens. ISR also enhances plant growth and development. Caveat is that PGPR treatment lacks reproducibility in field settings. Therefore, we have identified a key mobile signal of ISR, 2,3-dinor-12-oxo-phytodienoic acid (dnOPDA) that is produced in roots upon PGPR interactions and travels throughout the whole plant. In systemic tissues, it is received by a receptor, CYCLOPHILIN 20-3 (CYP20-3). We now aim at overexpressing CYP20-3 in Arabidopsis to amplify dnOPDA signaling and examine if these transgenic plants could pre-prime ISR against emerging disease spreads. This study will provide novel insights into how plants can orchestrate a broad-spectrum resistance while coordinating energy allocations into defense and growth at the same time.

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Altering the terminal inverted repeat sequences of the soybean CACTA transposable element dTgm9 inhibits its transposition

Transposable elements (TEs) are mobile DNA sequences that have significant roles in generating genetic variation and altering gene expression. The CACTA-family of TEs has highly conserved terminal inverted repeats (TIRs) composed of the sequence CACTA on both ends of the element. The TIRs are recognized by the transposase enzyme that binds the TIRs and catalyzes transposition. We developed a yeast transposition assay for a 2000 bp version of the soybean CACTA element, Tgm9, called dTgm9. Our goal was to determine the role of the TIRs in the transposition of the dTgm9 element. We hypothesized that they are required for transposase binding and/or catalysis because they are highly conserved across eukaryotes. We altered the first 'C' nucleotide of the dTgm9 TIR to an A, T, or G on the 5', 3', and 5'+3' ends and transformed them into yeast. By performing yeast transposition assays, we determined that all the modified constructs showed a significant decrease in transposition. This indicates that the TIRs play a critical role in dTgm9 transposition. However, a higher transposition frequency was observed for 3' modifications compared to 5' modifications, indicating that alterations to the 3' TIR are slightly less disruptive. This suggests that transposition complex formation may initiate at the 5' TIR. By continuing to study the role of the dTgm9 terminal inverted repeats, we hope to identify which other bases are critical for transposition.

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Functional Redundancy in PIF4-Mediated Thermosensory Transcriptional Regulation

Plants adjust architecture to modest temperature elevations through thermomorphogenesis, a growth program driven by coordinated transcriptional reprogramming. Multiple thermosensory transcription factors contribute to this response, yet PHYTOCHROME-INTERACTING FACTOR 4 (PIF4) occupies a central position: loss of PIF4 causes a pronounced failure of warm-temperature hypocotyl and petiole elongation. This strong genetic requirement has often been interpreted to mean that PIF4's canonical transcription-factor features—sequence-specific DNA binding and transactivation—must be indispensable for thermomorphogenetic gene expression. Here, we present evidence for a different framework built around functional redundancy within transcriptional assemblies. Using structure–function perturbations of PIF4 combined with genetic complementation and transcriptional readouts, we find that PIF4 variants with compromised intrinsic DNA-binding or transactivation capacity can still support thermosensory growth in a partner-replete context. These results suggest that, in vivo, the activities typically assigned to an individual activator can be distributed across a multiprotein complex, with DNA-binding and transactivation functions supplied in trans by collaborating factors. In contrast, perturbations that disrupt PIF4's ability to assemble through its helix–loop–helix (HLH) module strongly attenuate thermomorphogenetic output, highlighting oligomerization competence as a key requirement for productive partnerships. We further leverage partner-limited genetic backgrounds to probe how redundancy shapes apparent "requirements" for individual domains. Under reduced partner availability, intrinsic features of PIF4 become more consequential for target-gene induction, consistent with a model in which thermosensory transcription is buffered by cooperative

assemblies whose composition can shift with network context. Together, these findings motivate a view of PIF4 as an organizer of warm-temperature transcriptional programs: its essential role stems less from acting alone as a self-sufficient activator and more from enabling assembly of partner-dependent transcriptional complexes that distribute core functions across multiple proteins. This redundancy-based logic provides a conceptual framework for how plants achieve robust temperature-responsive growth despite fluctuating cellular conditions and variable transcription factor availability.

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Investigating the roles of small RNAs in regulating drought, heat, and combined drought and heat stress in Sorghum

Sorghum (Sorghum bicolor) is a cereal crop known for its resilience to drought and heat compared to other cereal crops. Therefore, it is crucial to understand the molecular mechanisms sorghum displays under these abiotic stresses to develop climate-resistant crops. This study will focus on elucidating the roles of small RNA (sRNA) such as microRNAs (miRNAs) and small interfering RNAs (siRNAs) in mediating drought, heat, and combined drought and heat stress in sorghum. In total, we have identified 75 miRNA loci in sorghum seedlings, of which 15 were novel, with most of them being 21 nucleotides in length. As expected, in plants, small interfering RNAs (siRNAs) made up most sRNA data, of which 19762 clusters were identified, with most being 24 nucleotides in length. Differential expression analysis of these sRNAs showed that there were unique responses in each stress condition for both miRNA and siRNA, with some sRNAs being differentially expressed in only one stress condition but not the other two. In total, there were 35 differentially expressed miRNAs, with 5,1, and 11 being unique to drought, heat, and combined, respectively. While there were 1390 differentially expressed siRNAs, with 296, 211, and 694 being unique to drought, heat, and combined, respectively. Following this, an additional differential expression analysis at the gene and transcript level was conducted to see the inverse correlation between the sRNAs and associated genes. With miRNAs targeting transcripts related to various aspects of a plant's growth and development. While siRNA clusters overlapped to genes encoding for various transcription factors, enzymes involved in metabolic processes, and stress signaling. By better understanding miRNA and siRNA regulatory mechanisms in sorghum, we hope this study provides a deeper understanding of how plants can adapt to abiotic stress.

