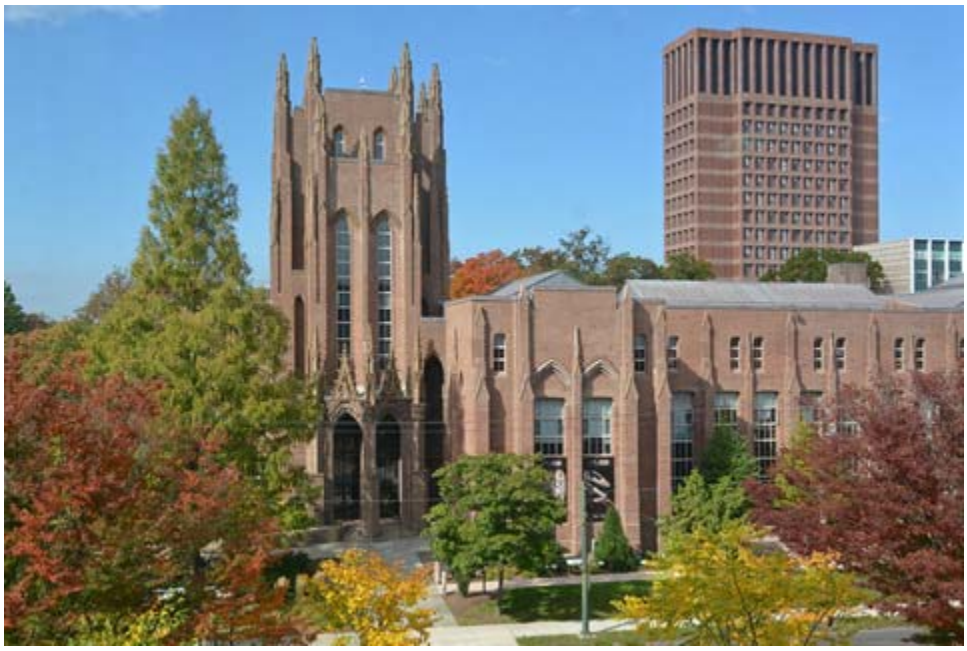
NEASPB 2017 | Northeast Regional American Society of Plant Biologists Conference

Yale University • New Haven, CT April 22-23, 2017

American Society of Plant Biologists

Cultivating a better future through plant biology research.

Yale University



Schedule and Abstract Book

NEASPB 2017 Northeast Regional American Society of Plant Biologists Conference

Yale University • New Haven, CT April 22-23, 2017

American Society of Plant Biologists

Cultivating a better future through plant biology research.

Yale University

Agenda

Saturday April 22, 2017

12:15-1:00	Registration	OML Lobby
1:00-1:15	Opening	OML 202
1:15-2:00	Keynote Speaker 1: Abby van den Berg Research Assistant Professor Department of Plant Biology Proctor Maple Research Center and University of Vermont	OML 202
2:00-2:45	Keynote Speaker 2: Miguel Pineros Research and Adjunct Professor Agricultural Research Service and School of Integrative Plant Science USDA and Cornell University	OML 202
2:45 – 3:15	Coffee Break	OML Lobby
3:15-3:30	You are invited to attend a group photo to support of the March for Science New Haven.	OML/Kroon Courtyard
3:30-4:15	Keynote Speaker 3: Vivian Irish Professor and Chair Molecular, Cellular and Developmental Biology Yale University	OML 202
4:15-5:00	Keynote Speaker 4: Carolyn W.T. Lee-Parsons Associate Professor Chemical Engineering & Chemistry and Chemical Biology Northeastern University	OML 202
5:00-5:15	Walk to the Peabody Museum	Sachem Street
5:15-9:00	Reception/Poster Session	Peabody Museum 1st floor
9:00	Executive Committee Meeting	OML 250

NEASPB 2017 Northeast Regional American Society of Plant Biologists Conference

Yale University • New Haven, CT April 22-23, 2017

American Society of Plant Biologists

Cultivating a better future through plant biology research.

