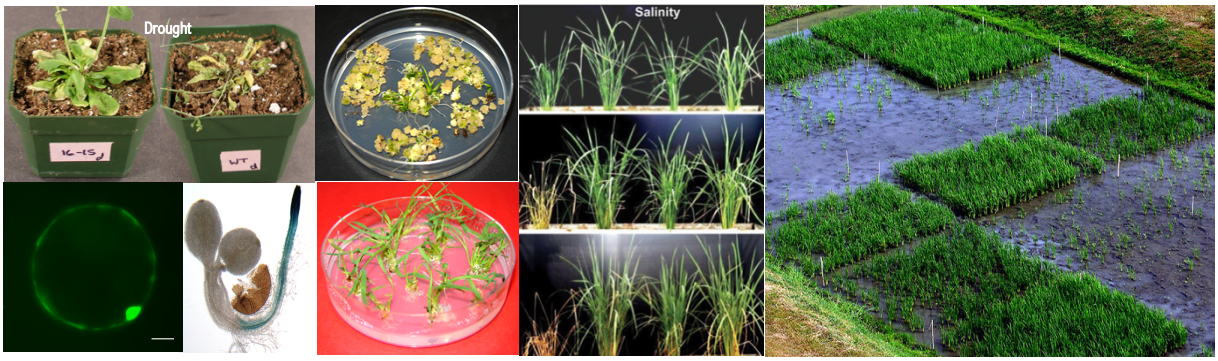
82nd Annual Meeting of the Northeast Section of the American Society of Plant Biologists



Translational Research for Crop Improvements

April 28-29, 2018

University of Massachusetts Amherst

82th Annual Meeting of the Northeast Section of the American Society of Plant Biology

Symposium Schedule

	Saturday April 28, 2018	
Time	**Activities**	**Location**
11:00-11:30	Registration	ILC 1st floor Foyer
1:00-1:15	Welcome- Om Parkash Dhankher and Prof. John McCarthy, Provost, UMass Amherst	ILC Lecture Hall room N151
1:15-2:00	**Prof. Danny Schnell, MSU East Lansing, MI** *A Systems Level Analysis to Understand the Control of the Metabolic and Genetic Networks Controlling Seed Oil Production Using the Model Oilseed Crop Plant, Camelina sativa*	ILC Lecture Hall N151
2:00-2:45	**Randy Allen, OSU, Ardmore, OK** *Translational research on abiotic stress tolerance and fiber development in cotton*	ILC Lecture Hall N151
2:45-3:15	**Coffee Break**	ILC 1st floor Foyer
3:15-4:00	**Subhash Minocha, UNH, Durham, NH** *Living with high putrescine: Metabolic Engineering of the Interacting Pathway of Glu-Orn-Arg-Pro-polyamines and GABA*	ILC Lecture Hall room N151
4:00-4:45	**Kristi Snell, Yield10 BioScience, Woburn MA** *Technologies for increasing plant yield and oil content: The Yield10 Bioscience Platform*	ILC Lecture Hall room N151
4:45-5:00	**Walk to Poster session and Poster set up**	**Amherst Room**, Campus Center 10th floor
5:00-7:00	**Poster session and Reception**	Amherst Room, Campus Center 10th floor
	5:00-6:00 Even Poster number	
	6:00-7:00 Odd Poster number	
7:00-9:00	**Banquet and Entertainment**	**Marriott Room**, Campus Center 11th floor
8:30-9:15	NEASPB Executive Committee meeting	**Marriott Room**, Campus Center 11th floor

	Sunday April 29, 2018	
7:30-8:30 AM	**Continental Breakfast**	ILC 1st floor Foyer
	Oral Presentations	
8:30-8:45	**Srinivasan Krishnan**, Postdoc, Boyce Thompson Institute, Cornell *Structure-Function Studies on Plant Membrane Proteins involved in Key Agronomic Traits by Center for Research On Plant TransporterS (CROPS)*	ILC room N151
8:45-9:00	**Heng-Hsuan Chu**, Postdoc, Dartmouth College, NH *A Point Mutation of Arabidopsis Vacuolar-Iron-Transporter1-Like-5 Protein Confers Iron Deficiency Tolerance and Improves Iron Accumulation in Seeds*	ILC room N151
9:00-9:15	**Minsoo Kim**, Postdoc, UMass Amherst *MTERF18/SHOT1 Protein Is Involved in Mitochondrial Nucleoid Organization by Binding Directly to the Mitochondrial DNA and ATAD3 Proteins in Arabidopsis*	ILC room N151
9:15-9:30	**Kwanghee Lee**, Postdoc, UConn, Storrs *The a Aurora kinases function in vascular development in Arabidopsis*	ILC room N151
9:30- 9:45	**Arielle Chaves,** Research Technician, University of Rhode Island CESA Domains Conferring Class Specific Function in Physcomitrella patens	ILC room N151
9:45-10:00	**Annett Richter, Postdoc, Boyce Thompson Institute, Cornell** *Indole-3-Glycerolphosphate, a Possible Branchpoint of Secondary Defense Compounds from the Tryptophan Biosynthetic Pathway in Zea Mays.*	ILC room N151
10:00-10:20	**NEASPB Business meeting**	ILC room N151
10:20- 10:45	**Coffee Break**	ILC room N151
10:45-11:00	ASPB Student Ambassador program information	ILC room N151
11:00-11:15	**Sanda Zolj**, Graduate student, Boston University *The Arabidopsis alf3-1 Mutation Causes Autoimmunity in the Root and Identifies a TIR Domain Protein*	ILC room N151
11:15-11:30	**Rania El-tanbouly**, Graduate Student, UConn Storrs *Elucidation of Involvement of Jasmonate in Shade Response of Perennial Ryegrass.*	ILC room N151

11:30-11:45	**Kirk MacKinnon**, graduate student, UMass Amherst *Exploring Diurnal Rhythmic Gene Expression in Brachypodium distachyon*	ILC room N151
11:45-12:00	**Roshani Budhathoki**, Undergraduate student, Eastern Connecticut State University *Characterization of a Novel chicken foot-like nodules (cfn) Mutant Defective in Root Architecture and Symbiotic Nitrogen Fixation in the Model Legume Plant Medicago truncatula*	ILC room N151
12:00- 12:15	**Jeeyon Jeong**, Assistant Prof., Amherst College *Mitochondrial Ferropotin and Iron Homeostasis in Plants*	ILC room N151
12:15- 12:30	**Sibongile Mafu**, Assistant Prof., UMass Amherst Discovery of a new diterpenoid pathway involved stress response in maize	ILC room N151
12:30-12:45	**Best Presentation and Poster Awards**	ILC room N151
12:45 PM	Closing Remarks and Adjourn	

Symposium Keynote Speakers

Keynote Speaker 1

A Systems Level Analysis to Understand the Control of the Metabolic and Genetic Networks Controlling Seed Oil Production Using the Model Oilseed Crop Plant, *Camelina sativa*

Danny J. Schnell
Department of Plant Biology, Michigan State University, East Lansing, MI 48840

Our collaborative program aims to understand the metabolic and genetic mechanisms that control seed oil production in the non-food oilseed crop plant, *Camelina sativa*. To this end, we are employing a tissue-specific and whole-plant systems approach to identify the major regulatory mechanisms that limit carbon fixation in photosynthetically active source tissues (leaves), the transport of fixed carbon from source to sink tissues (seeds), and the allocation of fixed carbon to TAG production in seeds. We are using a number of newly discovered traits that impact each of these processes to perform tissue-specific and whole-plant metabolic flux and transcriptional regulatory network analyses in an effort to understand the underlying physiological basis of their impact on oil yields. These studies are also being used for the development of predictive, dynamic metabolic and gene regulatory models to accelerate the identification of additional metabolic bottlenecks, transcriptional regulators and/or post-translational mechanisms that control seed yields. I will provide an overview of one study that highlights our approaches and demonstrates the critical role of chloroplast-mitochondrial metabolic networks in maintaining photosynthesis in source tissues under non-ideal environmental conditions. We have identified a mitochondrial metabolite transporter, Organellar Carrier Protein 1 (OCP1), which increases carbon dioxide assimilation by 20-30% and seed yields by 38-50%. As such, Camelina^{OCP} plants provide an excellent system to investigate the metabolic networks of central carbon metabolism in source tissues and to identify the control points that limit carbon capture and constrain photoassimilate export for seed production in a crop plant. The OCP1 plants also maintained lower stomatal conductance and reduced leaf gas exchange, resulting in a ~35% increase in photosynthetic water use efficiency (WUE) and a significant increase in photosynthetic Nitrogen Use Efficiency (NUE). I will present the details on the metabolic and physiological parameters affected by OCP1 activity and describe our hypothesis for the systems-level impact of OCP1 on growth and seed production under non-ideal environmental conditions.

Dr. Schnell is the Professor and the Chairperson of the Department of Plant Biology, Michigan State University, East Lansing, MI. Prof. Schnell received doctorate in Biochemistry from the University of California and Postdoctoral training at the Rockefeller University, New York. Prof. Schnell is also the fellow of the American Association for the Advancement of Science (AAAS).

Keynote Speaker 2

Translational research on abiotic stress tolerance and fiber development in cotton

Randy D. Allen
Department of Biochemistry & Molecular Biology and Institute for Agricultural Biosciences, Oklahoma State University, Ardmore, OK 73401

Cotton is the world's leading natural fiber and is cultivated commercially in more than 70 countries around the world with top production in China, India and the U.S. Cotton production has had an enormous impact on global economic development and cotton remains an important contributor to the world economy. Cotton is usually cultivated during the summer in arid and semiarid regions where water availability is often limited. Therefore, drought stress is a major environmental limitation on cotton productivity with serious impacts on yield and fiber quality. Beginning more than 20 years ago, research in my laboratory has been concerned with the use of reverse genetics to improve abiotic stress tolerance and fiber quality in cotton. We have developed and tested transgenic cotton plants with increased expression of stress-associated antioxidants and a range of regulatory proteins including, transcription factors, ubiquitin ligases, and protein kinases. Our recently published analysis of plants that over-express the ubiquitin ligase SAP5 or the transcription factor ABF3 provide examples of this approach. In addition, we have tested a number of genes involved in fiber development in an effort to improve cotton fiber quality. Following a brief overview of completed research in these areas, I will discuss ongoing research projects.

Dr. Randy Allen is a Professor and Sitlington Endowed Chair at the Department of Biochemistry and Molecular Biology and also the Resident Director of Institute for Agricultural Biosciences Oklahoma State University, Stillwater, OK. Prof. Allen received a doctorate in biology from the Texas A&M University, postdoctoral training from the Washington University, Saint Louis, MO, master's in biology from the University of Texas, Arlington, and bachelor's degree in biology from the Southwestern Adventist College.

Keynote Speaker 3

Living with high putrescine: Metabolic Engineering of the Interacting Pathway of Glu-Orn-Arg-Pro-polyamines and GABA

Subhash C. Minocha
Department of Biological Sciences, University of New Hampshire, Durham, NH 03824

Rakesh Minoicha, USDA Forest Service, Northern Research Station, Durham, NH 03824
Our research is focused on evaluating the feasibility of enhancing carbon assimilation through genetic manipulation of nitrogen metabolism in plants, specifically with the aim of increasing biomass accumulation in short-rotation tree crops like a hybrid poplar (*Populus nigra x maximowiczii* - NM6), which is used for bioenergy production and phytoremediation. The results show that genetic manipulation of a single step in the polyamine biosynthetic pathway (i.e. ornithine$\rightarrow$putrescine) in poplar cells as well as in *Arabidopsis thaliana* plants can lead to increased assimilation of both nitrogen and carbon. While ornithine is typically not an abundant amino acid, the metabolic flux of nitrogen through this amino acid is presumably quite rapid and high because of the cellular contents of the products for which it serves as the substrate. Likewise, putrescine (one of the common polyamines) is an essential metabolite for tolerance to drought, freezing, salinity, and oxidative stress among other type of abiotic stresses, and also biotic stresses. In addition to their role as stress-protective compounds, polyamines participate in key developmental processes mediated by specific signaling pathways involving gamma-aminobutyric acid (GABA), NO, and ethylene. Using the techniques of transcriptomics and metabolomics, we found that increased accumulation of putrescine is accompanied by alterations in the expression of a broad spectrum of genes; many of which are involved in transcription, translation, membrane transport, osmoregulation, shock/stress/wounding, and cell wall metabolism. The most noteworthy differences in metabolic makeup of the cells were in organic acids, carbohydrates and nitrogen-containing metabolites. The results provide valuable information about the role of polyamines in regulating nitrogen and carbon use pathways in plants. The results also provide guidance in designing transgenic plants with increased nitrogen use efficiency, especially in non-food/feed plants.

Dr. Subhash Minocha is a Distinguished Professor of Plant Biology and Genetics in the Department of Biological Sciences, University of New Hampshire, Durham, NH. Dr. Minocha received a doctorate in plant physiology from the University of Washington, and master's honors and bachelor's honors degree in botany from the Punjab University Chandigarh, India.

Keynote Speaker 4

Technologies for increasing plant yield and oil content: The Yield10 Bioscience Platform

Kristi D. Snell and Oliver Peoples
Chief Scientific Officer and Vice President of Research, Yield10 BioScience, Woburn MA 01801

Step-change increases in crop yield will require us to build better plants with both increased carbon fixation and targeted carbon deposition to the desired organ, either harvestable seed or biomass depending on the crop. Yield10 Bioscience has been using a multifaceted approach to discover gene targets to provide step-changes increases in plant productivity that include the use of *in silico* analyses of plant metabolism and gene networks. These approaches move our trait discovery program beyond the mass screening and testing of thousands of individual plant genes that have been typically employed in the crop industry over the last 20 years, with a low return on investment, and instead rely on rational design strategies for plant metabolic engineering. We have also collaborated with academic laboratories to validate and move promising early stage scientific discoveries forward to field tests. Specific examples of efforts to increase crop yield in the Yield10 pipeline will be discussed.

Dr. Kristi Snell is the Chief Scientific Officer and Vice President of Research at the Yield10 BioScience (formerly Metabolix), Woburn, Massachusetts, MA. Dr. Snell received her doctorate in organic chemistry from Purdue University, bachelor's degree in chemistry from the University of Michigan and postdoctoral training in biochemistry at the Massachusetts Institute of Technology, Boston, MA.

POSTER SESSION

Poster No.	Presenter	Title of the Poster
P1	Vijaykumar Veerappan, Roshani Budhathoki, Ramis Saleem, Vincent Brown, Jiangqi Wen and Kirankumar S. Mysore	Characterization of Tnt1 Mutants Defective in Root Architecture, Nodule development and Symbiotic Nitrogen Fixation in the Model Legume Plant *Medicago truncatula*
P2	Antonius R. Chess Jr., Brandon Charles Miller, and Cheryld L. Emmons	Evaluating the Stress responses of *Panicum millaceum* to Nitrogen Deficiency Under Central Haitian Climate Conditions
P3	Covel R. McDermot, Rakesh Minocha, Vincent D'Amico III and Tara LE Trammell	Native Red Maple (Acer rubrum L.) Tree Physiology: Dying or Thriving in Urban Environment?
P4	Desiree Bojanowski, Isaiah Greenwald, and Cheryld L. Emmons	*Panicum miliaceum* Growth in Alkaline Conditions
P5	Julia Miller, Alison Coluccio, Jan Niklas Offenborn, Anette Mähs, Jörg Kudla, Leon Kochian, Miguel Piñeros	A Multidrug and Toxin Efflux (MATE) Transporter Involved in Aluminum Resistance is Modulated by a CBL5/CIPK2 Calcium Sensor/Protein Kinase Complex
P6	Xiaotong Chen, Melissa Snare, Lynda McMaster-Schuyler, and Peiyu Zeng	Genetic Engineering Drought Tolerant Switch-grass by Over-expressing AVP1
P7	Ramis Saleem, Roshani Budhathok, Vincent Brown, Jiangqi Wen, Kirankumar S. Mysore and Vijaykumar Veerappan	Characterization of a Novel Mutant trapezia with Enhanced Anthocyanin Accumulation in the Model Legume Plant *Medicago truncatula*
P8	Hongxing Xu, Xingwei Wang, Shusheng Liu, Xiaowei Wang	A Salivary Protein of the Whitefly Affects its Phloem-feeding on Host Plants
P9	Vincent Brown, Roshani Budhathoki, Ramis Saleem, Jiangqi Wen, Kirankumar S. Mysore and Vijaykumar Veerappan	Secondary Screening and Characterization of vbn (very brown nodule) and gsun (green supernodulator) Mutants Defective in Symbiotic Nitrogen Fixation in the Model Legume Plant *Medicago truncatula*
P10	William E. Latour III, Joshua Lapham and Cheryld L. Emmons	PH Effects on Root Development in *Amaranthus gangeticus*
P11	Melissa Snare, Janel Cross, Yeying Zhou, Lynda McMaster-Schuyler, Peiyu Zeng	Soybean Transformation with Cysteine Protease Inhibitor (CPI1) Gene for Resistance and Tolerance
P12	Jing Wei, Sue Sherman-Broyles, Jeff J. Doyle, and Georg Jander	Aphid Resistance in Perennial Soybeans: Two Genomes Are Better than One
P13	Leiting Wang, Melissa Snare, Lynda McMaster-Schuyler, Peiyu Zeng	Genetic Transformation of Switchgrass Plants with FNR-FLD Flavodoxin Genes for Drought Resistance and Salt Tolerance (In Progress…)
P14	Chen Chang, Melissa Snare, Lynda McMaster-Schuyler, and Peiyu Zeng	Development of High Yield Switchgrass Cultivar by Agrobacterium-Mediated Transformation with InsP-5-Ptase Gene (In Progress…)
P15	Mingming zhu, Melissa Snare, Lynda McMaster-Schuyler, Peiyu Zeng	The improvement of Switchgrass by Agrobacterium-Mediated Transformation

