2017 Nebraska Research & Innovation Conference

PREDICTIVE CROP DESIGN: GENOME TO PHENOME

Message from the Nebraska EPSCoR Director

Welcome to the 2017 Nebraska Research & Innovation Conference (NRIC)! Thank you to our speakers for sharing their time and expertise with us, and thanks to the program committee for their recruitment of this excellent slate of speakers.

This event extends an annual series of conferences and symposia that Nebraska EPSCoR has been organizing to advance research activities in this state. This year's conference supports Nebraska's Center for Root & Rhizobiome Innovation (CRRI), a five-year project funded by the National Science Foundation.

In CRRI's Year 1, this symposium gathers leaders from academia and industry, with international perspectives and regional connections at the forefront.

Please enjoy NRIC's knowledge transfer and networking opportunities, and be sure to visit Thursday's poster session for a look at this area's exciting future.

Best,

F. Fred Choobineh, Ph.D., P.E.
Director, Nebraska EPSCoR
Blackman Distinguished Professor of Electrical Engineering, UNL

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Program Committee

Ed Cahoon, James Schnable, David Hyten, Ruth Welti, Robert Sharp, Pat Schnable, Senthil Subramanian

Nebraska EPSCoR Staff

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Notes:

PREDICTIVE CROP DESIGN: GENOME TO PHENOME

2017 Nebraska Research & Innovation Conference | Lincoln Marriott Cornhusker Hotel

AGENDA

DAY 1 - Thursday, April 6

7:30 am	Conference materials pick up and continental breakfast
8:15 am	WELCOME | University of Nebraska-Lincoln Chancellor Ronnie L. Green
8:30-9:10 am	PLENARY TALK: Challenges facing crop production and potential solutions | Pat Schnable

9:10 am - Noon | GENETICS & GENOMICS (Chair: David Hyten)

9:15-9:55 am	Underground signaling networks | Philip Benfey
9:55-10:10 am	Break
10:10-10:40 am	Genome-environment associations in sorghum landraces predict adaptive traits | Geoff Morris
10:45-11:15 am	Understanding variation that persists in the genome of elite maize inbred lines | Candice Hirsch
11:20-11:50 am	Transgene mediated epimutagenesis leads to heritable phenotypic variation | Robert Schmitz
11:50am - 1 pm	Lunch

1:00-2:55 pm | ENGINEERING & COMPUTATIONAL BIOLOGY (Chair: James Schnable)

1:05-1:45 pm	Digital agriculture: today and tomorrow | Calden Carroll Stimpson
1:50-2:20 pm	High throughput plant phenotyping in greenhouse and field: toward translational research from gene discovery to crop improvement | Yufeng Ge
2:25-2:55 pm	Deep learning for high-throughput phelotyping of 'complex' traits in wheat | Jesse Poland
3:00-3:20 pm	Break

3:20-4:50 pm | AGRICULTURAL ENTREPRENEURSHIP (Chair: Sally Mackenzie)

3:15-3:45 pm	Contemplating commercial implications of plant epigenetics research | Sally Mackenzie
3:50-4:50 pm	PANEL DISCUSSION: Agricultural entrepreneurship
5:00-6:45 pm	POSTER SESSION AND RECEPTION

FOR DAY 2 (FRIDAY) AGENDA, SEE NEXT PAGE

PREDICTIVE CROP DESIGN: GENOME TO PHENOME

2017 Nebraska Research & Innovation Conference | Lincoln Marriott Cornhusker Hotel

AGENDA

DAY 2 - Friday, April 7

7:30 am   Conference materials pick up and continental breakfast

| 8:15-11:50 am | SYSTEMS & SYNTHETIC BIOLOGY I (Chair: Senthil Subramanian) |

8:20-9:00 am   Precise engineering of plant genomes | Daniel Voytas

9:05-9:35 am   Applying RNA synthetic biology to study plant-microbe interactions | Ming Chen Hammond

9:40-10:10 am   Plant metabolic models: from model building to 'omics' data integration and answering important biological questions | Rajib Saha

10:10-10:30 am Break

10:30-11:00 am Integrated metabolomics for deciphering metabolic pathways and emerging solutions for addressing the grand challenges of metabolomics | Lloyd Sumner

11:05-11:35 am Linking lipidomics and genetics for crop improvement | Ruth Welti

11:45am -12:45 pm   Lunch

| 12:50 - 2:45 p.m | SYSTEMS & SYNTHETIC BIOLOGY II (Chair: Ed Cahoon) |

12:55-1:35 pm   Advanced fuels from advanced plants | Jay Keasling

1:40-2:10 pm   Application of high-resolution, functional genomic methods to study soybean root traits | Gary Stacey