Aaron M. Rashotte (Department of Biological Sciences, Auburn University)

Different Cytokinins and their Roles in Delaying Leaf Senescence

Cytokinin is a well known plant hormone that can delay leaf senescence, yet the mechanisms behind how this occurs is unclear. To better understand what is happening we examined transcriptome (RNA-seq) and cytokinin hormone profiling over a range of timepoints that paralleled physiological examinations of leaf senescence. This was conducted using the classic cytokinin Dark-Induced Senescence bioassay in Arabidopsis leaves after treatment with a number of distinct cytokinin bases, iP, tZ, DHZ, cZ and their N-conjugate forms to determine unique/overlapping cytokinin roles in the delay of senescence processes. From this we have been able to detect specific patterns related to bases vs N-conjugates, as well as distinct transcriptome effects at early, middle, and late stages of senescence seen as GO term categories. Moreover, changes in

cytokinin levels were measured across senescence, which indicate flow patterns that occur in the biosynthetic pathway, as well as how they are altered by the external application of specific cytokinin forms in this assay. Interesting novel cytokinin senescence related targets were identified and are being pursued.

Bryce Redfern Department of Biological Science Florida State University

How strain-specific EPS variants shape host permissiveness and immune modulation in Medicago symbiosis

This project investigates how strain-specific differences in rhizobial exopolysaccharides (EPS) influence host permissiveness and symbiotic compatibility in Medicago species. Although EPS I is classically required for nodule invasion, preliminary data reveal that EPS II substitution is strain- and host-dependent, occurring in Sinorhizobium medicae–Medicago truncatula interactions but not in the corresponding S. meliloti partnership.By generating targeted exoY and wgaAB mutants in Sinorhizobium medicae WSM419, this project directly tests how distinct EPS variants influence host recognition and invasion efficiency. Defining the molecular rules that govern EPS-dependent compatibility will advance our understanding of host–microbe specificity, illuminate evolutionary pressures shaping symbiotic signaling, and inform strategies to improve nitrogen-fixing partnerships in legumes.

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Investigating mPing transposition in Camelina sativa

DNA transposable elements are found in virtually all eukaryotic organisms and can jump around the genome using a cut and paste mechanism. mPing is a Tourist-like miniature inverted repeat transposable element from rice that is being developed into a targeted insertion tool for genome editing in plants. It has been shown that mPing, mobilized by Pong transposase proteins, can be inserted into Cas9-cleaved sites. Previous experiments showed that the mPing-based transposase-assisted target site integration (TATSI) system functions in Arabidopsis and soybean. Our goal was to identify additional crops that show evidence of mPing transposition. We chose Camelina sativa, an easily transformed oil crop that has been identified as a potential source of biofuel. To test for TATSI compatibility, we tested different aspects of mPing transposition in Camelina: its excision frequency, excision site repair efficiency, and presence of heritable excision. Using a GFP reporter and PCR analysis, we were able to confirm mPing activity in our transformed Camelina. Sequencing of the resulting excision sites allowed us to see how precisely the DNA is being repaired. For genome editing using mPing to work, the alterations must be passed down to its progeny. Analysis of the following generation of plants showed that multiple lines exhibited whole-plant GFP, consistent with heritable excision. We are currently investigating these plants to confirm if the mPing element transposed to a new location.

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Evaluation of Arabidopsis thaliana Genotype and Root Phenotype in LMS-2 and Calcium-Supplemented Soil

Lunar regolith presents major constraints for plant growth due to nutrient scarcity and unfavorable physical and chemical properties. The lunar mare regolith simulant LMS-2 is formulated from Apollo-derived compositional data to model basaltic maria surfaces, and is comparatively calcium-rich because it incorporates calcium-bearing volcanic minerals. Calcium serves as both a structural component and a signaling molecule in plants. Structurally, calcium aids in stabilizing cell walls and membranes, contributing to root integrity and development. As a secondary messenger, calcium translates environmental signals into cellular responses. Specifically, calcium-specific spikes activate signaling proteins such as calcium-dependent protein kinases (CDPKs), such as CPK1, which regulate stress responses and developmental processes. The goal of this study was to evaluate how a calcium-sensitive mutant (CPK2) and wild-type Arabidopsis thaliana (Col-0) respond to calcium-rich substrates, such as LMS-2. This study focused primarily on the impact of elevated calcium levels in LMS-2 on root development and gene expression. Plants were grown for four weeks in a controlled-environment chamber under four different substrate conditions: nutrient-balanced soil, calcium-supplemented soil, LMS-2 as a nutrient-poor substrate, and LMS-2 supplemented with a balanced nutrient solution. RNA sequencing was performed and calcium signaling genes (CPK1, CML24, TPC1) as well as auxin transport genes (PIN1, ARF7, TIR1) were targeted. Calcium supplementation markedly enhanced root system development, as the wild-type plants grown in calcium-supplemented soil displayed lateral root lengths of 33.4cm by week 4, compared to 18.6cm from the plants grown in LMS-2. Calcium supplementation also increased expression of the calcium-signaling genes CPK1 and CML24, particularly in the wild-type plants. For example, CPK1 expression peaked at 245 normalized counts under calcium-supplemented conditions, compared to 112 in LMS-2. The auxin transport genes PIN1 and ARF7 showed similar calcium-dependent upregulation, supporting the idea that calcium enhances auxin-mediated root development. Notably, CPK1 and ARF7 expression were moderately correlated under calcium-supplemented conditions (r= 0.56), suggesting coordinated regulation between calcium signaling and auxin pathways. Overall, these results indicate that calcium supplementation can partially offset growth limitations imposed by nutrient-poor lunar regolith simulants, and may inform substrate and nutrient management strategies for bioregenerative life support systems in long duration missions.

Gabrielle Rust (UNT Biology Department) Brandon Deeb (UNT Biology Department) Patrick Horn (UNT Biology Department) Hanbee Choi (UNT Biology Department)

Viability of genetically altered cyclic fatty acids expression in cotton

Cotton is an important agricultural product, farmed for both the textile use of its boll and the oils produced in its seeds. It is one of the few plants found in nature that produces cyclic fatty acids (CFAs). However, much is still unknown about the biochemical pathway that generates CFAs and their functional role in cotton. This project aims to identifying the long-term viability and effects of increased CFA level in cotton. Transgenic cotton lines were created to ensure a permanent alteration to CFA's production pathway. The impact the genetic alterations had on CFA levels (specifically dihydrosterulic acid) was determined by extracting the lipids from seed embryos, and analyzing the fatty acid composition using gas chromatography to identify an impact the genetic alterations had on CFA levels. A mature leaf assay investigated how conserved the CFA

upregulation was throughout the plant's development. Elucidating the effects of increased CFA is a key step in increasing the production and supply of CFAs, which may have benefits for plant defense, human and livestock nutrition, and industrial bioproducts.