P16	Javed Ahmad, Humayra Bashir, Rita Bagheri, Affan Baig, Asma Al-Huqail, Mohamed M. Ibrahim, M. Irfan Qureshi	Drought and salinity induced changes in ecophysiology and proteomic profile of *Parthenium hysterophorus*
P17	Hanwang Lu, Lei Cao, Yifeng Zhao, Lynda McMaster-Schuyler and Peiyu Zeng	Development of Tissue Culture System for Transformation System in Hops (*Humulus lupulus*)
P18	Yuka Konishi, Jun Oshika, Ryuichi Nishihama, Kimitsune Ishizaki, Takayuki Kohchi, Hideyuki Matsuura, Kosaku Takahashi	A Gene Encoding LRR-RLK Is Involved in OPDA Signaling of *Marchantia polymorpha*
P19	Navindra Tajeshwar, Luqian Chen, Alexander Heyl	Towards Understanding the Origin and the Evolution of Cytokinin Signaling
P20	Sandra P. Romero-Gamboa, Pubudu P. Handakumbura, Gina M. Trabucco, Samuel P. Hazen.	The Function of *Brachypodium distachyon* SECONDARY WALL ASSOCIATED MYB4 in the Transcriptional Regulation of Secondary Cell Wall Biosynthesis
P21	Leila Feiz, Susan R. Strickler, Linyong Mao, Alexa Rodriguez, Poornima Ghourabathini, Zhangjun Fei and David B. Stern	Photosynthetic mutants of the C4 model, *Setaria viridis*, link chloroplast RNA metabolism to intercellular communication and C4-cell-specific differentiation
P22	Danielle McGinty and Estelle Hrabak	Characterization of a Protein S-Acyltransferase Mutant, pat3, from *Arabidopsis thaliana*
P23	John McLarney and Estelle Hrabak	Characterization of a Protein Acyltransferase-14 Mutant in *Arabidopsis thaliana* Using Proteomics and Growth Assays
P24	Hoang Vo, Reza Abdavies, and Aleel Grennan	The Influences of Chloroplast Sizes on Plant Growth and Development
P25	Yan O. Zubo, Ivory Clabaugh Blakley, Maria V. Yamburenko, Jennifer M. Worthen, Ian H. Street, José M. Franco-Zorrilla, Wenjing Zhang, Kristine Hill, Tracy Raines, Roberto Solano, Joseph J. Kieber, Ann E. Loraine, and G. Eric Schaller	Type-B ARRs Target WUSCHEL to Control Shoot Initiation.
P26	Kanza Tahir, Leeann Thornton	Using Arabidopsis Mutants to Examine the Role of CYP72A Enzymes in Defense Against Environmental Stresses
P27	W.M.Medini Weerasinghe and Subhash C. Minocha	Designing Poplar for Increased Nitrogen and Carbon Assimilation and Biomass Yield
P28	Sara Shakir, Mahdiyeh Bigham, Wenbo Chen, Yu Mei, Steve Whitham, and Georg Jander	Development of Aphid-transmitted Viral Vectors for Transient Gene Expression in Maize
P29	Azam Noori, Joseph Colbert, Adam Ngo	*Lycopersicon esculentum* Physiological and Molecular Responses to Silver Nanoparticles
P30	Mahdieh Mirzaei, Suzy Strickler, Adrian Powell, Pavan Kumar, Lukas Mueller, Tobias Züst, and Georg Jander	Investigation of the Cardiac Glycoside Biosynthesis Pathway Using Genomic, Metabolomic and Transcriptomic Analysis of *Erysimum cheiranthoides*

P31	Jenna Lesnikowski, Alexandra Zink, Rachael Bernstein, Michelle Dacosta and Elsa Petit	Cold Hardiness of European-American Hybrid Grape Varieties in a Changing Climate
P32	Adam Saffer and Vivian Irish	Pectin suppresses the helical growth of plant cells
P33	Nisha Sanghani, Leeann E. Thornton	Understanding the Role of the Arabidopsis CYP72A14 Enzyme in Chemical Defenses Against Environmental Stress
P34	Jonathan D. Mahoney, Thao Hau and Mark H. Brand	Sexual and apomictic reproduction in Aronia species and lack of genetic diversity in commercial Aronia production
P35	Mercedes Harris	The Impact of Intraspecific Density on Garlic Mustard (*Alliaria petiolata*) Sinigrin Concentration
P36	Michelle R. Jackson, Erin Coates-Connor, Karina Martinez and Kristina Stinson	Effect of garlic mustard management on exotic earthworms and native plant diversity
P37	Shrimika Madhavan and Subhash C. Minocha	Acrolein Toxicity in Mammalian and Plant Cells
P38	Rachael Bernstein, Michelle DaCosta, Geunhwa Jung and Jeffery Scott Ebdon	Differential Gene Expression Associated with Winter Survival of *Lolium perenne*.
P39	Tahalia Lozano and Christos Noutsos	Effects of OrgDNA to Genes in 34 Different Plant Species
P40	Samuel Breselge, Diana Bernal-Franco, Erin J. Cram, Carolyn W. T. Lee-Parsons	Establishment of an Efficient Transient Seedling Transformation Protocol for *C. roseus*
P41	John Bortz, William Lee and Daniel Carter	Investigating Sorghum Bicolor Physiology in the Conditions of the Central Plateau Region of Haiti
P42	Asa Budnick, Samuel Breselge, Diana Bernal-Franco, Erin J. Cram, Carolyn W. T. Lee-Parsons	Investigation of Agrobacterium-mediated Stable Transformation Methods for *Catharanthus roseus*
P43	Ralph McNeilage and Steven M Theg	Translocation along the TAT Pathway
P44	Ahmed Ali and Om Parkash Dhankher	Characterization of Rice Plasma Membrane Intrinsic Protein Ospip1;3, Ospip2;7, and Their Roles in Arsenic and Boron Transport in Rice Plants.
P45	Natalie Marchi, Michael Caron, Mitchell Lacaire, Aleel K. Grennan, Peter M. Bradley	Can Parsnip Plants (*Pastinaca sativa*) and Carrot Plants (*Daucus carota*) Regenerate Shoots from Cultured Callus Cells in Mixed Co-cultures?
P46	Adriana Del Grosso, Sophia Pitti-Daly, Susan Witherup and Peter Melcher	Pollen movement between introduced and endemic coastal plants in the genus Scaevola in Puerto Rico
P47	Parika Chauhan and Leeann Thornton	Using Molecular Genetics to Study the Role of CYP72A Enzymes in *Zea mays* Stress Response
P48	Jazmin Abraham, Amanda Lavelle, and Madelaine Bartlett	Analysis of Protein-protein Interaction Profiles of Maize MADS-box Evolutionary Variants
P49	Gurpal Singh, Ayousha Shahi and Om Parkash Dhankher	Characterizing Genes Involved in Glutathione Homeostasis for Improving Tolerance to Multiple Abiotic Stresses in Plants
P50	Reza Abdavies, Hoang Vo, Aleel K. Grennan, Ursula Ruiz Vera, Donald R. Ort	Impacts of Elevated CO_2 on Cassava Leaf Anatomy

P51	Ian McCahill, Ian P. Whitney, Pubudu P. Handakumbura, Kathryn Brow, Samuel P. Hazen	Does WALL REGULATOR INTERACTING bHLH Modulate Biosynthesis of the Secondary Cell Wall in Response to Environmental Cues
P52	Imran Rauf, Shaista Javaid, Rubab Zahra Naqvi, Tanveer Mustafa, Imran Amin, Zahid Mukhtar, Georg Jander and Shahid Mansoor	Synergistic Insecticidal Activity of Hvt-lectin Provides Protection to Plants Against Hemipteran and Lepidopteran Insects
P53	Noroza Umer, Muhammad Asif, Georg Jander	Cloning of an *Allium sativum* leaf agglutinin gene under constitutive and phloem specific promoters to provide resistance against sap sucking insect pests
P54	Jade Doan, Quinn Bazinet, Kathryn Vescio, Li-Jun Ma	Variable Phenotypes of *Arabidopsis thaliana* Ecotypes in Response to Pathogenic *Fusarium oxysporum*
P55	Sefali Acharya and Nrisingha Dey	Designing and Testing Efficient Promoters for Enhanced Molecular Farming of Life Saving Therapeutics in Plants
P56	Anna C. Haber, Sefali Acharya and Subhash C. Minocha	Metabolic Engineering of Polyamines in Rice: Their Role in Drought and Salt Tolerance
P57	Deicy Carolina Munoz Agudelo and Aleel Grennan	Embryonic Callus Transformation of *Setaria viridis* (Green foxtail
P58	Meera Nair, Victoria Pook, KookHui Ryu, James C. Arpin, John Schiefelbein, Kathrin Schrick, and Seth DeBolt	Membrane bound UDP-Glc:Sterol Glycosyltransferase (80B1) is required for positioning of SCRAMBLED receptor in Arabidopsis roots
P59	Kelly S. Allen, Li-Jun Ma, Robert L. Wick	Survival of Sporangia of the Basil Downy Mildew Pathogen *Peronospora belbahrii*
P60	Sam Corcoran and Masoud Hashemi	Tropical Sunn Hemp in a Temperate Region for Animal and Vegetable Production Systems
P61	Jose Alfredo Guzman, June Simpson, and Jennifer Fletcher	AtGlsA/ZRF1 is Essential for Maintenance of Meristem Integrity by Regulating WUS
P62	A. S Chandrakala and Subhash C. Minocha	Abiotic stress and expression analysis of S-Adenosylmethionine decarboxylase in Arabidopsis
P63	Liam Iorio, Jonathan D. Mahoney, Mark H. Brand, Huanzhong Wang	Functional genomics of Aronia fruit polyphenol biosynthesis
P64	Michelle Heeney, Amanda Schrager-Lavelle, Madelaine Bartlett	Exploiting Grass Flower Development: Understanding Awns
P65	Yanjun Li, Rahul Kumar, and Yi Li	Manipulation of Different Chemicals to Enhance Agrobacterium Infection Efficiency and Increase Shoot Regeneration of Juvenile Citrus
P66	Jefferson Lu, Rachael Bernstein, Lindsey Hoffman and Michelle DaCosta	Examining the Role of Chemical Priming for Improved Drought Tolerance in Creeping Bentgrass
P67	Guoyong Huang, Hongqing Hu, Om Parkash Dhankher, and Baoshan Xing	Cu Accumulation and Speciation in Castor-oil Plant (*Ricinus Communis* L.) in Response to the Cu Stress

Oral Presentations from Selected Abstracts

O-1

STRUCTURE-FUNCTION STUDIES on PLANT MEMBRANE PROTEINS INVOLVED in KEY AGRONOMIC TRAITS by Center for Research On Plant TransporterS (CROPS)

Srinivasan Krishnan[1], Julia Miller[2], Aaron P. McGrath[3], Leon V. Kochian[4], Geoffrey Chang [3,5] and Miguel Piñeros[1,2,6]

[1]Boyce Thompson Institute, Cornell University, Ithaca NY, USA

[2]School of Integrative Plant Science, Plant Biology Section, Cornell University, Ithaca NY, USA; [3]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California at San Diego, La Jolla, California, USA

[4]Global Institute for Food Security, University of Saskatchewan, Saskatoon, Canada; [5]Department of Pharmacology, School of Medicine, University of California at San Diego, La Jolla, California, USA

[6]Robert W. Holley Center for Agriculture and Health, United States Department of Agriculture–Agricultural Research Service, Cornell University, Ithaca, NY, USA

Membrane proteins mediate the transport of ions and other hydrophilic molecules across cell membranes in plants. Although many of these proteins have been shown to underlie key agronomic traits key for plant abiotic stress resilience, the fundamental biochemical, functional, and structural characteristics of these proteins are largely unknown. CROPS (Center for Research On Plant TransporterS) is an NSF-PG funded initiative dedicated to: a) the expression and purification of large (milligram) quantities of functional membrane transport proteins, b) generation of single-domain antibodies with high target affinity/specificity and, c) the molecular structure determinations of membrane transporters. Here were present recent results obtained for two different plant membrane targets: a Ca2+ permeable ion channel and a multidrug efflux transporter, involved in mediating Ca2+ fluxes associated with drought stress response signaling process and extrusion of toxic metals, respectively. We have successfully purified these proteins, demonstrated their functionality using droplet-interface bilayer technique, and determined their oligomeric state in proteoliposomes by subunit-counting using Total Internal Reflection Fluorescence Microscopy. We present data on the identification of target specific nanobodies and validation of their usefulness in detecting the target protein *in vivo*.

O-2

A Point Mutation of Arabidopsis Vacuolar-Iron-Transporter1-Like-5 Protein Confers Iron Deficiency Tolerance and Improves Iron Accumulation in Seeds

Heng-Hsuan Chu[1], Joe Morrissey[2], Ivan R. Baxter[3], David E. Salt[4], and Mary Lou Guerinot[1]

[1]Department of Biological Sciences, Dartmouth College, Hanover, NH, USA

[2]MARS Inc., USA

[3]Donald Danforth Plant Science Center, Louis, MO, USA

[4]School of Biosciences, University of Nottingham, Nottingham, UK

A fast neutron mutant, 118:65, is able to thrive and produces more seeds with higher iron concentration when grown on alkaline soil. Although this mutant grows better on alkaline soil, its shoot iron concentration is similar to wild type. 118:65 exhibits strong rhizosphere acidification that may explain the ability to thrive on alkaline soil, and the increased acidification response appears to be due to an increase

secretion of protons by the AHA2 proton pump. Identification of the causative mutation showed that 118:65 has a single nucleotide change in its coding sequence (g253a) which leads to increased expression of a vacuole Fe transporter, VTL5. Assays in yeast show that the g to a nucleotide change of VTL5 leads to increased Fe transporter activity. Disruption of VTL5 does not affect rhizosphere acidification, while vtl5 loss of function mutant expressing VTL5.g253a and VTL5 overexpression lines exhibit increases rhizosphere acidification, thus confirming the phenotype of the original 118:65 mutant. This gene will be useful for our goal of breeding crops that are tolerant to alkaline soil and that have increased Fe nutrition in the edible parts that are consumed by humans.

O-3

MTERF18/SHOT1 Protein Is Involved in Mitochondrial Nucleoid Organization by Binding Directly to the Mitochondrial DNA and ATAD3 Proteins in Arabidopsis

Minsoo Kim[1], Vincent Schulz[2], Kristina Kühn[2], and Elizabeth Vierling[1]
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Mitochondria play critical roles not only in primary metabolism as a central organelle for ATP generation, but also in sensing biotic/abiotic stresses and relaying information to the nucleus to properly respond to the stresses. MTERF (Mitochondrial Transcription tERmination Factor) families of proteins are important nuclear factors for maintaining mitochondrial homeostasis. The founding member of the mTERF family, human mTERF1, binds specific sites in the mitochondrial genome and regulates transcription termination. Plants have undergone a dramatic expansion of this family during evolution, with 35 members in Arabidopsis, most of which are targeted to plastids and/or mitochondria. We previously identified a mutation in the Arabidopsis MTERF18/SHOT1 (Suppressor of hot1-4 1) gene in a screen for a suppressor of a heat sensitive mutant, a dominant-negative allele of chaperone HSP101 (hot1-4). shot1 mutants survive better under heat stress, presumably due to reduced oxidative damage, but the exact molecular mechanism of thermotolerance is unknown. In order to understand the mechanism of thermotolerance caused by shot1 mutations, it is critical to identify the molecular targets of SHOT1 protein. In our study, we found that shot1 mutations cause an overall increase in mitochondria-encoded transcripts and translation rate, which is likely a compensatory response to overcome reduced oxidative phosphorylation (OXPHOS). Proteomics analysis of shot1-2 compared to wild type detected 22 mitochondrial-encoded proteins, showing proteins involved in OXPHOS were decreased, while ribosomal proteins were increased in shot1-2. ATAD3 proteins which have been known to be involved in nucleoid organization in animals were identified as interacting partners of SHOT1. Immunoprecipitation followed by qPCR experiments also revealed that SHOT1 binds to mitochondrial DNA. With the evidence of diffuse mitochondrial nucleoids in shot1-2 mutant, SHOT1 appears to be an important protein for mitochondrial nucleoid organization, possibly bridging ATAD3 proteins to mitochondrial DNA in Arabidopsis.

O-4

The α Aurora kinases function in vascular development in Arabidopsis

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The Aurora kinases are serine/threonine kinases with conserved functions in mitotic cell division in eukaryotes. In Arabidopsis, Aurora kinases play important roles in primary meristem maintenance, but their functions in vascular development are still elusive. We report the identification of a dominant xdi-d mutant showing xylem development inhibition (XDI). Gene cloning and transgenic over-expression experiments indicated that the activation of the Arabidopsis Aurora 2 (AtAUR2) gene is responsible for the XDI phenotype. In contrast, the aur1-2aur2-2 double mutant plants showed enhanced differentiation of phloem and xylem cells, indicating the Aurora kinases negatively affect xylem differentiation. Key regulatory genes in vascular cell differentiation, i.e. ALTERED PHLOEM DEVELOPMENT (APL), VASCULAR-RELATED NAC-DOMAIN 6 (VND6) and VND7, were upregulated in the aur1-2 aur2-2 double mutant, but downregulated in xdi-d mutants, further support the functions of α Aurora kinases in vascular development. Gene mutagenesis and transgenic studies showed that protein phosphorylation and substrate binding, but not protein dimerization and ubiquitination, are critical for the biological function of AtAUR2. These results indicate that α Aurora kinases play key roles in vascular cell differentiation in Arabidopsis.

