

MJ 1–1–Unlocking the secrets of medicinal crops : from artemisinin to morphine, why are plants still better than bugs at making these drugs?

Speaker	Ian Graham, FRS	Organization	Professor, University of York
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Opium poppy (*Papaver somniferum*) remains one of the most important medicinal plants in the world. The discovery of a 10 gene cluster responsible for the production of the anti-cancer compound noscapine in opium poppy provided the tools for molecular breeding of new commercial varieties. The discovery of a novel P450 – oxidoreductase gene fusion described the last unknown step in synthesis of the painkiller drugs morphine and codeine proving a valuable tool for development of bespoke, high yielding poppy varieties.

The Chinese medicinal plant *Artemisia annua* (Sweet Wormwood or Qing Hao) is the primary source of the leading anti-malarial drug artemisinin. Characterisation and genetic mapping of traits responsible for production of artemisinin has enabled development of F1 hybrid seed that can deliver a robust source of this vital anti-malarial drug for the developing world. Genetic dissection of artemisinin synthesis demonstrated the importance of nonenzymatic conversions in the final steps of artemisinin synthesis in *A. annua* with significant implications for future production in native versus heterologous host systems.

Noscapine, morphinans and artemisinic acid (an artemisinin precursor) have all been targets for metabolic engineering in heterologous host systems. In this talk I will compare these different production routes with high yielding plant based field production that currently delivers active pharmaceutical ingredient (API) in the price range of \$200–300 per Kg.

Many other plant species also produce valuable bioactive molecules but in amounts that are not commercially viable. For example the Euphorbiaceae or spurge family produce a diverse range of diterpenoids, many of which have pharmacological activity. We are elucidating diterpenoid biosynthetic pathways from the spurge family and developing new production platforms for their synthesis. I will reflect on the different production routes for high value chemicals from plants.

MJ 1–2– From Arabidopsis to canola: Solving the pod shattering problem

Speaker	Martin Yanofsky, PhD	Organization	Distinguished Professor of UCSD
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For most crops, farmers have informally selected for plants that fail to disperse their seeds in order to maximize seed yield at harvest. For example, wild varieties of rice actively disperse their seeds at maturity by a process called shattering, whereas most cultivated rice varieties are non-shattering. However, for some crop species, shattering continues to represent a huge obstacle for optimal harvest by farmers. One example is canola, an important Brassica oilseed crop, where pod shattering can severely impact seed yield, particularly under adverse weather conditions. In an effort to solve this problem, we used the reference plant *Arabidopsis thaliana* to identify the major regulatory genes that control seedpod opening. *Arabidopsis* fruit, like those of canola, develop a highly specialized region called the valve margin to ensure normal fruit opening at maturity. These valve margin cells separate at maturity, allowing for the fruit to open and for seed dispersal. Using *Arabidopsis*, we identified a number of genes that are required for valve margin differentiation. Among these genes is *INDEHISCENT (IND)*, which encodes a putative bHLH transcription factor. *IND* is specifically expressed in cells that will form the valve margin, and mutations in *IND* reduce or eliminate valve margin formation, resulting in fruit that fail to open normally. These studies suggested that a reduction of *IND* activity could reduce the pod shattering issue associated with canola fruit. After many years of painstaking research, scientists at Bayer CropScience were indeed successful at identifying an allele of *IND* that results in shatter resistant canola pods. I will discuss the long and winding road that began with the basic science of fruit development in *Arabidopsis* and ended with the application of this technology to positively impact the way canola farmers harvest their precious crop.

MJ 1–3– Flood–tolerant rice as an example of the potential impact of plant biology research

Speaker	David Mackill, PhD	Organization	Adjunct Professor, University of California, Davis
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Rice is one of the major world staple crops, cultivated on a massive scale, and primary calorie source of the poor. Discoveries in basic plant biology can have major impacts even if they confer relatively small advantages to the plant. Submergence stress effects less than 10% of world rice production but is still estimated to result in billion-dollar losses annually. Detailed studies of traditional rice germplasm allowed scientists to identify a few varieties with of a high level of tolerance. However, successful use of this knowledge occurred only after the SUB1 gene was mapped and marker assisted backcrossing could be applied. This approach can allow rapid introgression of a trait into a popular variety without changing its other properties. Sub1 varieties were shown to have 1–3 t/ha yield advantages over susceptible varieties when flooding occurred. This encouraged rapid scale up and cultivation by millions of farmers. Current discoveries should allow us to solve more intractable problems; for example, develop varieties with higher yield, tolerance of biotic and abiotic stresses, improved cooking and nutritional quality, and reduced impacts on the environment. However, partnerships among plant biologists, field breeders, and other agricultural scientists need to be increased for translating these discoveries into improvements for farmers.

2017 Charles Albert Shull Award Recipient |

Non-coding RNA in plants: the long and the short of it

Speaker	Blake Meyers	Organization	Professor, Division of Plant Sciences Donald Danforth Plant Science Center
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Plant genomes generate innumerable small RNAs, the majority of which are products of non-coding RNAs processed by Dicers. For example, 21 or 22-nt microRNAs (“miRNAs”) are produced from fold-back, non-coding mRNA precursors. Phased “secondary” siRNAs (phasiRNAs) are generated from mRNAs targeted by a typically 22-nt “trigger” miRNA, with the phasiRNAs produced as either 21- or 24-nt small RNAs via genetically separable pathways. Work in monocot anthers has demonstrated the temporal and spatial distribution of two sets of “reproductive phasiRNAs”. These molecules are extraordinarily enriched in the male germline of the many angiosperms, yet their functions are not well characterized. Both reproductive phasiRNA classes are produced from generally long, non-coding mRNAs, and are generated from hundreds to thousands of loci, depending on the species. The prototypical phasiRNA locus is TRANS-ACTING SIRNA 3 (TAS3), one of few long, non-coding RNAs that is conserved back to the emergence of land plants. The work of my lab is focused on understanding the diverse functions, evolution, and biogenesis of plant small RNAs, their RNA precursors and their targets.

2017 Stephen Hales Prize Winner | Riding the wave: from stress to resilience

Speaker	Julia Bailey-Serres	Organization	Professor of Genetics; Director, Center for Plant Cell Biology University of California Riverside
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Our group has deciphered genetic mechanisms that underlie responses to transient water stresses, including flood and drought, from the cellular to the organismal level in rice and Arabidopsis. The tuning of gene regulation from chromatin to translation is critical during short-term acute stress and post-stress recovery. Recent studies provide insights into cellular plasticity that promotes physiological acclimation or developmental adaptation that foster productivity in challenging environments.

**MJ-2-O-Major Symposium II: CSPB President's Symposium,
Integrating Signals in Plant Cell Biology and Development,
Overview by Organizer Geoffrey Wasteneys, CSPB President**

Speaker	Goeffrey Wasteneys, PhD	Organization	Professor, University of British Columbia, Department of Botany
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Plants have evolved complex cellular mechanisms that optimize their development and enable them to perceive and respond effectively to both endogenous and environmental cues. This symposium will highlight the latest discoveries on sensory, transcriptional and physiological responses in plants. The topics encompass mechanical sensing, pollen selection and rejection, transcriptional networks under the control of auxin, and the endomembrane-mediated processes that drive cellular expansion.

MJ 2-1- Stretching the Imagination: Mechanosensitive Channels in Plants

Speaker	Elizabeth Haswell, PhD	Organization	Associate Professor, HHMI Faculty-Scholar Washington University in Saint Louis
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A long-standing question is how biological systems sense and perceive mechanical signals such as osmotic pressure, gravity, and touch. One well-established molecular mechanism for force sensing is the activation of mechanosensitive (MS) ion channels. The Mechanosensitive channel of Small conductance (MscS) from *E. coli* functions as a hypo-osmotic safety valve, opening in response to increased membrane tension and preventing cellular rupture. Genes predicted to encode MscS homologs are found in genomes from all three kingdoms of life. We have been characterizing the structure, function, and regulation of ten MscS-Like (MSL) proteins in the model plant *Arabidopsis thaliana*. Based on their modest homology to MscS and high topological diversity, we have proposed that MSLs might (1) sense and respond to sources of membrane tension other than environmental hypo-osmotic shock; (2) be regulated by mechanisms in addition to membrane tension; and (3) signal in ways that are separable from ion flux. Evidence in support of all three of these hypotheses will be presented.

MJ 2-2- Auxin transcriptional networks from beginning to end

Speaker	Mark Estelle, PhD	Organization	Distinguished Professor and Chair, UC San Diego
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Auxin controls growth and diverse physiological processes through a complex transcriptional network that includes thousands of genes. Auxin regulates gene expression by promoting the degradation of transcriptional repressors called Aux/IAA proteins. The 29 Aux/IAA genes in Arabidopsis exhibit unique but partially overlapping patterns of expression. Although some studies have suggested that individual Aux/IAA genes have specialized function, genetic analyses of the family have been limited by the lack of loss-of-function phenotypes, presumably because of overlapping function. Further, with a few exceptions, our knowledge of the factors that regulate Aux/IAA expression is limited. We hypothesize that transcriptional control of Aux/IAA genes plays a central role in the establishment of the auxin-signaling pathways that regulate organogenesis, growth, and environmental response. To identify transcription factors that regulate the Aux/IAA genes, we performed a yeast-1-hybrid screen with 15 Aux/IAA promoters against ~2000 Arabidopsis TFs. Our results indicate that the Aux/IAA genes are regulated by many transcription factors implicated in diverse processes. We have focused on regulation of Aux/IAA by the DREB2A/B transcription factors. The DREB2 proteins have been described as master regulators of ABA-independent responses to drought, heat and cold. Consistent with this, our genetic studies indicate that several Aux/IAA genes are required for drought tolerance. In my talk I will describe results that explain this requirement.