2:15-2:45 pm   Developing integrated products to improve crop performance, efficacy, and durability | Wendy Pline-Srnic

2:45-3:00 pm   Break

3:00-4:00 pm   PANEL DISCUSSION: Future of biotechnology for crop improvement | Chair: Jim Alfano

4:05-4:45 pm   PLENARY TALK: What can plant metabolic engineering do for human health? | Cathie Martin

4:45 pm   WRAP-UP & OPTIONAL TOUR: Phenotyping greenhouses at Nebraska Innovation Campus

THURSDAY, APRIL 6

Plenary Talk: Challenges facing crop production and potential solutions

PAT SCHNABLE, Iowa State University

8:30 - 9:10 A.M.

BIO: Pat Schnable is a distinguished professor at Iowa State University where he holds an endowed chair and directs the Plant Sciences Institute that fosters collaborations among plant scientists, engineers and computational scientists. He is also a ChangJiang Scholar Professor at China Agriculture University. Schnable received his B.S. in Agronomy from Cornell University and his Ph.D. in Plant Breeding and Cytogenetics from Iowa State University; he conducted post-doctoral research in Molecular Genetics at the Max Planck Institute in Köln, Germany. His wide-ranging investigations of the maize genome have resulted in >120 peer-reviewed publications and an h-index of 63. He is a fellow of the American Association for the Advancement of Science, serves as a consulting editor for PLoS Genetics (Impact Factor 8.7), is a past chair of the American Society of Plant Biology's Science Policy Committee, and a past chair and current member of the Maize Genetics Executive Committee. He is also the co-lead of the Genomes to Fields Initiative. Schnable is also a co-founder and managing partner of Data2Bio LLC, which provides research support for the breeding industry; of Dryland Genetics LLC; which is developing crops for arid environments via next-generation breeding; and of DecisionPx LLC which generates image-based decisions for crop production and breeding. He also serves on the scientific advisory boards of several other companies.

GENETICS & GENOMICS SECTION

CHAIR: DAVID HYTEN, University of Nebraska-Lincoln

9:10 A.M. - NOON

Underground signaling networks

PHILIP BENFEY, Duke University

9:15 - 9:55 A.M.

ABSTRACT: To understand the progression from stem cells to differentiated tissues we are exploiting the simplifying aspects of root development. We have developed new experimental, analytical and imaging methods to identify networks functioning within different cell types and developmental stages of the root. We are particularly interested in a subnetwork that regulates a key asymmetric cell division of a stem cell and the regulatory networks that control differentiation of the stem cell's progeny. These networks are partially dependent on cell-to-cell signaling through movement of transcription factors. To quantify dynamic aspects of these networks, we are employing light-sheet microscopy to image accumulation of their different components. To find additional signaling molecules we performed ribosome profiling and identified putative peptide ligands. We have also uncovered a clock-like process responsible for the positioning of lateral roots along the root primary axis. Two sets of genes were identified that oscillate in opposite phases at the root tip and are involved in the production of prebranch sites, locations of future lateral roots. A derivative of the carotenoid biosynthesis pathway appears to act as a new mobile signal regulating root architecture.

BIO: Philip Benfey is an HHMI Investigator and the Paul Kramer Professor of Biology at Duke University. His research focuses on plant developmental genetics and genomics. He is a fellow of the American Association for the Advancement of Science and a member of the US National Academy of Sciences. He received his Ph.D. from Harvard University and a DEUG (Diplome d'Etudes Universitaire Generale) from the University of Paris. He co-founded a spin-off company, GrassRoots Biotechnology, which was sold to a large multinational. He now leads a new company, Hi Fidelity Genetics, which applies sophisticated data analytics to plant breeding.

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Genome-environment associations in sorghum landraces predict adaptive traits

GEOFF MORRIS, Kansas State University

10:10 - 10:40 A.M.

ABSTRACT: Improving environmental adaptation in crops is essential for food security, but phenotyping adaptive traits remains a major bottleneck. If associations between SNP alleles and environment of origin in crop landraces reflect adaptation, then these could be used to predict phenotypic variation for adaptive traits. We tested this proposition in the global food crop sorghum, characterizing 1943 georeferenced landraces at 404,627 SNPs and quantifying allelic associations with bioclimatic and soil gradients. Environment-associated SNPs predicted genotype-by-environment interactions under experimental drought stress and aluminum toxicity, suggesting genomic signatures of adaptation may be useful for germplasm identification and marker-assisted selection. (Modified from Lasky, et al. 2015 Sci. Adv.)