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Reconstruction of induced systemic tolerance to engineer drought tolerant plants

Drought is the deadliest abiotic factors for crops. For decades, substantial efforts have been made to find drought-responsive genes (DRGs). However, their ectopic expressions bring growth penalty. To resolve this pitfall, we are exploring plant growth-promoting rhizobacteria-mediated induced systemic tolerance (IST), which is a state of heightened defense throughout the whole plant against various abiotic stresses such as drought, salinity and extreme temperatures, while maintaining optimal growth. Toward that, we have identified that Paenibacillus polymyxa CR1 mediates IST against drought in soybean and Arabidopsis by upregulating the expression of two DRGs, Response to Desiccation 29A (RD29)A and RD29B genes, before encountering drought stress. RD29A is a circadian clock transcriptional regulator (TR), and RD29B is a circadian oscillator of RD29A. Hence, we are trying to overexpress RD29A, in a circadian rhythmic manner, in Arabidopsis to test if these transgenic plants stably prime IST without growth penalty. The successful validation of this hypothesis will allow us to apply the same technique for economically important crops in engineering 'for-profit' drought tolerance.

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Conserved Mechanisms of Plant Lipidome Remodeling under Heat and Cold Stresses Revealed through Meta-Analysis

Increasing temperature fluctuations threaten crop productivity worldwide, emphasizing the need for a deeper understanding of plant adaptation to such extremes. Lipids are fundamental biological molecules that furnish structural, metabolic, and regulatory roles in plant growth and development, and responses to environmental stresses. The potential of lipids as key targets for crop improvement under changing climates is emerging. This systematic review and meta-analysis are comprehensive syntheses of current knowledge on plant lipidome responses to heat and cold stresses. The analysis reveals conserved lipidomic responses to heat and cold stresses across plant species, tissue types, and growth stages. The decreased levels of lipids with relatively smaller head groups (e.g., MGDG, PE) that promote membrane bilayer structure, a decrease in unsaturation index in membrane lipids, and sequestration of polyunsaturated acyl chains into neutral lipids (e.g., TG) emerged as conserved strategies for heat adaptation. Also, very long-chain fatty acids were identified as important in heat stress adaptation, as their presence is likely to counteract excessive membrane fluidity caused by high temperature and to maintain membrane stability under heat

stress. Under cold stress, the levels of membrane lipids containing polyunsaturated acyl chains were elevated, likely as an adaptive shift favoring more fluid, flexible membranes. Further, the levels of bilayer-forming lipids (e.g., DGDG) increased and non-bilayer-forming lipids (e.g., MGDG) decreased. Overall, this review synthesizes knowledge of lipidome remodeling in plants and its role in resilience to temperature stress, identifying priority areas for future research to support climate-resilient agriculture.

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Hormone crosstalk at the interface of CRF mediated flower and root development.

Abiotic stress widely regulates plant growth and development. Cytokinin Response Factors (CRFs) are a subgroup of the AP2/ERF transcription factor family. CRFs are downstream components of the cytokinin signaling cascade involved in regulating plant growth and development processes under different abiotic stresses. Our study suggests new roles for two Arabidopsis CRFs: CRF5 in lateral root growth under abiotic stresses and both CRF4 and CRF5 in flower development. CRF5 is reported to be expressed throughout the vasculature of the plant, but little work has been conducted on its role in roots. Upon examination, we found increased lateral root length and number in CRF5 overexpression (CRF5OE) lines compared to Wild-type, Col-0 (WT) and crf5 mutant. A similar trend was observed when CRF5OE lines were treated with drought, salt and a combination of drought and salt stress. Drought and salt-treated promoter::CRF5-GUS lines showed a reduction in GUS expression in leaves under stresses with a shift in expression towards the lateral root tip. crf5 also shows altered root gravitropic response and has fewer starch statoliths layers at the root tip. N-1-naphthylphthalamic acid (NPA) and trans-Zeatin (tZ) alter the root gravitropic response and starch statoliths layer formation at root tip in crf5 compared to WT and CRF5OE suggesting an auxin-cytokinin mediated root gravitropic response. We are currently generating crosses of CRF5 with auxin reporter lines DR5::GUS and PIN::GUS to check auxin regulation during lateral root development. CRF4 and CRF5 were also found to have a different role connected to regulating inflorescence development. CRF5 mutant and CRF4 overexpression lines show early bolting and flowering compared to Col-0, while crf4 mutants and CRF5OE are delayed. This suggests a new role for CRF4, which has previously been connected to cold and freezing responses. External Gibberellic acid (GA3) and tZ treatment speed up flowering time in crf4 and CRF5OE suggesting GA-Cytokinin mediated crosstalk. We are further interested in looking at how CRF4 and CRF5 interact with the Gibberellic acid pathway to regulate flower development. Together, these results shed light on the expanding roles of CRFs in roots and flowering.

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ISS-Derived Bacterial Inoculates for Plant Growth Promotion

With technology steadily advancing, humanity's interest in space exploration and long-term habitation has increased, creating a growing need to understand how biological systems function and adapt under spaceflight conditions. Beyond understanding these effects, it is also necessary to

develop strategies to mitigate the negative impacts of microgravity; one major challenge being impaired root gravitropism due to the absence of a gravity vector. Within the ISS's VEGGIE Unit, several species of bacteria have been found to engage in plant mutualism – these species were isolated and analyzed for plant-growth promoting phenotypes, as well as possible pathogenicity. This work evaluates the effectiveness of using ISS-derived bacterial isolates in helping Arabidopsis thaliana germinate and grow in simulated microgravity. To complete this work, seed inoculations at an optical density of 0.2 with relevant bacteria were performed and grown for 14 days on 0.25x Hoaglands agar. Plant inoculants with the most favorable results are then to be tested in simulated microgravity (using a 3D clinostat) to see if they remained beneficial.