MJ 2-4- Vacuoles – pumping up the plant volume

Speaker	Karin Schumacher, PhD	Organization	Professor, Heidelberg University
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Plant architecture follows the need to collect CO₂, solar energy, water and mineral nutrients via large surface areas. It is by the presence of a central vacuole that fills much of the cell volume that plants manage to grow at low metabolic cost. In addition vacuoles buffer the fluctuating supply of essential nutrients and help to detoxify the cytosol when plants are challenged by harmful molecules. Despite their large size and multiple important functions, our knowledge of vacuole biogenesis and the machinery underlying their amazing dynamics is still fragmentary. In my presentation, I will share our insights into the process of vacuole biogenesis as well as a surprising link between vacuolar proton-pumps, metabolism and stress-tolerance that we recently uncovered.

CS-1-1 – Nutrient sensing via O-GlcNAcylation in plants

Speaker	Shouling Xu	Organization	Principle Investigator, Carnegie Institution for Science
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Nutrient sensing is important to both plants and animals. One important nutrient sensing pathway is through O-linked N-acetylglucosamine transferases (OGTs), which modify and modulate target proteins using donor substrate UDP-GlcNAc derived from nutrients through the hexosamine biosynthetic pathway. Genetic studies have shown essential functions of O-GlcNAc modification in plants. However, the proteins and sites subject to this post-translational modification were largely unknown. Using lectin weak affinity chromatography to enrich modified peptides, followed by mass spectrometric analysis, we reported the first large scale proteomic identification of O-GlcNAc-modified proteins and sites in the model plant *Arabidopsis thaliana* (1). Our study generates a snapshot of the O-GlcNAc modification landscape in plants, indicating functions in many cellular regulation pathways and providing a powerful resource for further dissecting these functions at the molecular level. I will report a further improved method to enrich O-GlcNAc modified proteins, and our progress on understanding substrates, function and regulation of O-GlcNAcylation in plants.

1. Xu SL, Chalkley RJ, Maynard JC, Wang W, Ni W, Jiang XY, Shin K, Cheng L, Savage D, Hühmer AFR, Burlingame AL, Wang ZY. Proteomic analysis reveals O-GlcNAc modification on proteins with key regulatory functions in *Arabidopsis*. 2017. PNAS, PMID: 28154133.

Co-Authors

Zhi-yong Wang, Professor – Carnegie Institution for Science

CS-1-2 – Putative Plastid Rhomboid Protease Plays a Role in Phosphatidate Metabolism in *Arabidopsis thaliana*

Speaker	Anastasiya Lavell	Organization	Graduate Student, Michigan State University
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The thylakoid membranes of the chloroplast house the photosynthetic machinery that converts light into chemical energy. Chloroplast membranes are unique from other plant organelles in their lipid makeup, which is dominated by mono and digalactosyldiacylglycerol (MGDG and DGDG). The predominant galactolipid, MGDG, can be made through both plastidic (prokaryotic) and ER (eukaryotic) pathways in *Arabidopsis*, resulting in two distinct species of lipid. Phosphatidate has been shown to be the first acylated lipid species in the plastid galactolipid biosynthetic pathway, providing a pool of diacylglycerol for MGDG Synthase. The enzymatic reactions yielding these galactolipids have been well-described, however, regulation of these steps is unknown at this time. Intramembrane proteolysis, as demonstrated by members of the rhomboid-like family of proteins, is one example of regulation through proteolysis. One such rhomboid-like protein 10 (RBL10), found in the chloroplasts of *Arabidopsis thaliana*, may be involved in maintaining biosynthesis of MGDG through the plastidic pathway. Plants disrupted in the gene encoding RBL10 have greatly decreased 16:3 and increased 18:3 acyl chain abundance in MGDG in leaves. Additionally, *rbl10* mutants show reduced ¹⁴C – acetate incorporation into MGDG during the first hour of pulse-chase labeling, indicating a reduced flux through the prokaryotic galactolipid biosynthesis pathway. While plastid MGDG biosynthesis is reduced in *rbl10* mutants, they are capable of synthesizing PA, as well as making normal amounts of MGDG by compensating with ER lipid precursors. Though the molecular mode of action remains to be described, these preliminary findings link this protease to utilization of PA for galactolipid biosynthesis and give an opportunity to characterize a novel lipid regulatory mechanism.

Co-Authors

John Froehlich – Michigan State University; Olivia Baylis – Michigan State University; Anthony Rotondo – Michigan State University; Christoph Benning – Michigan State University

CS-1-3- Sex-dependent variation of pumpkin (*Cucurbita maxima* cv Big Max) nectar and nectaries as determined by proteomics and metabolomics

Speaker	Elizabeth Chatt	Organization	Graduate Student , Iowa State University
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Nectar is a floral reward that sustains mutualisms with pollinators, which in turn, improves fruit set. While it is known that nectar is a chemically complex solution, extensive identification and quantification of this complexity has been lacking. *Cucurbita maxima* c.v. Big Max, like many cucurbits, is monoecious with separate male and female flowers. Attraction of bees to the flowers through the reward of nectar is essential for reproductive success in this economically valuable crop. In this study, the sex-dependent variation in composition of male and female nectar and the nectary were defined using a combination of GC-MS based metabolomics and LC-MS/MS based proteomics. Metabolomics analysis of nectar detected 88 metabolites, of which 40 were positively identified, and included sugars, sugar alcohols, aromatics, diols, organic acids, and amino acids. There were differences in 29 metabolites between male and female nectar. The nectar proteome consisted of 46 proteins, of which 70% overlapped between nectar types. Only two proteins were unique to female nectar, compared to 10 specific to male nectar. The nectary proteome, defined using iTRAQ labeling, was composed of 339 proteins, 71% of which were descriptively annotatable by homology to *Plantae*. The abundance of 45 proteins differed significantly between male and female nectaries. This rich dataset significantly expands the known complexity of nectar composition.

Co-Authors

Patrick von Aderkas – University of Victoria; Clay Carter – University of Minnesota Twin Cities; Derek Smith – UVic Genome BC Proteomics Centre; Monica Elliott – UVic Genome BC Proteomics Centre; Basil Nikolau – Iowa State University

CS-1-4 – Comparative genomics of nectaries and nectars in the dicots reveals key conserved modules involved in nectar synthesis and secretion

Speaker	Clay Carter	Organization	Associate Professor, University of Minnesota
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Plants attract mutualistic animals by offering a reward of nectar. Specifically, floral nectar (FN) is produced to attract pollinators, whereas extrafloral nectar (EFN) mediates indirect defenses through the attraction of mutualist predatory insects to limit herbivory. Nearly 90% of all plant species, including 75% of domesticated crops, benefit from animal-mediated pollination, which is largely facilitated by FN. Moreover, EFN represents one of the few defense mechanisms for which stable effects on plant health and fitness have been demonstrated in multiple systems, and thus plays a crucial role in the resistance phenotype of plants producing it. In spite of its central role in plant-animal interactions, the molecular events involved in the development of both floral and extrafloral nectaries (the glands that produce nectar), as well as the synthesis and secretion of the nectar itself, have been poorly understood until recently. To date, a holistic and coordinated characterization of nectar secretion from a comparative genomic and molecular perspective has been lacking. Toward this end, we have evaluated the transcriptomes and proteomes of floral and extrafloral nectaries throughout development across twelve dicotyledonous species and identified core sets of genes and modules involved in the synthesis and secretion of nectar across species, as well as its regulation. Key conserved modules include hormonal biosynthesis and response pathways, as well as genes involved in carbohydrate metabolism and transport. Similarly, metabolite profiling coupled with transcriptomic and reverse genetics approaches identified specific loci responsible for nectar characteristics that influence mutualist visitation. For example, genes and pathways required for the synthesis of sucrose-rich and proline-rich nectars across species were identified.

Co-Authors

Rahul Roy – University of Minnesota; Elizabeth Chatt – Iowa State University; Erik Solhaug – University of Minnesota; Anthony Schmitt – University of Minnesota; Jason Thomas – University of Minnesota; Marshall Hampton – University of Minnesota Duluth; Robert Thornburg – Iowa State University; Basil Nikolau – Iowa State University

**CS-1-5- Type III PKS and biodiversity of plant secondary metabolites:
Can we manipulate it for the production of novel molecules?**

Speaker	Soniya Eppurath	Organization	Scientist F, Rajiv Gandhi Center for Biotechnology
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Type III Polyketide synthases (PKSs) forms a group of ‘fascinating biosynthetic enzymes’ involved in the biosynthesis of varied polyketides with numerous applications in pharmaceutical industry. These enzymes catalyze the production of various secondary metabolites in plants such as chalcones, acridones, quinolones, curcuminoids etc. Structurally, they are homodimeric proteins, where the active site in each monomeric subunit iteratively catalyzes the priming, extension and cyclization reactions to produce an array of plant secondary metabolites. The simple structure, catalytic versatility and wide-ranging substrate specificity of type III PKSs make them as one of the best candidates for the engineering of biocatalysts. They can accept a number of unnatural substrates and produces novel structural scaffolds with intense therapeutic potential.

In our studies we have identified and characterized a quinolone and acridone forming type III PKS from Indian Bael tree (*Aegle marmelos* Correa) (AmQNS). The reaction involves decarboxylative condensation of malonyl-CoA with N-methylantraniloyl-CoA to form an intermediate, which spontaneously cyclize by amide formation to yield 4-hydroxy- 2(1H)-quinolone. AmQNS can also synthesize benzalacetone by using p-coumaroyl-CoA as starter substrate. Modeling and structural analysis suggested that the CoA-binding tunnel and the catalytic triad (C-H-N) are maintained in AmQNS, with minute alterations (CHS-conserved residues Thr132, Ser133, and Phe265 are replaced by Ser132, Ala133, and Val265, respectively) in the functionally important region. Kinetic studies revealed that the catalytic efficiency of AmQNS to accept larger acyl-CoA’s are several fold higher than that for smaller substrates. The catalytic and structural significance of active site residues were investigated through site-directed mutagenesis. Modeling studies suggested that AmQNS might have emerged by the gain of function (by the substitution of two active site residues) mutation from a structural homolog ‘chalcone synthase (CHS), a type III protein’ and provided an insight into the enzymatic mechanism that could be used to produce pharmaceutically significant products.

