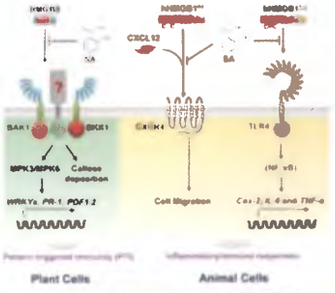
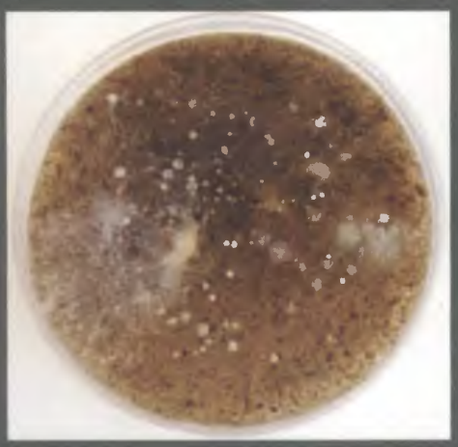
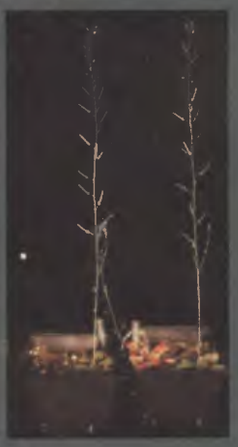
32nd Mid-Atlantic Plant Molecular Biology Society

August 18-19, 2015

Schematic of SA's mechanisms of inhibition of immune-related activities of HMGBs in plant and animal cells







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Lots of people provide the support and staffing for this meeting! Many thanks to all of them for the fine job they are doing.

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WELCOME

Welcome to the 32nd annual Mid Atlantic Plant Molecular Biology meeting. Thank you for coming!!! This year's meeting is dedicated to the memory of Dr. Leslie Wanner, who was our wonderful co-organizer for many years. Those of you who attended past MAPMBS meetings remember her warm, friendly personality, her sharp intellect, and generous spirit. I am sure she is here with us at this year's meeting.

We are delighted so many new and returning faces are here today, and we hope this meeting is a good way to share the excitement of new scientific thinking and resources and help all of us in keeping up-to-date in the ever-broadening world of ideas, tools and advances in the plant (molecular) biological sciences. We have an outstanding group of speakers for this year's meeting, and we hope this meeting will be stimulating for all of you.

Our intention for this meeting is to provide an accessible, affordable high quality (and short) meeting in the mid-Atlantic region in a small and informal atmosphere so that scientists at all levels from undergraduate and graduate students to researchers and scientists in industry, universities and government can meet and mingle. We therefore provide lunch and breaks at the meeting so each participant has the opportunity to meet invited speakers and presenters.

Many people are involved in the planning and organizing of this meeting (see the previous page), and we thank them all for their efforts in making this another successful and productive meeting. We especially wish to thank our sponsors, and the exhibitors who furnish us with up-to-date products and services, and help to defray the cost of the meeting.

We always welcome your participation, comments and suggestions. Also, if you are interested please join next year's organizing team and volunteer your services in planning next year's MAPMBS meeting. This meeting was initiated 32 years ago, and several folks have participated all 32 years. Several of us are nearing retirement, and we especially hope to encourage more of you younger participants to attend the business meeting (Tuesday right before lunch) and step up and play a role in continuing this MAPMBS tradition. All are welcome at any stage of the planning and organizing process!

We thank you for your continued support and participation in the Mid Atlantic Plant Molecular Biology Society. You can keep up with MAPMBS on our website:

www.mapmbs.com

Benjamin F. Matthews and John Hammond
Co-chairs

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2015 MAPMBS 32nd Annual Meeting Schedule

Tuesday, August 18, 2015

9:10 Registration and poster set-up
9:25 Welcome Ben Matthews and David Puthoff

Session I **Plant pathogen/ host interactions**
Moderators: Bret Cooper and Mark Tucker
USDA-ARS Soybean Genomics and Improvement Lab

9:30 Joonyup Kim
A functional study of root knot nematode IDA-like (IDL) peptide putatively secreted into the host plant.
Soybean Genomics and Improvement Lab, USDA-ARS, Beltsville MD

10:00 Olga Postnikova
Gene expression profiling of alfalfa (*Medicago sativa*) infected with root-knot nematode *Meloidogyne incognita*
Molecular Plant Pathology Lab, USDA-ARS, Beltsville MD

10:20 James Kilcrease
Elucidating plant pathogen interactions through correlative microscopic imaging.
Floral and Nursery Plants Research Unit, USDA-ARS, Beltsville MD

10:40-11:15 Coffee break: Posters and Exhibitors

11:15 Wei Wei
Phytoplasma induced reprogramming of plant stem cell destiny.
Molecular Plant Pathology Lab, USDA-ARS, Beltsville MD

11:45 Jeffrey Gardner
Systems biology approaches to understanding polysaccharide degradation at the plant-microbe interface
Dept. of Biological Sciences, University of Maryland-Baltimore County, Baltimore MD

12:15-1:30 Lunch break: Posters and Exhibitors

MAPMBS business meeting (Please attend if you want to get more involved in the planning and execution of this meeting)

1:30 Michelle Cilia
Aphids modulate Polerovirus transmission efficiency in a host-dependent manner
Boyce Thompson Institute for Plant Research and *Emerging pests and Pathogens Research Unit, USDA-ARS, Ithaca NY*

2:00 Kelly Elkins
"Legal high" plant species differentiation using a high resolution PCR melt assay
Chemistry Dept., Towson University, Towson MD

2:20-2:55 Coffee break: Posters and Exhibitors

2:55 Introduction of Keynote speaker: Bret Cooper
USDA-ARS Soybean Genomics and Improvement Lab

3:00 The Leslie Wanner Keynote address
Daniel Klessig
Salicylic acid and its binding proteins in plant and human health
Boyce Thompson Institute for Plant Research, Ithaca NY

4:20 Close of day; depart the Visitor Center (building closes at 4:30)

{Speaker dinner in evening, for Invited speakers and MAPMBS program committee}

Wednesday, August 19, 2015

9:00 Registration, posters, exhibitors

Session II **Plant development - genetics, genomics, and gene regulation**
moderators: Ben Matthews, *USDA-ARS Soybean Genomics and Improvement Lab*
David Puthoff, *Dept. of Biology - Frostburg State University*