Yale University

Sunday April 23, 2017

7:45-8:30	Continental Breakfast	OML Lobby
8:30-8:45	Speaker 1: Alexander Heyl, Adelphi University *Evolutionary Patterns in the Perception and Signal Transduction of Cytokinin*	OML 202
8:45-9:00	Speaker 2: Kathleen Hefferon, Cornell University *Plant Virus Nanoparticles: New Applications for Developing Countries*	OML 202
9:00-9:15	Speaker 3: Vijaykumar Veerappan, Eastern Connecticut State University *Forward Genetic Characterization of Tnt1 Mutants Defective in Nodule Development and Symbiotic Nitrogen Fixation in the Model Legume Medicago truncatula*	OML 202
9:15-9:30	Speaker 4: Saima Shahid, Pennsylvania State University *Examining mobile small RNAs exchanged between the parasitic plant dodder and its host*	OML 202
9:30-9:45	Speaker 5: Taylor Hoffman, SUNY at Old Westbury College *Affects of norgDNA into Cannabis genomes*	OML 202
9:45-10:00	Speaker 6: Allison Oakes, SUNY-ESF *The Return of the American Chestnut*	OML 202
10:00-10:30	NEASPB Business Meeting	OML 202
10:30-11:00	Coffee Break	OML Lobby
11:00-11:15	Speaker 7: Ellen Zelinsky, University of Massachusetts *On the Stability of Zonation in the Root Growth Zone*	OML 202
11:15-11:30	Speaker 8: Hesham Abdullah, University of Massachusetts Amherst *Comparative Transcriptome and Metabolome Analysis of Camelina sativa Transgenics Exhibiting Improved Seed and Oil Qualities*	OML 202
11:30-11:45	Speaker 9: Gabriella Angelini, University of New Hampshire *Protein Phosphatase 2A Regulates Root Response to Salt Stress in Arabidopsis thaliana via a Cytoskeleton-Dependent Mechanism*	OML 202

11:45-12:00	Speaker 10: Matthew Grasso, University of Vermont *Engineering Mechanically Tunable Microenvironments for Individual Plant Cells*	OML 202
12:00-12:15	Speaker 11: Jimi Miller, Yale University *A Novel Negative Regulatory Protein Mechanism to Maintain Immune Homeostasis*	OML 202
12:15-12:30	Speaker 12: Gonzalo Villarino, Yale University *Epigenetic Regulation of DNA Replication by Histone H3 Variants*	OML 202
12:30-12:45	Poster/Speaker Award Presentation and Book Raffle	OML 202
12:45	Adjourn	

NEASPB 2017 Northeast Regional American Society of Plant Biologists Conference

Yale University • New Haven, CT April 22-23, 2017

American Society of Plant Biologists

Cultivating a better future through plant biology research.

Yale University

Poster Session

Presenter	Organization	Poster Title
Chin-Mei Lee	Yale University	F-box decoys reveal the genetic and biochemical roles of plant E3 ubiquitin ligases in plant circadian clock
Harry Klein	University of Massachusetts Amherst	The rapunzel (rzl) Genes Regulate Growth Suppression in Maize Florets
Sydney O'Shaughnessy	Ithaca College	A Physiological Approach to Understand Invasiveness of Scaevola taccada in Coastal Habitats on the Islands of Puerto Rico
Ann Feke	Yale University	The ZTL Kelch-Repeat Domain is Involved in E3-ligase Dimerization and Substrate Recognition
Christopher Adamchek	Yale University	Circadian F-box Decoy Protein TLP2 Provides a Novel link to Endoreduplication and Cellular Expansion
Adriana Morales	Ithaca College	Population Genetics of Scaevola in the islands of Puerto Rico
Ahmed Ali	UMass Amherst	Characterization of Plasma Membrane Intrinsic Protein Members PIP1-3 and PIP2-6, and Its Roles in Arsenic and Boron Transport in Rice Plants
Alaaeldin Helaly	Stockbridge School of Agriculture - UMass Amherst	Phytochemical Analysis and Yield Characterization of Eight Cichorium intybus L. Landraces
Alaaeldin Helaly	Stockbridge School of Agriculture - UMass Amherst	Impact of Mycorrhizae and Polyethylene Mulching on Growth, Yield and Seed Oil Production of Bottle Gourd (Lagenaria siceraria)
Alaaeldin Abdallah	Stockbridge School of Agriculture - UMass Amherst	Enhancement Growth, Yield Production and Yield Quality of Kale Plants by Using Plant Growth Promoting Bacteria

NEASPB 2017 Northeast Regional American Society of Plant Biologists Conference

Yale University • New Haven, CT April 22-23, 2017

American Society of Plant Biologists

Cultivating a better future through plant biology research.