**CS-1-6 – JAZ proteins mitigate the metabolic cost of plant defense
against insect herbivores**

Speaker	Qiang Guo, PhD	Organization	PhD student, Michigan State University
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The plant hormone jasmonate activates anti-insect defense responses that are metabolically costly and often linked to reduced growth. Although it is known that jasmonate exerts its effects by triggering the degradation of JASMONATE ZIM DOMAIN (JAZ) transcriptional repressor proteins, genetic redundancy within the JAZ family has hampered efforts to understand the biological consequences of unleashing the jasmonate response over extended developmental time scales. Here, we combined mutations within the 13-member Arabidopsis JAZ gene family to investigate the relationship between defense, growth, and reproduction under conditions of chronic JAZ depletion. A jaz decuple line (jazD) harboring mutations in ten JAZ genes exhibited hyper-resistance to attack by insect larvae, strongly reduced vegetative growth rate, and compromised seed production. Metabolic phenotypes of jazD discerned from global protein and transcript profiling were indicative of elevated carbon allocation to protein- and amino acid-based defense traits controlled by both the jasmonate-MYC and ethylene-ERF branches of immune signaling. The strong defense sink in jazD leaves was linked to increased respiration and hallmarks of carbon starvation, whereas area-based photosynthetic efficiency was unaffected. We propose that JAZ proteins flexibly adjust growth-defense conflict to match anticipated changes in resource availability, potentially avoiding the detrimental effects of carbon limitation that may arise during growth-to-defense transitions.

Co-Authors

Ian Major – Michigan State University Yuki Yoshida – The University of Tokyo Kun Wang – Michigan State University Koichi Sugimoto – Michigan State University George Kapali – Michigan State University Christoph Benning – Michigan State University Gregg Howe – Michigan State University

CS-7-4- Large-scale comparative epigenomics reveals hierarchical regulation of non-CG methylation in Arabidopsis

Speaker	Jixian Zhai	Organization	Associate Professor, Southern University of Science and Technology
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Genome-wide characterization by next-generation sequencing has greatly improved our understanding of the “landscape” of epigenetic modifications. Since 2008, whole-genome bisulfite sequencing (WGBS) has become the gold standard for DNA methylation analysis and a tremendous amount of WGBS data has been generated by the research community. However, the systematic comparison of DNA methylation profiles to identify novel regulatory mechanisms has yet to be fully explored. Here, we re-processed the raw data of over five hundred publicly available Arabidopsis WGBS libraries from various mutant backgrounds, tissue types, and stress treatments, and also filtered them based on sequencing depth and efficiency of bisulfite conversion. This enabled us to identify high-confidence differentially methylated regions (hcDMRs) by comparing each “test” library to over fifty high-quality “wild-type” controls. We developed statistical and quantitative measurements to analyze the overlapping of DMRs and to cluster libraries based on their impact on DNA methylation. In addition to confirming existing relationships, we revealed novel connections between well-known genes. For instance, MET1 and CMT3 were found to be required for the maintenance of asymmetric CHH methylation at non-overlapping regions of CMT2 targeted heterochromatin. Our comparative methylome approach has established a framework for extracting biological insights via large-scale comparison of methylomes, and can also be adopted for other omics datasets.

Co-Authors

Yu Zhang – Souther University of Science and Technology; Jake Harris – University of California, Los Angeles; Qlkun Liu – University of California, Los Angeles; Haifeng Wang – Fujian Agriculture and Forestry University; Steven Jacobsen – University of California, Los Angeles

**MJ-3-0- Major Symposium III: CSPB/ASPB Joint Symposium,
Opening Research Avenues through New Technologies,
Overview by Co-Organizers Anja Geitmann and Phil Taylor**

Speakers	Anja Geitmann, PhD	Organization	Professor & Canada Research chair, McGill University
	Phil Taylor, PhD		New Investments Lead, Monsanto

Major Symposium III: Opening Research Avenues through New Technologies (organized by Anja Geitmann and Phil Taylor) will highlight a series of novel technologies being developed in order to expand the tool-box available to researchers working on both fundamental aspects of plant biology or developing concepts for more applied research. The speakers, Karen Tanino, Amy Marshall-Colon, Dan Voytas and Todd Mockler will cover breakthroughs in exciting new topics across phenotyping, imaging, genome editing and computational tools that have enabled new research methodologies to address a variety of critical questions in modern plant biology.

MJ 3-1- Integrating sorghum pan-genomic information with high-resolution phenotyping to accelerate trait discovery and crop improvement

Speaker	Todd Mockler, PhD	Organization	Geraldine J. and Robert L. Virgil Distinguished Investigator; Principal Investigator, Donald Danforth Plant Science Center
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Sorghum bicolor is a cereal crop and emerging cellulosic biofuel feedstock and serves as a model system for other bioenergy and food crops. Currently, sorghum is the focus of the ARPA-E TERRA program, which is currently developing and operating cutting-edge remote sensing platforms, complex data analytics tools, and conducting high-throughput plant phenotyping in both controlled greenhouses and field sites. Genomic re-sequencing of the sorghum bioenergy association panel (BAP), a diverse panel of ~400 sorghum lines, was performed in order to accelerate trait discovery and breeding. The sorghum BAP encompasses all five major races, all 16 intermediate races, as well as vast geographic ranges and climates. Through the sorghum BAP, we are exploring the scope of natural variation in the sorghum pan-genome for copy number variation (CNV), structural variation (SV), and presence/absence variation (PAV). De novo assembly of the sorghum pan-genome expands the sorghum gene space by >15%. Our analysis indicates that the core genome of sorghum comprises ~35,000 genes with ~15,000 additional genes comprising the variable or accessory genome not present in all accessions of a sorghum. Pan genomic information is being leveraged to inform genotype-phenotype association studies using robust sensor-based phenotypic data collected in the ARPA-E TERRA program. Population substructure analysis reveals 5-6 unique subpopulations within sorghum containing potentially adaptive gene sets that may be useful for allele mining approaches. The combination of precision field and greenhouse phenotyping on this diverse collection will allow for accelerated identification of genomic elements controlling agronomically important phenotypes including yield, growth rate, biomass accumulation, water-use efficiency, drought and disease resistance. Using pan-genomic information will maximize the available genetic resources to map key traits and accelerate breeding approaches to enhance this globally important crop.

**MJ 3–2– Integrative modeling and visualization for the development of
in silico crops**

Speaker	Amy Marshall-Colon, PhD	Organization	Assistant Professor, University of Illinois Urbana–Champaign
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Current crop models predict an increasing gap between food supply and demand over the next 50 years. Technology is needed to predict the fitness of various crops in response to climate and resource availability, and also aid in the design of crop ideotypes. I will highlight our efforts to generate virtual plant models that capture whole system dynamics in response to in silico environmental and genetic perturbations, using the Crops in silico (Cis) computational framework. The Cis multi-scale modeling platform was used to: i) integrate models of gene expression, photosynthetic metabolism, and leaf physiology to evaluate the effect of photosynthesis and transpiration under various environmental conditions. ii) Link a functional-structural root model to a process-based canopy model of maize to explore crop response to environmental inputs. iii) Combine modeling and advanced visualization approaches to make direct observations about changes in plant structure, biomass, and yield in response to environmental perturbations. Outcomes of these efforts include i) an improved prediction accuracy for soybean photosynthesis rate in the context of perturbed atmospheric CO₂ levels; ii) enhanced estimates of sink-source dynamics in maize under nutrient limited conditions; and iii) refined canopy-level photosynthesis rate predictions resulting from a more accurate simulation of leaf area and leaf angle using 3D visualization tools. The improved accuracy of model predictions and the realistic rendering of model simulated plants is an important step toward the in silico “testing” of ideotype designs under different environmental conditions, whereby dozens of observations about ideotype performance under varying scenarios can be made by researchers. In silico exploration has the potential to help researchers target components of the underlying crop genetics for engineering to ultimately enhance crop yield and nutritional quality.

MJ 3-3- Applications of Synchrotron Technology in Plant Biology Research

Speaker	Karen Tanino	Organization	Professor, University of Saskatchewan
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While synchrotron techniques are powerful tools in material and environmental sciences, they are underutilized in plant research. Relative ease of sample preparation, non-destructive analysis, high spatial resolution and multiple response measurements within a single sample are among advantages. Illustrations will include Fourier transform mid infrared spectromicroscopy, high resolution X-ray fluorescence imaging and X-ray absorption spectroscopy. For example, auxin transporters from PIN-FORMED family of membrane proteins were recently implicated in plant responses to specific elemental exposure. Conventional elemental analysis of bulk tissues showed PIN2-deficient *A. thaliana* mutant exhibited large differences in arsenic root accumulation relative to wild-type when exposed to arsenite in the growth medium, but details of tissue distributions were unclear. Preliminary X-ray Fluorescence Imaging and X-ray Absorption Spectroscopy data in live plant samples demonstrated that the arsenic is localized in the root tip meristem of the mutant plant in the As(III) thiolate-bound form, and the pattern of As distribution in tissues is consistent with the hypothesis that PIN2 may indeed facilitate transportation of arsenicals in plants. Synchrotron-based phase contrast imaging was also combined with Fourier Transform mid-Infrared Spectroscopy to identify structural and biochemical factors localized to the apoplasts of florets and rachis in wheat resistant to Fusarium Head Blight. Additional examples range from non-destructive imaging of corn roots in soil; spatial localization of protein secondary structure and compositional analysis of pollen surface lipids; spatial localization of methyl-esterified homogalacturonan pectin of the apoplast and simultaneous non-destructive localization of multiple nutrients in leaves. Mid-IR spectral corn leaf analysis indicated differential levels, composition of cuticular wax deposition among glossy lines. Arabidopsis mutant and overproducing lines enabled identification of a gene critical for cuticular wax accumulation under low-temperature stress. Multiple diverse plant systems including corn, wheat, Norway spruce buds, Arabidopsis will demonstrate use of synchrotron technology.