O-5

CESA Domains Conferring Class Specific Function in *Physcomitrella patens*

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Cellulose synthases (CESAs) make cellulose, a polysaccharide component of plant cell walls consisting of β-1,4-linked glucose. *Physcomitrella patens*, a bryophyte model organism, has two functionally distinct classes of CESA isoforms based on the ability to rescue the PpCESA5 knockout mutant (ppcesa5KO). We have investigated the role of the N-terminal and C-terminal regions in determining class-specific function in PpCESAs, using a complementation system based on ppcesa5KO, which is unable to produce gametophores. Gametophore production in ppcesa5KO is restored by constitutive expression of PpCESA5, but not by constitutive expression of PpCESA4. Vectors that drive constitutive expression of chimeric PpCESA proteins consisting of domain swaps between PpCESA5 and PpCESA4 were tested for their ability to rescue the ppcesa5KO phenotype. Expression of PpCESA4 with the hypervariable region 1 (hvr1) of PpCESA5 partially rescued the ppcesa5KO phenotype, indicating that hvr1 plays an important role in class specific function. Expression of PpCESA4 with the hvr1 and C-terminus of PpCESA5 fully rescues ppcesa5KO, suggesting that the C-terminus also plays a role in class specific function. In contrast, the highly conserved Zn-binding RING (Zn) domain is fully interchangeable between isomers with no change in function. Deletion of the Zn domain impairs PpCESA5 function, resulting in stunted gametophores, indicating that this putative protein-protein interaction domain plays a role in PpCESA function. This research was supported as part of The Center for LignoCellulose Structure and Formation, an Energy Frontier Research Center funded by the U.S. Department of Energy, Office of Science, Office of Basic Energy Sciences under Award Number DE-SC0001090.

O-6

Indole-3-Glycerolphosphate, a Possible Branchpoint of Secondary Defense Compounds from the Tryptophan Biosynthetic Pathway in *Zea Mays*.

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Benzoxazinoids are an important class of defensive metabolites in maize and other grasses. The benzoxazinoid biosynthesis pathway is well studied, with nine proteins (BX1-BX9) catalyzing the formation of the most basal benzoxazinoid, DIMBOA-Glc (2,4-dihydroxy-7-methoxy-1,4-benzoxazine-3-one glucoside), from indole-3-glycerol phosphate. BX1 and two other maize enzymes, IGL1 and TSA, catalyze the formation of indole, which is subject to metabolic channeling for the formation of benzoxazinoids, tryptophan, auxin, and other maize metabolites. A family of three indole-3-glycerolphosphate synthase enzymes (IGPS1, IGPS2, and IGPS3), may be a branch point for the biosynthesis of different indole-derived metabolites. The function of all three maize IGPS genes was confirmed by complementing the auxotrophy of an E. coli mutant. Global gene expression network analysis suggested that IGPS1 is co-expressed with BX genes. Herbivore feeding on maize seedlings induces expression of both IGPS1 and IGPS2, suggesting their involvement in the formation of benzoxazinoids and/or volatile indole, a maize defense signaling molecule. To investigate whether there are two distinct IGPS activities, one for the tryptophan biosynthesis and another for the indole-derived secondary metabolites, all three IGPS proteins were localized in a maize protoplast expression system. Interestingly, the localization pattern of IGPS3 in the plastids correlates with that of the TSA protein, which is part of the tryptophan biosynthesis complex. On the other hand, IGPS1 and IGPS2 have expression patterns similar to BX1, suggesting an involvement in plant defense. For a better understanding how maize tryptophan biosynthesis and defenses are regulated by the three IGPS genes, metabolite analysis of an igps1 igps2 double mutant, in combination with transient overexpression of each gene in maize seedlings, is in progress. Knowledge gained from this research can be used to increase the natural defenses of maize plants, thereby providing enhanced protection against pests and pathogens in the field.

O-7

The Arabidopsis alf3-1 Mutation Causes Autoimmunity in the Root and Identifies a TIR Domain Protein

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Plant defense responses vary depending on the pathogen and intensity of the attack and are mediated primarily through two levels of defense. PAMP-triggered immunity (PTI) is triggered in response to host recognition of pathogen-associated molecular patterns (PAMPs). However, pathogens can evade PTI by secreting effector molecules into the host cell that block PTI. In turn, effector molecules can be inhibited by a second line of plant defense called effector-triggered immunity (ETI). In ETI the plant uses effector-specific resistance proteins to block the effector. ETI results in gene expression changes that lead to the hypersensitive response (HR), a form of cell death, and to the plant-wide systemic acquired resistance. Previously we identified a dominant Arabidopsis thaliana mutant, alf3-1 (aberrant lateral root formation 3), whose primary and lateral roots die unless the growth medium is supplemented with auxin or the plants are grown at high temperature. Based on gene expression profiling, we found that many immune and defense response genes were expressed more highly in alf3-1 compared to WT. These genes include salicylic acid (SA)-responsive genes such as PR1 and PBS3 as well as several WRKY transcription factors, a

gene family implicated in plant defense. Consistent with these findings, alf3-1 mutants have greatly increased sensitivity to SA as well as increased production of defense compounds. In addition, we found that the vast majority of defense-related phenotypes dysregulated in alf3-1 returned to WT levels when the mutant was rescued by auxin or growth at high temperature. Using whole genome sequencing we found that the ALF3 gene encodes an uncharacterized TIR domain protein. Because characterized plant TIR domain proteins have been shown to function in plant innate immunity, we hypothesize that alf3-1 is a gain-of-function mutation that causes an HR in roots even in the absence of a pathogenic trigger.

O-8
Elucidation of Involvement of Jasmonate in Shade Response of Perennial Ryegrass.

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Shade tolerance in turf grasses is a desired trait, however the mechanism of the plant shade tolerance is not well understood. It has been reported that gibberellin and auxin are involved in the plant shade response. It has also been observed that if plants are subjected to shade, jasmonate (JA) levels are reduced. Previous studies have suggested that there is a link between JA and plant's light responses using JA deficient mutant plants. In this study, using perennial ryegrass as experimental materials, we show that higher levels of JA in a shade-tolerant mutant line, shadow-1, may play an important role in the observed shade tolerance. We have also observed that exogenous applications of JA to wild-type plants can lead to reduction the of shade-induced etiolation of leaves. Applications of JA-biosynthesis-inhibitor (phenidone) to wild-type plants enhanced their shade-induced etiolation of leaves. In addition, phenidone applications revertedshadow-1mutant to wild-type phenotype. Expression of CORONATINE INSENSITIVE 1 (COI1), an essential gene for JA-mediated responses, was significantly enhanced upon JA applications to wild-type plants and reduced by phenidone applications in shadow-1mutant plants. Thus, our results strongly suggest that JA can be an important endogenous regulator in shade tolerance of perennial ryegrass.

O-9
Exploring Diurnal Rhythmic Gene Expression in *Brachypodium distachyon*

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Plants are continuously exposed to varying environmental conditions; some anticipated diurnal changes in light and temperature and others far less predictable. Key to adaptation to a diurnal environment is the anticipation provided by the circadian clock, which coordinates broad changes in gene expression with a period of about 24 h. Here we present the analysis of RNA sequencing to measure transcript abundance in time courses from *Brachypodium distachyon* entrained in photo- and thermocycles and then transferred to photocycles or thermocycles alone, or constant light and temperature conditions. We found 2.8% of

the transcripts exhibited circadian changes in transcript abundance and on an individual gene level, 3.8%, far fewer than what has been reported in comparable datasets from *Arabidopsis thaliana*, maize, Setaria, and cotton. A similar proportion of genes cycled under diurnal conditions. We also examined the changes in alternative splicing that occurred between conditions, and quantified the shifts that resulted in a secondary transcript superseding the primary transcript. The timing of peak expression, phase, for individual genes was fairly consistent across all conditions with the exception of free-run where we observed a lengthening of period and a resulting shift in the phase of the cycling transcripts. Exploring the rhythmic transcripts by phase we found conserved gene ontology terms associated with particular times of the day. Many of the known circadian clock genes appear to remain rhythmic under all four conditions, with several also demonstrating a period shift under free-run. Furthermore, we identified sequence motifs enriched in the promoters of similarly phased genes and used published DNA affinity purified sequencing datasets to associate the motifs with potential upstream transcription factors influencing the rhythmic expression. In doing so we hope to elaborate on *B. distachyon* responses to changes in its environmental conditions.

O-10

Characterization of a Novel chicken foot-like nodules (cfn) Mutant Defective in Root Architecture and Symbiotic Nitrogen Fixation in the Model Legume Plant *Medicago truncatula*

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Plants such as soybeans, pea and lentils belong to the legume family known for their symbiosis with the soil bacteria rhizobia (*Sinorhizobium melliloti*). Symbiotic nitrogen fixation (SNF) occurs inside the plant root nodules where atmospheric nitrogen is captured and converted into bioavailable forms. SNF is important for reducing the manufactureand use of chemical fertilizers. A forward genetic screen was performed by screeningTnt1mutant population to discover novel genes essential for SNF in model the legume plant *Medicago truncatula*. One of the mutants chicken foot-like nodules(cfn) shows abnormal root and nodule architecture. The mutant was named after its clustered nodule-like structures on roots that looks similar to a chicken foot. Cfn mutant roots occasionally transform into white nodule-like structures. cfn shows nitrogen deficiency symptoms such as white nodules, reddish-purple shoot and defective SNF. Comparison of root and nodule phenotypes of cfn with previously characterized *M. truncatula* root architecture and root-nodule organ identity mutants nodule root (noot), compact root architecture1 (cra1), and cra2 indicates that cfn is a novel mutant. Segregation analysis of cfn mutant using R2(Regeneration 2) population confirms that cfn phenotype is controlled by a single, recessive mutation. Cfn mutants are seedling lethal and should be maintained in heterozygotes. To find the mutation responsible for cfn mutant phenotype, I will mine Medicago Tnt1 mutant database and also perform whole genome sequencing. I will test co-segregation of mutations in candidate genes that are highly expressed in roots and nodules with the cfn mutant phenotype. Identification of causative mutation in cfn mutant will expand our knowledge on novel mechanisms controlling root architecture and SNF in legumes.

O-11
Mitochondrial Ferropotin and Iron Homeostasis in Plants

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Mitochondria are the powerhouses of the cell and organelles of high iron demand, but highly susceptible to iron-induced oxidative stress. However, mitochondrial iron trafficking in plants is not well-studied despite its significance at the cellular and organismal level. We have identified that Arabidopsis Ferroportin 3 (FPN3) is a targeted to the mitochondria. Assays using FPN3 expressed in yeast suggest that FPN3 is most likely exporting iron from the mitochondria. Phenotypic analyses and gene expression studies with Arabidopsis fpn3 loss of function mutants and fpn3 vit1double mutants suggest that FPN3 function is critical for proper iron homeostasis.

O-12
Discovery of a new diterpenoid pathway involved stress response in maize

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Specialized diterpenoids are major constituents of biotic and abiotic defenses in maize (*Zea mays*), yet knowledge of their diversity and biosynthesis remains incomplete. In maize, two distinct groups of inducible terpenoid phytoalexins, zealexins and kauralexins, were recently discovered that form a key wall of defense against major maize pathogenic fungi, and kauralexins further function as feeding deterrents against insect pests and accumulate under drought-stress conditions. Two enzyme classes, diterpene synthases (diTPS) and cytochromes P450 monooxygenase (P450), are the major engines driving diterpenoid phytoalexin diversity. The world's major crops, maize, rice and wheat, have expansive diTPS families with roles in phytoalexin biosynthesis. Here, we report the discovery and biochemical characterization of two cytochromes P450 that hydroxylate diterpene precursors' *ent*-(iso)-kaure-16-ene, and β- macrocarpene en route to the formation of kauralexins and zealexins. In addition, CYP71Z16 reacts with recently identified dolabradiene to form intermediates to a novel diterpenoid pathway in maize that is suggested to play a role in mediating abiotic stresses in maize roots. This study highlights the combinatorial pathways of the diterpene synthases together with the promiscuity of the cytochromes P450 make for a diverse and highly dynamic network.

POSTER PRESENTATIONS

P1

Characterization of Tnt1 Mutants Defective in Root Architecture, Nodule development and Symbiotic Nitrogen Fixation in the Model Legume Plant *Medicago truncatula*

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Legume plants establish symbiotic relationship with the soil bacteria rhizobia and form unique structures on the roots called nodules to convert the inert atmospheric nitrogen into a bioavailable form. *Medicago truncatula* (barrel medic) is an elite legume model plant with extensive genetic and genomic resources. To identify novel genes essential for nodule development and symbiotic nitrogen fixation (SNF), we have isolated 60 *M. truncatula* Tnt1 retrotransposon mutants by forward genetic screening during Medicago Tnt1 mutant screening workshop organized by Noble Research Institute in the summer of 2016 and 2017. We confirmed the defective phenotypes of several mutants using a soil free aeroponic root phenotyping system. Some of the mutants show abnormal root architecture, nodule development and white colored nodules while other mutants show dark-brown/green nodules indicating premature death of rhizobia, early nodule senescence and defective SNF. Phenotypic characterization of mutants including nitrogen deficiency symptoms (purple shoot caused by anthocyanin accumulation), nodule morphology and nodule occupancy (X-Gal stained sections of nodules harboring rhizobia constitutively expressing lacZ reporter) will be presented. Efforts are underway to identify the causal genes of select mutants by mining the Medicago mutant database for the publically available Tnt1 insertion flanking sequence tags and also by whole genome sequencing to recover additional Tnt1 insertions from the mutants. Co-segregation analysis and reverse genetic characterization of additional independent Tnt1 insertion alleles will be performed to confirm the causative mutations.

P2

Evaluating the Stress responses of *Panicum millaceum* to Nitrogen Deficiency Under Central Haitian Climate Conditions

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Haiti needs a sustainable crop that meets their nutritional needs and can survive in their harsh conditions in order to help mitigate their malnourishment. Porso Millet also contains more protein and iron than corn and wheat, which is exactly what the Haitian people need. Porso Millet also contains more protein and iron than corn and wheat, which is exactly what the Haitian people need. Finding the lowest amount of nitrogen that can be available for successful stress avoidance will allow Haitian farmers to grow Porso Millet without stress from nitrogen depletion; as well as potentially save money on fertilizer. From September 2017 to November, 2017 we started growing Millet inside of a climate-control lab facility set to simulate Haiti's conditions. There were 5 total groups; 2 control groups, and 3 experimental groups. Each group consisted of 8 total Proso Millet plants and a different concentration of nitrogen consisting of of calcium nitrate, potassium nitrate, magnesium sulfate, monopotassium phosphate, FeNaEDTA, and microelements. We measured average shoot length, root length, leaf area, and seed production. We recorded a p-value of 0.94 showing no significant differences in any of these measured variables with the application of varied concentrations of nitrogen. Further experimentation needs to be performed in order to show its significance.

P3
Native Red Maple (Acer rubrum L.) Tree Physiology: Dying or Thriving in Urban Environment?

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Anthropogenic stressors are the main driving forces behind fundamental shifts in foliar metabolism in urban forest ecosystems. Urban forests are ideal surrogates for investigating the simultaneous-cumulative effects of global change factors on tree physiology and adaptive plasticity. Physiology based stress indicators have received inadequate attention in urban-plant ecology research. The objective of this study was to determine if red maple (A. rubrum) foliar metabolism responds to city size and sub-canopy Rosa multiflora invasion. We hypothesized that shifts in red maple metabolism will be greater in Philadelphia, PA (Urban) than Newark, DE (Suburban) forests due to evolved physiological plasticity to greater urban pressures. We used a long-term urban forest ecology study, FRAME (Forest Fragments in Managed Ecosystems), to test our hypotheses. We sampled soils and mid-upper canopy sun lit leaves from 77 adult red maple trees (experiencing sub-canopy R. multiflora invasion presence/absence) from ten different forested sites across Newark, DE (5 sites) and Philadelphia, PA (5 sites). We analyzed leaves for pigments, polyamines, amino acids, nitrogen, soluble nutrients, and heavy metals. Soils were analyzed for nutrients, bulk density, and heavy metals. Observed foliar chlorophyll, carotenoids, nitrogen, natural abundance nitrogen isotopic content (δ15N), polyamines (putrescine, spermidine) and amino acids (arginine, proline, glutamic acid) and sub-canopy soil metals (Pb, Al, Na, Zn) were significantly higher in red maple trees in Philadelphia as compared to Newark. The concentrations of these elements at Philadelphia correlated with greater nitrogen sources, elevated temperature, and metal stress. Thus while factors associated with urbanization influenced red maple foliar metabolism and nutrition, the edaphic conditions created by a sub-canopy R. multiflora invasion did not (data not shown). Data suggest urban trees can physiologically acclimatize in response to environmental drivers. These accommodations however, often comes at a cost in terms of productivity.