9:30 **Sona Pandey**
Phosphorylation-dependent regulation of G-protein cycle during nodule formation in soybean
Donald Danforth Plant Science Center, St. Louis

10:00 **Chong Zhang**
The circadian clock component LUX ARRHYTHMO regulates Arabidopsis defense through salicylic acid
Dept. of Biological Sciences, University of Maryland-Baltimore County, Baltimore

10:20-11:00 **Coffee break: Posters and Exhibitors**

11:00 **Robert Stupar**
Genetic and genomic insights gained from soybean fast neutron mutagenesis
University of Minnesota

11:30 **Burkhard Schulz**
Genomic and molecular approaches to herbicide resistance – giant ragweed case study
University of Maryland, College Park

12:00-1:30 **Lunch break: Posters and Exhibitors**

1:30 **Mary Locke**
Inherent variability in crop plant composition
DuPont-Pioneer, Wilmington DE

2:00 **Jason Miller**
Araport: the community-extensible portal for Arabidopsis data
J.Craig Venter Institute, Rockville MD

2:20 **Close of meeting – Poster takedown**

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Posters – **Titles and Authors** (Please view posters during lunch, breaks, etc)

Poster #	Abstract on page:	Title, Authors
1	25	**THE ARAPORT 11 UPDATE TO THE ARABIDOPSIS THALIANA TRANSCRIPTOME** Chia-Yi Cheng, Vivek Krishnakumar, Erik Ferlanti, Maria Kim, Irina Belyaeva, Benjamin Rosen, Jason Miller, Agnes Chan, Christopher Town
2	25	**CELL WALL ARCHITECTURE DURING DEVELOPMENT OF THE LEGUME-*RHIZOBIUM* SYMBIOSIS** Cherish Warner and D. Janine Sherrier
3	26	**INTERACTION WITH HOST TRANSCRIPTIONAL REGULATORS ALTERS THE PHLOEM TRANSLATOME AND CONFERS A MOVEMENTADVANTAGE TO *TOBACCO MOSAIC VIRUS*** Tamara D. Collum and James N. Culver
4	26	**INOCULATION AND CHARACTERIZATION OF NATIVE US RHIZOBIAL STRAINS FOR THE USE AS COMMERCIAL INOCULANTS OF LIMA BEAN (*PHASEOLUS LUNATUS* L.)** Usha Bishnoi and D. Janine Sherrier
5	27	**PHYCOBILIPROTEIN AND PHOTOSYNTHETIC PIGMENT ACCUMULATION IN WILDTYPE AND HALOTOLERANT *FREMYELLA DIPLOSIPHON*** Giwa-Otusajo, J., Tabatabai, B., Enitan, O., Adusei, A., and Sitther, V
6	28	**SUGAR BEET GENES ENCODING POLYGALACTURONASE-INHIBITING PROTEINS AND THEIR FUNCTION IN PLANT DEFENSE** Haiyan Li, Senthilkumar Padmanaban and Ann C. Smigocki
7	28	**GENETIC STUDIES ON THE OPPOSING ROLES OF TWO PHOPHOLIPASE D ISOFORMS IN PLANT INNATE IMMUNITY** Qiong Zhang, Robert Berkey, Xuemin Wang & Shunyuan Xiao
8	29	**MOLECULAR IDENTIFICATION OF JAPANESE BARBERRY CULTIVARS USING MICROSATELLITE MARKERS** Kerry Lambert and Samuel Obae
9	30	**DEVELOPMENT OF A PCR-BASED DIAGNOSTIC ASSAY FOR THE DETECTION OF *MAGNAPORTHE ORYZAE TRITICUM* PATHOTYPE, THE CAUSAL AGENT OF WHEAT BLAST** Michael L. Pieck, Li Chen, Amy L. Ruck, Gary L. Peterson, Mark L. Farman, Barbara Valent, Kerry F. Pedley
10	30	**DESIGNING DISEASE RESISTANT PLANTS** Reham Youssef and Benjamin F. Matthews

Speaker Abstracts

A functional study of root knot nematode IDA-like (IDL) peptide putatively secreted into the host plant

Joonyup Kim[1,2], Ronghui Yang[1], Caren Chang[2], and Mark L. Tucker[1]
[1] Soybean Genomics and Improvement Lab, USDA-ARS, Beltsville, MD, USA
[2] Department of Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, USA

Inflorescence deficient in abscission (*IDA*) is a gene that is essential to the regulation in Arabidopsis floral organ abscission. The *IDA* gene encodes a small, secreted peptide that binds to two redundant receptor-like kinases (HAESA and HAESA-like 2), which alters the expression of KNOX transcription factors. IDA-like genes are conserved in every dicot genome and four monocots we have examined. Root-knot nematodes (RKN), *Meloidogyne* spp., are costly pathogens of many agriculturally important crops. In addition to the plant species, we identified *IDA*-like (*IDL*) genes in the genomic sequence for *Meloidogyne incognita* and *M. hapla*. Expression of *MiIDL1* is very low in RKN eggs and pre-parasitic J2 but rapidly increases after inoculation of tomato roots and then declines at approximately 14 days post inoculation. Five and three prime RACE of RNA from *M. incognita* infected roots revealed a sequence of 392 nt with a 47 aa open reading frame (ORF) including a putative 28 aa N-terminal signal peptide. Synthetic peptide for the MiIDL1 ORF minus the signal peptide and transgenic Arabidopsis harboring the full-length ORF both complement the delayed abscission phenotype of the *ida* mutant. Furthermore, application of the synthetic MiIDL1 peptide to Arabidopsis roots promoted root growth that indicates a possible role for the RKN peptide in root development, which could support RKN infection of roots. Transgenic lines of RNAi that over-express *MiIDL1* (MiIDL1i) and *GUS* (GUSi) were generated and tested for host infection in Arabidopsis. Preliminary results suggest that suppression of the *MiIDL1* gene in the nematode delays gall development and the numbers of galls that form. We propose that IDA-like peptides are conserved throughout the plant kingdom and that the nematode MiIDL1 peptide is a novel effector, which functions as a signaling peptide in the host plant.