Co-Authors

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MJ 3-4- Editing the Plant Genome

Speaker	Daniel Voytas, PhD	Organization	Professor and Director, Center for Precision Plant Genomics University of Minnesota
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The ability to precisely modify plant genomes through homologous recombination (HR) promises to advance both basic and applied plant biology. However, even with the use of sequence-specific nucleases, which stimulate HR by creating targeted DNA double-strand breaks, there are only a handful of studies that report precise editing of endogenous plant genes. Our group has been focusing on two efforts to more effectively modify plant genomes through HR. In one, we are developing new vectors to deliver sequence-specific nucleases and DNA repair templates to plant cells. Specifically, we have been using geminivirus replicons, which function in both monocots and dicots, to amplify nuclease-encoding cassettes and DNA repair templates. In a second effort, we are attempting to achieve HR by either genetically manipulating DNA repair pathways or delivering nucleases and repair templates to cells proficient in HR. Progress on our efforts to optimize gene targeting strategies will be reported.

CS-12-4- The impact of autophagy and oxidative stress on the turnover of selective proteins in Arabidopsis

Speaker	Harvey Millar, PhD	Organization	Director-ARC Center of Excellence in Plant Energy Biology The University of Western Australia
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We are using progressive ^{15}N labelling of Arabidopsis to provide a birds-eye view of the activity of the proteolysis network as it maintains and sculpts the plant proteome. Using peptide mass spectrometry, the progressive labelling of new peptides and the decrease in the abundance of peptides with natural isotope profiles enabled the degradation rate of specific leaf and root proteins to be quantified. This allows deep insights in selective proteolysis of proteins in vivo in different mutant backgrounds. It also enables analysis of the selective degradation of subunits of protein complexes, giving information on the regulation and maintenance of these structures. We will present new evidence of the changes in turnover rate of specific proteins in leaves and roots in several atg mutants in Arabidopsis which are altered in autophagy. This shows the selective effect of pathways in autophagy on the fate of organelle types and on biochemical functions in leaves and roots. We will also show the effect of oxidative stress on turnover rates of 80S ribosome and 26S proteasome subunits in Arabidopsis following purification of the complexes from ^{15}N labelled Arabidopsis cells.

CS-11-5- Structure and mechanism of isopropylmalate dehydrogenase from *Arabidopsis thaliana*: insights on leucine and aliphatic glucosinolate biosynthesis

Speaker	Soon Goo Lee	Organization	Postdoctoral Associate, Washington University in St. Louis
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Isopropylmalate dehydrogenase (IPMDH) and 3-(2-methyl-thio)ethylmalate dehydrogenase catalyze the oxidative decarboxylation of different β -hydroxyacids in the leucine- and methionine-derived glucosinolate biosynthesis pathways, respectively, in plants. Evolution of the glucosinolate biosynthetic enzyme from IPMDH results from a single amino acid substitution that alters substrate specificity. Here, we present the x-ray crystal structures of *Arabidopsis thaliana* IPMDH2 (AtIPMDH2) in complex with either isopropylmalate and Mg^{2+} or NAD^+ . These structures reveal conformational changes that occur upon ligand binding and provide insight on the active site of the enzyme. The x-ray structures and kinetic analysis of site-directed mutants are consistent with a chemical mechanism in which Lys232 activates a water molecule for catalysis. Structural analysis of the AtIPMDH2 K232M mutant and isothermal titration calorimetry supports a key role of Lys232 in the reaction mechanism. This study suggests that IPMDH-like enzymes in both leucine and glucosinolate biosynthesis pathways use a common mechanism and that members of the β -hydroxyacid reductive decarboxylase family employ different active site features for similar reactions.

Co-Authors

Ronald Nwumeh – Washington University; Joseph Jez, Ph.D. – Washington University

CS-16-1- Network-based pattern classification associates temporal dynamics of the transcriptome with circadian regulation of plant fitness

Speaker	Kathleen Greenham, PhD	Organization	Postdoctoral Researcher, Dartmouth College
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The synchronization of metabolic and physiological processes with the environment results in time-of-day dependence (gating) of responses to stress. Temporal gating is thought to maximize stress resistance while minimizing growth costs. The temporal coordination of environmental signals with plant physiology requires an endogenous circadian oscillator. Latitudinal gradients in circadian clock period among natural populations and highly bred crops support the role of the clock as a central regulator of plant adaptability. To understand the underlying transcriptional network contributing to drought response we performed a two-day RNAseq time course experiment in the crop *Brassica rapa* comparing drought with well-watered conditions, where circadian regulation results in time of day-dependent changes in stomatal conductance and CO₂ assimilation.

A comparative network-based approach provided the temporal resolution to correlate co-expressed modules with dynamic changes in physiology. Early drought perception causes extensive rearrangement of the gene regulatory network that is best characterized by altered gene expression patterns. Classifying these changes by assessing differential expression at each time point fails to capture daily transcriptome dynamics. To retain the pattern of transcript abundance over time we used the module membership measures from the network analysis to test for altered expression patterns under drought. We associated specific responses to drought of circadian clock regulated genes assigned based on two 48 h circadian RNAseq datasets collected following either photocycle or thermocycle entrainment with 2 h sampling. In addition to support for circadian involvement in drought response, this pattern discovery approach identified examples of divergence among homeologs. These represent candidates for subfunctionalization following genome triplication since diverging from *Arabidopsis thaliana* and supports previous work showing preferential retention of circadian clock genes in *B. rapa*. This analytic pipeline for assessing changes in expression pattern can be applied to any time series dataset and will be available as a package in R.

Co-Authors

Ryan Sartor – North Carolina State University; Ping Lou – Dartmouth College; Patrick Edger – Michigan State University; Robert VanBuren – Michigan State University; C. Robertson McClung – Dartmouth College

**CS-16-2- Modeling degrees of genetic redundancy among paralogs
in *Arabidopsis thaliana***

Speaker	Siobhan Cusack	Organization	Graduate student, Michigan State University
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Genetic redundancy refers to paralogous genes maintaining seemingly redundant functions; a single gene mutant (single mutant) may not show an apparent phenotype until additional paralogs are knocked out in combination (i.e. double or higher-order mutants). In *Arabidopsis thaliana*, many single mutants have no reported phenotype. This may be due to genetic redundancy or because they have conditional or extremely subtle phenotypes, among other possibilities. Here, a machine-learning approach is applied to build a model for prediction of the extent to which an *A. thaliana* gene pair is genetically redundant based on evolutionary conservation, duplication patterns and mechanisms, epigenetic and post-translational modifications, gene expression patterns, and network properties of paralogous gene pairs. The predictions are then tested using hold-out, published phenotype data and a library of *A. thaliana* Mitogen Activated Protein Kinase single and double mutants. To capture subtle and/or conditional phenotypes in single mutants, we impose low-level abiotic stress and examine growth rate, photosynthetic efficiency, and most importantly, lifetime fitness estimates that measure the combined impact of subtle phenotypes on reproductive success. With this comprehensive phenotyping, a fine-scale measure of the degree of genetic redundancy between these gene pairs is generated. The genetic redundancy model sheds light on characteristics that may contribute to long-term maintenance of paralogs that are seemingly functionally redundant. It additionally allows for more targeted generation of functionally informative double mutants, advancing the study of gene functions.

Co-Authors

Fanrui Meng – Michigan State University; Peipei Wang – Michigan State University; Bethany Moore – Michigan State University; Paityn Donaldson – Michigan State University ; Jeffrey Conner – Michigan State University; Patrick Krysan – University of Wisconsin-Madison; Melissa Lehti-Shiu – Michigan State University; Shin-Han Shiu – Michigan State University

CS-16-3- Tripal: an open-source, standards-based toolkit for construction of online biological databases

Speaker	Stephen Ficklin	Organization	Assistant Professor, Washington State University
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With the availability of large-scale, high-throughput data, challenges exist for research communities who desire to create online data repositories. The financial, physical and personnel resources needed to create, maintain and improve a community database can be overwhelming in comparison to the ease at which data is increasingly obtained. These online databases fill an important niche specific to their respective research community by combining data with tools, custom searches, and visualizations not provided by larger online repositories. Tripal is a popular, open-source toolkit developed to assist with the construction of online biological data repositories. It is well suited for creation of genomics, transcriptomics and breeding databases and uses community-developed standards to provides data pages, search tools, and a graphical interface for site-specific customizations. In addition to its default features, Tripal provides an Application Programming Interface (API) to allow a site developer to create new customizations, or extensions, that are specific for an individual site. Moreover, an active community site developers share code, experience and expertise. Therefore, custom extensions can be shared with others, and this exchange helps decrease costs, ensure cross-site compatibility, and ensures long-term sustainability of all Tripal sites. Recently, the Tripal Gateway Project, funded by the US National Science Foundation (NSF) award #1443040, has added functionality to address challenges related to storage, transfer, and analysis of large data. Specifically, three new capabilities are provided: 1) mechanisms for exchange of data between sites, 2) best practices for optimizing data transfers, and 3) integration with the Galaxy Project (an interface for execution of complicated scientific workflows) for large data workflow analysis. Thus Tripal offers new sites model-organism style functionality, and supports large-data needs, but requires fewer resources.