P4
***Panicum miliaceum* Growth in Alkaline Conditions**

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The grass crop *Panicum miliaceum* was among a select few plant species selected to be tested in conditions relating to the natural environment of Haiti. Environmental pH levels of Haiti may be higher than what *P. miliaceum* would normally be able to tolerate. Growing *P. miliaceum* in pH conditions akin to Haiti would provide a better understanding of the plant and its potential to be a productive crop for Haitian people. Testing strictly between a control of pH 6 and a tested control of pH 8, several methods of result collecting took place to gather as much data as possible. The plants are susceptible to spider mites and were able to survive water deficit conditions for weeks. The pH differencing results pointed pH 8 plants as being the more proactive plants with higher seed counts, more soluble protein and a higher water use efficiency when compared to pH 6 plants.

P5

A Multidrug and Toxin Efflux (MATE) Transporter Involved in Aluminum Resistance is Modulated by a CBL5/CIPK2 Calcium Sensor/Protein Kinase Complex

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Members of the ALMT (Al-activated malate transporter) and MATE (multidrug and toxin efflux) families confer plant aluminum resistance on acid soils by mediating organic acid (OA) anion efflux, thereby immobilizing toxic aluminum (Al3+) ions in the rhizosphere. Although similar in function, ALMT and MATE structure and regulation are remarkably different: while ALMT transport activity in heterologous systems is dependent on and enhanced by extracellular Al3+, the MATE transporter mediates constitutive and Al3+-insensitive transport, suggesting that in planta the MATE transport activity is modulated by additional cellular mechanisms associated with an upstream Al3+ signaling cascade. Functional (i.e., electrophysiological) approaches allowed us to screen for and identify the calcineurin B-like (CBL5)/protein kinase (CIPK2) complex as a modulator of AtMATE1 activity. BiFC analysis in *Xenopus* oocytes and in planta validated the specificity of the protein-protein interactions among CBL5, CIPK2 and AtMATE, and suggests a mechanism by which the CIPK2/CBL5 complex alters the trafficking of AtMATE1 into and out of the plasma membrane. We identify CBL5–CIPK2 as part of a Ca2+-regulated pathway involved in the Al-resistance response, by which phosphorylation of the downstream target protein (AtMATE1) limits unnecessary carbon loss via unregulated citrate exudation, thereby regulating the abiotic stress tolerance response in a temporal and spatial manner.

P6

Genetic Engineering Drought Tolerant Switch-grass by Over-expressing AVP1

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Switchgrass (*Panicum virgatum*) is an important biofuel crop, salinization and scarce water availability have been major constraints to switchgrass production and yield. Developing drought resistant switchgrass has become an important agronomic issue recently. AVP1, a pyrophosphate-driven proton pump protein, transports ions in and out of plant cell vacuoles. It has been reported overexpressing AVP1 gene in Arabidopsis increases vacuolar solute accumulation in plant leaf tissue, which leds to increased water retention and confers drought and salt tolerant (Gaxiola et al., 2001). Tomoto plants engineered to overexpress the vacuolar H+-pyrophosphatase AVP1(AVP1-OX) also shows enhanced tolerance to salinity and drought stress (Park et al., 2005). These observations suggest that AVP1 overexpressing crops would be useful in water deficient regions. We are attempting to overexpress AVP1 to introduce the drought and salt tolerant trait into this important biofuel crop and have successfully produced transgenic plants. We are now conducting molecular, physiological and progeny analysis.

P7

Characterization of a Novel Mutant trapezia with Enhanced Anthocyanin Accumulation in the Model Legume Plant *Medicago truncatula*

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Anthocyanins are one of the most abundant pigments found in plants. The colors of anthocyanins range from hues of blue-purple-red and belong to the flavonoid family of biomolecules. The roles of anthocyanins are tissue and organ specific. Anthocyanins protect seeds from harmful UV radiation, attract fruit dispersers and pollinators. Anthocyanins confer tolerance to abiotic and biotic stresses in plants. In humans, antioxidant and pharmacological benefits of anthocyanins have been well documented. Uniquely, anthocyanins can cross the blood brain barrier to reach neural cells and slow down neural degeneration along with other early-onset neurological diseases such as Alzheimer's. To discover the novel regulators of anthocyanin accumulation in plants, ~500 plants from aTnt1mutant population in the model legume *Medicago truncatula* were screened to identify mutants displaying abnormal anthocyanin pigmentation in leaves and other organs. One of the mutants, trapezia (tpz) was named after its characteristic red spots which are similar to the red-spotted guard crab (genus Trapezia, a protector of coral reefs). Tpz mutant displays increased number of large reddish-purple anthocyanin spots on both top (adaxial) and bottom (abaxial) sides of the leaves compared to the wild-type. Phenotypic characterization of tpz mutant will be presented. To identify the mutation underlying the tpz mutant phenotype, I will mine Medicago Tnt1 mutant database as well as purifying DNA from tpz mutant for whole-genome sequencing to recover additional insertion events in candidate genes. Elucidating novel genes and mechanisms involved in biosynthesis and regulation of anthocyanin accumulation will allow us to engineer anthocyanin rich plants to enable stress tolerance in crops and improved human health.

P8

A Salivary Protein of the Whitefly Affects its Phloem-feeding on Host Plants

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Whiteflies inject saliva in plant tissues and gain access to phloem sap during feeding. Some protein components of the saliva, which may either induce or repress plant responses, are crucial to whitefly feeding on host plants. Combining whitefly salivary gland transcriptomics with saliva proteomics, we identified a whitefly salivary protein and arbitrarily named it Bt56. Using RNAi-based transcript knockdown and transient overexpressionin planta, we discovered that Bt56 is important for the survival and reproduction of B. tabaci on host plants. The Bt56 gene encodes a ~10 kDa protein that the whitefly injects into host plant during feeding. qRT-PCR and immunohistochemistry analyses showed that the transcript and the protein are localized to a special region of the primary salivary glands. Monitoring by electrical penetration graph showed that, compared to control whiteflies, in Bt56-knockdown whiteflies both the number of individuals that successfully fed from phloem and the total phloem feeding duration were significantly reduced. Therefore, we conclude that the Bt56 protein is a salivary effector promoting whitefly colonization.

P9

Secondary Screening and Characterization of vbn (very brown nodule) and gsun (green supernodulator) Mutants Defective in Symbiotic Nitrogen Fixation in the Model Legume Plant *Medicago truncatula*

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Nitrogen (N2) is an essential nutrient for the survival of all organisms because it is required to synthesize important biomolecules such as proteins and nucleic acids. Atmospheric air contains 78% N2but it is not bioavailable. Legume plants establish a relationship with the soil bacteria rhizobia, forming unique structures called nodules, allowing the plant to convert the inactive nitrogen (N-2) into bioavailable form by symbiotic nitrogen fixation (SNF). Numerous mutants defective in SNF were isolated by Dr. Veerappan to identify novel genes controlling SNF by screening theTnt1retrotransposon mutant population in the model legume plant *Medicago truncatula* (barrel medic). I am characterizing two mutants vbn (very brown nodule) and gsun (green supernodulator). Nodule formation in wild type legume plants appear pink and ovoid shape with green shoots whereas vbn mutants show brown nodules and are defective in SNF. gsun shows green nodules and also increased nodule numbers. I will be presenting data on the secondary screening and phenotypic characterization of vbn and gsun mutants. To find the causative mutation, I will examine theTnt1databasefor specific mutants to identifyTnt1insertion sites. To find more mutations, whole genome sequencing will be performed. Understanding novel genes responsible for defective phenotypes can allow us to transfer SNF to other non-legume plants such as rice and corn.

P10

PH Effects on Root Development in *Amaranthus gangeticus*

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Soil pH plays a vital role in the health of a plant. Small changes in pH can alter a plants overall health as well as other physical traits. In the central plateau region of Haiti, the soil pH can range between 6.8 to 8.3 (Stewart 2012). Haiti also suffers from deforestation, flooding, and erosion. This is what has become the focus for this study; Does soil pH alter the root physiology of *Amaranthus gangeticus*? The experiment observed a total of 32 plants; half being grown in root boxes and the other half being grown in pots. Each group treated four plants to four pH levels. Data was collected observationally as well as with the use of a LICOR 6400 XT Portable Photosynthetic System. The number of adventitious roots per root box plant proved to be significantly affected when a one-way ANOVA test was performed. The most significant and possibly the most relevant data collected from this study was the number of adventitious roots. There was an apparent trend of increased root growth in both slightly acidic and alkaline conditions. This supports our original hypothesis that root structure would be positively impacted when place under pH stresses.

P11
Soybean Transformation with Cysteine Protease Inhibitor (CPI1) Gene for Resistance and Tolerance

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Soybeans (*Glycine max*) are one of the major agricultural important crops in the United States. These legumes have a variety of uses, including food and industrial applications. Soybean growth is susceptible to drought, pest infection, and bacterial disease. These conditions strain soybean growth worldwide, dampening the effect that soybeans have on the economic network. It has been reported that the introduction of an active Cysteine Protease Inhibitor gene (CPI1) originally identified in Arabidopsis thaliana, will enhance soybean disease resistance and drought tolerance. The CPI1 gene helps the soybean combat programed cell death, which occurs when soybeans are exposed to unfavorable conditions and stress. Protease enzymes, released during cell death, break down the proteins and peptides necessary for the cell to live. Therefore, with the introduction of the CPI1 gene into soybean DNA protease levels can be controlled to help overcome programmed cell death. This will produce a heartier soybean that will more readily survive in a variety of adverse environmental conditions. The transgenic soybeans overexpressing CPI1genes will promote grow the transgenic soybeans formed will promote soybean growth and its role in the economy.

P12
Aphid Resistance in Perennial Soybeans: Two Genomes Are Better than One

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Wild relatives of Glycine max (cultivated soybean) are a potential source of genes that can be used to enhance resistance to aphids and other insect pests. The allotetraploid perennial soybean *Glycine dolichocarpa* has resistance to both *Aphis glycines* (soybean aphid) and *Acyrthosiphon pisum* (pea aphid), whereas its diploid progenitors, *Glycine tomentella* D3 and *Glycine syndetika*, show resistance to only *A. glycines* or *A. pisum*, respectively. Using transcriptomic and metabolomic approaches to compare responses of these three perennial soybean species to aphid infestation, we found that they vary in their responses to *A. glycines* and *A. pisum*. Perennial soybeans resistant to *A. pisum* accumulate more isoflavones in response to aphid attack, whereas those resistant to *A. glycines* accumulate more flavones. This is recapitulated in artificial diet assays, where isoflavones have a greater negative effect on *A. pisum* and flavones have a greater negative effect on *A. glycines*. Correlative analysis of gene expression and aphid resistance in the three perennial soybean species identified likely resistance (R) genes. The functions of two leucine rich repeat receptor kinases were confirmed by showing that expression silencing and overexpression, respectively, have significant effects on aphid reproduction. Together, the observation of additive effects of flavonoids and R genes in aphid resistance support the hypothesis that allotetraploidy in perennial soybeans provides an evolutionary advantage through the combination of two plant defense systems. The identified R genes could be transferred to G. max, where breeding for enhanced aphid resistance has been hampered by low genetic diversity and the rapid evolution of aphid biotypes that can overcome the known resistance genes.

P13

Genetic Transformation of Switchgrass Plants with FNR-FLD Flavodoxin Genes for Drought Resistance and Salt Tolerance (In Progress…)

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Switchgrass (*Panicum virgatum* L.) is a warm-grass is native to North America's prairies. It is a common forage grass and high potential biofuel crop. To produce the maximum number of biofuels, the switchgrass plants must have favorable conditions including water and heat; otherwise; the plants yield will be low and an economic loss in agriculture. To improve the survival abilities of switchgrass by Agrobacterium-mediated transformation with the FNR-FLD, a flavodoxin gene with pea peptides. Studies have shown that creeping bentgrass plants have successfully transformed the FNR-FLD gene into the DNA of the plants genes, giving the plants an advantage during unfavorable conditions. This gene decreases susceptibility to drought and salt, allowing the plants to flourish and have maximum yields of various products that are useful in the industry. Transgenic switchgrass has been achieved and is continually undergoing analysis by physical and molecular processes.

P14

Development of High Yield Switchgrass Cultivar by Agrobacterium-Mediated Transformation with InsP-5-Ptase Gene (In Progress…)

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Switchgrass is an important warm season grass in Northern America, often used in the production of biofuels. By manipulating the switchgrass genome, we can increase the yield of desired products, including ethanol. Introducing the foreign gene into the callus will give the plants an ability to grow in poor soil, making it a very valuable biofuel crop. In this research, we infect the plants with a transgenic agrobacterium used as a binary vector for the desired plasmid. Transgenic switchgrass plants have been obtained and continue to undergo molecular, physiological and progeny analysis. This experiment has five steps: callus incubation, agrobacterium preparation, cocultivation, selection and regeneration, and then do the gene analysis.

P15
The improvement of Switchgrass by Agrobacterium-Mediated Transformation

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Switchgrass which is a C4 perennial warm-season grass with high biomass yields native to the North America. It has been reported as a significant biofuel crop. Several studies show that transgenic plants overexpressing CodA gene can strengthen stress tolerance. In the project, CodA gene which is located in PHL093 is overexpressed in switchgrass to increase its stress tolerance. In addition, the aggregation of glycinebetaine can enhance the freezing tolerance of plants. The strength of freezing tolerance is not related to the expression of cold-regulated genes by Northern blot analysis. The results indicate that biosynthetic glycinebetaine by Agrobacterium-mediated transformation technology with the CodA gene is an effective method to increase the tolerance of plants. Several regenerated plants have grown successfully in the project and the expression of gene in switchgrass has been proved by PCR and molecular analysis.

P16
Drought and salinity induced changes in ecophysiology and proteomic profile of *Parthenium hysterophorus*

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Parthenium hysterophorus is a plant that tolerates drought and salinity to an extremely high degree. Higher expression of stress-responsive proteome contributes for greater defence against abiotic stresses. Thus, *P. hysterophorus* could be a rich source of genes that encode stress-imparting mechanisms and systems. The present study utilizes comparative physiological and proteomic approaches for identification of key proteins involved in stress defence of *P. hysterophorus*. Thirty-days-old plants were exposed to drought (10% PEG 6000) and salinity (160 mM NaCl) for 10 days duration. Both stresses induced oxidative stress estimated in terms of TBARS and H2O2. Levels of both enzymatic and non-enzymatic antioxidants were elevated, more by drought than salinity. Particularly, SOD, GR, CAT and GST proved to be assisting as very commendable defence under drought, as well as salinity. Levels of ascorbate, glutathione and proline were also increased by both stresses, more in response to drought. Comparative proteomics analysis revealed a significant change in relative abundance of 72 proteins under drought and salinity. Drought and salinity increased abundance of 45 and 41 proteins and decreased abundance of 24 and 26 proteins, respectively. Drought and salinity increased and decreased abundance of 31 and 18 proteins, respectively. The functions of identified proteins included those related to defence response (26%), signal transduction (13%), transcription and translation (10%), growth and development (8.5%), photosynthesis (8.5%), metabolism (7%), terpenoid biosynthesis (5.5%), protein modification and transport (7%), oxido-reductase (4%) and Miscellaneous (11%). Among the defence related proteins, antioxidants and HSPs constituted 26% and 21%, respectively. Present study suggests a potential role of defence proteins. Proteins involved in molecular stabilization, formation of osmolytes and wax and contributing to stress-avoiding anatomical features emerged as key and complex mechanisms for imparting stress tolerance to *P. hysterophorus*.

P17
Development of Tissue Culture System for Transformation System in Hops (*Humulus lupulus*)

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Hop (*Humulus lupulus*) is widely used in the brewing industry because the female flower improves the aroma and flavor of beer. It is hard to cultivate hops in New York state since the hop is very sensitive to fungi and bacteria. A gene which could confer fungus resistance to Hop would be useful. The goal of our project is to develop a tissue culture protocol which can be used to grow single cell hops capable of Agrobacterium-mediated transformation. We have established a tissue culture system for regeneration by using MS-B5 medium supplemented with 1.43µM IAA and 9.08µM TDZ, resulting in successful shoot induction. Small (0.5cm) shoots and green calli induced from shoot internodes in vitro have resulted in transplantable Hop.

P18
A Gene Encoding LRR-RLK Is Involved in OPDA Signaling of *Marchantia polymorpha*

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12-Oxo-phytodienoci acid (OPDA) is an intermediate of jasmonic acid (JA) biosynthesis in plants. Jasmonates are biosynthesized from a-linolenic acid via octadecanoid pathway under biotic and abiotic stresses and play important roles in flowering plants. OPDA has beenshown to have JA-dependent and/or JA-independent biological functions. *Marchantia polymorpha* (*M. polymorpha*) belongs to liverwort which is considered as the first land plant family and JA does not inhibit its growth even though OPDA does, so OPDA signaling pathway in *M. polymorpha* is important to understand how plants have dealt with environmental stresses in plant evolution. To clarify the mechanism of OPDA signaling, T-DNA insertion mutants of *M. polymorpha* were generated. In a mutant line, whose growth was not significantly inhibited by OPDA, T-DNA was inserted in 3'-UTR of the gene encoding putative LRR-RLK (Mapoly0098s0059.1). To make sure the effect of the gene, knockout mutants of the LRR-RLK gene were generatedby homologous recombination-mediated strategy. OPDA inhibited the growth of the knockout mutants less than that of wild-type, and OPDA did not induce the expression of MpAOC, which encodes an OPDA biosynthetic enzyme, in the knockout mutants unlike in the case of wild-type. Moreover, a recombinant protein of the kinase domain of the putative LRR-RLK showed in vitro kinase activity. These results indicate that LRR-RLK is involved in OPDA signaling especially in feedback on OPDA biosynthesis in *M. polymorpha*.