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Characterizing Unknowns in Plants and Pathogens

The era of big data has opened new opportunities for research with unknown sequences, structures, and datasets waiting to be explored. These sources can provide a low barrier and flexible introduction to research through student projects ranging from high school science fairs to master's theses. Presented here is a sampling of student projects that used similar tools and strategies to explore diverse unknowns across species. Transcriptomics data indicate members of the RER protein family in cotton (Gossypium hirsutum) are differentially expressed in abiotic stress and fiber studies. A pair of high school students investigated the similarities and differences between subgroups within this family to demonstrate differential expression, localization, and motifs along with a potential new subgroup within the family. In addition to numerous uncharacterized protein sequences, there are also many experimentally solved protein structures of proteins of unknown function. An undergraduate thesis project centered on an intriguing uncharacterized protein structure from Staphylococcus aureus in PDB (3NU6). Bioinformatic analysis and docking placed the protein within the ABC transporter F-1 class of substrate-binding proteins with a unique active site containing two Zn2+ cofactors. Another uncharacterized protein structure was studied computationally and experimentally by a master's student. A protein from Salmonella typhimurium on PDB (3M07) was listed as a putative alpha-amylase. However, initial computational studies indicated the protein was a maltooligosyl trehalose trehalohydrolase (MTHase) belonging to a trehalose synthesis pathway along with maltooligosyl trehalose synthase (MTSase). Computational characterization of both MTSase/MTHase along with basic enzymatic activity assays support that this trehalose synthetic pathway is functional in this bacterial strain. In addition to knowledge gained from these student projects, all the students continued their studies in science, pursuing undergraduate and PhD degrees. With more data to explore being generated daily and students eager to engage in meaningful research, further implementation of these mutually beneficial projects is an exciting prospect.

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Effects of plant composition (neighbor presence and maternal lineage), and inundation regime on black mangrove (Avicennia germinans) growth

Black mangroves (Avicennia germinans) are expanding into salt marshes along coastal Louisiana due to a reduction in extreme cold events, replacing the historical foundation saltmarsh grass, Spartina alterniflora. Given this shift in foundation species, A. germinans is increasingly considered for planted restoration efforts to replace or supplement S. alterniflora. However, restoration outcomes using mangroves have been variable, and the drivers of establishment success remain unclear. Prior studies have shown that S. alterniflora can exert both competitive and facilitative effects when planted with A. germinans. Environmental context may underpin the variability in these interactions, with facilitation becoming more likely under higher abiotic stress. In coastal marshes, tidal inundation presents a key stress as it creates anoxic soil conditions. S. alterniflora can increase rhizosphere oxygenation, suggesting that any facilitative effects may emerge primarily under prolonged inundation. Additionally, individuals within species can also vary in morphological and physiological traits. Consequently, A. germinans maternal identity may impact A. germinans growth in response to inundation and neighbor presence. We plan to conduct a year-long fully-factorial mesocosm experiment testing the interactive effects of inundation duration (i.e., long vs. short), plant composition (i.e., presence vs. absence of S. alterniflora), and A. germinans maternal lineage on A. germinans growth and survival. We will measure A. germinans canopy area, height, leaf count, and stem count monthly. At the end of the experiment, we will measure above- and belowground biomass of both plant species. We collected propagules from 20 maternal A. germinans trees located in Port Fourchon, LA that are currently growing in the greenhouse prior to transplantation into the experiment in spring 2026. Currently, we are measuring germination rate to explore links between maternal tree traits and propagule growth rate. Preliminary results indicate strong variation in propagule mass between maternal lineages. Further, there is a weak correlation between increased propagule size and quicker germination. Our results aim to inform restoration practices to improve success when incorporating mangroves into future projects. Specifically, we will establish whether strategies should consider incorporating plant neighbors, tidal elevation, and maternal lineages with high performing propagules into the broader environmental context of restoration.

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Plant Growth Responses to International Space Station-Derived Microbes in Simulated Microgravity by Clinorotation

Long-term human space exploration depends on viable plant cultivation, a critical factor in psychological wellness, supplemental life support, and food production. However, plant growth in the spaceflight environment is greatly inhibited by stressors such as radiation exposure and microgravity. When faced with stressors in Earth environments, plants utilize interactions with plant growth-promoting (PGP) microorganisms to improve growth and yields through methods such as increased nutrient uptake and stress reduction. We propose that these plant/microorganism interactions could be similarly utilized in the spaceflight environment to mitigate stressors faced by plants on long-term space exploration missions. Current protocols in the spaceflight environment focus on the elimination of microorganisms, yet microbes continue to persist in wide distributions across both surfaces and hosts, including the presence of PGP bacteria in association with plants present on the International Space Station. These microbes may be utilized to mitigate stressors and improve plant yields in the spaceflight environment, including lunar or Martian missions. The

present study examines the ability of mixed cultures of PGP microbes (Bacillus subtilis, Pseudomonas fulva, and Paenibacillus pabuli) isolated from the ISS to improve plant growth in simulated microgravity by clinorotation. Our findings are interpreted in the context of engineering mixed microbial systems capable of supporting long-term missions across a range of extraterrestrial challenges.