Co-Authors

Chun-Huai Cheng – Washington State University; Shawna Spoor – Washington State University; Ming Chen – University of Tennessee; Abdullah Almsaeed – University of Tennessee; Bradford Condon – University of Tennessee; Nick Mills – Clemson University; Nick Watts – Clemson University; Connor Wytko – Washington State University; Lacey-Anne Sanderson – University of Saskatchewan; Emily Grau – University of Connecticut; Nic Herndon – University of Connecticut; Brian Soto – Washington State University; Sook Jung – Washington State University; Alex Feltus – Clemson University; Margaret Staton – University of Tennessee; Jill Wegrzyn – University of Connecticut; Dorrie Main – Washington State University

CS-16-4- Mutagenomics:

a high throughput strategy for screening of mutant lines

Speaker

Charles Hodgens

Organization

UNC Chapel Hill

In a mutagenetic screen, often a cumbersome task is the identification of causal genes. Generally, this necessitates the creation of a mapping population where the co-segregation of the mutant genotype with genetic markers is assessed. The mapping process has been greatly accelerated with the use of mapping-by-sequencing methods. However, these methods require the user to generate a segregating population, requiring two generations of growth and the selection of plants with the mutant phenotype from the F2 population. Further, such approaches focus on small set of target genes at a time. We present a strategy, dubbed “mutagenomics,” for screening through uncharacterized, uncrossed mutant lines in a parallel fashion. This strategy has the potential to reduce the number of candidate genes from mutant lines without requiring the researcher to perform back-crosses. Mutagenomics is a two-stage, two-prong strategy. After resequencing the genome of mutant lines, the first stage is the removal of lines with mutations in known genes. The second stage is a dual strategy which assesses whether any genes are mutated more often than expected by chance (i.e. identification of multiple alleles) and whether any genes are found to be mutated in multiple lines of common descent. This method does not preclude the use of mapping-by-sequencing technologies or traditional marker-based mapping. Either method can be used to map mutations in lines where mutagenomics did not identify a candidate mutation.

We have applied mutagenomics to mutant lines from a screen for hyposensitivity to the hormone cytokinin, a critical regulator of diverse set of biological processes in plants. A pool of 28 mutant lines have been sequenced and mutations in *ahk4* and *hy5* were identified as very strong candidates for causal mutations. We anticipate this strategy will accelerate the pace and utility of genetic screens.

Co-Authors

Joseph Kieber – UNC Chapel Hill

CS-16-5- MVApp - Multivariate Analysis Pipeline for Streamlining the Identification of New Plant Traits with Significant Contribution to Stress Tolerance

Speaker	Magdalena Julkowska	Organization	PostDoc, KAUST
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Plants are master shape-shifters, constantly adapting their architecture to enhance resource acquisition, ensuring reproductive success. These metamorphoses are governed by genotype and environment (GxE) interactions. Understanding the full range of plant's morphological versatility, environmental triggers and adaptive relevance often requires a thorough assessment of large numbers of genotypes under various conditions. Recent advances in phenotyping technologies allow the high-throughput quantification of traits reflecting plant size, shape, photosynthetic efficiency and transpiration rate. With increasing number of phenotypes it is becoming increasingly crucial, and proportionally complicated, to identify redundancy, correlations, and impact in phenotypic datasets. Therefore, we developed the MVApp (mvapp.kaust.edu.sa), a user-friendly multivariate analysis tool for large or small datasets. The MVApp features include:

Curve fitting for plant growth estimation

Data curation for possible outlier values

Data examination for significant differences between genotypes or treatments

Correlation analysis across different traits

Principle Component Analysis

Clustering analysis

We show how MVApp enhanced the understanding of traits contributing to salt stress responses in large *Arabidopsis thaliana* natural diversity panels. We think that MVApp will serve the scientific community streamlining laborious multivariate analysis and enhancing transparent data curation and analysis.

Co-Authors

Stephanie Saade - KAUST; Mariam Awlia - KAUST; Gaurav Agarwal - KAUST; Ge Gao - KAUST; Mitchell Morton - KAUST; Yveline Paillies - KAUST; Mark Tester - KAUST

CS-16-6- Leveraging More from de novo Transcriptome Assemblies Using Machine Learning

Speaker	Matt Stata	Organization	PhD Candidate, University of Toronto
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Plant genomes are often large and costly to sequence compared with other eukaryotic systems. For many research applications, working with transcriptomes rather than full genomes represents a much more cost-effective alternative. However, in the absence of a reference genome de novo assembly of RNA-seq data represents a considerable computational challenge: gene expression can lead to transcript abundance levels that vary by several orders of magnitude, complicating error detection, while alternative splice isoforms are very difficult to resolve. Here, I will present a classification method based on machine learning to distinguish genuine paralogous gene copies from either splice isoforms or variant assemblies of the same gene. Features used in classification include pairwise alignment details and BLAST statistics, which are easy to obtain. This method is applicable for both single species and groups of related species, with a more robust feature set being possible in the latter case. I will show how this method has been successfully used to obtain primary coding sequences for the transcriptomes of two related species of *Atriplex* without the aid of a reference genome.

Co-Authors

Tammy Sage – University of Toronto; Rowan Sage – University of Toronto

CS-21-1- Metabolite transport between cellular organelles in photorespiration and C4 photosynthesis

Speaker

Andreas Weber

Organization

Heinrich Heine University

Plastids are metabolically extraordinarily active and versatile organelles that are found in all plant and algae cells. Plastidial metabolism is tightly interfaced with that of the surrounding cytoplasm via solute transporters that reside in the inner of two layers of envelope membrane that circumference the plastid. Particular tight metabolic connections exist between chloroplasts, peroxisomes, and mitochondria during photosynthesis since these organelles cooperate in photorespiration, the metabolic repair process that detoxifies 2-phosphoglycolic acid (2-PG). The photorespiratory pathway not only detoxifies the oxygenation product of the Rubisco reaction, it also recovers part of the carbon contained in 2-PG and it transfers redox power from the chloroplasts to the mitochondria. Further, photorespiration provides a stepping stone for the evolution of the highly efficient biochemical carbon concentrating mechanism of C4photosynthesis.

We will here report on our recent findings on the role of organellar solute transporters in facilitating metabolic flux in photorespiration and C4photosynthesis, with particular emphasis on the role of inter-organellar and inter-cellular transport processes in the evolution of C4photosynthesis.

CS-21-2– Sugar transport to guard cells is required for stomatal opening and plant growth

Speaker

Diana Santelia, PhD

Organization

**Group Leader,
University of Zurich**

CO₂ for photosynthesis enters plants via stomata – small adjustable pores on the leaf surface. Stomatal opening is promoted by increase in the turgor pressure of the two flanking guard cells through accumulation of osmotically active inorganic (K⁺, Cl⁻) and organic (malate²⁻ and sugars) solutes. Given that CO₂ fixation within guard cells can only provide a limited amount of carbon, symplastically isolated guard cells likely rely on external carbon sources to fulfil their metabolic needs. Here, we investigated the role of sugar import in stomatal opening in *Arabidopsis thaliana*. We show that the synergistic action amongst members of the plasma membrane monosaccharide/proton symporters STP family is required for stomatal opening and CO₂ uptake driving photosynthesis and biomass production. Furthermore, we reveal that the uptake of apoplastic sugars into guard cells provides the main source of carbon for guard cell starch accumulation. Thus, at the start of the day, guard cell metabolism for stomatal opening relies predominantly on mesophyll-derived sugars imported into guard cells in the form of monosaccharides. This study highlights that a tight coordination between mesophyll and guard cell carbohydrate metabolism is critical to promote stomatal opening and plant growth.

Co-Authors

Arianna Nigro – University of Zürich; Klára Panzarová – Photon Systems Instruments

CS-21-3- Is Elevated Carbon Dioxide-triggered Stomatal Closure Mediated via Absciscic Acid Signaling?

Speaker	Julian Schroeder, PhD	Organization	Professor, Division of Biological Sciences, UC San Diego
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Regulation of stomatal apertures in response to changing environmental conditions controls CO₂ fluxes and water loss between plants and the atmosphere. Elevated [CO₂] and the plant hormone abscisic acid (ABA) trigger stomatal closure, but remains a matter of debate whether elevated [CO₂]-triggered stomatal closure is mediated via a rapid rise in ABA concentration and it remains unknown where these pathways converge. To address these questions, stomatal CO₂ responses were analyzed in ABA synthesis mutants and in ABA receptor mutants. Time-resolved gas exchange analyses show that ABA synthesis mutants and ABA receptor mutants respond to [CO₂] elevation, whereas the response kinetics are altered. However, these analyses do not distinguish whether CO₂ elevates ABA in guard cells or whether CO₂ and ABA transduction converge further downstream at a defined point. We have pursued additional experiments in several mutant backgrounds and report patch-clamp analyses of guard cell anion channel regulation and guard cell biochemical analyses of ABA and CO₂ signaling. Further, we have used newly developed real-time ABA FRET nano-reporter plants to determine whether CO₂ concentration changes cause rapid ABA concentration changes in guard cells. Taken together these interdisciplinary investigations point to a new and unexpected understanding of how CO₂ signaling and ABA signaling both close stomata.

Co-Authors

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**CS-21-4- Chloroplasts ion transport mechanisms and their role
in photosynthesis and organellar function**

Speaker	Henning Kunz, Diploma, PhD	Organization	Assistant Professor, Washington State University
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Chloroplast ion homeostasis impacts essential processes inside the organelle such as cofactor availability, membrane potentials, and stromal and luminal pH. Consequently, the plastid's internal ion status is critical for chloroplast development and proper function of biochemical pathways, most importantly photosynthesis. Because of the central importance of the plastid for plants, disturbances in plastid ion homeostasis often affect plant physiology as a whole. Early investigations had revealed specific ion flux mediated by ion channels and ion carriers across envelope and thylakoid membranes. However, at that time, the lack of genome sequencing and tools did not allow to identify the transport genes.