BIO: Geoff Morris is an assistant professor in the Department of Agronomy at Kansas State University. He received his Ph.D. from the Department of Ecology & Evolution at the University of Chicago. The goal of his research is to develop genomic knowledge and tools that accelerate the genetic improvement of climate-resilient crops. His group's research is focused on the genomics of climate adaptation in sorghum. Ongoing projects include improving chilling tolerance of grain sorghum for the Great Plains, building genome-phenome maps of ecophysiological traits for energy sorghum, and developing genomics-enabled breeding pipelines to improve drought adaptation of dual-purpose sorghums in West Africa and Haiti.

Understanding variation that persists in the genome of elite maize inbred lines

CANDICE HIRSCH, University of Minnesota

10:45 - 11:15 A.M.

ABSTRACT: Maize is a species with extensive diversity from the genome to the phenome, and as such is an excellent model system to study natural variation and the relationship between various levels of natural variation such as the genome versus the transcriptome. We recently developed a second maize genome assembly to compliment the existing B73 reference genome assembly. Using these assemblies and transcriptome profiling throughout development we have been able to extensively mine the variation that exists between elite inbred lines at the genome and transcriptome levels. The relationship and impact of promoter variation, transcribed allelic variation, structural variation, and spatial and temporal transcriptional variation will be discussed.

BIO: Candy Hirsch is an assistant professor in the Department of Agronomy and Plant Genetics at the University of Minnesota, where she focuses on maize translational genomics. She received her B.S. in Genetics and Ph.D. in Plant Breeding and Plant Genetics from the University of Wisconsin-Madison and did her post-doc at Michigan State University. Her research involves the integration of big data including high throughput genome and transcriptome sequencing, high throughput phenotyping, and extensive environmental measurements with the end goal of improving corn as a crop plant. She and her team have projects in the lab examining the maize pan genome including dissecting natural mechanisms that create genome content variation and the impacts on phenotypic variation. She's also interested in understanding the interaction of genotype and environment and the impact on plant performance and elucidating the molecular mechanisms underlying heterosis in maize.

Transgene mediated epimutagenesis leads to heritable phenotypic variation

BOB SCHMITZ, University of Georgia

11:20 - 11:50 A.M.

ABSTRACT: There exists extensive natural epigenetic and cryptic variation in plant genomes, some of which is linked to heritable phenotypic variation. Accessing this source of variation to improve plant traits is cumbersome as it often relies on the identification and incorporation of rare events into breeding programs. We describe a novel methodology termed "epimutagenesis" to rapidly generate phenotypic variation by randomly demethylating the genome of Arabidopsis thaliana via transgenic expression of a DNA demethylase. Not only does this system lead to widespread loss of DNA methylation, it also leads to the production of heritable phenotypic variation. Application of epimutagenesis to other plant species will lead to expression of alleles typically silenced by DNA methylation, uncovering previously hidden genetic variation.

BIO: Bob Schmitz earned his B.Sc. in Molecular & Cellular Biology from the University of Arizona and his Ph.D. in Genetics from the University of Wisconsin-Madison. His postdoctoral training was performed at the Salk Institute. In 2013, he joined the Genetics Department at the University of Georgia where his lab is studying how phenotypic plasticity and diversity are driven by natural epigenetic variation. His lab uses a combination of molecular genetics and epigenomic approaches on plant populations to understand the impact that natural epigenetic alleles (epialleles) have on life history traits.

LUNCH
11:50 A.M. - 1:00 P.M.

ENGINEERING & COMPUTATIONAL BIOLOGY SECTION

CHAIR: JAMES SCHNABLE, University of Nebraska-Lincoln

1:00 - 2:55 P.M.

Digital agriculture: today and tomorrow

CALDEN CARROLL STIMPSON, Climate Corp.

1:05 – 1:45 P.M.

ABSTRACT: Today, agriculture systems are receiving boosts in productivity and efficiency from advanced seed genetics, biotechnology and crop protection technologies while vast amounts of data collected on the farm through a wide array of precision ag equipment, field implements, weather stations, and soil and plant measurements. These inputs are augmented by new, advanced sensors of increasing capability and sophistication. The confluence of data science and precision agriculture promises to help farmers manage large amounts of data, enabling more integrated and refined decision-making on the farm. Data analytics is transforming the agriculture industry as we know it today and advanced technologies will further enable enhanced decision making, improved efficiency and maximized productivity.