P19
Towards Understanding the Origin and the Evolution of Cytokinin Signaling

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Cytokinins are adenine derivatives and as such they are found in every organism. However, only plants use them as signaling molecules. Plants transduce the cytokinin signal via a variant of the two-component signaling system. Although this signaling system is very common in bacteria, it is unique to plants among higher eukaryotes. Cytokinins are detected by a hybrid-histidine kinase receptor, and the signal is transduced by a multi-step phospho-relay system of histidine phospho-transfer proteins and different classes of response regulators. To shed light on the origin and evolution of the members of this signaling system, comprehensive similarity and domain-based phylogenetic studies across the relevant kingdoms were conducted. Surprisingly, a novel subfamily of cytokinin receptors was identified and members subsequently experimentally characterized. Further experiments in both, the moss *Physcomitrella patens* and the charophyte *Coleochaete scutata*, hint at an origin of the cytokinin signaling in charaphyceae algae and thus before the conquest of land by plants.

P20
The Function of *Brachypodium distachyon* SECONDARY WALL ASSOCIATED MYB4 in the Transcriptional Regulation of Secondary Cell Wall Biosynthesis

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Vascular bundle arrangements and cell wall composition varies between eudicots and monocots suggesting divergent transcriptional regulation. In Arabidopsis thaliana, R2R3 MYB proteins are a large family of plant transcription factors involved in the regulation of plant processes and several MYBs are key regulators of secondary cell wall biosynthesis. SECONDARY WALL ASSOCIATED MYB4 (SWAM4) is an R2R3 MYB highly expressed in stems compared to roots and leaves, typical of genes that are associated with secondary cell wall development, and it was selected as candidate regulator of secondary cell wall in *B. distachyon*. Yeast one-hybrid experiments showed that SWAM4 protein binds upstream of the cellulose synthase genes CESA4, CESA7, CESA8, the lignin genes CAD1, COMT, and an AC-element. Reverse genetic approaches were used to generate plants that constitutively overexpress the full-length coding region of SWAM4 and dominant repressor lines containing a 39bp dominant repressor domain (SWAM4 DR). SWAM4 DR lines were dramatically shorter than control plants with significantly lower stem and leaf biomass. SWAM4-DR stem cross sections stained with phloroglucinol-HCL indicated reduced lignin and decrease cell wall thickness. Our findings suggest that SWAM4 has a role in secondary cell wall transcriptional regulation in and our research aims to further functionally characterize SWAM4 by collecting genetic and biochemical evidence that contribute to understand its role in the transcriptional network.

P21

Photosynthetic mutants of the C4 model, *Setaria viridis*, link chloroplast RNA metabolism to intercellular communication and C4-cell-specific differentiation

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The hallmark of C4 photosynthesis is two differentiated leaf cell types, bundle sheath (BS) and mesophyll (M), each with specialized chloroplasts and cell-type specific proteins. Yet, molecular mechanisms that regulate this differentiation are amongst the most intensively studied, but most poorly understood in plant science. To identify factors involved in BS specificity of Rubisco, a mutant screen was conducted in *Setaria viridis* expressing YFP specifically in BS chloroplasts. Phenotypes sought included Rubisco deficiency, and mislocalization of YFP to M as well as BS chloroplasts. From a subpopulation of chlorotic mutants, two of them accumulated YFP in both BS and M chloroplasts. The causative mutations were determined to be in genes encoding a novel chloroplast-targeted splicing factor, and a known chloroplast-targeted exoribonuclease, both of which have essential roles in chloroplast RNA metabolism. Additional experiments showed that in these mutants, YFP migrates freely from BS to M cells, due to modification in normal cell-to-cell communication mediated by plasmodesmata (PD). Structural characterization of the PD in the BS/M interface showed that the cell-type specificity mutants have modified PD structure and size exclusion limit relative to the WT and a control mutant. PD deformation in the size exclusion mutants was linked to a retrograde signaling pathway, which was shown to regulate nuclear genes encoding PD-localized proteins and proteins with substantial roles in cell plate formation and cell wall biosynthesis, possibly mediated by ABA.

P22

Characterization of a Protein S-Acyltransferase Mutant, pat3, from *Arabidopsis thaliana*

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Protein palmitoylation or S-acylation is the reversible, covalent, post-translational lipid modification of cysteine residues with the 16-carbon fatty acid palmitic acid. Protein S-acyl transferases (PATs) catalyze this reaction. PATs are integral membrane proteins with four to six transmembrane domains and a cytoplasmic DHHC motif that is essential for enzymatic activity. Palmitoylation promotes membrane association of cytosolic proteins, regulates protein activity, or impacts protein stability. S-acylation influences cell size, growth, and polarity within eukaryotic cells; however, knowledge of the roles of S-acylation in plant cells is limited in comparison to other organisms. We use the model plant *Arabidopsis thaliana* to study the role of S-acylation in plants. Arabidopsis has 24 PAT genes. I am studying PAT3 using homozygous pat3-2 and pat3-3 mutants. T-DNA mapping by PCR showed a deletion in the cytosolic tail after the fourth transmembrane domain. This area contains several regions that are conserved across all PAT proteins and thus may affect enzyme activity. To detect transcript from the pat3-2 and pat3-3 mutants, I am using reverse transcriptase PCR. Finally, the GUS reporter gene system is being used to determine where and when PAT3 is expressed in Arabidopsis. Once the quality of the pat3-2 and pat3-3 mutants is determined, the search for pat3 mutant phenotypes will begin with the ultimate goal of determining the normal function of PAT3 in this plant.

P23

Characterization of a Protein Acyltransferase-14 Mutant in *Arabidopsis thaliana* Using Proteomics and Growth Assays

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Cells employ various enzymes that modify discrete sets of target proteins. Protein S-acyltransferases modify their targets by the reversible, covalent addition of a saturated fat, usually the 16-carbon fatty acid palmitate. Among other effects, palmitoylation can direct the target protein to one of the cell's membrane systems, facilitate new protein-protein interactions, or modify the target protein's function. The model plant Arabidopsis thaliana has 24 protein S-acyltransferases. Protein S-acyltransferase-14 (pat14) mutants in *Arabidopsis thaliana* exhibit premature leaf senescence. The aim of my research is to identify target protein(s) of PAT14 with the long-term goal of understanding the role of PAT14 and its substrates in cell physiology and senescence. To accomplish this, a proteomics approach was used. Tissue from both wildtype and pat14 mutants was fractionated by Acyl-Biotin Exchange to enrich for palmitoylated proteins, which were then identified by mass spectrometry. By comparing data from wildtype and the pat14 mutants, a set of palmitoylated proteins, which should include potential PAT14 targets, was generated. In addition to the proteomics approach, the effect of environmental factors on the development of the pat14 senescence phenotype was investigated. pat14 plants were grown either in pots containing a soilless, peat-based potting medium with commercial fertilizer or in petri dishes containing plant culture medium solidified with agar under aseptic conditions. The characteristic early senescence symptoms did not develop under the latter growth conditions. Assays are in progress to identify the variables (growth conditions and nutrient composition) that affect the early senescence phenotype of pat14 mutants.

P24

The Influences of Chloroplast Sizes on Plant Growth and Development

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Plants are able to survive on their own through photosynthesis, the process where plants utilize sunlight energy to convert carbon dioxide and water to produce sugar and oxygen. Photosynthesis takes place in the chloroplasts located on the leaves of plants. Light absorption and utilization by the chloroplast are part of a signaling cascade regulating plant developmental responses. Knowing how the chloroplast influence plants growth and development, we can propose further experiments and apply those to real life agriculture. In this experiment, we predict that differences in chloroplast sizes could influence plant growth and development due to changes in how much light is absorbed by the leaves. To support our hypothesis, *Arabidopsis thaliana* plants with artificially enlarged chloroplasts were grown in the greenhouse under the same environmental conditions. Growth rate and development between the mutant lines and the wild-type plants will be measured as well as chloroplast size, leaf thickness, cell number and vein spacing.

P25

Type-B ARRs Target WUSCHEL to Control Shoot Initiation.

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The plant hormone cytokinin affects a diverse array of growth and development processes and responses to the environment. How a signaling molecule mediates such a diverse array of outputs and how these response pathways are integrated with other inputs remain fundamental questions in plant biology. To this end, we characterized the transcriptional network initiated by the type-B ARABIDOPSIS RESPONSE REGULATORs (ARRs) that mediate the cytokinin primary response, making use of chromatin immunoprecipitation sequencing (ChIP-seq), protein-binding microarrays, and transcriptomic approaches. By ectopic overexpression of *ARR10*, Arabidopsis lines hypersensitive to cytokinin were generated and used to clarify the role of cytokinin in regulation of various physiological responses. ChIP-seq was used to identify the cytokinin-dependent targets for ARR10, thereby defining a crucial link between the cytokinin primary-response pathway and the transcriptional changes that mediate physiological responses to this phytohormone. Binding of ARR10 was induced by cytokinin with binding sites enriched toward the transcriptional start sites for both induced and repressed genes.

WUSCHEL (*WUS*) gene was identified as a direct target of ARR10. *WUS* is a homeodomain transcription factor that plays a key role in the establishment and maintenance of the shoot apical meristem. Analysis of single- and double- mutant combinations of type-B ARRs reveal functional overlap in the gene family such that *ARR1*, *ARR10*, and *ARR12* all play roles in mediating the cytokinin-dependent induction of *WUS*. Hormonal induction of *WUS* expression was strongly elevated in *35S:ARR10:GFP* hypersensitive lines. Additionally, hypocotyls from *35S:ARR10:GFP* lines were able to form shoots on callus-induction medium bypassing the usual requirement for shoot-induction medium.

Results from our analyses shed light on the physiological role of the type-B ARRs in regulating the cytokinin response, mechanism of type-B ARR activation, and basis by which cytokinin regulates diverse aspects of growth and development as well as responses to biotic and abiotic factors.

P26

Using Arabidopsis Mutants to Examine the Role of CYP72A Enzymes in Defense Against Environmental Stresses

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When plants are stressed they respond by producing defensive metabolic compounds. A group of enzymes called Cytochrome P450s (CYPs) are involved in the biochemical pathways induced by this stress response. Our lab studies the CYP72A subfamily of these enzymes by comparing the phenotypic response of mutants in CYP72A genes with wild type plants. CRISPR/Cas9 was used to make mutants in genes encoding for CYP72As. Using publicly available gene expression data we identified unique expression patterns of these genes, and then hypothesized which stresses would result in the biggest phenotypic difference when comparing mutant plants to wild type. For example, the gene CYP72A8 is induced by drought so we expect mutant plants to be more sensitive to drought stress. The mutant and wild type plants were exposed to different stresses, among which were drought, caterpillar herbivory, and heat stress. We measured chlorophyll concentration for drought stress, the change in mass of the caterpillar for herbivory stress, and anthocyanin accumulation for the heat stress. Under heat stress experiment the cyp72a8 mutants had significantly lower and the cyp72a11 mutants had significantly higher anthocyanin production than the wild type. This suggests that the CYP72A8 enzyme may play a part in producing anthocyanin, whereas the CYP72A11 enzyme may be involved in breaking down anthocyanin. By studying how this model plant responds to stress we are contributing to a better understanding of how plants induced chemical defense in to stressful environments.

P27

Designing Poplar for Increased Nitrogen and Carbon Assimilation and Biomass Yield

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An important component for plant growth and regulation is Nitrogen (N). N fertilization plays an important role in increasing crop yield. However, oxidized and reduced form of N are the most common and most costly input nutrient that often limits carbon (C) assimilation in plants. Moreover, N is also a cause for environmental pollution by leaching and run offs into streams and lakes. Carbon is a predominant component of plants which plays a major role in inorganic N usage in leaves and distribution of assimilated C between organic acids, starch and sugars. Polyamines are aliphatic amines that are present in all living organisms and are an obligatory requirement for survival. In higher plants, the most prevalent polyamines are spermidine (Spd), spermine (Spm), and their diamine precursor, putrescine (Put). A variety of roles have been proposed for polyamines in the growth, development, and stress response. Past research in the our lab has found out that by genetically manipulating the polyamine synthesis pathway, accumulation of C and N can be enhanced. Using the hybrid poplar plant (*Populus nigra* x maximowiczii - NM6) my research focuses on producing transgenic plants with genes that regulate the polyamine biosynthesis and to test if they showed N and C assimilation, and show increased growth and biomass accumulation. We are also testing whether foliar application of N Increases N assimilation in transgenic plants, thereby further promoting higher C assimilation and biomass production.

P28
Development of Aphid-transmitted Viral Vectors for Transient Gene Expression in Maize

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Maize (*Zea mays*) is the most economically important field crop in the United States. Both abiotic factors such as drought and frost, and biotic factors such as pests and diseases significantly affect crop yield. Given the unpredictable nature of these threats to agricultural productivity, we are developing Sugarcane mosaic virus (SCMV, a ssRNA potyvirus), as an aphid-transmitted viral vector to express transgene(s) that can mitigate previously unforeseen threats in real time. Corn leaf aphids (*Rhopalosiphum maidis*) transmit a GFP-expressing version of this virus (SCMV-GFP) to maize plants with high efficiency. In further work, SCMV will be engineered to overexpress protein-producing transgenes to directly counter relevant threats, up-regulate gene expression to enhance endogenous resistance, introduce RNA that interferes with essential gene expression in pest insects, and induce mutations in the maize genome using CRISPR/Cas9 or related nucleases to enhance resistance to drought and pests. We have sequenced the *R. maidis* genome, with the goal of identifying genes that can be manipulated to improve virus transmission by these aphids, as well as to create auxotrophic mutations that can limit further spread of *R. maidis* in natural settings. The outcomes from this project will not only help to mitigate existing threats from biotic and abiotic stress, but also can be used to counter emerging threats to the maize crop. Furthermore, the viral vectors that we are developing will be important research tools for investigating the functions of endogenous maize genes. Key words: Maize, biotic and abiotic stresses, insect vectors, virus vectors, aphid transformation protocols.

P29
Lycopersicon esculentum Physiological and Molecular Responses to Silver Nanoparticles

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Nanoparticles, in particular silver nanoparticles, have been used frequently in industry (e.g., electronics, energy sectors), in medicine (e.g., cancer therapy, antibacterial agents) and in agriculture (e.g., herbicides and pesticides). Nanoparticles that are released into soil and water can be taken up by plants and subsequently can enter the human body through the food chain. Understanding the effects of nanoparticles on plants and the mechanism by which they are taken up is important to protect agriculture and human health. This study focuses on the physiological responses of tomatoes (*Lycopersicon esculentum*) to silver nanoparticles. *L. esculentum* were exposed to 10, 20 or 30 mg/kg of 20 nm pvp coated silver nanoparticle (Ag-NP), silver ion (Ag) or silver nitrate (AgNO3) dissolved in Hoagland media. Physiological responses were studied in plant leaves by measuring plant growth, chlorophyll, total flavonoids, anthocyanins, hydrogen peroxide and MDA content, and the activity of antioxidative enzymes including peroxidase and catalase. The result showed that exposure to a higher concentration of silver in the form of nanoparticle or nitrate resulted in lower plant growth and higher ROS generation compared to the control group. To better understand the impact of nanoparticles on plants, the expression of Phenylalanine Ammonia Lyase (PAL) and Universal Stress Protein (USP) was studied in leaves using q-PCR. The result showed significantly higher expression of PAL in exposed plants to 30mg/kg of Ag-NPs compared to the control while there was no significant difference in the expression of USP.

P30

Investigation of the Cardiac Glycoside Biosynthesis Pathway Using Genomic, Metabolomic and Transcriptomic Analysis of *Erysimum cheiranthoides*

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Erysimum is the only crucifer genus that produces cardiac glycosides, a class of defense-related plant metabolites that has evolved independently in at least twelve plant families. Despite the medical applications of cardiac glycosides, their biosynthetic pathways have not yet been identified in any plant species. Due to its close phylogenetic relationship with Arabidopsis, fast growth, and self-fertility, we chose *Erysimum cheiranthoides* (wormseed wallflower) for a multi-omics approach to elucidate the cardiac glycoside biosynthesis pathway. Pacific Biosystems (PacBio) sequencing of a 7th-generation inbred line of *E. cheiranthoides* variety Elbtalaue was used to generate a high-quality genome, representing 150x coverage of 174.5 Mb total sequence length, with an N50 length of 1.5 Mb. Chromosome-scale assembly was achieved using Hi-C technology, resulting in 98.7% of the original assembly being assigned to eight scaffolds, corresponding to the eight chromosomes of *E. cheiranthoides*. A total of 31,095 gene models were annotated. Quality assessment of the genome assembly identified 94.6% of BUSCO orthologs, indicating a high level of completeness. Measurement of tissue-specific metabolite abundance showed that cardiac glycosides are differentially accumulated in *E. cheiranthoides*. With the exception of old leaves and roots, treatment with the defense elicitor methyl jasmonate did not significantly increase cardiac glycoside levels. In parallel, transcript profiling (RNAseq) was conducted with the same *E. cheiranthoides* tissue types. Based on gene co-expression network analysis of the transcriptomic and metabolomic datasets, candidate genes for the biosynthetic pathway were identified. Agrobacterium rhizogenes-mediated root transformation was optimized in *E. cheiranthoides*, and will be used to confirm the function of candidate genes for cardiac glycoside biosynthesis. The functionally of confirmed genes will provide a firm basis for the further research into cardiac glycoside biosynthesis and function, as well as practical applications in improving drug design for use in human medicine.