The discovery of genes encoding for three chloroplast K⁺/H⁺ exchangers from the KEA family but also of plastid ion channels from the TPK and MSL family have revived this research recently. The studies of respective plant mutants provided exciting insights into the physiological significance of K⁺ transport processes across the inner envelope, and the thylakoid membranes. The data combined reveal a current gap in knowledge regarding the chloroplast K⁺ import mechanism(s). Furthermore, a closer look at previously published plastid TPK points towards important questions regarding its membrane localization.

To overcome these limitations we established an amiRNA library tool allowing for forward genetics on chloroplast-targeted gene products coupled to ionomic studies on intact isolated chloroplasts. Supported by transcriptomics we have started to characterize gene candidates for chloroplast K⁺ importers. Lastly, older and our own physiological studies indicate that K⁺ loss from the chloroplast contributes to decreased photosynthetic efficiency in glycophytes during early stages of salt-stress. We therefore envision to gain a holistic understanding of the chloroplasts K⁺ transport network and design plants with higher photosynthetic performance under salt stress by carefully modulating stromal and lumen K⁺ level. We have initiated a first phase to test the feasibility of this endeavor in crop plants.

**CS-21-5- Early plant evolution:
stress signalling circuits in the algal ancestors of land plants**

Speaker	Jan de Vries	Organization	Postdoctoral Fellow(DFG Research Fellow), Dalhousie University
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All land plants evolved from a streptophyte algal progenitor in a monophyletic event. Zygnematophyceae are, of all extant streptophyte algae, those that are most closely related to the algal land plant progenitor. One of the major questions revolving around the algal ancestors of land plants is what features enabled only this particular organism to conquer land on a global scale. A prime candidate feature is the ability to ward off terrestrial stressors, including drought, high light, and rapid chilling stress. Using comparative transcriptomics, we investigated streptophyte algal stress response signaling towards the latter two stressors. For this, we analyzed one representative of each of the six major classes of streptophyte algae, including the Zygnematophyceae Zygnema. As in land plants, high light and cold stress impacted plastid biology as indicated by differential gene expression of a variety of plastid and photosynthesis-associated genes. Zygnema further invested the highest transcript budget into plastid biology-associated gene expression. This suggests that the plastid of streptophyte algae might be an equally important hub in stress-response as in land plants. While our data pinpoint the presence of many stress signaling circuits known from land plants in various streptophyte algae, Zygnema particularly stands out: only Zygnema has the full genetic repertoire for sensing the stress phytohormone abscisic acid and mounting its canonical signaling pathway. This not only underscores the phylogenetic position of the Zygnematophyceae but is also directly relevant for the inferences of the algal land plant progenitors stress signaling capacities. From these data, we infer that embryophytic stress signaling circuits were among those features that helped the algal land plant ancestor during terrestrialization.

Co-Authors

Bruce Curtis – Dalhousie University; Sven Gould – Heinrich-Heine-Universität Düsseldorf;
John Archibald – Dalhousie University

**CS-21-6- Identification of SLAC1 anion channel residues
that function in CO₂ signaling in Arabidopsis guard cells**

Speaker	Jingbo Zhang	Organization	Postdoctoral researcher, University of California, San Diego
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Plants control CO₂ exchange and water loss to the atmosphere in response to endogenous and environmental stimuli via stomatal pores. Atmospheric [CO₂] elevation triggers stomatal closure by Cl⁻ efflux mediated via S-type anion channels in the guard cell plasma membrane encoded by the SLAC1 gene. Previous research suggested that bicarbonate (HCO₃⁻) can directly up-regulate reconstituted SLAC1 channel activity and that the transmembrane domain of SLAC1 is involved in the stomatal CO₂/HCO₃⁻ response. The mechanism by which HCO₃⁻ regulates the SLAC1 anion channel activity and whether this regulation is relevant in planta is unknown. Here, we computationally seek to predict candidate bicarbonate binding sites within the SLAC1 anion channel through long-timescale Gaussian accelerated molecular dynamics (GaMD) simulations. Mutations of two putative HCO₃⁻ -interacting residues abolished the enhancement of the SLAC1 anion channel activity by CO₂/HCO₃⁻, while SLAC1 activation by other stimuli remained intact. Furthermore, gas exchange experiments with complemented *slac1* mutant plants expressing mutated SLAC1 proteins revealed that one of these SLAC1 residues is required for the stomatal CO₂ response, but not the ABA response, in planta. Patch clamp analyses of guard cells showed that activation of the S-type anion channel activity by CO₂/HCO₃⁻ was impaired, while ABA activation was intact, further showing a role of this SLAC1 site for CO₂ signaling. This study indicates that SLAC1 not only mediates anion efflux from guard cells, but also suggests that SLAC1 could contribute to biologically relevant CO₂/HCO₃⁻ sensing. Results from this study provide important insights into how plants respond to daily C_i changes and the continuing atmospheric rise in [CO₂].

Co-Authors

Nuo Wang – University of California, San Diego; Yinglong Miao – University of Kansas, Lawrence; Felix Hauser – University of California, San Diego; Wouter-Jan Rappel – University of California, San Diego; J. McCammon – University of California, San Diego; Julian Schroeder – University of California, San Diego

CS-26-1- Putting plant RuBisCO together in E. coli

Speaker	Manajit Hayer-Hartl, PhD	Organization	Group Leader, Max Planck Institute of Biochemistry
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Ribulose 1,5-bisphosphate carboxylase/oxygenase (RuBisCO) is responsible for the fixation of atmospheric CO₂ in photosynthesis. It is the most abundant enzyme in nature, owing in part to its low catalytic turnover rate and limited specificity for CO₂ versus O₂. Thus, RuBisCO has long been a target for reengineering with the goal of increasing crop yields. However, genetic manipulation has been hampered by the failure to express plant RuBisCO in a bacterial host.

The major form of RuBisCO (form I) is hexadecameric, consisting of 8 large (RbcL) and 8 small (RbcS) subunits. In recent years it has become evident that the RuBisCO enzyme requires a tremendous amount of help from chaperones to fold and assemble into the functional holoenzyme. We found that seven chaperones – the chloroplast chaperonin system Cpn60/Cpn20, RuBisCO accumulation factors 1 and 2 (Raf1 and Raf2, respectively), Ribulose-bisphosphate-carboxylase factor X (RbcX) and the protein bundle-sheath defective-2 (BSD2) – mediate the folding and assembly of *Arabidopsis thaliana* RuBisCO when co-expressed in *E. coli*. Our biochemical and structural analysis revealed the role of BSD2 in stabilizing an assembly intermediate of eight RbcL subunits until the RbcS subunits become available. The ability to produce plant RuBisCO recombinantly will facilitate efforts to improve the enzyme through mutagenesis.

Co-Authors

Harald Aigner – Max Planck Institute of Biochemistry; Robert Wilson – Max Planck Institute of Biochemistry; Andreas Bracher – Max Planck Institute of Biochemistry; Javaid Bhat – Max Planck Institute of Biochemistry; F. Ulrich Hartl – Max Planck Institute of Biochemistry

**CS-29-1- Building climate resilience in agricultural crops
by manipulating CO2 fixation**

Speaker	Robert Sharwood	Organization	Senior Lecturer, Australian National University
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With significant increases in the global population and the accelerating changes in climate, maintaining future increases in yield potential of food and fibre crops is coming under serious threat. The impact of climate change will intensify with the continued reductions in arable land and the availability of water that is often limiting for crop production. Future climates are predicted to increase the intensity and frequency of extreme events, such as heatwaves and varying rainfall patterns associated with droughts. To cope with future uncertain climates, agricultural crops will now need to be equipped with flexible strategies to cope with variable environments to mitigate declines in productive yields. One such target is CO₂ fixation, which is mediated by the key rate-limiting enzyme Rubisco (ribulose-1,5-bisphosphate carboxylase / oxygenase). Through the interrogation of C₄ grasses we have discovered Rubisco enzymes within Paniceae and Andropogon that will provide improvements in CO₂ fixation under future conditions of elevated temperature and CO₂. The catalytic properties of Rubisco were more favourable from grasses originating PCK and NADP-ME subtypes and it is evident the catalytic variation resides within the small subunit of Rubisco. To extend this research, we have now began screening wild-relatives of food and fibre crops and provenances of Eucalyptus trees that arose from varying climates of origin to identify new yield traits resulting in improved CO₂ assimilation under abiotic stress. An update of the progress will be presented.

Co-Authors

Oula Ghannoum – Western Sydney University; Spencer Whitney – Australian National University

CS-29-2- Leaf carbon isotope composition in *Setaria*: a genetic contribution and potential for high throughput screening for water use efficiency in C4 plants

Speaker	Asaph Cousins	Organization	Associate Professor, Washington State University
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Increasing whole plant water use efficiency (yield per transpiration; WUE_{plant}) through plant breeding can benefit the sustainability of agriculture and improve yield under drought. To select for WUE_{plant} a high throughput method of phenotyping must be developed, and the genetic architecture of traits such as transpiration efficiency (TE_i; rate of CO₂ assimilation relative to stomatal conductance) must be better understood. Leaf carbon stable isotope composition ($\delta^{13}\text{C}_{\text{leaf}}$) has been proposed as a high throughput proxy for TE_i, and there is a negative correlation between $\delta^{13}\text{C}_{\text{leaf}}$ and both WUE_{plant} and TE_i in the C4 model grass species *Setaria*. Therefore, a water limitation experiment was conducted where transpiration, biomass, WUE_{plant}, and $\delta^{13}\text{C}_{\text{leaf}}$ were measured on a recombinant inbred line (RIL) population of *Setaria viridis* and *S. italica* to better define the genomic control of WUE_{plant} and TE_i. Three quantitative trait loci (QTL) for $\delta^{13}\text{C}_{\text{leaf}}$ were co-localized with transpiration and biomass, but not with WUE_{plant}. However, $\delta^{13}\text{C}_{\text{leaf}}$ was negatively correlated with WUE_{plant} when WUE_{plant} was calculated for allele classes based on the allele combinations of the three QTL for $\delta^{13}\text{C}_{\text{leaf}}$. This negative relationship suggests that variation in WUE_{plant} across allele classes is in part due to differences in TE_i. In this C4 grass population, multiple traits can influence WUE_{plant}; however, the analysis of $\delta^{13}\text{C}_{\text{leaf}}$ provides insights into how TE_i contributes to WUE_{plant}. The data presented here suggests that $\delta^{13}\text{C}_{\text{leaf}}$ can be used in marker-assisted breeding to select for TE_i and to better understand the genetic architecture of TE_i and WUE_{plant} in C4 species.