Claire Taylor (Department of Biology, Texas State University), Sunethra Dharmasiri (Department of Biology, Texas State University), Nihal Dharmasiri (Department of Biology, Texas State University)

Investigating an ethylene insensitive mutant in the model plant Arabidopsis

As environmental extremes intensify, unraveling the molecular mechanisms of plant stress responses has become essential for sustaining agricultural productivity. Environmental stresses enhance the biosynthesis of ethylene, a stress hormone that balances the growth and defense responses and causes plant senescence. Interestingly, a commercially used herbicide, picloram, is known to exert its herbicide activity through the enhancement of ethylene production in the affected plants. We have isolated a picloram resistant mutant (designated pic20) in the model plant Arabidopsis. Subsequent mapping located the mutation to the first exon of EIN4 gene, which codes for an ethylene receptor. Our experiments have confirmed that pic20 mutant seedlings are moderately insensitive to ethylene. Additional experiments demonstrated that pic20 mutant seedlings are hypersensitive to osmotic stress, salt stress, and exogenous application of Abscisic acid (ABA), another stress induced hormone in plants. To confirm whether these phenotypes are due to the mutation in EIN4 gene, we overexpressed the wild-type EIN4 gene in pic20 mutant plants for complementation assays. Additionally, we are investigating the expression pattern of EIN4 gene under different abiotic stresses, and generating transgenic lines expressing GUS reporter gene fused with EIN4 to understand the developmental and stress-induced regulation of EIN4 expression. Our results will enable the elucidation of specific role/s of EIN4 protein in stress responses in plants, leading to substantial reduction in crop losses and amelioration of crop yields in stressful conditions, positively impacting the sustainable agriculture in a changing world.

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Exploring the function of plant immune receptors in regeneration

After wounding, plants must decide which route to take and where to allocate resources for - defense and regeneration – two fundamental biological processes essential for plant adaptability and survival. Two forms of regeneration include - de novo root regeneration (DNRR), in which adventitious roots develop at the wound sites, and wound induced callus formation (WIC), which includes formation of mass of undifferentiated cells at the wound site. However, the influence of immunity and environmental factors such as temperature on regeneration remains underexplored. To investigate the impact of immunity and temperature on regeneration, DNRR and WIC were studied in Col-0 (wild-type) and Chitin Elicitor Receptor kinase 1 (CERK1) mutants. CERK1 is a well-characterized pattern recognition receptor (PRR) located in plasma membrane that recognizes fungal cell wall components such as chitin and β-glucans and activates plant innate immunity and defense responses. Effects of two temperature conditions (22 °C and 28 °C) on DNRR and WIC formation were investigated. In context of DNRR, CERK1 mutants showed consistently higher DNRR as compared to Col-0 at 28 °C. On the other hand, mutants showed higher WIC as compared to Col-0 at both 22 °C and 28 °C. We conclude that CERK1 might be playing a role in balancing

regeneration and immunity, as coordinated responses to tissue damage. Understanding the regeneration responses might provide valuable insight into plant regenerative mechanisms and broaden the scope of future regeneration research.

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Integrated Physiological and Transcriptomic Analysis of Oxidative Stress Responses in Duckweed (Lemnaceae)

Environmental stressors, including elevated temperatures, drought, and flooding, severely disrupt plant growth and productivity by inducing oxidative stress. Excess accumulation of reactive oxygen species (ROS) damages lipids, proteins, and nucleic acids, ultimately compromising cellular integrity and yield stability. While oxidative stress mechanisms have been extensively characterized in the dicot model Arabidopsis thaliana, comparable omics-level insights in monocots remain limited. Addressing this gap is essential for developing climate-resilient crops. Our research establishes duckweed (Lemnaceae), a rapidly growing aquatic monocot with exceptional stress adaptability, as a powerful system to dissect oxidative stress responses. Through comparative physiological analyses across multiple Lemnaceae species, ROS accumulation, chlorophyll degradation, and antioxidant enzyme dynamics were analyzed under diverse oxidative stressors. Distinct stress-tolerant and stress-sensitive phenotypes among species were identified, highlighting natural variation in redox buffering capacity and adaptive potential. Moreover, to uncover the underlying regulatory networks, bulk RNA sequencing was used to profile transcriptomic reprogramming under oxidative stress. Differential expression and pathway enrichment analyses identified coordinated activation of ROS-scavenging enzymes, glutathione metabolism, detoxification pathways, and stress-responsive transcription factors. These findings provide insight into monocot-specific regulatory modules governing redox homeostasis and cellular protection. Importantly, candidate stress-tolerance regulators were identified, generating valuable targets for functional validation and translational applications. By integrating physiological phenotyping with systems-level transcriptomics, our research advances duckweed as an efficient monocot model for oxidative stress biology. Collectively, this research delivers foundational physiological and omics resources to identify key regulators of stress tolerance. These findings have broad implications for crop improvement, phytoremediation, and sustainable biotechnological innovation in the face of accelerating environmental stress.

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Rice expressing AtDREB1A transcription factor improves Nitrogen Use Efficiency

Use Efficiency (NUE) in major crops such as rice (Oryza sativa) would help to reduce the effects on the environment generated by the excessive use of fertilizers. Arabidopsis Dehydration Responsive Element Binding (AtDREB1A) is a transcription factor for tolerance to abiotic stresses, e.g., cold, drought, and salinity. In the other side, OsDREB1C is a transcription factor present in rice that recently has been shown to boost nitrogen uptake and rice grain production. We hypothesize that AtDREB1A directly or indirectly upregulates OsDREB1C in the transgenic lines. To determine the impact of AtDREB1A on rice production, this study evaluated NUE of the AtDREB1a-expressing transgenic line using two experimental designs. The first experiment was conducted in a hydroponic system with low and normal N levels, and the second experiment was performed under greenhouse conditions with 0 N and 100 N treatments. Chlorophyll content (SPAD), photosynthetic rate (LI-COR), biomass production, leaf N content, and grain yield were assessed in order to find out the impact of AtDREB1A on these traits. The results showed that AtDREB1A transgenic lines maintain higher SPAD values during the vegetative stage and higher photosynthetic rates than wild-type plants. Under N limitation, transgenic plants often showed greater leaf N content at the reproductive stage. Additionally, transgenic plants showed increased grain yield or no yield penalty under the different N treatments. Overall, the results suggest that AtDREB1A plays a key role in optimizing NUE possibly through upregulation of OsDREB1C leading to improved agronomic performance of plants, especially under low N rates as well as normal or optimal N rates. This approach may mitigate environmental pollution, decrease rice production costs, and integrate stress tolerance with enhanced grain yields.