Yale University

Presenter	Organization	Poster Title
Sophie LaRochelle	SUNY Cobleskill	Development of a Nematode Resistance cultivar of Glycine max Via Agrobacterium-Mediated Transformation of the Cysteine Protease Inhibitor 1 Gene
Yao Chen	SUNY Cobleskill	Development of Drought and Salinity Tolerance cultivar of Panicum virgatum by Over Expressing SIZ1 E3 Ligase Gene
Wanlu Zeng	SUNY Cobleskill	Development of Drought and Stress Tolerant Switchgrass (Panicum virgatum L) Cultivar Via Agrobacterium-mediated Transformation of a Bacterial Choline Oxidase A Gene (CoxA)
Kai Yun	SUNY Cobleskill	Development of a Drought and Stress Tolerant Switchgrass (Panicum virgatum L.) Cultivar by Agrobacterium-Mediated Transformation of the InsP-5-Ptase Gene
Dhanasekaran Dharumadurai	Department of Microbiology Bharathidasan University	Diversity of Frankia from the actinorhizal plant Casuarina equisetifolia, South India
Adam Saffer	Yale University	Rhamnose-Containing Cell Wall Polymers Suppress Helical Plant Growth Independently of Microtubule Orientation
Analysa Frederick	State University of New York at Cobleskill	Over Expression of Valerophenone Synthase (VPS) in Humulus Lupulus (Hops) for Enhanced Lupulin Production
Chuan-Jie Zhang	University of Connecticut	Evaluation of Camelina species life histories for ecological risk assessment
Benoit Lacroix	Stony Brook University	T-DNA Transfer Mediated by Rhizobium etli and Regulation of its Virulence Genes
Navindra Tajeshwar	Adelphi University	Effect of Plant Hormone Cytokinin on Green Algae Choleochaete scutata
Trevor Donnelly	Merrimack College	The Impact of Silver Nanoparticles on Plant Physiological Responses
Xingxing Li	University of Rhode Island	Functional Analysis of Cellulose Synthase (CESA) Isoforms Provides Insight into the Composition of Cellulose Synthase Complexes (CSCs) in Physcomitrella patens
Alexis Grebenok	Canisius College	Determination of Sterol Species and Levels that Provide Localized Enhancement of Electron Transport Rates in Tobacco Thylakoid Membranes
Joshua Harkins	Canisius College	Cholesterol Oxidase Expressed in the ER of A. thaliana

NEASPB 2017 Northeast Regional American Society of Plant Biologists Conference

Yale University • New Haven, CT April 22-23, 2017

American Society of Plant Biologists

Cultivating a better future through plant biology research

Yale University

Presenter	Organization	Poster Title
Patrick Treffon	University of Massachusetts Amherst	Posttranslational Modification of Cysteines by Reactive Nitrogen Species - Linking S-nitrosoglutathione Reductase (GSNOR) to Redox Homeostasis
T. Page Owen	Connecticut College	Comparison of Nepenthes Nectary Glands at Three Locations
Maria Buanafina	Pennsylvania State University	The Impact of Reduced Cell Wall Feruloylation on Cell Wall Turnover and Plant Growth
Camille Martin	Northeastern University	Investigating the Transcriptional Regulation of Alkaloid Biosynthesis in Catharanthus roseus Hairy Root Cultures
Casey Lewicki	Pennsylvania State University	The impact of reduced cell wall feruloylation in flowering stems of Brachypodium distachyon
Lianna Wodzicki	Penn State University	Effect of Auxin Antagonist PEO-IAA on Aphid Feeding Behavior and Fecundity
Arielle Chaves	University of Rhode Island	Determinants of Cellulose Synthase (CESA) Class-Specific Function in Physcomitrella patens
Wei Liu	Yale University	Characterization of a Novel Circadian Clock Regulator in Arabidopsis
Wei Liu	Yale University	Characterization of a Novel Circadian Clock Regulator in Arabidopsis
Brenden Barco	Yale University	Evolution and Transcriptional Regulation of a Novel Secondary Metabolic Pathway in Arabidopsis thaliana
Samuel Breselge	Northeastern University	Effect of the Promoter on Long-term Expression Stability in Chlamydomonas reinhardtii
Ramis Saleem	Eastern Connecticut State University	Characterization of Medicago truncatula Mutants Defective in Symbiotic Nitrogen Fixation
Jie Dong	Yale University	Plant seedlings emerging from darkness into the light environment undergo photomorphogenesis.
Chandra Ganash	UMass Amherst	Expression analysis of three *Arabidopsis thaliana* S-adenosylmethionine decarboxylase genes in response to abiotic stress

NEASPB 2017 Northeast Regional American Society of Plant Biologists Conference
Yale University • New Haven, CT April 22-23, 2017

American Society of Plant Biologists
Cultivating a better future through plant biology research.
Yale University

Key Note Speakers

Sustainable tapping guidelines for modern maple sap collection practices

Abby van den Berg
Research Assistant Professor
Department of Plant Biology
Proctor Maple Research Center and University of Vermont