Gene Expression Profiling of Alfalfa (*Medicago sativa*) Infected with Root-Knot Nematode *Meloidogyne incognita*

Olga A. Postnikova[1], Maria Hult[2], Jonathan Shao[1], Andrea Skantar[2] and Lev G. Nemchinov[1*], USDA-ARS, Beltsville Agricultural Research Center, [1]Molecular Plant Pathology Laboratory and [2]Nematology Laboratory, Beltsville, MD 20705.
*corresponding author: lev.nemchinov@ars.usda.gov

Root-knot nematode (RKN) *Meloidogyne incognita* or southern root-knot nematode is one of the most damaging crop pathogens in the world. Prior to this work, no studies have been published on global gene expression profiling in alfalfa infected with RKN or any other plant parasitic nematode. We performed root transcriptome analysis of resistant (Moapa 69) and susceptible (Lahontan) alfalfa cultivars infected with RKN *M. incognita.* A total of 1,701,622,580 pair-end reads were generated on an Illumina Hi-Seq 2000 platform from the roots of both cultivars and assembled into 45,595 and 47,590 transcripts in cvs Moapa 69 and Lahontan, respectively. Bioinformatic analysis revealed a number of common and unique genes that were differentially expressed in susceptible and resistant lines as a result of nematode infection. Although the susceptible cultivar showed a more pronounced defense response to the infection, feeding sites were successfully established in its roots. Basal gene expression levels under normal conditions differed between the two cultivars as well, which may confer advantage to one of the genotypes toward resistance to nematodes. Functional roles of the differentially expressed genes were predicted. Candidate genes that contribute to protection against *M. incognita* in alfalfa were proposed.

Elucidating Plant Pathogen Interactions through Correlative Microscopic Imaging

James P. Kilcrease[1,2], John Hammond[1]
[1]USDA ARS, United States National Arboretum, USNA, Floral and Nursery Plants Research Unit, FNPRU, Beltsville, MD
[2]Oak Ridge Institute of Science and Education, Oak Ridge, TN
james.kilcrease@ars.usda.gov

Plant pathogens are wide spread and have detrimental effects on many economically important plant species. The symptomatic progression of disease is an expansive complex with physical interactions between plants, viruses and/or vectors including parasitic nematodes, fungi, and protists. Many issues arise in attempting to elucidate a complete picture of an infection cycle, especially when multiple pathogenic entities / vectors contribute to a single disease, or a physical barrier such as the virus-soil complex is encountered. Imaging is a vital component to successfully acquiring the most complete scope of a host-pathogen interaction whereby multiple microscopic techniques with various modes of processing are used in correlation with one another. Therefore the objectives of this research are to; 1) utilize a liquid agar fixative medium to aide in the stabilization of soil / host biological complexes in their native conformation with regards to viruses and fungi and 2) determine interactions / localizations of pathogenic vectors and viral co-infections. Laser scanning confocal microscopy (LSCM) and wide-field fluorescent (WF) imaging in conjunction with scanning and transmission electron (SEM and TEM) microscopy methods were used to investigate the effects of *Potato virus X* (PVX) and *Alternanthera mosaic virus* (AltMV) co-infections in leaf samples of *Nicotiana benthamiana*. Root-soil samples of Asiatic / Oriental lilies (*Lilium* sp.) and *Nicotiana benthamiana* infected with *Plantago asiatica mosaic virus* (PlAMV) were analyzed via TEM utilizing an agar assisted fixation protocol to stabilize the natural conformation of soil in direct contact with roots. Additionally, the agar assisted embedding method was applied to leaves infected with pathogenic fungi. These findings demonstrate the architecture / interactions / modes of entry for viruses and fungi in host plants. Successful confirmation of PlAMV infection in *Lilium* sp. and *N. benthamiama* was determined via leaf dips, negatively stained soil preparations, ELISA, and PCR. Confirmation of PVX and AltMV infections in *N. benthamiama* was confirmed utilizing multiple microscopic approaches. The PlAMV root-soil embedded tissue using the agar assisted procedure resulted in composite TEM samples containing both root and soil entities with undisturbed architecture while procedures for LSCM and TEM applied to PVX / AltMV co-infections demonstrated viral interactions on a sub-cellular level. This method of utilizing a liquid agar fixative solution has been demonstrated to be very useful in the TEM visualization of the root-soil interface and fungal/leaf matrices but could also be used in instances of soil-borne vector and/or other pathogen interaction with roots as well as a stabilizer in pre-embedment processing for bacterial colonies or other unstable targets. The correlative imaging of plant pathogens using multiple microscopic techniques reveals more detailed information about host-pathogen-vector etiology.

Phytoplasma induced reprogramming of plant stem cell destiny

Wei Wei, Robert E. Davis, and Yan Zhao
Molecular Plant Pathology Laboratory, ARS-USDA, 10300 Baltimore Ave, Beltsville, MD20705
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Phytoplasma-infected plants often exhibit diverse symptoms such as excessive shoot proliferation, witches'-broom growth, general stunting, and abnormal floral development, but mechanisms underlying development of these symptoms have only recently been explained. Using the Columbia Basin potato purple top (PPT) phytoplasma and its alternative host tomato as a model system, we identified four mutually distinct symptoms exhibited by infected plants. We found that each symptom type is linked to a specific derailment of the genetically preprogrammed destiny of meristem cells. Such stem cell fate modification includes premature floral meristem termination, suppressed floral meristem initiation, delayed vegetative-to-inflorescence meristem conversion, and repetitive initiation of lateral vegetative meristems. Remarkably, transcriptional reprogramming of key meristem switching genes occurred prior to symptom appearance. Based on these findings, we hypothesize that reprogramming of meristem fate may represent a unifying mechanism underlying diverse phytoplasmal disease symptoms that involve alterations of plant architecture and morphology. In testing our hypothesis in the present study, we identified additional symptoms in PPT phytoplasma-infected tomato plants, and we determined expression profiles of an array of meristem switching genes in relation to the emergence and development of these symptoms. Our results provide new mechanistic insights into the coupling of each phytoplasmal symptom to a corresponding alteration of gene expression, and consequently of meristem fate. Elucidation of a unifying mechanism that explains development of diverse symptoms opens new avenues for devising practical strategies against phytoplasmal diseases.