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Unravelling the molecular mechanism of chalkiness by transcriptomic analysis of rice targeted in VPP5 gene

Chalkiness, the white opaque region in the rice endosperm, affects the quality of rice. The major QTL of chalkiness in indica rice is called VPP5 that encodes vacuolar H+ pyrophosphatase. However, its role in the chalkiness of japonica rice is unknown. Previously, in a japonica rice Nipponbare, VPP5 was targeted in the promoter region. The resulting vpp5 mutants displayed lower chalk content under ambient condition or high nighttime temperature. In this study, transcriptomic analysis of vpp5 mutant was carried out using the caryopses collected at 5 and 10 days after flowering (DAF). RNAseq analysis of these caryopses showed that expression pattern of VPP5 was modulated in the mutant towards generally a higher expression at both stages. 8430 and 2188 genes were differentially expressed in 5DAF and 10DAF, respectively, in the mutant. Among which 1292 genes are commonly expressed between 5 and 10DAF. Heatmap analysis and enrichment analysis shows that heat shock proteins are downregulated in the mutant at both stages whereas prolamine genes are downregulated in 5DAF and upregulated in 10DAF. In comparison to WT, HSP, starch and sucrose metabolism genes are more downregulated at 5DAF in the mutant, than at 10DAF. Specifically, FLO, Starch Branching Enzyme, ADP-glucose pyrophosphorylase, and amylase genes are more downregulated at 5DAF in the mutant than at10DAF. In genotype comparison, mutant has lower expression of HSPs at both stages and lower prolamine expression at 5DAF. These observations point to a differential accumulation of grain components including starch and

proteins. Further, the improved grain quality traits in vpp5 mutant are reflected in the transcriptome of the caryopses and the list of differentially-expressed genes are foundational in understanding how modulation of VPP5 leads to reduced chalkiness.

Ying Wang (Plant Pathology Department, University of Florida)

Preparing for the outbreaks of viroid diseases in crops

Spillover events expand the host range of pathogens and increase the risks of new disease outbreaks. The biological basis underlying the spillover of plant viral diseases remains poorly understood. Potato spindle tuber viroid (PSTVd) is a noncoding subviral RNA that causes production loss of potato and tomato. Recently, a fortuitous observation uncovered that high temperature permitted PSTVd infection in a non-host plant, Arabidopsis thaliana, and the titer was further increased in the NONEXPRESSOR OF PATHOGENESIS-RELATED GENES 1 (NPR1) loss-of-function plants. One mutation (G201U), which was reported in other PSTVd spillover events, emerged during the infection, and this mutation didn't lead to any new RNA motif. Further analysis showed that salicylic acid (SA) immunity represses PSTVd infection by degradation of key factors for its replication. As a counter activity, the NPR1 nuclear import was impaired in the PSTVd-infected host plants, attributed to the repressed expression of nucleoporins and nuclear transport receptors. Our data expands the effectiveness of SA-immunity to a new class of pathogens that do not encode any pathogen factors. This study also sends an alarming message regarding the increased likelihood of PSTVd spillover to new hosts during the global climate change and pinpoints the direction of molecular breeding for PSTVd resistant plants.

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Vermiculture: Creating Viable Regolith-Substrate Using Earthworms

Successful space crop production requires a sustainable agriculture system capable of supporting the dietary needs of mission crews. Rather than using more fuel and cargo space to haul heavy equipment for hydroponic systems on missions, it can be far more cost-effective and sustainable to instead fix regolith on-site to be a viable substrate, which leverages many aspects of traditional soil-based agriculture systems. However, the toxic and inhospitable nature of regolith presents challenges for plant growth and development. We propose using earthworms, specifically Eisenia fetida and Perionyx excavatus, for use in ameliorating regolith through vermiculture. Earthworms aerate, fertilize, and generally improve the structure of the soils they live in; moreover, they can ingest and immobilize heavy metals, effectively removing them from soils. This quality is of great interest concerning regolith, which contains high levels of heavy metals that make it incredibly inhospitable to plant life. In the present study, these worms were introduced to both sand and Lunar Highland Simulant (LHS) samples, mixed with manure, and incubated for a period of four months. The resulting substrates, along with the appropriate controls, were sifted to remove the worms and used as a substrate for the growth of Capsicum annuum, hot peppers, until fruits were harvested. We discuss our findings in terms of the viability of the approach, the changes to regolith as a growth substrate (pH, redox potential, etc.), and the general impacts on plant growth as well as edible fruit production.

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A Guide or an Escort? Role of IBR5 in auxin signaling pathway in Arabidopsis

Plant growth and development is fine-tuned by a wide array of exogenous and endogenous factors. Among them, phytohormones play a key role as an endogenous factor. Auxin is one of the major phytohormones that affects almost every aspect of plant growth and development. Auxin is perceived by a co-receptor system that includes TIR1/AFB F-box proteins and Aux/IAA repressor proteins. In the presence of auxin, Aux/IAAs interact with TIR1/AFBs and this interaction results in the degradation of Aux/IAA repressors leading to auxin induced gene expression. Earlier studies identified IBR5 as a component of the auxin response pathway, as ibr5 mutants exhibited reduced primary root sensitivity to indole-3-butyric acid (IBA), a precursor of IAA in plants. This mutant phenotype is consistent with an accumulation of Aux/IAA repressors. Interestingly though, Aux/IAA repressor proteins are degraded faster in ibr5 mutants, our studies indicate that IBR5, which encodes a dual specificity phosphatase, potentially controls the localization of the components of SCF(TIR1/AFBs) complex, and thereby regulates the degradation of Aux/IAA repressors. Additionally, it appears that IBR5 potentially interacts with Aux/IAAs further affecting their stability. Thus, it is possible that IBR5 regulates Aux/IAA degradation through multiple mechanisms. Broadening our understanding on such complex hormone signaling pathways will open doors to successful manipulation of plant growth and development towards human benefit.