The profitability and long-term economic sustainability of maple syrup production depend entirely on the sustainability of annual sap extraction from trees. To help ensure their practices result in sustainable outcomes, maple producers follow tapping guidelines, a set of best practices including minimum tree diameter and dropline length, and maximum taphole width and depth. However, the amount of sap that can be extracted annually from trees for maple syrup production using current equipment and practices is more than double the typical yields achievable when current maple industry tapping guidelines were developed. To assess whether the existing tapping guidelines represent a sustainable approach when applied with these current "high-yield" practices, the growth rates of trees tapped with these practices at 18 sites in Vermont were measured, and a model that estimates the availability of conductive wood in the tapping zone of a tree over time was used to determine whether these growth rates were sufficient for the replenishment of conductive wood to remain at sustainable levels when following the current maple industry tapping guidelines. The basal area increments of healthy, codominant or dominant trees across the sites ranged from 1.8 in^2/yr in 10-in. diameter trees, to 3.5 in^2/yr in 18-in. diameter trees. Estimated minimum growth rates required ranged from 1.4 in^2/yr in 10-in. trees, to 2.6 in^2/yr in 18-in. trees. These results suggest that the growth rates of many trees tapped with high-yield sap collection practices are sufficient for this activity to remain sustainable when current tapping guidelines are followed. However, an average of 35% of sampled co-dominant and dominant trees, 38% of smaller-diameter (8.0-9.9-in dbh) trees, and between 50 and 82% of trees with intermediate or suppressed canopy position, had growth rates below the estimated minimums. This indicates that for some trees, tapping practices must be modified from those specified in the current guidelines in order ensure adequate replenishment of conductive wood is maintained. Likewise, this indicates that to be certain sustainable tapping practices are implemented, radial growth rates must be measured.

NEASPB 2017 Northeast Regional American Society of Plant Biologists Conference
Yale University • New Haven, CT April 22-23, 2017
American Society of Plant Biologists
Cultivating a better future through plant biology research.
Yale University

A Journey from Plant Physiology to Structure-Function Studies of Membrane Transporters Underlying Abiotic Stress Responses

Miguel Pineros
Research and Adjunct Professor
Agricultural Research Service and School of Integrative Plant Science
USDA and Cornell University

There is growing awareness that plant transporters play a central role in facilitating plant adaptation to adverse environments. For instance, some plants species overcome aluminum (Al) phytotoxicity by releasing organic acid anions (OA) from the root, which chelate and immobilize Al3+ ions in the rhizosphere. Al toxicity constitutes a major limitation to crop productivity in acid soils, which represent about half of the world's arable lands. Members of the ALMT (Al-activated malate transporter) and MATE (multidrug and toxic compound efflux) transporter families are the key transporters underlying the release of OA's in response to Al stress. My current research focuses on understanding how the structural features of these membrane proteins determine their functional characteristics (i.e. transport properties). We have integrated electrophysiological analysis with cellular imaging approaches to conduct a structure-function analysis aimed at determining the transporters' topology, stoichiometry, function and regulation. Although ALMT and MATE proteins underlie analogous Al resistance mechanisms, their structural and functional properties are very distinct. These studies are providing a new framework for understanding the function of plant transporters in the context of their roles in planta, with the ultimate goal of "engineering" their functional characteristics to enhance their ability to confer higher levels of Al resistance to crop plants grown on acid soils.

Development with a twist

Vivian Irish
Professor and Chair
Molecular, Cellular and Developmental Biology
Yale University

We are using the Arabidopsis petal as a simple, tractable, system for investigating the molecular mechanisms controlling plant organogenesis. Petal growth depends on a wave of cell divisions followed by cell expansion and differentiation. We have characterized the role of

RABBIT EARS (RBE), encoding a zinc finger transcriptional repressor, which is a master regulator of these processes. Using RNAseq approaches, we identified a number of genes regulated by RBE. Through these analyses, we have shown that RBE regulates primordium specification through modulating the expression of a family of transcription factors that are implicated in growth control. To explore the mechanisms by which petals differentiate, we identified a mutation that disrupts the patterning of petal epidermal cells. This mutation, which we call dairy queen, causes dramatic left-handed helical growth of petal epidermal cells, leading to twisted petals. The dairy queen mutation disrupts the RHM1 gene that encodes a UDP-L-rhamnose synthase; rhamnose is a major component of pectin, a major structural component of the cell wall. The rhm1 mutants display decreases in the levels of the pectic polysaccharide rhamnogalacturonan-I. rhm1 mutant roots also display left-handed helical growth and, unlike other mutants with a similar phenotype, rhm1 does not alter the orientation of microtubule arrays. Our findings reveal a novel source of left-handed growth in plants caused by changes in cell wall composition that is independent of microtubule orientation; we propose that an important function of rhamnogalacturonan-I is to suppress helical twisting of expanding plant cells. We suggest that many instances of helical growth in nature may be due to naturally occurring alterations in the levels or organization of cell wall components.