P31

Cold Hardiness of European-American Hybrid Grape Varieties in a Changing Climate

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In face of unpredictable climate change, maintaining a sustainable agriculture depends on the availability of genetically diverse cultivars. The traditional European grapes (e.g. Pinot Noir) are cultivars of a single species and have little cold hardiness. In contrast, emerging grape cultivars (European-American hybrids) take advantage of the tremendous genetic diversity of native American grape species (about 30 species). Yet, little is known regarding the effect of large fluctuations of temperatures on emerging hybrids but the hybrids appear to show variable level of survival. Hybrids might lose hardiness (de-acclimate) earlier than they use to in response to the increased mean temperatures in the winter due to climate change. The response of these hybrids to new warm weather patterns are complex and need to be understood. It is critical to identify varieties that are predisposed to early de-acclimation and therefore more susceptible to early spring frost.

We sampled two cold hardy grape varieties from the UMass Cold Spring Orchard late winter at regular times. In order to quantify deacclimation, we exposed the cuttings to decreasing temperatures below freezing and quantified the temperature at which half the buds are able to survive.

P32
Pectin suppresses the helical growth of plant cells

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Specific organs in some plant species exhibit helical growth patterns of fixed or variable handedness, but most plants organs are not helical. Previous work has implicated the organization of the cytoskeleton as a basis for helical growth. We report that changes in cell wall composition can also cause helical growth. Mutations in Arabidopsis RHAMNOSE BIOSYNTHESIS 1 (RHM1) decreased the amount of rhamnose in the cell wall and caused dramatic left-handed helical twisting of roots and petals. Rhamnose is a major component of certain pectins, and a combination of genetic and biochemical experiments showed that the helical growth of rhm1 mutants is likely a consequence of decreased levels of the pectin rhamnogalacturonan-I. Unlike other mutants that exhibit helical growth of fixed handedness, the orientation of cortical microtubule arrays was unaltered in rhm1 mutants, indicating that the left-handed growth of rhm1 mutants was independent of microtubules and revealing a novel source of chiral plant growth caused by changes in cell wall composition. We also found that rhamnose-containing cell wall polysaccharides are required in multiple organs to promote cell expansion. While others have suggested that some rhm1 defects result from decreased flavonol rhamnosylation, we showed that changes in flavonol rhamnosylation do not directly affect cell expansion, but instead act indirectly by altering the partitioning of rhamnose between flavonols and cell wall polysaccharides. Our results indicate that rhamnose-containing pectins are broadly important for promoting expansion of plant cells and suppressing the emergence of chiral twisting in those expanding cells.

P33
Understanding the Role of the Arabidopsis CYP72A14 Enzyme in Chemical Defenses Against Environmental Stress

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Abiotic and biotic stresses are causes of major losses in crop yield resulting in less food for consumers. We can improve our understanding of stress tolerance in plants by studying the enzymes that are activated for secondary metabolism. We are studying the function of a highly conserved family of enzymes known as cytochrome P450s in Arabidopsis thaliana. The focus is on the subgroup CYP72A, and the particular gene of interest for this study is CYP72A14. It is known that heat stress, osmotic stress, and *Pseudomonas syringae* stress activate this gene in wildtype plants; however, the role of the enzyme in these stress responses is unclear. If mutant plants lacking the CYP72A14 enzyme are exposed to such stresses, we expect that they will be more severely impacted than wildtype plants exposed to the same conditions. To study heat stress, plants were exposed to 40℃ and 42℃ for 3 hours. For osmotic stress, seedlings were grown on 50mM and 100mM mannitol plates. In studying the bacterial stress, plants were inoculated with *P. syringae* in the underside of their leaves and the number of colonies grown were measured on Day 0 and Day 3 or 4. There were no significant differences in heat stressed or osmotic stressed mutant and wildtype plants. The *P. syringae* stress resulted in a slight trend indicating that mutant plants allowed less growth than wildtype plants. By studying the function of this gene, we will have a better understanding of how plants cope with different stresses in their environment and how secondary metabolites are protecting them.

P34

Sexual and apomictic reproduction in Aronia species and lack of genetic diversity in commercial Aronia production

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Native to eastern regions in North America, the genus Aronia is a group of deciduous shrubs in the Rosaceae family, subtribe Pyrinae. Very little has been accomplished with genetic improvement of polyploid Aronia genotypes due to the suspected apomictic reproductive mechanisms in this genus. The objectives of this study were: 1) elucidate the reproductive mechanisms of Aronia species and reveal the occurrence of apomixis within the genus and 2) determine the genetic diversity of commercial cultivars of *A. mitschurinii*. For experiment I, 20 Aronia accessions (five *A. melanocarpa* [2x], four *A. melanocarpa* [4x], three *A. prunifolia* [3x], four *A. prunifolia* [4x], three *A. arbutifolia* [4x], one *A. mitschurinii* [4x]) were used in this study. Intra-accession variability was evaluated by growing out progeny from an open-pollinated maternal accession and comparing Amplified Fragment Length Polymorphism (AFLP) profiles between the progeny and maternal accession. Diploid accessions produced a significant amount of genetic variation (0.6-0.8 Jaccard's similarity coefficient) in progeny which was indicative of sexual reproduction. Seedlings from tetraploid accessions had very little genetic variation (0.90-0.98 Jaccard's similarity coefficient) in comparison to their maternal accession. The very limited genetic variation observed in tetraploid progeny suggests that apomictic diplospory with one round of meiotic division is occurring. Triploid accessions appear to reproduce via sexual reproduction and apomictic diplospory. For experiment II, genetic similarities were determined for nine *A. mitschurinii* cultivars that are commonly used in commercial fruit production. All cultivars, except for 'Nero', were genetically identical, with 'Nero' producing a Jaccard's similarity coefficient of 0.97. We propose that the same genotype has been renamed repeatedly by growers. Nero is likely a seedling of the primary clone in commerce, since it has a similarity coefficient that is equivalent to what we observed in tetraploid Aronia progeny.

P35

The Impact of Intraspecific Density on Garlic Mustard (*Alliaria petiolata*) Sinigrin Concentration

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Garlic mustard (*Alliaria petiolata*, Brassicaceae) is a biennial herb that produces glucosinolates, a class of constituent secondary metabolites that defend against herbivores and pathogens allowing it to grow at high densities in invaded regions. The glucosinolate sinigrin is predominant in garlic mustard and aids in its competitiveness as an invasive species. In North America, garlic mustard can grow at high densities and form dense monocultures which may increase its apparency to herbivores and therefore increase its sinigrin production. I measured leaf sinigrin concentration in garlic mustard populations of different densities in the field and in greenhouse experiments to evaluate the response of sinigrin concentration and growth to density and light. Sinigrin concentrations of second-year plants were negatively correlated with growth metrics across all field densities; indicating a cost to sinigrin production. In the greenhouse density experiment with high and low rosette stem densities, sinigrin differed significantly by rosette density category. A factorial greenhouse experiment with light and density treatments discerned significant differences in sinigrin concentration by density. These findings suggest that sinigrin concentration may be influenced by intraspecific density across different light environments.

P36

Effect of garlic mustard management on exotic earthworms and native plant diversity

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The invasive plant *Alliaria petiolata* (Garlic Mustard) can disturb aboveground diversity of native forest ecosystems in Massachusetts. Exotic earthworms have been hypothesized to promote *A. petiolata* invasion, but the mechanism of coinvasion is not understood, nor are the impacts of both species on native biodiversity. We conducted an eradication study at two sites in Massachusetts to test the responses of exotic earthworms and native plant communities to *A. petiolata* removal. This work was conducted at the Harvard Forest (central MA) and McLennan Reservation (western MA), where we established replicate plots without Garlic Mustard (control), reference plots with Garlic Mustard, and plots where Garlic Mustard was eradicated by hand one year earlier. We measured native plant diversity and earthworm biomass in the field from each treatment. Post-hoc analyses discerned earthworm biomass a highest in the invaded treatment and declining to uninvaded levels in the Garlic Mustard eradication treatments (Tukey's test p<0.05). Results from a regression analysis also demonstrated a marginally significant interaction effect between eradication treatment and earthworm biomass on native plant diversity (p<0.01). Our findings suggest that *A. petiolata* populations may be facilitating earthworm invasion, contrary to previous studies suggesting the opposite relationship. Moreover, sites eradicated of Garlic Mustard had lower earthworm biomass than invaded sites, which posits this method as possible dual management strategy to control earthworm and Garlic Mustard invasions. We also show that native plant diversity is negatively correlated with earthworm biomass in invaded plots but positively so in eradicated plots, further supporting previous research that garlic mustard eradication as a tool can preserve aboveground diversity at least for some sites.

P37

Acrolein Toxicity in Mammalian and Plant Cells

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Polyamines are small, nitrogen-rich, aliphatic compounds present in all living cells and play a multiple roles in cellular processes. Acrolein, a toxic organic aldehyde is a byproduct of polyamine metabolism, produced both in plants and animals. It was initially known to be produced mainly though lipid oxidation in mammalian cells, and by burning or charring of plants. Acrolein has been shown to be a useful biomarker for early diagnosis in stroke, and causes apoptosis of cells at the site of infarction. In collaboration with scientists at Chiba University in Japan, we tested the effects of different N-acetyl cysteine derivatives on acrolein treated cells to measure cell recovery. N-acetyl-S-ethyl-L-cysteine was found to be the most effective at protecting the cells through glutathione conjugation mechanism. In plant cells, acrolein causes cell death when plants are subjected to abiotic stress. Acrolein is also a major toxic compound produced in forest fires. In our lab, we have produced several transgenic lines of Arabidopsis thaliana with genes for ornithine decarboxylase, which results in 10-30-fold increase in cellular polyamines. Currently, we are studying the relationship between polyamine content, abiotic stress response and acrolein production in these plants.

P38
Differential Gene Expression Associated with Winter Survival of *Lolium perenne*.

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Perennial ryegrass (*Lolium perenne* L.) is an economically important perennial grass used for turf and forage purposes, but often exhibits poor winter survival compared to other cool-season grasses. Further research into the mechanisms required for freezing tolerance and resistance to deacclimation is needed to help facilitate breeding of cultivars better adapted to northern climates. Temperature regulated gene expression has shown to be critical in determining cold acclimation capacity and winter survival in perennial grasses. The objectives of the research were to examine temperature-induced changes in freezing tolerance and associated gene expression during cold acclimation and deacclimation for two perennial ryegrass genotypes differing in freezing tolerance, hereby referred to as Freezing Tolerant (FT) and Freezing Sensitive (FS). Plants were exposed to seven temperature treatments including: (1) non-acclimated control at 20°C for 2 weeks, (2) cold acclimated 2°C for 2 weeks, (3) cold acclimated -2°C for 2 weeks, (4) deacclimated at 4°C for 1d, (5) deacclimated at 4°C for 5 d, (6) deacclimated at 8°C for 1d, (7) deacclimated at 8°C for 5d. Following each temperature treatment, leaves and crowns were harvested for evaluation of freezing tolerance (lethal temperature resulting in 50% mortality, LT50) and gene expression using qRT-PCR. Genes were selected based on previous research demonstrating their importance in cold acclimation including C-repeat binding factor 3 (CBF-3), ice recrystallization inhibitor-a (IRI-a), sucrose-sucrose-1-fructyltransferase (Prft1), and plasma membrane intrinsic protein 1 (PIP1). The FT genotype exhibited higher freezing tolerance during cold acclimation and deacclimation, which was associated with higher expression of CBF-3, IRI-a and Prft1. The FS genotype exhibited higher expression of PIP1, which could predispose this genotype to water uptake in response to mid-winter warming events. Our results suggest that greater freezing tolerance and deacclimation resistance are associated with expression of genes involved in transcription, ice inhibition, and fructan synthesis.

P39
Effects of OrgDNA to Genes in 34 Different Plant Species

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Endosymbiosis is an ongoing process that has been quantified recently using experimental approaches. Up to now the effect that organelle DNA (orgDNA) has to the nuclear genome is largely unknown. There is a hypothesis that orgDNA might be involved in the creation of new genes. Once the orgDNA is integrated to the nucleous is name nuclear organelle DNA (norgDNA), recent studies supported with experimental data demonstrated that newly functional genes could be created by the incorporation of orgDNA into existing genes. In this study we have used a systematic approach to study the effect of orgDNA in the genomes of 34 different plants. We have identified many genes affected positively by orgDNA by comparing closely related orthologous genes. We found that most of the norgDNA is located to introns and 3' UTR regions of genes. We have validated whether those genes are functional using two methods: 1) Finding homolog genes in other species that do or do not have the norgDNA insertion into their structure 2) By finding expression data for those specific genes. In this presentation we will be presenting our findings.

P40

Establishment of an Efficient Transient Seedling Transformation Protocol for *C. roseus*

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The medicinal plant *Catharanthus roseus* produces terpenoid indole alkaloids (TIAs) of great importance. The two key TIAs, vinblastine and vincristine, are commonly used as anti-cancer drugs. However, vinblastine and vincristine are only produced at a very low level (0.0001 – 0.001% by weight) and costs ~$4 - $20 million/kg. The expression of TIA pathway genes is tightly regulated and understanding this regulation would lead to strategies for improving TIA production. Studying gene function in *C. roseus* is limited by the availability of certain tools. The development of stable hairy root lines is a commonly used method, but the establishment of a transgenic line requires 4 to 6 months. Furthermore, processes which are specific to photosynthetic active tissue cannot be studied in hairy roots. The development of a transgenic plant is labor intensive, inefficient, and difficult. Therefore, transient methods are the preferred choice for evaluating gene function. Virus induced gene silencing can be used to knock down genes of interest but overexpressing genes of interest by Agrobacterium infiltration into *C. roseus* leaves results in only low transformation efficiencies. Here we present an efficient and reliable Agrobacterium-based transient seedling transformation protocol for evaluating gene function in *C. roseus*. We systematically optimized the infiltration method (vacuum versus syringe-infiltration), age of the seedlings, OD of *A. tumefaciens*, and the best time point for tissue collection to improve seedling transformation. Further optimization and methods for normalization of transgene expression will also be explored. Our findings are on the way to establish an efficient and reliable seedlings transformation protocol, which can be used to functionally test the overexpression of genes, study promoter function in leaf tissue and further applications.

P41

Investigating Sorghum Bicolor Physiology in the Conditions of the Central Plateau Region of Haiti

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The objective of the experiment was to find a plant that could not only act as a food source for the people of Haiti, but could also provide financial stability by selling the yield of the plant. The group decided to test Sorghum bicolor because of its many uses and nutritional value. To test if Sorghum would survive the environmental conditions of Haiti, plants were placed in a chamber that was held constant at 36.7° C during the day and then would drop to 26°C at night. The plants were also watered with 185ml of water daily to determine if they would do well with substantial amounts of water. The results show there were not many statistically significant differences, and the test plants were like the control plants. With these results, it can be concluded that Sorghum bicolor would be able to survive in the harsh environmental conditions of Haiti.

P42

Investigation of Agrobacterium-mediated Stable Transformation Methods for *Catharanthus roseus*

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Catharanthus roseus is a medicinal plant which produces biologically active alkaloid compounds known as terpenoid indole alkaloids (TIAs). Two of these, vincristine and vinblastine, are effective chemotherapeutics for various cancers, including leukemias and lymphomas. However, the low yield of these compounds extracted from grown *C. roseus* leads to high prices and limits the medical impact of these chemotherapeutics. Various groups are studying the TIA metabolic pathway by which vinblastine and vincristine are produced in the hopes of understanding the regulation of the pathway and eventually using metabolic engineering to increase the production of the alkaloid chemotherapeutics. The work of these groups has been hindered by the lack of adequate genetic transformation protocols for *C. roseus*. The work reported here is to evaluate and develop effective Agrobacterium-based transformation methods for *C. roseus*. Two main approaches were investigated: 1) the traditional approach of callus induction, transformation of callus by Agrobacterium, and subsequent regeneration; and 2) Agrobacterium-mediated transformation of seeds and embryos to generate transgenic seedlings without requiring regeneration. Seed and seedling based Agrobacterium transformation was attempted with sonication and vacuum infiltration of seeds, and liquid co-culture of Agrobacterium and germinating seeds of *C. roseus*. In the callus regeneration investigation, callus lines were stably and efficiently transformed by Agrobacterium but the efficiency of generating shoots from calli was limiting. In the Agrobacterium-seed infiltration investigation, consistent transient transformation efficiencies of >20% occurred but no transformation of the meristematic tissue necessary to achieve whole plant transformation was shown. Co-culture of germinating seedlings with Agrobacterium showed some meristematic transformation and greatly improved the basal transformation rate compared to the seed infiltration approach. The goal of our research is to further develop this methodology for generating whole transgenic plants.

P43

Translocation along the TAT Pathway

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The Twin Arginine Translocase (TAT) translocates folded proteins across the thylakoid membrane of the chloroplast utilizing a Proton Motive Force (PMF) as its only energy source. The translocon consists of only three proteins: Tha4, Hcf106, and TatC. Tha4 and Hcf106 are structurally similar and composed of an N-terminal transmembrane domain embedded in the membrane, a hinge, an amphipathic helix domain that lies along the surface of the membrane, and an unstructured C-terminal domain. TatC has six transmembrane domains and both termini face the stroma. The PMF thins the thylakoid membrane. The mechanism for TAT transport is poorly understood. Here, we make use of Cell Penetrating Peptides (CPP) to simulate the thinning activity of the PMF. We find that CPPs stimulate translocation across the TAT pathway.