Jing-Ke Weng

Integrated Omics for Studying Plant Metabolism in the Age of AI

Plants have evolved a dazzling array of lineage-specific specialized metabolic traits that enable them to cope with diverse ecological pressures and interact with other organisms, including humans. Our lab studies the origin and evolution of plant specialized metabolism at the enzyme, pathway, and systems levels, and applies this knowledge toward bioengineering strategies for drug discovery, sustainable chemical production, crop improvement, and climate remediation. Elucidating plant biosynthetic pathways is central to these efforts, as it provides access to complex natural products through synthetic biology. While genomic, transcriptomic, and metabolomic approaches have generated vast datasets, much of this multi-omics information remains underutilized. In this talk, I will highlight state-of-the-art strategies that integrate diverse omics layers with emerging computational tools to address challenges in pathway discovery. Specifically, I will discuss workflows that combine molecular networking, reaction pair analysis, and gene expression patterns to enhance data interpretation, as well as the transformative potential of artificial intelligence (AI) in streamlining both discovery and validation. By integrating multi-omics data, chemical insights, and advanced algorithms, we can accelerate our understanding of plant metabolism and unlock new opportunities for engineering valuable natural products. I will present a few of the latest examples from our own lab that demonstrate the power of this integrated omics and AI-driven approach.

Audrey Widmier (Department of Plant Biology, University of Georgia), CJ Tsai (Warnell School of Forestry and Natural Resources, University of Georgia)

Establishing simulated growth chamber conditions to bypass annual field cycles for the mechanistic dissection of seasonal growth arrest in Populus

Transition to seasonal growth arrest in perennial trees requires precisely timed transcriptomic, metabolic, and phenotypic changes. We developed a growth chamber system to bypass the unpredictability of field conditions and capture these changes in high resolution. Using this system, we successfully induced responses in tissue-cultured Populus tremula × alba INRA 717-1B4 that reflect the early autumnal phenology of field-grown counterparts. Platform validation using wild-type plants revealed a coordinated program of seasonal response at multiple levels. Within three weeks of treatment, primary stem growth plateaued, coinciding with the progressive closure of the shoot apical meristem and the vascular cambium transition to a definitive resting state. Metabolic profiling identified a priority in production of protective non-structural carbohydrates, raffinose and sugar alcohols, by the first week in treatment conditions. Transcriptomic data revealed significant shifts in gene expression within the first week of treatment related to environmental sensing, with later significant shifts toward genes associated with resource management and metabolism, while genes associated with active growth were downregulated. These data suggest that the simulated growth chamber system successfully captures the seasonal response and growth cessation similarly examined in field-grown trees. Current work is moving toward the use of this system to functionally validate genetic factors of early autumnal response through the screening of CRISPR knock-out mutants. By drastically reducing the experimental timeline and reducing reliance on field trials, this platform enables a rapid, efficient study of molecular machinery involved in initiating the early transition into seasonal dormancy.

Jack D Williams (School of Biological Sciences, University of Louisiana Lafayette) Robyn A Zerebecki (School of Biological Sciences, University of Louisiana Lafayette)

Assessing plant diversity across salt marsh restoration and the cascading effects on ecosystem function

Salt marshes are intertidal grasslands that provide numerous ecosystem services, including coastal protection, filtering of nutrients, carbon sequestration and providing habitat for a variety of economically valuable and ecologically important species; yet, these ecosystems are currently threatened and being lost by a host of anthropogenic forces including sea-level rise, land use change, altered hydrology, and coastal development. Consequently, this has prompted diverse restoration strategies aimed at reestablishing these ecosystems. Along the US Gulf Coast, restoration can take many approaches. For instance, containments are large plots of dredged sediment, contained in diked walls, usually allowed to colonize by neighboring marsh. Alternatively, terraces are small, segmented ridges built in open water to stabilize soil and grow marsh environment. The variation in size and connectivity among these techniques may lead to differences in diversity, as larger and more connected areas tend to support more species. Increased species richness can have positive effects on ecosystem function. Salt marshes along the Gulf coast are dominated by a single foundation plant, Spartina alterniflora, in the low and mid intertidal zones. Spartina exhibits natural variation in small-scale genotypic diversity and both genotypic identity and diversity can have positive ecological effects (e.g., plant production, associated invertebrate community). However, marshes in SW Louisiana tend to be more brackish to intermediate salinity, creating moderate environmental stress that may promote higher plant

species richness. Here, we examine how both inter- and intraspecific plant diversity varies across restoration techniques in SW Louisiana as well as the cascading effects diversity may have on ecosystem function. We sampled six sites throughout the region that each contained a terrace, containment, and natural marsh. At each marsh surveyed, we quantified Spartina productivity (e.g., biomass), plant community composition (e.g., species richness), and environmental parameters (i.e., soil redox, salinity, tidal elevation). Spartina genetic samples were also collected across spatial scales to evaluate whether genetic diversity patterns vary among restoration types and whether this corresponds to functional differences. By linking plant diversity—both inter- and intraspecific—to ecosystem function across restoration contexts, this study advances restoration science while integrating biodiversity–ecosystem function theory to inform long-term wetland management.

Li Yang (Department of Plant Pathology, University of Georgia); Joseph Balem (Department of Plant Pathology, University of Georgia); Chenjiao Tan (Department of Agricultural and Biological Engineering, University of Florida); Nathália Cássia Ferreira Dias (Luiz de Queiroz College of Agriculture, University of São Paulo); Mariah Arnold (Department of Plant Pathology, University of Georgia); Sorrel Tran (Department of Plant Pathology, University of Georgia); Paul M. Severns (Department of Plant Pathology, University of Georgia) Paulo J.P.L. Teixeira (Luiz de Queiroz College of Agriculture, University of São Paulo); Changying Li (Department of Agricultural and Biological Engineering, University of Florida);

Plant Wound Healing: From Biophysical Cues to Hormonal Signaling

Tissue repair is essential for plant survival, yet the mechanisms governing the completion of wound healing remain poorly understood. In this study, we report that mechanical injury in Arabidopsis leaves induces a transient, localized cooling response caused by evaporative water loss. Water evaporation is accompanied by a rapid activation of cold-responsive genes. We developed a thermal image-based workflow that leverages computer vision and deep learning to monitor spatiotemporal cooling patterns and gene expression dynamics. Using this platform, we demonstrate that CBF transcription factors act as key transducers linking injury-induced cooling to the activation of wound healing programs. This work uncovers a biophysical cue—evaporative cooling—as a signal in plant tissue repair and highlights the power of combining molecular genetics with deep learning–based phenotyping.