Engineering the Production of Medicinal Natural Products from Plant Tissue Cultures

Carolyn W.T. Lee-Parsons
Professor
Chemical Engineering Department
Chemistry & Chemical Biology Department
Northeastern University

Many plant-derived pharmaceuticals are currently supplied by extracting the plant material. Due to the slow growth rates or low product concentrations in plants, finding an alternative route for supplying these critical drugs is necessary. The overall vision of this research is to enhance the production of critical plant-derived pharmaceutical compounds through plant cell cultures, specifically using the production of terpenoid indole alkaloids (TIAs) from cultures of Catharanthus roseus as a model system. The C. roseus plant produces several highly valued pharmaceuticals, including the anti-cancer drugs vincristine and vinblastine. The high cost and need for these pharmaceuticals motivate this research to better understand their biosynthesis

and ultimately overproduce these compounds using C. roseus cultures. In this talk, I will present our research in exploring how TIA biosynthesis is regulated and how this knowledge leads to developing strategies for manipulating TIA production.

The plant hormone jasmonate (JA) is known to regulate TIA production by inducing the expression of the transcriptional activators ORCA and repressors ZCT, which bind to the promoter regions of TIA biosynthetic genes and regulate their expression. Our research shows that JA regulates TIA production in a dose-dependent manner by controlling the expression levels of Orca to Zct, which consequently alters the expression levels of the TIA biosynthetic genes. Interestingly, at high JA dosages, significantly elevated levels of Zct to Orca were induced and correlated with a repression in TIA biosynthesis. The repressing role of Zct was similarly observed in the literature where the overexpression of Orca in C. roseus cultures did not increase TIA biosynthesis but dramatically induced Zct expression.

We propose a model for the transcriptional control of TIA biosynthesis, which includes this feedback regulatory mechanism. In this proposed regulation, significantly elevated levels of ORCA proteins will induce the expression of Zct genes; hence attempts to increase the expression of TIA biosynthetic genes by ORCA will also activate an opposing response by inducing Zct genes, leading to the observed tight regulation of TIA biosynthesis. This hypothesized mechanism suggests that TIA biosynthesis could be enhanced by manipulating the expression levels of the transcriptional activators Orca to repressors Zct with JA dosage and RNA silencing. In this talk, I will present the outcome of this strategy and the next steps in understanding the regulation of TIA biosynthesis.

NEASPB 2017 Northeast Regional American Society of Plant Biologists Conference
Yale University • New Haven, CT April 22-23, 2017
American Society of Plant Biologists
Cultivating a better future through plant biology research.
Yale University

Oral Abstracts

Oral Presentation 1: Evolutionary Patterns in the Perception and Signal Transduction of Cytokinin

Alexander Heyl
Adelphi University, Garden City, NY

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. The ubiquitous distribution of the signaling molecule and the widespread use of the type of signaling system, combined with the fact that only plants use cytokinin and the two-component system as a signaling circuit, make the cytokinin signal transduction system an ideal model for the analysis of the evolution of signaling systems. To shed light on the origin and the evolutionary patterns of the members of this signaling system, a comprehensive domain-based phylogenetic study was conducted. This study revealed a more complex path for the evolution of this pathway than previously anticipated. Surprisingly, each of the four components of this signaling pathway showed individual evolutionary patterns. While the cytokinin receptors seemed to be the most conserved in terms of copy number, other members of this pathway seemed to be less constrained and thus evolved more freely. The results of this study will be discussed in the context of recent experimental findings in this research area.

Oral Presentation 2: Plant Virus Nanoparticles: New Applications for Developing Countries

Kathleen Hefferon
Cornell University, Trumansburg, NY

For over two decades now, plants have been explored for their potential to act as production platforms for biopharmaceuticals, such as vaccines and monoclonal antibodies. Without a doubt, the development of plant viruses as expression vectors for pharmaceutical production have played an integral role in the emergence of plants as inexpensive and facile systems for the generation of therapeutic proteins. More recently, plant viruses have been designed as non-toxic nanoparticles which can target a variety of cancers and thus empower the immune system to slow or even reverse tumor progression. The following presentation describes the employment of plant virus expression vectors for the treatment of some of the most

challenging diseases known today. The presentation concludes with a projection of the multiple avenues by which virus nanoparticles could impact developing countries.

Oral Presentation 3: Forward Genetic Characterization of Tnt1 Mutants Defective in Nodule Development and Symbiotic Nitrogen Fixation in the Model Legume Medicago truncatula

Vijaykumar Veerappan
Eastern Connecticut State University, Willimantic, CT

Legume plants establish symbiotic relationship with the soil bacteria rhizobia and form unique structures on the root 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 30 M. truncatula Tnt1 retrotransposon mutants by forward genetic screening during Medicago Tnt1 mutant screening workshop in the summer of 2016 organized by the Samuel Roberts Noble Foundation. A secondary screening is underway using aeroponic phenotyping system to confirm the defective nodule formation and SNF phenotypes. 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 expressing lac Z reporter) will be presented. To study the inheritance of the mutant phenotypes and also to generate BC1F2 population for linkage analysis of candidate Tnt1 insertions, mutants will be backcrossed into wild type R108 ecotype. We will mine the Medicago mutant database (http://medicago-mutant.noble.org/mutant/database.php) for the publicly available Tnt1 insertion flanking sequence tags and also will perform whole genome sequencing to recover additional Tnt1 insertions from the mutants. A combination of genomic, genetic and transgenic approaches will be used to identify the causal genes of the mutants defective in nodule development and SNF.