Systems Biology Approaches to Understanding Polysaccharide Degradation at the Plant – Microbe Interface

Jeffrey G. Gardner
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The expression of bacterial enzymes that degrade complex polysaccharides (glycoside hydrolases) inside of plant tissues is one strategy to create transgenic crops with desirable traits for renewable fuel and chemical production. However, it is still unclear what bacterial enzymes would be best to express in plants because our knowledge of how bacteria efficiently degrade plant material is incomplete. Most lignocellulose degrading bacteria have hundreds of glycoside hydrolases, but it is unknown which are essential for lignocellulose degradation. Enzymes that are well suited for industrial processes are unlikely to also be appropriate choices for expression in transgenic plants. Therefore, data on what bacterial enzymes are effective for degrading plant-specific lignocellulose is required. To addresses this knowledge gap, our research group uses the saprophytic bacterium *Cellvibrio japonicus* to understand the mechanisms and regulation of efficient lignocellulose depolymerization using a comprehensive *in vivo*, *in vitro*, and *in silco* approach. Recently our studies have uncovered a complex response for the degradation of crystalline cellulose in *C. japonicus*. Specifically, our data indicate that despite the presence of 13 glycoside hydrolases of the GH5 class, only one (Cel5B) is essential for cellulose degradation. Efficient cellulose degradation is also dependent on the cellobiohydrolase Cel6A, as well as the lytic polysaccharide mono-oxygenases *Cj*LPMO10B. Several studies have examined the expression of microbial cellulases in plants, however the expression of LPMO enzymes in plant tissues would be a novel approach to decrease cellulose recalcitrance in a transgenic crop. Additional work in our laboratory is examining the glycoside hydrolases essential for degrading the lignocellulose in important bioenergy crops such as corn and switchgrass.

Aphids modulate Polerovirus transmission efficiency in a host-dependent manner

Patricia Pinheiro[1,2,3], Murad Ghanim[4], **Michelle Cilia**[3,5,6]
[1] Embrapa Rice and Beans, Santo Antônio de Goiás, 75375-000, Brazil
[2] Department of Entomology, Cornell University, Ithaca, NY
[3] Boyce Thompson Institute for Plant Research, Ithaca, NY
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[5] Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Ithaca, NY
[6] Emerging Pests and Pathogens Research Unit, USDA Agricultural Research Service, Ithaca, NY

This talk will highlight the first example wherein the virus transmission efficiency of an insect vector is modulated according to interactions with its plant host. Aphids, in the order Hemiptera, are among the most prolific insect vectors of plant viruses. The green peach aphid, *Myzus persicae*, is an efficient vector of the circulative *Potato leafroll virus* (PLRV). PLRV transmission efficiency was significantly reduced when a clonal lineage of *M. persicae* was reared on turnip (*Brassica napa*) as compared to the weed physalis (*Physalis floridana)*. The effect on transmission efficiency was relatively transient and due to a host-switch response. Although turnip and physalis-reared aphids (T- and P-Myzus, respectively) acquired similar levels of PLRV, T-Myzus were larger and had a fitness advantage. Using 2-D Difference Gel Electrophoresis (DIGE) and nanoflow liquid chromatography coupled to high-resolution mass spectrometry, we revealed multiple size and charge isoforms of the cysteine protease cathepsin B as up-regulated in T-Myzus. The expression and up-regulation of at least two protein isoforms in T-Myzus as compared to P-Myzus was validated using selected reaction monitoring mass spectrometry. We tested the effect of cathepsin B inhibition using the cysteine protease inhibitor E-64 on PLRV transmission by T-Myzus and P-Myzus. After feeding aphids on a diet with E-64, PLRV transmission from P-Myzus was decreased. In contrast, after feeding aphids on a diet with E-64, T-Myzus showed an E-64 dose-dependent increase in transmission efficiency. Immunostaining in the gut of T-Myzus revealed co-localization of cathepsin B and PLRV on aphid midgut brush border cell membranes, the site of PLRV acquisition. By varying enzyme and substrate concentration, we showed that the enzyme activity was biphasic and regulated differently in the insects on different hosts, suggesting the presence of a cathepsin B co-factor or inhibitor in P-Myzus. While our results do not rule out the potential involvement of additional gut-localized cysteine proteases in PLRV transmission, they indicate that there is an optimal level of cathepsin B activity inside the aphid midgut that is required for the transmission of PLRV by *M. persicae*.

"Legal High" Plant Species Differentiation Using a High Resolution PCR Melt Assay

Kelly M. Elkins, Anjelica C. U. Perez and Alicia Quinn
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Efforts to detect and control substance abuse in the United States are ongoing. We have developed high resolution PCR melt assays for four plant species: *Cannabis sativa* (marijuana), *Papaver somniferum* (poppy), *Ipomoea purpurea* (morning glory), *and Datura stramonium* (jimson weed). Marijuana and poppy are the two most prevalent internationally-abused herbal highs; poppy seeds can be purchased at garden stores and jimson weed can be collected outdoors here in Maryland. These species are acquired, crushed and ingested whole, brewed in teas or smoked to illicit "legal highs" in several countries worldwide. To differentiate the plants, we designed PCR primers specific for each plant using public genome data. Each set of PCR primers produce an amplicon from the plant of interest with a specific melt temperature that differs from amplicons produced with primers for the other plants. In this presentation, we will show data demonstrating the specificity, selectivity, sensitivity, and reproducibility of the assays. Progress in multiplexing primer sets to simultaneously detect one or more of the species will be presented.

Keynote address

Salicylic acid and its binding proteins in plant and human health

Klessig D.F.[1], Choi H-W.[1], Tian M.[1], Manohar M.[1], Moreau M.[1], Park S-W.[1], Song F.[2], Venereau E.[3], Nagy P.D.[4], Harraz M.M.[5], Snyder S.H.[5], Schroeder F.C.[1], Montelione G.T.[2], and Bianchi M.E.[3]