P44

Characterization of Rice Plasma Membrane Intrinsic Protein Ospip1;3, Ospip2;7, and Their Roles in Arsenic and Boron Transport in Rice Plants.

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Aquaporins (AQPs) are integral membrane channel proteins with major roles in tranporting water and small solutes. Plant aquaporins are divided into four major subfamilies: plasma membrane intrinsic proteins (PIPs), NOD26-like intrinsic proteins (NIPs), tonoplast intrinsic proteins (TIPs), and small basic intrinsic proteins (SIPs). Members of AQPs are implicated in metalloids transporting into the plant. Metalloids are the elements with physical and chemical characteristics that are intermediate between metals and non-metals such as arsenic (As) and boron (B). Arsenic is a highly toxic element which classified as a group I carcinogen for humans. Unlike As, plants need B for many biological processes, but exceeded levels cause toxicity and significantly decrease the yield. Few studies on the role of PIP members and their engagement in transporting metalloids have been done. Previously, we have studied some of the rice (*Oryza sativa*) PIPs through overexpression of four PIPs (OsPIP1;3, OsPIP2;4; OsPIP2;6 and OsPIP2;7) members into Arabidopsis. Transgenic Arabidopsis lines showed strong tolerance to elevated concentration of arsenite (AsIII) and B, without significant accumulation compared to wildtype plants. Further, to understand the *in-planta* function of these OsPIPs in rice, we used RNAi approach to knockdown the expression of OsPIP1;3 and OsPIP2;6. RNAi lines showed a significant reduction in OsPIP1;3 and OsPIP2;6 mRNA transcripts. Seeds of T3 Homozygous lines were raised, and further analysis of these RNAi lines for metalloid transport and tolerance is in progress. We are also interested in characterizing the members of Arabidopsis PIPs for metalloids transport and potentially their role in drought and salt tolerance. Preliminary data for PIP 1A T-DNA mutants in Arabidopsis showed promising phenotypes under different concentration of As and B compared to the WT plants. PIP1a TDNA mutants showed strong sensitivity to As(III) and NaCl compared to WT plants. The qPCR analysis showed that AtPIP1A gene is regulated under Absecic acid treatments. These finding may point to the role played by PIP 1A in tolerating abiotic stresses.

In this research, the exact *in-planta* role of candidate OsPIP members in metalloids transport and tolerance will be investigated in rice at the molecular and biochemical levels through the application of RNA-Seq, metabolome profiling, and genome editing CRISPR/Cas9 tools. Further, As and B influx and efflux assays will be performed on the generated transgenic lines to investigate the involvement of these transporters in transport, translocate, and sequester of As and B, thus reducing their toxicity to rice plants. Additionally, we will overexpress these PIPs in rice and wheat for improved As and B tolerance, enabling these important food crops to grow on high As and B affected soils.

P45

Can Parsnip Plants (*Pastinaca sativa*) and Carrot Plants (*Daucus carota*) Regenerate Shoots from Cultured Callus Cells in Mixed Co-cultures?

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Plant tissue culture techniques can be used to culture plant cells. The presence or absence of plant hormones in the medium can induce regeneration of embryos, or shoots and roots from callus cells. In this study, carrot cells were cultured on B5 agar medium containing 1 mg/l of the auxin 2,4-dichlorophenoxyacetic acid (2,4-D). Transfer to medium lacking 2,4-D induced the formation of carrot shoots and roots from carrot callus. B5 medium with 2,4-D was also used to grow callus of parsnip. Various different plant hormone combinations were tried unsuccessfully to regenerate the parsnip plants from callus, thus, the formation of shoots was more difficult than with carrot cultures. Parsnip plants were finally regenerated from a mixed culture on agar medium lacking 2,4-D where plants were also regenerating from carrot cells at the same time. Shoots from parsnip and carrot were distinguished by the variation in leaf morphology. This preliminary study suggests a co-culture method to regenerate shoots from parsnip callus that does not rely on treatments with the addition of synthetic plant hormones. Did the presence of the regenerating carrot tissues stimulate the regeneration of the parsnip shoots? This study is continuing in order to test this hypothesis.

P46

Pollen movement between introduced and endemic coastal plants in the genus Scaevola in Puerto Rico

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The aim of this study was to determine if *Scaevola taccada* (ST), a recently introduced coastal species, is stealing pollinators from an endemic congener S. plumieri (SP) in Puerto Rico. The genus Scaevola originates from Australia and has since radiated to many regions globally, as the seeds are easily dispersed by birds and ocean currents. ST was dispersed to Indonesia, many Pacific islands, and the eastern coasts of Africa, but did not make it to the Caribbean naturally. SP on the other hand, made it to Africa and then crossed the Atlantic and naturalized in the Caribbean islands. We wanted to understand pollination interactions between the two species to determine if ST will have long-term negative or positive impacts on the fertilization of SP flowers by attracting or distracting pollinators from endemic SP plants. To study this interaction, we measured pollen crossover events from pollen samples collected from open flowers of both species from plants that were growing in close proximity to each other. We compared these measurements to pollen standards that were collected from closed flowers from the same individuals. We found ST pollen on SP flowers, but we did not find SP pollen on ST flowers. These findings suggest that either pollinators visiting SP flowers did not need additional supplemental nutrients from ST flowers, or there were so few SP flowers per plant compared to ST plants, that the probability of finding SP pollen on an ST flower would be a much rarer event. Pollinator visitation rate was also measured in the field on both species and we found that the visitation rate is higher for ST plants compared to SP plants.

P47

Using Molecular Genetics to Study the Role of CYP72A Enzymes in *Zea mays* Stress Response

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Abiotic and biotic stresses affect every plant differently, and as a result the plants can defend themselves using either physical or chemical, indirect or direct and induced or constitutive responses. Here, *Zea mays* was used to study induced chemical responses by studying the role of cytochrome P450 (CYP450) enzymes, specifically the CYP72A subfamily, in relation to caterpillar herbivory. We screened Ac/Ds transposon mutants for insertions in any of five CYP72A genes that are induced by insect attack. The mutants help us test the hypothesis that CYP72A enzymes produce metabolites needed for defense. Upon completing the necessary PCR for finding good stable mutants, the plants were exposed to *Spodoptera exigua*, beet armyworm, or *Spodoptera frugiperda*, fall armyworm, herbivory. Mutations in CYP72A6, also known as Ds 436, and CYP72A349, also known as Ds 309, were found and used for phenotypic experiments in relation to the W22 wildtype plants. Two feeding experiments were conducted allowing *S. exigua* to feed on Ds 436 and W22 plants for 24 hours and Ds 436, Ds 309 and W22 plants for 1 week. Metabolic profiling was done to determine chemical differences between W22 and mutant plants. A choice experiment was conducted to give *S. exigua* and *S. frugiperda* a choice of food among Ds 436, Ds 309 and wildtype plants. All of these experiments suggest that both species prefer mutant plants over W22 plants. This could be because the mutant plants produce less defense chemicals than W22 wildtype plants due to the Ds insertion that affected the metabolic profile of these plants. Overall, this work helps us to explore subtle chemical shifts that help plants survive under environmental stresses.

P48

Analysis of Protein-protein Interaction Profiles of Maize MADS-box Evolutionary Variants

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The regulatory network that controls floral development is complex, and still is not completely understood, especially in monocots. MADS-box transcription factors are important regulators specifying floral organ identity, and interactions between themselves and with other proteins are critical for DNA-binding. Grass B-class MADS-box differ in their protein–protein interaction profiles, and such differences might have profound effects in floral morphology and evolution. B-class proteins APETALA3 (AP3) and PISTILLATA (PI) of most species bind DNA as obligate heterodimers with one another, but interestingly, both homo and heterodimerization occurs particularly in monocots. We are using the maize PI ortholog STERILE TASSEL SILKY EAR1 (STS1) and evolutionary variants of STS1 to determine the mechanistic basis of the altered protein complexes of differential dimerization, both in planta and in vitro. Tassel samples from sts1 mutant and sts1 complemented with STS1-YFP heterodimer and with homodimer version are being compared by complex immunoprecipitation (IP) and quantitative proteomics. BiFC and gel shifts also will help to confirm interactions. Our results show interesting candidates in the STS1 complex, like B-class proteins and chromatin remodeling factors. IP of STS1 forming obligate heterodimers is being carried out. Comparison of proteins in the different complexes will help to identify differential interactions in the evolutionary variants. All together, our experiments will reveal the consequences of shifting protein-protein interactions to gene regulatory evolution, a fundamental, but poorly understood evolutionary process.

P49

Characterizing Genes Involved in Glutathione Homeostasis for Improving Tolerance to Multiple Abiotic Stresses in Plants

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Plants have various mechanism to adjust to abiotic stresses and one such pathway is glutathione (GSH) homeostasis. Glutathione, an antioxidant produced in the cells of both plants and animals, is a tripeptide made from cysteine, glycine, and glutamate via peptide linkages. It plays a vital role in the survival of the cell by protecting it from the action of reactive oxidative species (ROS) like free radicals, peroxides, lipid peroxides and in dealing with xenobiotics like heavy metals and pesticides. A steady level of GSH is maintained in the cell via glutathione homeostasis, the process of synthesis of glutathione, degradation, and recycling of its component amino acids via γ-glutamyl cycle**.** Previous studies using knockout t-DNA mutant and overexpression(OE) lines of GGCT2;1, a ChaC like Protein, in Arabidopsis proved the role of this pathway in increasing tolerance to heavy metals like arsenic and cadmium along with other abiotic and hormonal stresses. q-PCR studies showed a significant increase in expression level of GGCT2;1 under arsenic and cadmium. Heterologous expression of GGCT2;1 also established the direct relation of GGCT in GSH synthesis and thiol-reactive arsenic uptake**.** Both GGCT2;1 OE and t-DNA mutants lines showed increased biomass under heavy metal stresses. While t-DNA lines exhibited higher GSH synthesis by increased nitrogen uptake, OE lines had similar growth via glutamate recycling, therefore, suggesting a role in nitrogen use efficiency(NUE). Moving forward, our preliminary work in q-PCR analysis of the t-DNA mutants of paralog of GGCTs, GGCT1 and GGCT2;2, and leucyl aminopeptidase (LAP), another enzyme which breaks the peptide bond between cysteine and glycine, showed a strong upregulation of mRNA transcripts under arsenic and mercury stress. Further, the characterization of oxoprolinase (OXP1), which recycles the oxoproline, a precursor of glutamate, is also in progress.

Currently, we are working on fully characterizing the role of all the genes involved in GSH homeostasis by analyzing the phenotypic and differential expression of Arabidopsis t-DNA and overexpression lines under various abiotic stresses. Along with uncovering the layers of basic science involved in this, we are also translating this knowledge into commercial crops such as soybean and canola for improving productivity via enhanced tolerance to various abiotic stresses.

P50

Impacts of Elevated CO2 on Cassava Leaf Anatomy

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Carbon Dioxide is one ofthe main components that any kind of plant needs in order to fully grow and function properly. In this research, we wanted to determine how elevated CO2 impacts leaf growth and function in a variety of Manihot esculenta (Cassava) cultivars relative to cultivars grown in ambient CO2. The difference in leaf thickness, cell number and size, vein spacing, as well as the number and size of laticifers (specialized latex-producing organelle) will be compared. This study will help us determine how elevated CO2 will affect Cassava plants.

P51

Does WALL REGULATOR INTERACTING bHLH Modulate Biosynthesis of the Secondary Cell Wall in Response to Environmental Cues

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The plant secondary cell wall is a major component of plant biomass, and a key determinant of certain crop and bioproduct yields. WALL REGULATOR INTERACTING bHLH (WRIB) is a Brachypodium distachyon basic helix-loop-helix transcription factor implicated in the regulation of secondary cell wall biosynthesis. Phylogenetic analysis suggests WRIB is an ortholog of AtPIF7, a phytochrome interacting bHLH protein involved in light signaling and shade avoidance. In yeast, WRIB is capable of binding the promoters of several secondary cell wall biosynthetic genes, including BdCESA7, a secondary cell wall cellulose synthase and BdCAD, which is involved the production of monolignols through the phenylpropanoid pathway. Yeast two-hybrid assays show that WRIB participates in protein-protein interactions with several characterized cell wall transcription factors, as well as the Red/Far Red light sensor PHYB. At the transcript level, WRIB expression is strongly upregulated by a nighttime reduction in temperature, and this effect is independent of light conditions. In light of this thermoregulation, the observed interaction between WRIB and PHYB, and an emerging body of evidence that PHYB functions as a plant thermosensor, here we describe approaches to further characterize light and temperature effects on secondary cell wall deposition in Brachypodium, and identify a putative role for WRIB in modulating these responses.

P52

Synergistic Insecticidal Activity of Hvt-lectin Provides Protection to Plants Against Hemipteran and Lepidopteran Insects

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The development of advanced biotechnological control strategies opens a new era of environmentally friendly pest management. The current study is part of such an effort, in which we developed a control strategy based on gene pyramiding that confers resistance against both lepidopteran (Helicoverpa armigera and Spodoptera litura) and hemipteran (Myzus persicae, Phenacoccus solenopsis, and Bemisia tabaci) insect pests. Recently we reported a double gene construct consisting of Hadronyche versuta (Blue Mountains funnel-web spider) neurotoxin and Allium sativum (onion) leaf lectin (hvt-lectin) that is expressed in tobacco (Nicotiana tabacum) plants under a phloem-specific promoter and confers resistance against hemipteran insects. Here we have extended our studies by evaluating an advanced generation of these tobacco plants expressing hvt-lectin against lepidopteran insects. Tobacco plants expressing both toxins were tested against H. armigera and S. litura. Insect bioassay results showed 100% mortality of H. armigera within 48-72 hours and 100% mortality of S. litura within 72-96 hours. Our results suggest the use of both toxins as part of a gene pyramiding strategy for controlling both lepidopteran and hemipterans insects on a commercial basis to reduce use of chemical pesticides.

P53

Cloning of an Allium sativum leaf agglutinin gene under constitutive and phloem specific promoters to provide resistance against sap sucking insect pests

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Agricultural productivity losses by insect pests have been estimated to be 10-20% globally. Herbivorous insect pests include both chewing and sap sucking insect pests. Whiteflies (Bemisia tabaci), jassids (Amrasca devastans), thrips (Thrips tabaci), and aphids (Aphis gossypii) are destructive sap sucking insect pests that can cause up to 50% reduction in crop productivity. Different approaches, including the use of agro-chemicals, bio-pesticides, conventional breeding, and biotechnology, have been employed for the protection of crop plants from insect pests. Although, with the advent of genetic engineering, Bacillus thuringiensis (Bt) genes have been used extensively to develop insect resistant crops, they do not target sap sucking insect pests. Engineering plants with plant derived insect resistance genes is a promising approach to control sap sucking insect pests. Important insect resistance genes that have been characterized in various plant insect pest systems include lectins, R-genes, inhibitors of insect digestive enzymes, proteases, amino acid deaminases, plant secondary metabolites (PSMs) and polyphenol oxidases.In the present research work, a plant derived insect resistance gene, Allium sativum leaf agglutinin (ASAL) was isolated and cloned under constitutive (35S) and phloem specific promoter (rolC) in a binary vector (pGA482). Cloning transgenes under a phloem specific promoter is a novel and promising approach to controlling sap sucking insect pests. Phloem specific expression may provide better protection against sap sucking insects, and using transgenes with a plant origin is environmentally friendly it will also lessen the biosafety concerns.

P54

Variable Phenotypes of Arabidopsis thaliana Ecotypes in Response to Pathogenic Fusarium oxysporum

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Arabidopsis thaliana is a small flowering plant commonly used in plant biology research, mainly due to its easy and fast growing nature, as well as its well-mapped genome allowing locus-specific functionality. There are over 750 natural accessions (or ecotypes) of Arabidopsis thaliana, with the Columbia (Col-0) and Landsberg erecta (Ler) lines being the most commonly used in lab work. Other ecotypes, however, may possess properties that are useful for specific lines of research, such as plant pathogen research and stress research. Fusarium oxysporum is a common soil-borne ascomycete with many genetically diverse strains, some of which are pathogens. In plants, these pathogens induce vascular wilting and necrosis, ultimately causing the death of the plant host. For this project, a survey of 4 ecotypes were utilized for comparison to assess difference in susceptibility by examining biomass and disease score results when inoculated with a pathogenic and non-pathogenic strain of Fusarium oxysporum over the course of 2 weeks. There were statistically significant signs of susceptibility found in Sg-1 and indications of resistance in Per-1 when compared to Col-0 as a baseline. These differences indicate that other ecotypes may be significantly different in their disease and stress responses, and further investigation of these and other ecotypes may be useful for understanding how slight genetic differences can influence large variations in functionality and phenotype.