Oral Presentation 4: Examining mobile small RNAs exchanged between the parasitic plant dodder and its host

Saima Shahid
Penn State University, State College, PA

The obligate stem parasitic plant dodder (Cuscuta pentagona) invades a diverse range of dicotyledonous host plants using specialized feeding structures called haustoria. Besides nutrient and water uptake, haustoria also allow exchange of macromolecules and viruses

between dodder and its hosts. A large-scale transcriptomic study revealed that mRNA exchange through haustorial connections is bidirectional and involves thousands of different transcripts. Additionally, previous studies have shown that host-derived transgenic small RNAs can move across haustoria and silence dodder-specific genes. These results indicate that endogenous small RNAs such as microRNAs (miRNAs) may be also mobile between dodder and its host. To address this possibility, we generated small RNA-seq data from dodder-Arabidopsis associations. Our results show a striking predominance of 22 nt parasite miRNAs at the dodder-Arabidopsis interface. Most of these miRNAs were also detected in host tissue away from the point of haustorial connections. Additionally, several of these miRNAs triggered secondary small RNA production from at least six Arabidopsis mRNA targets. Examples of such targets include BIK1 (Botrytis Induced Kinase 1), an important player in plant immunity. Another target, SEOR1 (Sieve-Element-Occlusion-Related 1) encodes a protein thought to be involved in sealing phloem sieve elements after wounding. Furthermore, mRNAs encoding three auxin receptors, TIR1, AFB2, and AFB3 are targeted by a dodder miRNA and showed a unique pattern of secondary siRNA production in dodder-host interface. These data demonstrate that dodder-derived miRNAs target host mRNAs during parasitism, suggesting they may act as factors to enhance parasite fitness.

Oral Presentation 5: Affects of norgDNA into Cannabis genomes

Taylor Hoffman
SUNY at Old Westbury College, Old Westbury, NY

DNA transfer from the organelles to the nucleus is an ongoing process, observed in many species both in animal and plant kingdoms. It has been demonstrated that has impacts in functional areas of genomes, by being involved in the alternation of the coding proteins of pre-existing genes, or by being involved in the creation of new genes. It has also been detected to non-functional areas of the genome. The Cannabis species are of great importance since they are used in medicine and crosses of different species produce hybrids with more advantageous traits than the parental lines. The genome of the species is not yet well understood due to high divergence. In the current study we are using four different mitochondria and four different chloroplast genomes to search for nuclear organellar DNA insertions (norgDNA) into two variarities, the Cannabis sativa Purple Cash and the Cannabis sativa Finola genomes. In total 4.3Mb of DNA is inserted to the genomes out of which 10% is inserted to transcripts of Purple Cash and 16% to the transcripts of the Finnola. During our presentation, we will be demonstrating how genes are affected by norgDNA.

NEASPB 2017 Northeast Regional American Society of Plant Biologists Conference
Yale University • New Haven, CT April 22-23, 2017
American Society of Plant Biologists
Cultivating a better future through plant biology research.
Yale University

Oral Presentation 6: The Return of the American Chestnut

Allison Oakes
SUNY-ESF, Syracuse, NY

The American chestnut (Castanea dentata) was a keystone species of North America, making up over a quarter of the forests east of the Mississippi river. The arrival of Cryphonectria parasitica on Asian chestnut stock in the late 1800s introduced the chestnut blight to the continent, which devastated the chestnut population. The American Chestnut Research and Restoration Project has achieved pure American chestnuts able to withstand the chestnut blight chestnut by inserting the gene for oxalate oxidase into American chestnut embryos. The oxalate oxidase breaks down the oxalic acid secreted by Cryphonectria parasitica, the tree builds a wound periderm, and the infection is contained as merely a small, superficial canker instead of girdling and eventually killing the tree, allowing both organisms to live communally and reach reproductive maturity; presence of the transgene in resulting offspring also confers full blight resistance. As the American Chestnut Research and Restoration Project nears its goal of a publicly-available, fully blight resistant, performing environmental and safety testing and tree production is a top priority, and we will present our current findings on how non-target organisms may be affected by the inclusion of a novel transgene in American chestnut.