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Since our discovery in 1990 that SA regulates plant immunity, we have attempted to determine its mechanisms of action in plant immunity and other biological processes using genetic, molecular, and biochemical approaches. Over two dozen plant SA-binding proteins (SABPs) have been identified primarily through biochemical methods, including three high-throughput screens (see http://bioinfo.bti.cornell.edu/SA2010/). SA binding alters the biochemical and/or biological activities of these proteins, generally by inhibit them. We have extended this work to humans, since the most widely used medicine aspirin (acetyl SA) is rapidly converted to SA after ingestion and SA has most of the same pharmacological activities of aspirin. Two novel targets of SA/aspirin have been identified across the animal and plant kingdoms. Together the two human SABPs are associated with most of the major human diseases, including heart attack, stroke, sepsis, rheumatoid arthritis, inflammation-associated cancers, hepatitis, and neurodegenerative diseases. One of the identified human SABPs is High Mobility Group Box1 (HMGB1). In addition to its nuclear role in condensing DNA and regulating gene expression, extracellular HMGB1 is a damage-associated molecular pattern (DAMP), which activates immune and inflammatory responses. SA suppresses both the chemo-attractant activity of HMGB1 and the increased expression of pro-inflammatory cytokine and *COX-2* genes induced by HMGB1. An HMGB1 protein mutated in one of the SA-binding sites identified in the HMG-box domain by NMR analyses retained its chemo-attractant activity, but lost binding of and inhibition by SA, thereby firmly establishing that SA binding to HMGB1 directly suppresses its pro-inflammatory activities. Natural and synthetic SA derivatives also have been identified with greater potency for inhibition of the pro-inflammatory activities of HMGB1. Interestingly, our parallel study of the plant ortholog AtHMGB3 revealed that it also functions as a DAMP to activate plant immunity. Moreover, it binds SA and mutations in its corresponding HMG box suppress both SA binding and SA inhibition of its immune-inducing activity.

The second novel target in humans is Glyceraldehyde 3-Phosphate Dehydrogenase (GAPDH). In addition to its central role in glycolysis, human GAPDH participates in several pathological processes including neuronal cell death associated with Alzheimer's, Parkinson's, and Huntington's diseases. We discovered that SA, like the anti-Parkinson's drug deprenyl, suppresses nuclear translocation of GAPDH, an early step in cell death, as well as cell death induced by the DNA alkylating agent N-methyl-N-nitroso-N^1-nitroguanidine. Two synthetic SA derivatives and two natural compounds from the Chinese medicinal herb *Glycyrrhiza foetida* (licorice), glycyrrhizin and the SA-derivative amorfrutin, were identified which appear to not only more tightly bind GAPDH, but also more effectively suppress nuclear translocation of GAPDH and cell death than SA. In addition to GAPDH's role in neuronal cell death, some animal and plant viruses, such as human Hepatitis A, B, C Viruses

and Tomato Bushy Stunt Virus (TBSV), usurp this host protein for their replication. We discovered that SA binding to GAPDH inhibits its interaction with the TBSV minus RNA strand, thereby suppressing viral replication. This finding reveals a novel mechanism of SA action in defense against viral pathogens.

In summary, these studies demonstrate that SA can modulate both plant and human health via shared SABPs. Furthermore, the identification of human HMGB1 and GAPDH as pharmacological targets of SA/aspirin provides new insights into the mechanisms of action of one of the world's longest and most used natural and synthetic drug. It may also provide an explanation for the protective effects of low-dose aspirin usage. Moreover, the identification of natural and synthetic SA derivatives with greater potency for inhibition of HMGB1 and GAPDH provides proof-of-concept that new SA-based compounds with high efficacy are attainable.

Phosphorylation-dependent regulation of G-protein cycle during nodule formation in soybean

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Signaling pathways mediated by heterotrimeric G-protein complex comprising Gα, Gβ and Gγ subunits and their regulatory RGS (Regulator of G-protein Signaling) protein are conserved in all eukaryotes. We have shown that the specific Gβ and Gγ proteins of soybean G-protein complex are involved in regulation of nodulation. We now demonstrate the role of nod factor receptor 1 (NFR1)-mediated phosphorylation in regulation of G-protein cycle during nodulation in soybean. We also show that during nodulation the G-protein cycle is regulated by the activity of RGS proteins. Lower or higher expression of RGS proteins results in fewer or more nodules, respectively. NFR1 interacts with RGS proteins and phosphorylates them. Analysis of phosphorylated RGS protein identifies specific amino acids which when phosphorylated; result in significantly higher GTPase accelerating activity. These data point to a phosphorylation-based regulation of G-protein signaling during nodule development. We propose that active NFR1 receptors phosphorylate and activate RGS proteins, which help maintain the Gα proteins in their inactive, trimeric conformation, resulting in successful nodule development. Alternatively, RGS proteins might also have a direct role in regulating nodulation because overexpression of their phosphomimic version leads to partial restoration of nodule formation in *nod49* mutant.

The Circadian Clock Component LUX ARRHYTHMO Regulates Arabidopsis Defense Through Salicylic Acid

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Recent studies showed that two morning clock genes regulate Arabidopsis defense independently of the key defense signaling mediated by salicylic acid (SA). To further understand the defense role of the circadian clock, we tested a mutant impaired in the evening clock gene *LUX ARRHYTHMO* in defense responses. We found that the *lux---* mutant was compromised to both basal and R---gene mediated defense against *Pseudomonas syringae* and expression of the *LUX* gene was suppressed by *P. syringae*. We also found that *lux---1* had transiently reduced SA accumulation after infection with a virulent *P. syringae* strain. Consistent with this result, the double mutant *acd6---1lux---1* displayed suppression on dwarfism, cell death, and constitutive defense phenotypes, compared with *acd6---1*, which has been used as a convenient genetic tool in gauging the change of defense levels. We further found that two downstream targets of LUX also could modulate resistance to *P. syringae* via the SA pathway. Together our results showed that LUX regulates Arabidopsis defense, possibly through affecting SA signaling. These data further support crosstalk between the circadian clock and plant innate immunity and also reveal different molecular mechanisms underlying clock---defense crosstalk.

Genetic and genomic insights gained from soybean fast neutron mutagenesis

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Soybean (*Glycine max*) has a paleopolyploid genome with limited natural variation in the modern germplasm, due to successive genetic bottlenecks during domestication and modern breeding. While soybean is an important crop species, genetic research has lagged behind model plant systems. Furthermore, mutant populations have been difficult to develop, maintain and utilize. For these reasons, few soybean genes have been functionally characterized to date. The emergence of a reference soybean genome sequence and advances in bioinformatic methodologies has altered this landscape, providing a new toolbox to accelerate the cloning and characterization of DNA polymorphisms that cause phenotypic variation. Genome-wide structural variation, such as large deletions and duplications, are hypothesized to drive important phenotypic variation. Using microarray and re-sequencing technologies, we have screened genic structural variants across a panel of over 250 fast neutron mutant lines. Deletions and duplications associated with soybean gene models have been cataloged and archived in these populations. This seminar will focus on the general patterns observed across the structural genomic landscape, and promising leads in associating deletions and duplications at specific loci with phenotypic variation. This presentation will also feature case studies where bioinformatic approaches were used to accelerate the identification of DNA sequence polymorphisms underlying mutant phenotypes. The cloning of both natural and induced alleles will be demonstrated, spanning a wide range of phenotypes that may include plant architecture, seed composition, hairless leaves and chlorophyll deficiency mutants.