P55

Designing and Testing Efficient Promoters for Enhanced Molecular Farming of Life Saving Therapeutics in Plants

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We have developed few efficient chimeric/hybrid promoters namely FSgt-PFlt, PFlt-UAS-2X and MSgt-PFlt incorporating different important domains of Figwort Mosaic Virus sub-genomic transcript promoter (FSgt, -270 to -60), Mirabilis Mosaic Virus sub-genomic transcript promoter (MSgt, -306 to -125) and Peanut Chlorotic Streak Caulimovirus full-length transcript promoter (PFlt-, -353 to +24 and PFlt-UAS, -353 to -49). We demonstrated that these chimeric/hybrid promoters can drive the expression of reporter genes in different plant species including tobacco, Arabidopsis, petunia, tomato and spinach. On an average, the recombinant promoter showed 2-3 times stronger GUS activity when compared to the activity of the CaMV35S promoter. Whereas FSgt-PFlt, PFlt-UAS-2X and MSgt-PFlt promoters showed 3.0, 1.3 and 1.0 times stronger activities than the activity of the CaMV35S² (a modified version of the CaMV35S promoter with double enhancer domain) promoter, respectively, in Nicotiana tabacum. Furthermore, we confirmed that these chimeric promoters are inducible in the presence of salicylic acid (SA) and abscisic acid (ABA).

P56

Metabolic Engineering of Polyamines in Rice: Their Role in Drought and Salt Tolerance

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Abiotic stresses are important constraints on crop productivity. Paddy-grown rice is particularly susceptible to drought and salt stress, which have negative effects on carbon and nitrogen intake thus limiting plant growth and grain yield. Polyamines (PAs), mainly putrescine, spermidine, and spermine, are important molecules in plant metabolism and have been implicated in abiotic stress responses, both as protectors of plants from stress and preparing the plant for tolerance of stress. This has led to genetic manipulation of PA metabolism aimed at improving drought and salt tolerance in rice and several other crops. Prior to overexpressing PA biosynthetic genes in order to produce a multiple-stress-tolerant plant, we have profiled the response of a commercial rice variety to drought and salt stress in terms of changes in growth and PA content. We found that PAs may be involved in recovery from stress, but levels during stress appear to fluctuate widely. To minimize sampling errors, we also studied differences in PA contents among different parts of the long, morphologically heterogeneous rice leaf. The PA levels were significantly higher in the leaf blade than the sheath, which may have affected our abiotic stress results. Currently, we are using both whole in-vitro-grown plants and callus to study the effects of salinity and osmotically-induced water stress on changes in PAs, amino acids and total protein, etc. Together, the results will help us plan future strategies of transgenic rice plants with modified PA metabolism, which will ultimately increase scientific understanding of abiotic stress tolerance for plant improvement.

P57
Embryonic Callus Transformation of *Setaria viridis* (Green foxtail)

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Setaria viridis (green foxtail millet) is an emerging model plant which offers the combination of short stature and rapid life cycle with a close phylogenetic relationship with economically important crops such as sugar cane, wheat, and maize. During the last years, different transformation protocols for the green foxtail have been developed using Agrobacterium varying success. Agrobacterium-mediated transformation is particularly attractive because of its simplicity and well-established protocols to success. However, monocot plants offer the additional challenge of being hard to transform with Agrobacterium. In this project, the Agrobacterium-mediated transformation protocol by Martins et al. (2015) was used. However, MS medium, as called for in the protocol, was found not yield robust callus. Thus a study comparison of callus formation and plant regeneration on different growth media compositions was initiated.

P58
Membrane bound UDP-Glc:Sterol Glycosyltransferase (80B1) is required for positioning of SCRAMBLED receptor in Arabidopsis roots

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Sterols have been identified as major components of membrane lipids that are part of specialized membrane domains necessary for organizing events such as polar protein targeting and signal transduction in plants, fungi and animals. However, a common modification of sterols is the addition of sugar moieties via glycosylation abundantly found in plants. A physiological role for such diversification of sterols in plants is still unknown. Therefore, Arabidopsis plants deficient in UDP-Glucose:Sterol Glycosyltransferase gene, UGT80B1 were studied. Aberrant root hair patterning and reduction in number of root hairs in ugt80B1 plant roots was observed. Patterning of hair cells (H-cells, trichoblasts) and non-hair cells (N-cells, atrichoblasts) in the epidermis of Arabidopsis root involves signaling through SCRAMBLED (SCM), a plasma membrane localized leucine-rich repeat receptor-like (LRR-RL) kinase which is a positive regulator of H-cell. SCM-GFP was mislocalized to the cytoplasm of ugt80B1 in a cell-type independent manner instead of H-cell plasma membrane; explaining the reduction in root hairs in ugt80b1. Feedback regulation via the transcriptional regulatory complex containing R2R3-MYB transcription factor WEREWOLF (WER) represses SCM and activates the homeodomain-leucine-zipper protein GLABRA2 (GL2) in N-cells. Both WER::GFP and GL2::GUS were expressed in ugt80B1 in a cell-type independent manner. Moreover, sterol glucoside profiling in ugt80B1 roots reveal a significant deficiency in stigmasteryl glucoside. Thus, suggesting that deficiency in specific sterol glucosides disrupt cellular patterning and development and may have a role in plasma membrane targeting of specific proteins.

P59

Survival of Sporangia of the Basil Downy Mildew Pathogen Peronospora belbahrii

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Peronospora belbahrii causes downy mildew of sweet basil (*Ocimum basilicum*), threatening production in both field and greenhouse settings. In greenhouse production, destruction of an infected crop following a disease outbreak is recommended to reduce further infection. However, infective sporangia may endure on greenhouse benches, potting materials, and other surfaces. It is also hypothesized that sporangia can persist as a source of inoculum within seed lots. The pathogen requires extended periods of high relative humidity (RH) and leaf wetness to complete its infection cycle and no known resting spore stage is produced by the pathogen in North America. This study aims to define a timeframe of *P. belbahrii* sporangia survival under pathogen-optimal conditions. Two approaches were used to evaluate the long-term viability of *P. belbahrii* sporangia: an in vitro assay to assess germination following release, and a plant infection bioassay to determine infectivity. Sporangia were isolated from plants and stored for 24 hour intervals in 20 and 25°C temperatures and 84% and 96.5% RH in all pairwise comparisons. Significant reductions in germination in vitro were observed after 24 hours, and reduction of disease incidence was significant after 48 hours across all treatments. While relative humidity significantly affected survival of sporangia, no significant difference was observed between 20 and 25°C. Germination of sporangia and plant infection reached 0% after 13 days when kept at 96.5% RH and 8 days while at 84% RH. We recommend a safe re-entry interval of 8-13 days to resume basil production in a greenhouse following an epidemic during periods of high ambient RH. *P. belbahrii* survival in seed lots for extended periods of time would depend on an unidentified dormancy mechanism, and will require further investigation for development of effective control.

P60

Tropical Sunn Hemp in a Temperate Region for Animal and Vegetable Production Systems

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The tropical annual *Crotalaria junce*, or Sunn Hemp (SH), is globally coveted for its multi-purpose use as a nitrogen source, rapid biomass production, and forage potential. In temperate climates, SH also behaves as a rare summer cover crop. However, little research in the US has prepared growers to include this novel crop in their production system, particularly in New England. Following three years of preliminary work, this study formally addresses date of planting (DOP) ,dry matter (DM) production, rate of growth, N-fixation, and suitability as forage. From 30-90 days after planting (DAP), plants were harvested every 10 days; harvest ceased after the first frost and winterkill. The effect of weeds on growth over time was assessed, as was cutting time, and feed and fertilizer composition as a factor of plant anatomy and age. From this - and most importantly -DOP and harvest date were shown to be of critical importance for this crop in accordance with its intended use for subsequent fertilizer or animal feed. We have also identified important pathogens of this crop, measured plant regrowth, and elicted regionally uncharacteristic seed production.

P61
AtGlsA/ZRF1 is Essential for Maintenance of Meristem Integrity by Regulating WUS

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Identification of genes involved in shoot apical meristem (SAM) formation and maintenance, has a huge potential for plant reproduction improvement. The SAM is formed during embryogenesis and contains a stem cell reservoir that gives rise to almost all aerial part of the plants. Recently we reported an Arabidopsis thaliana gene called gonidialess A (AtGlsA/ZRF1), which is important for maintenance of SAM integrity. We functionally characterized the two genes encoding GlsA/ZRF1 orthologs annotated in the A. thaliana genome. Expression patterns showed that AtGlsA/ZRF1 genes are strongly expressed in SAMs and RAMs. Double mutants showed stunted growth of aerial and root tissue, formation of multiple ectopic meristems and defects on cotyledons, leaves, and flowers. Developing embryos in double mutants showed multiple changes in morphology. Some of the embryos showed development of two apical meristems and the planes of the cell divisions were affected. Expression domain of the genes WUS, CLV3, STM and CUC was misregulated in double mutants, and lack of AtGlsA/ZRF1 expression was also associated with changes in localization of auxin and cytokinin. These results suggest that GlsA/ZRF1 is an essential component of the machinery that maintains the integrity of SAM and RAM since the establishment of the meristem. The next goal is to identify proteins physically interacting with AtGlsA/ZRF1, to can construct a network in which it works.

P62
Abiotic stress and expression analysis of S-Adenosylmethionine decarboxylase in Arabidopsis

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S-adenosylmethionine decarboxylase (SAMDC) is a key enzyme in the biosynthesis of polyamines spermidine and spermine, which play a variety of physiological roles in plants. This monofunctional enzyme that decarboxylates SAM to produce decarboxylated SAM (dcSAM), which is the substrate for biosynthesis of spermidine and spermine, is encoded by a five-gene family in Arabidopsis thaliana. In order to understand the tissue and organ specificity of the three of these genes, we used the approach of promoter::GUS (β-glucuronidase) fusion and fluorometric MUG assay to measure the enzyme activity of GUS under the control of AtSAMDC1(A;B), AtSAMDC2(A; B), AtSAMDC3(A,B,C;D), AtSAMDC4(A,B,C;D), and AtSAMDC5(A,B;C) promoters in response to various forms of abiotic stress. Three-week old in-vitro grown plants were treated with 100 mM NaCl or 300 mM sorbitol or 0.1 mM AlCl3 or 0.5 mM CdCl2 or low (4.5) pH or low temperature (4˚C) for 0 h, 24 h and 48 h before histochemical and fluorescence assay. The results show a higher GUS enzyme activity in response to 0.1mM AlCl3, 0.5mM CdCl2, and low temperature stress, with relatively less effect of salinity and low pH stress for all the types of genes, at the same time lesser enzyme activity in AtSAMDC1A & AtSAMDC5B compared to other three types of constructs.

P63
Functional genomics of Aronia fruit polyphenol biosynthesis

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Native to eastern regions in North America, the genus Aronia is a group of deciduous shrubs in the Rosaceae family, subtribe Pyrinae. Interest in Aronia fruit has increased because of their high levels of antioxidants and polyphenols and wide adaptability to various geographic regions with few disease and pest issues. Using Illumina RNA-seq, this study is investigating the transcriptome of Aronia fruit development to understand the molecular mechanisms involved with Aronia fruit polyphenol biosynthesis. Six accessions of *A. melanocarpa*, 2x (black fruit) and three accessions of *A. arbutifolia*, 4x (red fruit) were collected at four developmental stages. The anthocoyanin content of *A. melanocarpa* was significantly higher than *A. arbutifolia*, and anthocyanin content tended to increase at each developmental stage for both species. The total number of trimmed reads ranged from 11.1 to 17.3 million paired- end reads in 36 libraries. About 63 to 69% of the trimmed reads were aligned to the Malus × domestica genome v1.0. Compared with stage 0, a total of 871 differentially expressed genes (DEGs) were identified in stage 2 fruit of *A. melanocarpa*, with 296 of these genes significantly up-regulated and 575 down-regulated. *A. melanocarpa* compared with *A. arbutifolia* stage 2 fruit showed a total of 1440 DEGs. Three DEGs were selected as candidate genes in the flavonoid pathway, MYB11, MYB9, anthocyanin regulatory C1 protein-like, MYB108-like and MYB114-like. All five genes showed significant up-regulation between the four developmental stages. Future studies will focus on functional annotation of DEGs, gene validation and function of structural and regulatory genes in the polyphenol biosynthetic pathways.

P64
Exploiting Grass Flower Development: Understanding Awns

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USDA studies have ranked wheat third among U.S. field crops in planted acreage and production (Bond, & Liefert, 2017). Ability to exploit naturally occurring processes in grain development will allow for increased production per plant, leading to a decrease in required acreage, and increased projected profit per acre. Grass flowers are contained within specialized branching structures called spikelets. Many grass spikelets have a bristle on each of the outer sheathing leaves, called an awn. Awns contribute photosynthate to seeds in wheat and barley (Schrager-Lavelle *et al,* 2017). This function is difficult to explore in wheat and barley. Thus, we are using the model system *Brachypodium distachyon*, which is a close relative of wheat and barley. I performed experiments analyzing whether awns contribute to grain loading in *B. distachyon* and mapped the presence and function of awns within the Pooideae. I found that in a larger context, once awn function is understood, it may be manipulated to optimize floral development in grass crops. This may impact grain weight, seed nutritional content, and the number of seeds produced per plant. Globally, the optimization of grain production would have effects in every major nation due to grain consumption.

P65

Manipulation of Different Chemicals to Enhance Agrobacterium Infection Efficiency and Increase Shoot Regeneration of Juvenile Citrus

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Success in creating CRISPR-mediated transgenic or non-transgenic mutant plant production depends on two major factors: Agrobacterium infection and explants regeneration. Agrobacterium infection is the base of highly efficient transient and stable expression of deliveries. Here we have used epicotyls of young seedlings of citrus as explants to study the effects of different chemicals on Agrobacterium infection and shoot regeneration. First, we have observed that including sulfamethazine(SMZ), lipoic acid(LA), paclobutrazol(PAT) and IAA plus N-1-naphthylphthalamic acid (NPA) in co-culture medium individually during Agrobacterium transformation processes has enhanced Agrobacterium infection by 1.6-fold, 1.8-fold, 2.0-fold and 2.5-fold by GUS staining. The results also showed that shoot regeneration is increased when SMZ, LA and PAT applied individually. This study also demonstrated that transformation efficiency is increase from 6.7% to 17.1% when IAA and PAT were added in co-culture stage, and to 28.1% when IAA and SMZ were added in co-culture stage. Based on these and other results, we have developed experimental manipulations to enhance efficiencies of Agrobacterium infection and shoot regeneration of epicotyl cuttings of citrus.

P66

Examining the Role of Chemical Priming for Improved Drought Tolerance in Creeping Bentgrass

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In turfgrass management, priming agents are often used alone or mixed with other products to enhance plant health and reduce pesticide usage. Previous work has shown that pretreatment with primers can improve turf health under reduced irrigation. Two commonly used priming agents include petroleum-derived spray oils (PDSO) and acibenzolar-S-methyl (ASM), which are reported to activate induced systemic resistance and systemic acquired resistance in plants, respectively. However, little is known about the physiological benefits and cost associated with the continuous activation of these resistance pathways. The objectives of this study were (i) to determine the effects of priming agents on two differentially drought-resistant creeping bentgrass cultivars, and (ii) to evaluate the effects of PDSO and ASM on turf health in response to reduced irrigation. The experiment consisted of twelve treatments, including two irrigation levels (a well-watered control and a mild drought treatment that received 50% of the water relative to the control), two cultivars 'Penncross' (sensitive) and '007' (tolerant), and three priming treatments (Untreated, PDSO, and ASM). Plants were pretreated three times with either PDSO (5.1mL m-2) or ASM (1.4mg m-2) before reduced irrigation commenced, two additional treatments were made during reduced irrigation. Plants were maintained in a growth chamber at $20^{o}/15^{o}$C day/night temperatures with a 14-hour photoperiod. The experiment concluded at 49 days of reduced irrigation when significant reductions in plant health were observed. Weekly measurements included visual assessment of turf quality (TQ), volumetric soil moisture content (VWC), leaf relative water content (RWC), and chlorophyll content index (CCI). We observed that 007 exhibited higher TQ, RWC, and CCI compared to Penncross. Plants under reduced irrigation and primed with either PDSO or ASM had a higher TQ, RWC, and VWC compared to non-treated controls. Our results demonstrated that priming agents improved plant health under reduced irrigation, possibly by mitigating water loss.

P67

Cu Accumulation and Speciation in Castor-oil Plant (*Ricinus Communis* L.) in Response to the Cu Stress

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To restore polluted soil, phytoremediation was found to be a feasible approach to eliminate contaminant in an eco-friendly manner by plants uptaking, sequestering and detoxifying the pollutants. Seeking high biomass and fast-growing plants with hyepraccumulation and tolerance to heavy metals is the key to the success of phytoremediation. Castor-oil plant (*Ricinus communis* L.) from *Euphorbiaceae* family was discovered recently as a Cu-tolerant plant with wide application prospects in heavy metal remediation due to its massive biomass and likely endurability to poor soil. We investigated the response of castor-oil plant to various Cu concentrations in hydroponic system on biomass, photosynthetic pigments, amino acids contents, Cu accumulation, and Cu speciation with the X-Ray Near-Edge Spectroscopy (XANES). Our results showed that the castor-oil plant has a strong tolerance to Cu and there was no significant difference between the photosynthetic pigment contents of leaves up to 4mg/L Cu^{2+} treatments, however, the plant biomass and photosynthetic pigment levels decreased at concentrations of Cu^{2+} exposure above 4mg/L. Castor-oil plant could accumulate high concentrations of Cu, most of which was accumulated in the root. In response to the Cu stress, levels of free amino acids found in the leaves, phloem and root of castor-oil plant also varied. The result from XAFS analysis revealed that Cu in castor-oil plant was mainly associated with citrate and arginine in roots and leaves, but speciation of Cu in the stems was present mainly as CuO and Cu-GSH. Our findings showed that castor-oil plant could be effectively used for phytoremediation of Cu and seed oil will be used for biofuel production.

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