BIO: Calden Carroll Stimpson joined the Climate Corporation in 2016, leading the company's development of novel in-field and in-ground sensors to enable the flow of high quality, high resolution data into Climate's FieldView. Prior to joining Climate, he was co-founder and President of SupraSensor Technologies, which was acquired by Climate in 2016. He received his Ph.D. in 2011 from the University of Oregon for work on the molecular sensor platform which is the underlying technology for the field sensors being developed today. As a post-doc, his team was awarded the top prize in the National Science Foundation's Innovation Corps program designed to take basic research out of the lab and into the private sector. He is a firm believer in the power of investment in the fundamental sciences as a tool to drive revolutionary societal changes, and takes particular pride in developing the nitrate sensor, a technology which can protect the fisheries where he spends so much of his free time today.

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High throughput plant phenotyping in greenhouse and field: toward translational research from gene discovery to crop improvement

YUFENG GE, University of Nebraska-Lincoln

1:50 – 2:20 P.M.

ABSTRACT: High throughput plant phenotyping is a frontier research field which bears the promise to unlock the full genetic potential of major food crops and boost yield. University of Nebraska-Lincoln has procured a LemnaTec automated imaging greenhouse. More recently, a Spidercam field phenotyping facility is also under development. The idea is to enable interdisciplinary translational research among various research communities with these state-of-the-art facilities. This talk will focus on a few phenotyping projects conducted in both greenhouse and field, with the emphasis on new image- and sensor-derived plant phenotypes. Lessons and perspectives gained from these studies will be discussed.

BIO: Yufeng Ge obtained his Ph.D. in Biological & Agricultural Engineering from Texas A&M University. After several years as a postdoc and research assistant professor there, he joined the Biological Systems Engineering Department at University of Nebraska-Lincoln in 2014. His research expertise is in instrumentation and sensing for agriculture and natural resources. He has been actively involved in several collaborative projects in high throughput plant phenotyping. He has received funding from such federal agencies as NSF and USDA-NIFA. He has authored and coauthored more than 35 journal articles in his career, and hold two patents regarding plants and soil sensing.

Deep learning for high-throughput phenotyping of 'complex' traits in wheat

JESSE POLAND, Kansas State University

2:25 - 2:55 P.M.

ABSTRACT: In field-based high-throughput phenotyping, the indirect measurement of plant phenology through canopy spectral reflectance offers insights to the overall status of the crop and opportunities to improve yield prediction models and selection approaches in the breeding program. To advance high-throughput phenotyping for assessment of more complex phenotypes such as plant morphology or developmental stages, new approaches are needed to measure these phenotypes in a manner that is analogous to how we, as humans, score traits in plants. Through training under the direction of an experienced breeder, we learn to rapidly and accurately through visual assessment score complex plant morphology, disease resistance, growth stages and a suite of other important plant characteristics. Analogous to this, we use deep learning approaches to train convolutional neural networks to directly score phenotypes of interest from field imaged collected by high-throughput phenotyping platforms. These CNNs are developed using "breeder-trained datasets" consisting of thousands of images that are geo-referenced to a single field plot and matched with a breeder defined score. With these types of datasets we have demonstrated 100% accuracy for plot-level scoring of awned / awnless and heading stage in wheat. The scope of using breeder knowledge to train neural networks has the possibility to enable phenotyping for any traits of interest, and via high-throughput. Such tools will enable new possibilities for breeding and genetics on a scale much larger than is currently possible.

BIO: Jesse Poland is an assistant professor at Kansas State University, director of the Feed the Future Innovation Lab for Applied Wheat Genomics, and associate director of the Wheat Genetics Resource Center. His research group focuses on wheat genetics, genomics and germplasm improvement. They work to develop new approaches in quantitative genetics, genomics and high-throughput phenotyping for use in breeding, diversity studies, and association genetics. In collaboration with public breeding programs, Dr. Poland applies use of genomic selection methods to accelerate wheat breeding. In the area of germplasm development, his group strives to develop new breeding lines with resistance to wheat's major pests--including stem rust, stripe rust, leaf rust and Hessian Fly--as well as understand the genetic basis of these traits. To complement advances in genomics, his lab pursues high-throughput phenotyping approaches for field-based evaluation of breeding lines with the primary focus being genetic characterization of heat and drought tolerance and development of improved germplasm.