Genomic and Molecular Approaches to Herbicide Resistance – Giant Ragweed Case Study

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Giant ragweed is a competitive annual weed found in agriculture fields and disturbed areas, and is a problematic weed in corn and soybean production. The introduction of glyphosate resistant crops ("Roundup®-ready") in 1996 provided a new tool to manage giant ragweed. The cellular mechanism of glyphosate is inhibition of EPSP synthase, the key enzyme of the shikimate pathway. Weed management with glyphosate led to recurring use of glyphosate. This use pattern resulted in high selection pressure for glyphosate resistance. Glyphosate-resistant giant ragweed (GRGR) has been reported throughout the U.S. We investigate the mechanism of glyphosate resistance in giant ragweed. The goal of our project is to determine genes responsible for glyphosate resistance in GRGR. We hypothesize that the basis of resistance in giant ragweed biotypes is related to reduced translocation of glyphosate combined with induced rapid necrosis of glyphosate exposed leaf tissue. GRGR plants show a unique response when treated with glyphosate by exhibiting initial rapid necrosis of mature leaves within 12 hours of treatment. These plants do not die from a glyphosate treatment but resume normal-growth from axillary meristems and reproduce. The progression of the response and symptoms resemble a typical hypersensitive response similar to that observed after pathogen attack. We investigated hallmarks of hypersensitive response reactions in plants such as reactive oxygen species (ROS) production and auto-fluorescence of chlorophyll, which is dramatically increased in resistant plants after treatment. Glyphosate sensitive plants (GSGR) plants do not exhibit rapid leaf necrosis but their leaves become slowly chlorotic, then necrotic and plants die over a 2-4 week period. We compared both biotypes for response to glyphosate up to 8 x field application rates (1x=0.84kg/ha). GRGR plants survived all applied spray rates whereas GSGR plants died at 1x and higher rates. To study the transcriptome of giant ragweed under glyphosate treatment, total RNA from both biotypes was analysed after glyphosate treatment in a time-course from 0 to 6 hours. Sequence data analysis showed differential gene expression in GSGR and GRGR plants upon glyphosate treatment. GO term analysis revealed that a great number of differentially expressed genes are involved in pathogen and stress responses. To our surprise we found that even in control plants differential expression of pathogenesis-related genes can be found. This indicates that the innate immunity and the hypersensitive response system of plants is involved in cellular reactions of GRGR plants toward glyphosate treatments.

Inherent Variability in Crop Plant Composition

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The vast number of intra-species variations seen in food crops is a consequence of multiple combinations of genetic and environmental factors. Differences in crop varieties are not just phenotypic, but can be observed on a compositional level. The oleic acid percentage in soybean, for example, can have an inherent range of 15.18-30.46% (OECD, 2012). This seminar will address what natural variability is, how it has come about, and the genetic and/or environmental factors that may affect the nutrient composition of a food crop. In addition, we will discuss how assessments of compositional comparability (between a GE event and its control) can be made within this context of wide natural variability.

ARAPORT: The Community Extensible Portal for Arabidopsis Data

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The Arabidopsis Information Portal (Araport) is an online resource for the plant genomics community. Centered on *Arabidopsis thaliana* , the portal integrates gene annotation with the latest highquality reference genome sequence. Araport supports sophisticated query and analysis operations while also presenting datarich report pages for individual genes and proteins. The portal hosts two GMOD software applications: the JBrowse genome browser and the InterMine data mining tool. These applications combine data from TAIR, UniProt, PubMed, BAR, EPICCoGe, IntAct, Atted II, KEGG, 1001 Genomes, and other sources. The portal currently hosts community curation of the draft "Araport11" update to the TAIR10 genome annotation. Araport is designed for growth. It warehouses and indexes a core information set but makes substantial use of web services to obtain and integrate data from remote databases at run time. It hosts tools and documentation designed to help community members develop additional web services and science apps and add them to the portal. Araport offers community developers the benefits of automatic indexing, caching, security, logging, scaling, styling, portability, and automatic documentation generation. Araport already offers a variety of web services for third party data and these boast a shared vocabulary and uniform documentation. Araport provides a model for sustainable growth of model organism resources with reliance on federated data, realtime integration, an opensource architecture, and communitycontributed software.

Poster abstracts

Poster 1

THE ARAPORT 11 UPDATE TO THE ARABIDOPSIS THALIANA TRANSCRIPTOME

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The flowering plant *Arabidopsis thaliana* is a major dicot model organism for genetic research. A comprehensive annotation paves the road for understanding the functions of genes, the modulation of transcriptional and translational activities, alternative splicing events, and RNA-directed gene regulation. Using an integrative annotation pipeline, we assembled developmental-specific RNAseq libraries to explore the features of coding RNA in 11 tissues or organs. The pre-release of the Araport11 protein-coding gene set contains 28,598 loci with 50,164 transcripts. 80.3% (28,429/35,385) of TAIR10 protein-coding gene models have been updated among which 3.3% (933) and 88.2% (25,079) have altered CDS and UTR respectively. 38.1% (10,906) of the genes in Araport11 have more than one splice variant as compared to 18% in TAIR10. 20.8% (5,713/27,416) of the TAIR10 loci have updated functional annotation. In addition, we annotated tens of thousands of non-coding RNAs, including small RNA, long intergenic RNA, small nucleolar RNA, natural antisense transcript, small nuclear RNA, and microRNA using published datasets and in-house analytic results. Together, our data uncover the landscape of coding and noncoding RNAs, untranslated regions, and splicing activities to be more complex than previously revealed. We present a refined Arabidopsis annotation, Araport11, with a substantially increased number of transcribed elements and improved resolution of the structures and dynamics of gene models.

Poster 2

CELL WALL ARCHITECTURE DURING DEVELOPMENT OF THE LEGUME-*RHIZOBIUM* SYMBIOSIS

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Although studies of whole organ systems have greatly increased our understanding of the developmental processes, they are limited by traditional methods of analysis used in plant tissue systems. One organ system that would directly benefit from such analysis is the legume symbiotic root nodule. During the legume-*Rhizobium* symbiosis, root nodules are formed and are the site of biological nitrogen fixation. Nodule cell types undergo extensive modifications during organ development. In pea (*Pisum sativum)* nodules, these modifications occur along the longitudinal axis of the organ. In the present study, a whole pea root nodule was analyzed for changes in the cell wall architecture occurring throughout each developmental stage using three-dimensional modeling software and a novel optical clearing technique.