Co-Authors

Patrick Ellsworth – Washington State University; Max Feldman – Donald Danforth Plant Sciences Center; Ivan Baxter – Donald Danforth Plant Sciences Center

CS-29-3- Sugar Loading Is Not Required For Phloem Transport In Plants

Speaker	Benjamin Babst, PhD	Organization	Assistant Professor, Arkansas Forest Resources Center, and College of Forestry, Agriculture and Natural Resources, University of Arkansas at Monticello
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Plant growth and productivity depends on transport of photoassimilates through the phloem from leaves to non-photosynthetic organs, such as the meristems, roots, and seeds. Thus, there is potential to attain societal benefits by manipulating phloem transport. Most evidence generally has been consistent with a pressure-flow mechanism of phloem transport, which was proposed over 85 years ago and, in all current models, is thought to require loading of sugars into the phloem to generate the osmotic potential that propels bulk flow. We used genetic and environmental manipulations in combination with state-of-the-art techniques to measure sieve tube pressures and photoassimilate transport dynamics to test unequivocally whether sugar loading is required as the driving force for phloem sap flow. Using carbon-11 radiotracer, we show that a maize sucrose transporter1 (sut1) loss-of-function mutant has severely reduced export of carbon from photosynthetic leaves (only ~5% the level of wild-type), even after leaf carbohydrates were reduced to wild-type levels by dark treatment. Remarkably, the sut1 mutant maintains the phloem sap flow at ~50-75% of wild-type velocities. In spite of the dramatic reduction in carbon export, pressure in sut1 mutant sieve tubes was similar to wild-type sieve tubes, suggesting that some other osmolyte can replace sucrose as the driver of phloem sap flow. The implications of these results for the transport of other phloem-mobile nutrients and signaling molecules independent of sugar transport will be discussed.

Co-Authors

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Michael Knoblauch – School of Biological Sciences, Washington State University
Kaare Jensen – Department of Physics, Technical University of Denmark

CS-29-4- A continued investigation of adaptations to the structural and biophysical properties of both whole leaves and root tissue of broad bean and tomato seedlings grown in an aquaponics system relative to the same species grown in soil

Speaker	Mazz Marry, MSC PhD	Organization	Assistant Professor, Minnesota State University Moorhead
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Aquaponics is the combination of aquaculture and hydroponics for food production that uses the nutrient rich water from fish culture to irrigate and fertilize a wide variety of plants, with less than 10% of total water volume replaced every day. The focus of this research is to understand what processes are evident to account for the reported increase in size, yield, and observed health of crop plants grown in an aquaponic based system, relative to plants grown in potting soils as controls. As yet, there have been no detailed studies to either quantify or qualify such physical vicissitudes in appearance, nor to determine what biochemical adaptations are being stimulated to account for these.

My working hypothesis is that the environment provided to growing economic crop plants by an aquaponic system will induce permanent, and beneficial, alterations to both the structural biochemistry of the plant cell walls and the basic cell physiology, relative to such plants grown in potting soil. Such modifications will not only be evident in leaf tissue, but also in root tissue, as the root cells adapt to the continuous presence of water and nutrients, compared to a relatively restricting soil environment. My initial work on aquaponics systems has strongly suggested an alteration of key structural components and energy producing components in the tissues of plants grown in an aquaponics system, relative to soil grown control plants.

CS-29-5- Image-Based Analysis to Dissect Vertical Distribution and Horizontal Asymmetry of Conspecific Root System Interactions in Response to Planting Densities, Nutrients and Root Exudates in *Arabidopsis thaliana*

Speaker	Jane Geisler-Lee	Organization	Southern Illinois University Carbondale
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Intraspecific competition is an important plant interaction that has been studied extensively aboveground, but less so belowground, due to the difficulties in accessing the root system experimentally. Recent in vivo and in situ automatic imaging advances help understand root system architecture. In this study, a portable imaging platform and a scalable transplant technique were applied to test intraspecific competition in *Arabidopsis thaliana*. A single green fluorescent protein labeled plant was placed in the center of a grid of different planting densities of neighboring unlabeled plants or empty spaces, into which different treatments were made to the media. The root system of the central plant showed changes in the vertical distribution with increasing neighbor density, becoming more positively kurtotic, and developing an increasing negative skew with time. Horizontal root distribution was initially asymmetric, but became more evenly circular with time, and mean direction was not affected by the presence of adjacent empty spaces as initially hypothesized. To date, this is the first study to analyze the patterns of both vertical and horizontal growth in conspecific root systems. We present a portable imaging platform with simplicity, accessibility, and scalability, to capture the dynamic interactions of plant root systems.

Co-Authors

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CS-29-6- A Simplified Strategy for Site-Directed Mutagenesis of the Rubisco Large Subunit in Tobacco

Speaker

Myat Lin

Organization

Research Associate,
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Rubisco (ribulose-1,5-bisphosphate carboxylase/oxygenase, EC number 4.1.1.39) catalyzes the first step in carbon fixation and a competing oxygenation reaction, which leads to photorespiration. Thus, Rubisco controls an important intersection in major metabolic pathways and has been a strategic target to improve photosynthetic efficiency. In plants, Rubisco is a complex made up of eight large subunits encoded by a chloroplast gene, *rbcl*, and eight small subunits expressed from a nuclear gene family and targeted to chloroplast stroma. The catalytic site is formed by residues in the large subunit. Chloroplast transformation technology is well established in tobacco, where *rbcl* can be readily replaced with a foreign homolog. However, site-directed mutagenesis of *rbcl* requires a special master line, where the native *rbcl* was already replaced with a foreign version, to prevent undesired homologous recombination between the wild-type and mutant *rbcl*. Here, we present a simplified strategy for site-directed mutagenesis of *rbcl* that does not require a special master line. First, we synthesized an *rbcl* gene that encodes the wild-type tobacco large subunit, but has 26 silent mutations and unique restriction sites. Then, we introduced into this modified *rbcl* gene different mutations that have been selected in the evolution of C4 photosynthesis and used them to replace the wild-type *rbcl* in tobacco. This strategy can be applied to site-directed mutagenesis of other chloroplast genes. (Funded by DOE Energy Biosciences DE-SC0014339)

Co-Authors

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**MJ 4-O– Major Symposium IV: ISPR/ASPB/CSPB Joint Symposium,
The Ecophysiology of Photosynthesis from the Leaf to Global Scale,
Overview by Organizer Thomas Sharkey**

Speaker	Thomas Sharkey, PhD	Organization	Professor, Michigan State University
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Photosynthesis provides energy and metabolic building blocks for nearly all life on Earth. Photosynthesis operates over an extremely broad range of scales both in time and space. Photosynthesis is studied in the sub nanosecond scale of light capture reactions to the geological scale, the best example of which is the oxidation of the Earth, which changed global geochemistry. In this symposium four experts will describe current research into the ecophysiology of photosynthesis at the organizational level of the leaf, plant, ecosystem, and whole Earth. Topics that will be addressed is how photosynthesis might be manipulated to better serve human needs for food, fuel, and fiber, the interplay between environmental change and photosynthesis, and how we can understand photosynthesis at ecosystem and global scales.

MJ 4-1- Leaf: Improving photosynthesis to maximize productivity

Speaker	Elizabeth Carmo-Silva, PhD	Organization	Lecturer, Lancaster University
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Field-grown plants experience an environment of constant fluctuation. The light level that reaches a leaf at the top of the canopy oscillates continuously, e.g. in response to cloud coverage, wind, and canopy movement. Leaf temperatures are also becoming increasingly variable as the global temperature and the occurrence of extreme temperature events increase. Plants respond to these environmental fluctuations and adjust rates of CO₂ assimilation to the prevailing conditions. However, current evidence suggests that the rate of photosynthetic response to changes in the environment is not optimal for crop productivity under fluctuating conditions. Central to photosynthesis, the activity of ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) is highly regulated and involves interaction with its catalytic chaperone, Rubisco activase (Rca). Rca activity is modulated by the chloroplast redox status and ADP/ATP ratio, thereby mediating Rubisco activation and photosynthetic induction in response to light. Our research focuses on exploiting natural diversity in the response of Rubisco and Rca to fluctuations in light and temperature amongst elite cultivars and wild relatives of crops such as wheat and cowpea to improve the climate resilience of CO₂ assimilation in current and future climates.