Allona Yehiav (APSS, Florida Institute of Technology) Frances A. Edmonson (OEMS, Florida Institute of Technology) Thiara Bento (BES, Florida Institute of Technology) John Z. Kiss (BES, Florida Institute of Technology) Andrew Palmer (OEMS, Florida Institute of Technology)

Kin Recognition in Simulated Microgravity by Clinorotation

As humanity starts establishing a presence on both the Moon and Mars in the upcoming decades, optimizing space-based agriculture will become more critical for life support. On Earth, plant growth under environmental stressors has been shown to be influenced by kin recognition (KR), which is the ability of plants to alter growth and other parameters based on the extent of genetic relatedness of their neighbors. KR has been implicated as a modulator of root and shoot growth and architecture as well as exudate production. KR also could have significant implications for many plants, whose life plan frequently involves growth in a community of closely related individuals. The 'strength' of this interaction has previously been shown to be regulated, in part, by

nitrogen and phosphorus availability suggesting this process could be tuned towards specific outcomes. This includes optimizing growth and yield in close quarters, such as those aboard the International Space Station (ISS) or similar structures in the future. However, the effects of microgravity on KR remain unknown. Understanding how gravity affects biological signaling is vital for designing and maintaining bioregenerative life support systems (BLSS) that will be used in upcoming space missions. If microgravity is shown to inhibit kin recognition, alternate spacing between plants or specialized nutrient-allocating units might be implemented to limit resource competition and improve yield. It might also affect the yield calculations for future crop models. This study evaluates the effects of simulated microgravity by clinorotation on KR in Arabidopsis thaliana, potentially impacting biomass yield in future space agriculture. We discuss our findings within the context of how this plant-plant interaction in space agriculture could direct space agriculture plans for future long-term operations in the space flight environment.

Yujeong Yeo (Department of Plant Pathology and Microbiology, Texas A&M University), Joseph Edwards (Department of Plant Pathology and Microbiology, Texas A&M University)

Understanding the ecological and genetic drivers of rice microbiomes across irrigation systems, cultivars and compartments

Rice is a staple food for more than half of the global population and is cultivated across a wide range of environments worldwide. Rice growers and consumers seek ways to increase the sustainability and resilience of this crop. One avenue to achieve this goal is through improving interactions with the rice microbiome. The rice microbiome plays a key role in soil health and plant fitness, affecting plant growth, nutrient acquisition, stress tolerance, greenhouse gas emissions, and disease resistance. Therefore, a key question to growers, plant breeders, and scientists is whether rice cultivars can be bred to enrich their microbiomes with beneficial microbes and whether these effects are robust across environments and cultivation practices. Nevertheless, how host genetics impacts rice microbiome assembly is unknown. In this study, we characterized microbial communities of rice rhizosphere soil, root, and leaves across two irrigation methods and multiple cultivars. Compartment was the strongest determinant of microbiome structure, reflecting marked ecological contrasts among plant microhabitats. Cultivar identity also explained significant variation, indicating that host genetic background is a powerful driver of microbiome assembly across environments. Importantly, we found that methane-producing archaea varied in abundance depending on rice cultivar, particularly for Methanobacteria, which was enriched in root rather than rhizosphere. These results indicate that host heritable variation exists for associations with microbes relevant to greenhouse gas emissions. In addition, we have established a collection of 2,243 bacterial isolates from seven major U.S. rice-growing regions. Our collection is diverse, encompassing 5 phyla, 60 families, 159 genera, and at least 389 unique bacterial species. We have captured many dominant bacterial strains making up the microbiome of rice plants in the field, demonstrating the ecological relevance of our collection. By screening this collection against Rhizoctonia and Pyricularia, we have identified dozens of strains with strong antagonistic activity against major rice fungal pathogens. This isolate resource provides a foundation for future studies of plant–microbe interactions and offers potential for testing microbiome functions. Overall, this study identifies the primary ecological and genetic drivers structuring rice microbiomes in field environments and introduces a valuable microbial resource for advancing functional and applied research.

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A novel RG-I acetyltransferase that functions in vascular tissue and root cap

Pectins are a group of plant cell wall polysaccharides that represent major components of the middle lamella and are often highly abundant in the primary walls and seed mucilage of dicots and nongraminaceous monocots. They play important roles in cell wall assembly and in maintaining wall integrity and extensibility. Pectins function in a wide range of biological processes, including cell-cell adhesion, organ initiation and elongation, asymmetric cell growth, and plant immune responses. There are four major types of pectin: homogalacturonan (HG), xylogalacturonan (XGA), rhamnogalacturonan I (RG-I), and rhamnogalacturonan II (RG-II). Pectins are frequently O-acetylated. The TRICHOME BIREFRINGENCE-LIKE (TBL) protein family is involved in O-acetylation of different plant cell wall polysaccharides. Here, we present the biochemical characterization of a novel TBL protein from Arabidopsis thaliana. Our mass spectrometry and NMR spectroscopy data demonstrate that this TBL protein functions as an RG-I acetyltransferase that acetylates the rhamnose residue at the O-3 position. Molecular docking analysis allowed us to identify residues surrounding the active site that are important for substrate binding and acetyltransferase activity. Transcriptional analysis indicates that this TBL gene is specifically expressed in vascular tissues during early developmental stages and in the root cap. Its expression is induced by exogenous auxin. Transient expression shows that this protein is localized to the apoplast of Nicotiana benthamiana epidermal cells. Previous studies have shown that alterations in pectin O-acetylation affect plant growth and development. However, there is still limited understanding of the enzymes responsible for pectin O-acetylation, the mechanisms regulating this modification, and how changes in pectin O-acetylation influence plant growth and responses to environmental cues. Based on our findings, we hypothesize that auxin induces the expression of this TBL gene, leading to increased RG-I O-acetylation in the cell wall. This modification may alter the cell wall architecture, thereby triggering vascular tissue formation and affecting root cap function.