Whole organ analysis using these techniques resulted in mature nodules which were cleared optically and imaged using confocal microscopy. Depth of imaging achievable in the z-axis increased two-fold as compared to tissue treated using standard methods. In addition, the three-dimensional modeling of whole nodules provided new insight and details about nodule organogenesis thus allowing for analysis of cell wall composition and architectural changes that occur during the development of legume-*Rhizobium* symbioses.

Poster 3

INTERACTION WITH HOST TRANSCRIPTIONAL REGULATORS ALTERS THE PHLOEM TRANSLATOME AND CONFERS A MOVEMENTADVANTAGE TO *TOBACCO MOSAIC VIRUS*

Tamara D. Collum and James N. Culver

The *Tobacco mosaic virus* (TMV) replication protein has been shown to interact with IAA26, an auxin transcriptional regulator. Promoter expression studies show IAA26 predominately accumulates in the nuclei of companion cells in the phloem vascular tissue. The companion cell nuclear localization of IAA26 is disrupted upon infection with TMV, but not upon infection with a non-interacting virus TMV-V10871. Viruses that cannot interact with IAA26 have a reduced apility to spread within the vascular tissue and are less competitive at systemic movement compared to an interacting virus. Similarly, over accumulation of IAA26 in the phloem by making the protein resistant to auxin mediated degradation but not disrupting its ability to interact with TMV, was found to reduce TMV accumulation. Translatome profiling with phloem specific promoters PSUC2 and PSULTR2;2, as well as a control CaMV 355 promoter further characterize how the phloem environment is altered during TMV infection. Results showed the down regulation of host defense genes involved in systemic acquired resistance, RNA interference, and callose deposition at plasmodesmata specifically within the vascular phloem in response to TMV infection. Taken together these results suggest that reprogramming the phloem environment gives TMV an evolutionary advantage by promoting phloem loading and systemic movement.

Poster 4

INOCULATION AND CHARACTERIZATION OF NATIVE US RHIZOBIAL STRAINS FOR THE USE AS COMMERCIAL INOCULANTS OF LIMA BEAN (*PHASEOLUS LUNATUS* L.)

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In recent years, biofertilizers have emerged as important resources for effective biological nitrogen fixation in legume crop production. They offer an economically-attractive and ecologically-sound route to augment nutrient supply for crops, and their use reduces the carbon footprint associated with crop production. Soil microorganisms are important in the cycling of nutrients from both inorganic and organic sources in the soil and also in the

maintenance of soil health and quality, and the microbial communities can be optimized through the use of microbial amendments to promote crop production and a sustainable agricultural system. The present study was conducted to evaluate the utility of 41 native US rhizobial strains for lima bean (*Phaseolus lunatus* L.) varieties C-Elite, Cypress, and Fordhook in greenhouse and field experiments. From greenhouse studies, we selected 15 strains that promoted growth, in terms of total biomass, and these 15 rhizobial strains were further considered for field study experiments. In subsequent field trials, we identified the top five performing rhizobial strains for baby lima and Fordhook varieties based on the yield, and these are currently being evaluated in bigger plot or whole field studies. The promising results from the field studies will be decisive in our future experiments for harnessing the positive influence of these different native rhizobacteria for the development of rhizobial inoculants for lima bean.

Poster 5

PHYCOBILIPROTEIN AND PHOTOSYNTHETIC PIGMENT ACCUMULATION IN WILDTYPE AND HALOTOLERANT *FREMYELLA DIPLOSIPHON*

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Fremyella diplosiphon, a fresh water-inhabiting cyanobacterium, is a widely studied model organism that can thrive at low light intensity and optimal temperature. In the present study, the photosynthetic efficacy of a genetically transformed halotolerant strain (HSF33) was compared to the wildtype (SF33). Cultures were grown in liquid BG-11/HEPES for seven days under fluorescent white light to an absorbance of ~0.6 at 750 nm, centrifuged, and flash frozen. Phycobiliproteins (phycocyanin, phycoerythrin, allophycocyanin) and photosynthetic pigments (chlorophyll *a*, carotenoids) from HSF33 and SF33 were extracted and quantified. While phycocyanin level in HSF33 was significantly lower than SF33, no variation in the amount of phycoerythrin and allophycocyanin was observed. Although both strains accumulated comparable levels of chlorophyll *a*, significantly higher amounts of carotenoids were observed in HSF33 than the wildtype, which accounts for the yellow coloration. Findings of this study indicate a similarity in photosynthetic efficacy between wildtype and halotolerant strain, but with altered pigment accumulation. Future studies will aim towards evaluating lipid content in the two strains, for use of the transformant in biofuel production.

Poster 6

SUGAR BEET GENES ENCODING POLYGALACTURONASE-INHIBITING PROTEINS AND THEIR FUNCTION IN PLANT DEFENSE

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Polygalacturonase-inhibiting proteins (PGIPs) are cell wall leucine-rich repeat (LRR) proteins that inhibit pathogen and pest polygalacturonases (PGs). Five sugar beet *PGIP* genes were cloned from breeding lines F1016, F1010 and FC607, namely *BvPGIP1*, *BvPGIP2*, *BvPGIP3*, *Bv(FC607)PGIP1* and *Bv(FC607)PGIP2*. The full-length cDNA sequences of the five *PGIP* genes encoded 382 or 384 amino acid peptides that were similar in length to five of the eight *PGIP* sequences found in the sugar beet reference genome (RefBeet). These peptides were 50-60 amino acids longer than all other known plant PGIPs except one. These additional amino acids were located in an LRR domain region. RT-PCR and quantitative real-time PCR (qPCR) analysis demonstrated varying levels of tissue-specific expression of the *BvPGIP* genes in leaves, petioles, hypocotyls and roots, with maximum expression being detected in roots. Significant up-regulation of *BvPGIP* transcripts by insect feeding and mechanical wounding was observed in leaves. An agarose diffusion assay was used to demonstrate inhibition of five different fungal PGs by sugar beet PGIPs. These findings will facilitate further studies on the role of PGIPs in plant defense.