AGRICULTURAL ENTREPRENEURSHIP SECTION

CHAIR: SALLY MACKENZIE, University of Nebraska-Lincoln

3:20 - 4:50 P.M.

Contemplating commercial implications of plant epigenetics research

SALLY MACKENZIE, University of Nebraska-Lincoln

3:20 – 3:45 P.M.

ABSTRACT: Contemplating commercial avenues for academic research can be challenging. Generally the process grows serendipitously and requires attention to practical implications of fundamental research. Consideration of licensing, selection of investor models, and plotting a plan toward commercialization are concepts in which academics are generally unfamiliar. My group has participated over the past two years in the initiation of a new company that addresses opportunities in epigenetic crop breeding. I will describe some of the research observations that prompted the pursuit of this path.

BIO: Sally Mackenzie is currently the Ralph and Alice Raikes Chair of Plant Science at University of Nebraska-Lincoln. Her research over the past several years has focused on the influence of non-genetic variation on plant behavior and whether it is feasible to capture agricultural value from exploiting crop epigenetic variation. Her laboratory has developed a system permitting the induction of epigenetic changes in plants that confer enhanced crop productivity and abiotic stress tolerance. Originally from California, she received graduate training at the University of Florida, and was on the faculty at Purdue University from 1988 to 1999. She was also Founding Director for the Center for Plant Science Innovation at UNL from 1999 to 2010. She currently serves as President for the American Society of Plant Biologists and Director for the National Plant Science Council.

Panel Discussion: Agricultural Entrepreneurship

CHAIR: SALLY MACKENZIE, University of Nebraska-Lincoln

3:50 – 4:50 P.M.

POSTER SESSION & RECEPTION

5:00 - 6:45 P.M.

FOR A LIST OF PRESENTERS, PLEASE SEE LATTER PAGES OF THIS PROGRAM.

FRIDAY, APRIL 7

SYSTEMS & SYNTHETIC BIOLOGY SECTION

CHAIR: SENTHIL SUBRAMANIAN, South Dakota State Univ.

8:15 - 11:35 A.M.

Precise engineering of plant genomes

DAN VOYTAS, University of Minnesota

8:20 - 9:00 A.M.

ABSTRACT: Plant agriculture is poised at a technological inflection point. Recent advances in genome engineering make it possible to precisely alter DNA sequences in living cells, providing unprecedented control over a plant's genetic material. Potential future crops derived through genome engineering include those that better withstand pests, that have enhanced nutritional value, and that are able to grow on marginal lands. In many instances, crops with such traits will be created by altering only a few nucleotides among the billions that comprise plant genomes. As such, crops created through genome engineering might prove to be more acceptable to the public than plants that carry foreign DNA in their genomes.

BIO: Dan Voytas is a professor in the Department of Genetics, Cell Biology and Development and the Director of the Center for Genome Engineering at the University of Minnesota. He graduated from Harvard College in 1984 and received his Ph.D. from Harvard Medical School in 1990, and conducted postdoctoral research at Johns Hopkins University School of Medicine. Prior to joining the University of Minnesota, he was a professor at Iowa State University (1992-2008). He currently serves as Chief Science Officer for Calyxt, a biotechnology company focused on making new crop varieties through genome engineering.

Applying RNA synthetic biology to study plant-microbe interactions

MING CHEN HAMMOND, University of California, Berkeley

9:05 – 9:35 A.M.

ABSTRACT: My lab develops RNA-based tools for gene regulation and molecular sensing. In this seminar, I will describe the development of a fully generalizable, robust, and orthogonal suicide exon system for gene regulation in dicots. Using this suicide exon, we were able to generate previously unattainable transgenic plants harboring bacterial effector genes that inducibly trigger the hypersensitive response. In the second half, I will describe the development of highly sensitive and bright RNA-based fluorescent biosensors for studying bacterial signaling. We recently applied these biosensors to make several exciting discoveries related to small molecule signals that control how certain environmental bacteria respond to biotic and abiotic surfaces, which has implications for host, community, and environmental interactions.

BIO: Ming Hammond is an assistant professor in the Departments of Chemistry and Molecular & Cell Biology at the University of California, Berkeley and a faculty scientist in the Biological Systems and Engineering division at Lawrence Berkeley National Laboratory. She is a founding PI for the NIGMS Center for RNA Systems Biology at UC Berkeley and has served as a grant reviewer for the NSF, JGI Community Science Program, and Biotechnology and Biological Sciences Research Council in the UK. She is a recipient of the NIH New Innovator Award and the BWF Career Award at the Scientific Interface.