Oral Presentation 7: On the Stability of Zonation in the Root Growth Zone

Ellen Zelinsky
University of Massachusetts, Amherst, MA

The developing root is divided into three zones: meristem, elongation zone, and maturation zone. In a root growing under constant conditions, the sizes of these growth zones are stable even as cells move rapidly from one zone to the next. Here, we attempt to find what enforces this stability by analyzing the spatial distribution of velocity. On a horizontal microscope, we imaged a growing root over a three-hour interval and obtained velocity profiles every 5 minutes. The profiles were obtained from a pair of images, separated by 30 seconds, by using a computer-vision algorithm called Stripflow. For a given root, the 37 velocity profiles overlapped closely, indicating that the zonation is stable over the sampled interval. However, a significant time-dependent oscillation emerged from principal component analysis, which appears to reflect a periodic change in the position of the boundary between meristem and elongation zone. To determine whether the oscillation is intrinsic to the growth zone, we excised the shoot. Surprisingly, roots without shoots grow vigorously for several days. Excision converts the

oscillation to a linear change, consistent with sustained meristem shortening. Thus, the stability of root zonation appears to depend on material arriving from the shoot.

Oral Presentation 8: Comparative Transcriptome and Metabolome Analysis of Camelina sativa Transgenics Exhibiting Improved Seed and Oil Qualities

Hesham Abdullah
University of Massachusetts, Amherst, MA

Among the seed oil-producing crops, Camelina sativa has attracted much interest in the last few decades as an emerging oilseed crop dedicated for biofuel and biodiesel applications as well as a source for edible oils. Its unique seed and oil qualities attract the researchers to engineer new varieties exhibiting improved oil quantity and quality. The overexpression of enzymes that catalyze the synthesis of the glycerol backbone and the sequential conjugation of fatty acids into this backbone appear to be far more promising targets for increasing the triacylglycerols (TAG, the main lipids in seeds). In our previous study, we combined the overexpression of two genes involved in TAG metabolism under the control of seed-specific promoters. The transgenic plants exhibited a higher percentage seed oil content, a greater seed mass, and overall improved seed and oil yields, on a per plant basis, than either the non-transgenic wildtype (WT) or manipulation of each gene individually. However, in order to further increase seed oil content in Camelina, we utilize metabolites profiling, in conjugation with transcriptome profiling during seed development in order to reveal the rate-limiting step(s) in TAG metabolism. The whole seed-specific transcriptome of transgenic lines revealed the identification of approximately 1,566 and 2,102 transcripts were differentially regulated in Camelina transgenics. Many of these transcripts were involved in various functional categories and controlling several metabolic routes in lipid metabolism. Further, we quantified the relative contents of over 240 metabolites by using GC/MS and LC/MS/MS platforms. The results indicate major metabolic switches in transgenic seeds, which are associated with significant changes in the levels of glycerolipids, phospholipids, most amino acids, TCA cycle and glycolysis-related metabolites. Collectively, the integration of transcriptome and metabolome can be highly useful to understanding the regulation of TAG biosynthesis and identifying the bottlenecks in TAG pathways, providing a precise selection of candidate genes for generating Camelina varieties with improved seed and oil yields.

Oral Presentation 9: Protein Phosphatase 2A Regulates Root Response to Salt Stress in Arabidopsis thaliana via a Cytoskeleton-Dependent Mechanism

Gabriella Angelini
University of New Hampshire, Durham, NH

Protein phosphatase 2A (PP2A) is required for normal root responses when Arabidopsis thaliana is grown under salt stress. The roots of some PP2A mutants skew or curl rather than grow straight on NaCl-supplemented growth medium. Root skewing can be caused by cell file rotation due to root cells with irregular shapes. To determine if the root skewing phenotype of PP2A mutants is due to changes in cell shape, cell file rotation was measured. Roots of PP2A mutants grown on NaCl-supplemented medium exhibited more cell file rotation than wildtype seedlings, and the amount of cell file rotation was correlated with the degree of skewing or curling. Because changes in cell shape can be caused by alterations to the cytoskeleton, microtubules and microfilaments were investigated. Cortical microtubules are normally oriented transverse to the axis of growth. After immunodetection, microtubules in seedlings grown on NaCl-supplemented medium had a wider range of orientations than untreated seedlings and favored an oblique arrangement. These microtubule patterns were more pronounced in PP2A mutant seedlings grown on NaCl-supplemented medium than in wildtype seedlings, which correlated with non-rectangular cell shape and cell file rotation. To study microfilaments, wildtype seedlings exposed to salt stress were treated with the actin polymerization inhibitor, Latrunculin B (LatB). LatB-treated wildtype seedlings phenocopied the root skewing phenotype of PP2A mutant seedlings. Experiments are in progress to observe changes in bundling and distribution of microfilaments in seedlings with and without NaCl treatment.