Poster 7

GENETIC STUDIES ON THE OPPOSING ROLES OF TWO PHOPHOLIPASE D ISOFORMS IN PLANT INNATE IMMUNITY

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Plants have evolved an effective immune system to fight against various pathogens. Despite tremendous progress towards an understanding of the molecular architecture of the immune system, many aspects of the underlying regulatory mechanisms remain to be elucidated. Phospholipase D (PLD) is a family of enzymes that hydrolyze phospholipids to generate phosphatidic acid (PA) and a free head group. Our genetic studies showed that pldα1-knockout (ko) plants displayed enhanced disease resistance whereas pldδ-ko plants exhibited enhanced disease susceptibility to powdery mildew, a biotrophic fungal pathogen, indicating that these two PLD genes serve opposing (negative for PLDα1 while positive for PLDδ) roles in regulating plant innate immunity. In addition, the infection phenotype of the pldα1/pldδ double mutant resembles that of the pldα1 single mutant, suggesting that PLDα1 may function downstream of PLDδ. Interestingly, neither of pldα1-ko nor pldδ-ko plants showed altered

disease phenotypes toward avirulent strains of bacteria and oomycete, implying that the two PLD genes are not involved in effector-triggered immunity (ETI). Genetic analyses of pldδ-ko in combination with mutations that impair SA synthesis or signaling suggest that PLDδ may function in an SA-independent (thus potentially novel) defense signaling pathway. Unexpectedly, overexpression of an YFP-tagged phosphatidylinositol 3-phosphate (PI3P)-binding protein (YFP-2xFYVE) can partially suppress pldα1-ko-mediated phenotypes, suggesting that (i) PI3P may be a substrate of PLDα1 and (ii) elevated PI3P level may promote defense signaling. Taken together, our results suggest that PLDα1 and PLDδ play opposing roles, possibly via modulation of subcellular PI3P and/or PA levels, in regulation of an SA-independent, basal defense signaling pathway that is engaged for resistance against powdery mildew.

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Poster 8

MOLECULAR IDENTIFICATION OF JAPANESE BARBERRY CULTIVARS USING MICROSATELLITE MARKERS

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Due to the growing concern for black stem rust (BSR) disease in wheat producing regions in the United States and Canada, sale and movement of barberry plants to "quarantined" regions is restricted to just a few cultivars approved as BSR resistant. Currently, the verification of a given barberry plant as "true-to-type" to the approved cultivar relies on comparing its morphological features to that of its reference cultivar. Often times, this approach leads to misidentification of cultivars given the similarity of morphological features among young plants. A technique that could be used at any stage of plant growth to reliably identify and verify cultivars during inspection is needed. In this study, the genetic diversity of barberry cultivars was assessed using microsatellite markers, and a molecular identification key was developed for the cultivars based on allele profiles at different microsatellite loci. A total of 43 alleles were generated at the seven microsatellite loci assessed, and all were polymorphic. Unweighted pair group method with arithmetic averaging (UPGMA) clustering based on Jaccard's coefficient of similarity matrix revealed that most of the cultivars are genetically different. Based on allele profiles at the seven microsatellite loci, a molecular identification key capable of differentiating 84.3% of the cultivars tested was developed. Ten of the eleven cultivars approved for import in Canada were successfully differentiated using the developed key. This key could be used by regulatory agencies to identify and offer "true-to-type" guarantees to cultivars destined to BSR "quarantined" regions, and to verify the uniqueness of new cultivars when issuing Plant Variety Protection certificates.

Poster 9

DEVELOPMENT OF A PCR-BASED DIAGNOSTIC ASSAY FOR THE DETECTION OF *MAGNAPORTHE ORYZAE TRITICUM* PATHOTYPE, THE CAUSAL AGENT OF WHEAT BLAST

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Magnaporthe oryzae (anamorph = *Pyricularia oryzae*) causes diseases on a wide variety of cultivated graminaceous species including cereal crops and turfgrasses. Wheat blast disease, caused by the *Magnaporthe oryzae Triticum* pathotype (MoT), is responsible for sporadic widespread losses of wheat production in Argentina, Bolivia, Brazil, and Paraguay. To date, wheat blast has only been reported in South America, but the potential for the introduction of the pathogen to the United States is a significant concern due to the lack of resistance in elite wheat cultivars and the ineffectiveness of fungicide treatments during outbreaks. As a first step towards preventing the spread of the South American MoT isolates into the U.S. we have developed a rapid, accurate and sensitive diagnostic assay that can distinguish between the MoT population from South America and the closely related *M. oryzae Lolium* pathotype and *M. oryzae Oryzae* pathotype populations that are endemic to the U.S. We used whole genome sequencing and a custom bioinformatics pipeline to identify 78 markers unique to the MoT genome. Using a subset of 22 markers, PCR primers were designed and tested against a panel of five *M. oryzae* isolates. From this analysis, 20 markers specifically amplified MoT isolates, and one marker, MoT3, was determined to be the most sensitive. MoT3 was selected for further development of the assay using a large set of *M. oryzae* isolates collected from seven different countries. The MoT3 marker was detected in 109 of 110 *M. oryzae* isolates collected from infected wheat heads, while 169 of the 170 *M. oryzae* isolates collected from 14 different non-wheat host species tested negative for the MoT3 marker. Pathogenicity testing of the two outliers revealed that the isolate collected from wheat that tested negative for MoT3 was only weakly pathogenic on wheat, and that the isolate collected from a non-wheat host that tested positive for MoT3 was strongly pathogenic on wheat.

Poster 10

DESIGNING DISEASE RESISTANT PLANTS

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Our understanding of plant pathways, signaling, and regulation involved in the plant resistance response to pathogens has greatly expanded over the past twenty years. My

laboratory has applied a portion of this knowledge to design soybean with resistance to two different genera of nematodes, the soybean cyst nematode (SCN: *Heterodera glycines*) and the root-knot nematode (RKN; *Meloidogyne incognita*). SCN is the major pathogen of soybean, and RKN is a highly destructive pathogen to a wide range of plants, including soybean. We designed over 200 DNA constructs based on data from gene expression studies and from the literature. These DNA constructs overexpress soybean or Arabidopsis genes, or they silence soybean genes or nematode genes. The constructs were transformed into cells at the base of soybean plants to form transgenic roots on composite plants. The transformed plants were inoculated with SCN or RKN to determine if the transgenic roots were more resistant to nematodes. Several constructs reduced SCN cysts and RKN galls more than 60%. It is likely that new approaches, such as these, can provide resistance in plants to an even broader range of pathogens.

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