MJ 4–2– Plant: Ecophysiology of plant response to environmental change over evolutionary time scales

Speaker	Joy Ward, PhD	Organization	Associate Dean of Science Research and Professor, University of Kansas
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Studying the responses of plants to changing atmospheric CO₂ concentration ([CO₂]) over tens of thousands of years allows us to better understand how changing carbon availability may alter photosynthesis and whole-plant functioning over evolutionary time. Paleoecological studies that involve low CO₂ conditions may also be useful for understanding the constraints that past evolutionary responses impose on plant response to future conditions. During the Last Glacial Maximum that occurred 20,000 years ago, atmospheric [CO₂] was as low as 180 ppm and has since risen to a current value of 402 ppm, and is expected to reach at least 700 ppm by the end of this century. In order to understand how changing CO₂ has influenced tree physiology over the last 50,000 years, we studied juniper specimens from the Rancho La Brea tar pits in southern California, kauri specimens from peat bogs in New Zealand, and an intact plant community preserved within packrat middens in the southwestern U.S. From carbon isotope ratios, we calculated leaf ci/ca (intercellular [CO₂]/atmospheric [CO₂]) and ci from annual tree rings and leaf tissue. In both kauri and juniper, mean ci/ca values remained constant over 50,000 years despite major climate and [CO₂] changes. We also observed that ci of juniper never fell below 90 ppm, suggesting this may represent a [CO₂] compensation point for whole-plant functioning and survival. Interestingly, our results with leaf specimens from middens suggest that plant species from the same family showed similar physiological responses over time and thus plant lineage seems to be an important factor in pre-determining plant response to climate change. Taken together, these results increase our understanding of the adaptation of plants to rising CO₂ and climate change and provide a means for understanding physiological traits that may lead to long-term species sustainability versus loss within a plant community over time.

MJ 4-3- Controls on ecosystem-scale photosynthesis

Speaker	Larry Flanagan, PhD	Organization	Professor of Biological Sciences, University of Lethbridge
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Photosynthesis provides the energy that drives most biological processes in terrestrial ecosystems. At the ecosystem-scale, photosynthesis rates can be determined from eddy covariance measurements of net ecosystem carbon dioxide exchange during the day and ecosystem respiration at night. Networks of eddy covariance towers in contrasting biomes across the globe have provided important insights into the interacting, climatic and biotic controls on ecosystem photosynthesis. In this presentation, I will describe new information obtained about controls on ecosystem-scale photosynthesis from syntheses of data from FLUXNET, a network of international eddy covariance studies. In addition, a few case studies in contrasting ecosystems will be presented to illustrate how ecosystem photosynthetic carbon acquisition can be altered by warmer temperatures, altered precipitation and other major global environmental changes.

MJ 4-4- Quantifying photosynthesis at regional and global scales

Speaker	Joseph Berry, PhD	Organization	Carnegie Institution for Science, Washington
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Photosynthesis sustains Earth's Biosphere and is essential for supporting the human population of the planet. The continued growth of our population will place increased demands on this productivity, while at the same time, the planet is undergoing significant climate and environmental change that can effect productivity. These effects on productivity are quite complex and may show large local variation. For example, some areas will experience increases in precipitation while other a decrease. Average temperatures will increase but not uniformly. Increasing CO₂ may stimulate photosynthesis in places where nutrients are abundant but have little effect in other areas. These complexities make it difficult to assess what may be happening to the "carrying capacity" of our planet from local scale monitoring of crop yield, net carbon flux or forest growth. Integrative monitoring of productivity writ large on regional, continental or even planetary scales are needed for this task. These large scale measurements rely heavily on spectroscopic measurements from Earth observing satellites, on networks that monitor the variation in the composition of trace gases in the atmosphere, and on models that link these observations to surface processes and the weather. I will review these approaches and highlight recent advances such as the new capability to monitor the emission of chlorophyll fluorescence from space and new satellite capabilities for monitoring atmospheric trace gases from space. These new approaches for monitoring photosynthesis from space are bringing us closer to being able to determine how climate and environment change is effecting this key planetary support system.

**MJ 5-1- The Acquisition of Novel Organelles Thorough
Endosymbiosis-Genomic, Cellular, and Physiological Consequences**

Speaker	Eva Nowack	Organization	Heinrich Heine University Duesseldorf
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The evolution of mitochondria and plastids generated novel cell types containing new bioenergetic and biosynthetic compartments. These evolutionary processes were initiated more than a billion years ago by the acquisition of bacterial endosymbionts. More recently established endosymbioses that engage a broad range of bacterial phyla are found across the eukaryotic tree of life and provide eukaryotic hosts with novel biochemical capabilities that allow colonization of new ecological niches. Over time, the genomes of vertically transmitted endosymbionts tend to reduce tremendously in size and coding capacity, indicating an intricate integration of metabolic processes between the partner organisms. Additionally, size and shape of a bacterial endosymbiont can greatly differ compared to its free-living ancestor and numbers of endosymbionts per host cell can be strictly controlled. Molecular mechanisms that mediate the metabolic and cellular integration of a genomically reduced bacterial endosymbiont, however, are largely unknown. We are interested in the molecular base and genetic repertoire needed for host/symbiotic interactions and the genomic and cellular changes that accompany the transition from endosymbiont to genetically integrated organelle. To explore these issues we use as model systems the cercozoan amoeba *Paulinella chromatophora* that contains cyanobacterium-derived evolutionary-early-stage photosynthetic organelles (termed “chromatophores”) and the trypanosomatid *Angomonas deanei* that contains nutritional β -proteobacterial endosymbionts. Genome and transcriptome analyses revealed highly complementary gene repertoires that are expressed from the host and endosymbiont genomes. Apparently, horizontal gene transfers from various bacteria to the host nucleus contributed to this complementarity and might have been critical for symbiont integration. Proteomic analyses identified in both systems sets of nuclear-encoded proteins that are specifically targeted to the endosymbiont/chromatophore. Particularly in *P. chromatophora*, control over the chromatophore proteome shifted significantly to the nucleus and a novel type of signal sequence evolved that seems to mark nuclear-encoded proteins for import into the chromatophore.

MJ 5-2- The role of horizontal gene transfer in the evolution of plants and their genomes

Speaker	Jeff Palmer, PhD	Organization	Distinguished Professor of Biology and Class of '55 Professor, Indiana University
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Horizontal gene transfer (HGT) – the transfer of genes between more-or-less distantly related organisms by non-sexual processes – is surprisingly common in plants. However the frequency of HGT, its adaptive consequences, and the universe of donor organisms vary significant among the three plant genomes. HGT is extremely common in mitochondrial genomes, indeed is a major force driving their evolution, yet is restricted to a relatively narrow range of donor organisms and genomes. Although many cases of adaptively significant HGT from a wide range of donors have been reported in plant nuclear genomes, the overall extent, frequency, and importance of HGT in the nucleus are poorly understand. Finally, HGT is unheard of in plastid genomes of land plants despite how many have been sequenced. I will briefly review the most salient findings relevant to these issues, as well as the mechanisms through which HGT occurs in plants. I will also present new data showing that HGT is far more common, pervasive, and important in plant mitochondrial genomes than is already thought to be the case. These data indicate that most adaptively important HGT in mitochondria occurs through the infiltration of native mitochondrial genes with foreign bits of mitochondrial homologs from other green plants via HGT-driven gene-conversion events that are very difficult if not essentially impossible to detect. These findings also support the growing body of evidence that most HGT in plants involves other plants as donors and occurs through direct physical contact of donor and recipient cells via processes such as illegitimate pollination, grafting, parasitism, and epiphytism.

**MJ 5–3– Polyploidy as Integrator Across Levels of Biological Organization:
From Cells to Ecosystems**

Speaker	Pamela Soltis, PhD	Organization	Founding Director of UFBI and Distinguished Professor and Curator, Laboratory of Molecular Systematics and Evolutionary Genetics Florida Museum of Natural History, University of Florida
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Polyploidy, or whole-genome duplication (WGD), has long been recognized as an important speciation mechanism in plants. However, WGD has biological effects that extend far beyond the generation of new species. WGD is a key integrator across levels of biological organization, with effects that range from the molecular and subcellular levels to those of the ecosystem and Tree of Life. The immediate impact of WGD is duplication of all nuclear genetic material, but over time, the component subgenomes become fractionated to yield a composite of duplicated and unduplicated loci. This loss of duplicate genes can begin to occur surprisingly quickly, in perhaps only a few generations. Through gene loss and shifts in gene expression, polyploid individuals originating from a single polyploidization event may become genetically and phenotypically unique, together forming a morphologically, physiologically, and/or ecologically polymorphic population, in contrast to classical views of allopolyploids as genetically identical and chromosomally fixed F1 hybrids. This array of genetic and phenotypic novelty may provide new variants that can potentially drive evolution in new directions, with consequences for the tempo of diversification at macroevolutionary scales. Case studies in *Tragopogon* (Compositae) will illustrate patterns of duplicate gene loss and shifts in gene expression in synthetic and natural allopolyploids of recent origin. On longer timescales, signatures of ancient WGDs in Compositae and across angiosperms are often associated with accelerated rates of species diversification, suggesting a causal role of WGD in the diversification of these clades. Although statistical support for co-localized WGD events and diversification rate shifts is low across all angiosperms, many individual WGDs appear to be associated with the origins of novel features and increased diversification, suggesting that features that arise via microevolutionary processes may translate into key innovations on macroevolutionary timescales.

MJ 5-4- Genes gone wild: Experimental genome evolution in plants

Speaker	Ralph Bock, PhD	Organization	Director of Organelle Biology, Biotechnology and Molecular Ecophysiology Department Max Planck Institute of Molecular Plant Physiology
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In my talk, I will describe experimental approaches to study genome evolution in real time. I will discuss three fundamental processes in eukaryotic genome evolution and show how they can be reconstructed in laboratory experiments: (i) the transfer of organellar (plastid and mitochondrial) genes to the nuclear genome, (ii) the horizontal movement of organellar DNA between plants, and (iii) the movement of nuclear genetic material between plants by horizontal genome transfer. I will discuss the underlying mechanisms and the implications for genome evolution and speciation. Finally, I will show also how horizontal gene transfer can be employed as a versatile tool in plant biotechnology and synthetic biology.