Oral Presentation 10: Engineering Mechanically Tunable Microenvironments for Individual Plant Cells

Matthew Grasso
University of Vermont, Burlington, VT

Although the importance of mechanical cues in plant development is appreciated, the field currently lacks tools that allow researchers to influence single cell mechanics in a controlled way. A technology that allowed researchers to isolate mechanical variables during cell growth and differentiation could reveal mechanisms of developmental regulation that were previously inaccessible. Over the past decade considerable advances have been made in engineering hydrogel microcapsules to be used in biomedicine and biomedical engineering. However, the technologies developed in these fields have not found significant applications in plant studies. In this study, individual plant protoplasts from a BY-2 tobacco suspension culture were isolated and captured in microbeads of agarose using a fluidic microdroplet system. These cell-containing agarose microbeads were then further reinforced with polyelectrolyte shells. The layer-by-layer deposition of these polyelectrolyte shells makes them mechanically tunable. The shelled hydrogel microbeads yield a biocompatible environment with the potential to

mechanically regulate the growth and development of individual cells. This technology has the potential to facilitate novel studies in plant cell biomechanics.

Oral Presentation 11: A Novel Negative Regulatory Protein Mechanism to Maintain Immune Homeostasis

Jimi Miller
Yale University, New Haven, CT

Recognition of pathogen-derived molecules by pattern-recognition receptors (PRRs) that subsequently activate mitogen-activated protein kinase (MAPK) cascades are common features in both animal and plant innate immune systems. The activation and amplitude of innate immune responses must be tightly regulated. Therefore, plants have evolved mechanisms to fine-tune immune signaling to maintain immune homeostasis. Here, we report that recognition of bacterial flagellin by the Flagellin Sensitive 2 (FLS2) receptor activates a novel negative signaling pathway in Arabidopsis. This pathway involves the Gα subunits of heterotrimeric G-protein complexes and Gβ-like proteins, which function upstream of the MAPK cascade. Additionally, receptor for activated C kinase 1 (RACK1) functions as a scaffold that binds to the Gβ-like proteins and all three tiers of the MAPK cascade, thereby linking upstream G-protein signaling to downstream inhibition of an MAPK cascade. The FLS2-G-protein-RACK1-MAPK cascade modules identified in these studies are distinct from previously described plant immune signaling pathways. Previous studies show RACK1 functions to link upstream G-protein signaling to downstream activation of a MAPK cascade, in contrast to our findings. The discovery of the negative G-protein-mediated circuit in plant immune signaling provides an alternative mechanism to regulate PRR complexes in addition to pseudokinases.

Oral Presentation 12: Epigenetic Regulation of DNA Replication by Histone H3 Variants

Gonzalo Villarino
Yale University, New Haven, CT

In the nucleus of eukaryotic cells, DNA is organized around a complex of histone proteins. Histones can be chemically modified by chromatin-modifying proteins, and these modifications have been shown to affect gene expression, DNA repair, and DNA replication. Proper regulation of all these biological processes is essential in both humans and plants. In plants, defects in DNA repair and/or DNA replication impair genome stability and can result in reduced agricultural yield. Previous work from our lab has shown that the two conserved histone H3 variants H3.1

and H3.3 provide very different functional properties to chromatin in plants. We have shown that DNA replication is specifically regulated by a specific modification on the H3.1 variant. The chromatin-modifying enzymes ATXR5 and ATXR6 (ATXR5/6) exclusively monomethylate lysine 27 of histone H3.1 (H3.1K27me1), and mutations in the ATXR5/6 genes result in over-replication of heterochromatin. Our findings indicate that the heterochromatic over-replication phenotype in atxr5/6 mutants is caused by the unmethylated H3.1 variant (H3.1K27me0). In order to further understand how chromatin regulates DNA replication, we used a histone replacement strategy to investigate the relationship between the H3.1 variant and DNA replication. Using this strategy, we have identified other residues in H3.1 involved in regulating DNA replication in plants. Our findings provide novel and important mechanistic insights into the regulation of DNA replication in plants, and possibly, in human.

NEASPB 2017 | Northeast Regional American Society of Plant Biologists Conference

Yale University • New Haven, CT April 22-23, 2017

American Society of Plant Biologists

Cultivating a better future through plant biology research.

Yale University

Conference Supporters

BioChambers

PROVIDING GROWTH TO RESEARCH.

NEW ENGLAND BioLabs® Inc.

PERCIVAL

Yale PEABODY MUSEUM

Yale Plant Molecular Biology

Yale Combined Program in Biological and Biomedical Sciences

Special thanks to Sinauer Associates, Inc. Biology, Psychology, & Neuroscience • Publishers since 1969 for the books donated to the raffle.