Plant metabolic models: From model building to 'omics' data integration and answering important biological questions

RAJIB SAHA, University of Nebraska-Lincoln

9:40 – 10:10 A.M.

ABSTRACT: A typical genome-scale metabolic model of a plant (or a plant tissue) contains gene-protein-reaction relationships, elemental and charge-balanced reactions, and incorporates experimental evidence pertaining to the biomass composition, compartmentalization, and flux constraints. Condition-specific biomass descriptions are sometimes introduced that account for amino acids, fatty acids, soluble sugars, proteins, chlorophyll, lignocellulose, and nucleic acids as experimentally measured biomass constituents. Compartmentalization of this sort of model is often based on proteomic/transcriptomic data and literature evidence. Transcriptomic and proteomic data can also be used to introduce regulatory constraints in the model in order to simulate specific environmental and/or genetic conditions. In this talk, we will discuss about the steps of model building, 'omics' data integration, and how such models can be useful in answering important biological questions.

BIO: Rajib Saha is a new assistant professor in the UNL Department of Chemical and Biomolecular Engineering. His research interests include reconstruction and analysis of genome-scale and community models, systems-level analysis of 'omics' data, development of genetic toolkit and engineering metabolic pathways, and redesign photosynthetic apparatus and carbon fixing mechanism. Prior to his current appointment he was post-doctoral research associate in the Himadri Pakrasi Lab in Biology department at Washington University in St. Louis. He graduated with his Ph.D. and M.S. in Chemical Engineering from the Costas Maranas Lab at The Pennsylvania State University in 2014 and 2011, respectively. Prior to that, he earned his bachelor degree in Chemical Engineering from Bangladesh University of Engineering and Technology with the top position in his graduating class. Throughout his multidisciplinary graduate research career, he has developed metabolic network models for photosynthetic organisms and subsequently utilized those for studying their physiology and also for metabolic engineering applications. His recent postdoctoral research includes study of light/dark behavior and development of efficient gene expression control system of a model cyanobacterial strain.

Integrated metabolomics for deciphering metabolic pathways and emerging solutions for addressing the grand challenges of metabolomics

LLOYD SUMNER, University of Missouri

10:30 - 11:00 A.M.

ABSTRACT: This presentation will first describe our metabolomics platform and how we are using metabolomics, correlated gene expression profiling and genome wide association studies (GWAS) for the discovery and characterization of novel saponin biosynthetic genes in the model legume Medicago truncatula. The presentation will also describe a new Plant Metabolite Annotation Toolbox (PlantMAT) for the large-scale prediction of metabolite identity using experimental xC-MS/MS and custom combinatorial databases. The presentation will then describe a sophisticated UHPLC-MS-SPE-NMR approach for automated purification and higher-throughput empirical metabolite identification. The combination of computational and empirical identification has been very successful in the identification of specialized metabolites.

BIO: Lloyd Sumner acquired his Ph.D. in analytical chemistry from Oklahoma State University in 1993. He joined the Samuel Roberts Noble Foundation in 1999 and rose to the rank of Professor within the Plant Biology Division. He moved to the University of Missouri, Columbia in January 2016 as a professor in the Biochemistry Department and director of the University of Missouri's Metabolomics Center. His research program focuses upon the development, integration, and application of large-scale biochemical profiling technologies (i.e., metabolomics, proteomics and transcriptomics) for the discovery and characterization of the molecular and biochemical components related to plant specialized metabolism.

Linking lipidomics and genetics for crop improvement

RUTH WELTI, Kansas State University

11:05 – 11:35 A.M.

ABSTRACT: A goal of lipid analysis by mass spectrometry is to link variations in plant lipid levels with natural or induced genetic variation, thus identifying genes encoding catalytic or regulatory proteins underlying the lipid variation. Welti will describe lipidomic analyses and their applications to identify the genetic and biochemical basis for alterations in lipids involved in plant responses to abiotic stresses.

BIO: Ruth Welti obtained her B.S. from the University of Connecticut and her Ph.D. from Washington University in St. Louis. She is a long-time lipid biochemist who assumed the role of plant biologist at the turn of the century. She currently serves as director of the Kansas Lipidomics Research Center and is a university distinguished professor and Lillian J. Brychta professor of biology at Kansas State University. She has been instrumental in developing mass spectrometry-based lipid analysis for the plant community.

LUNCH
11:45 A.M. - 12:45 P.M.

SYSTEMS & SYNTHETIC BIOLOGY II SECTION

CHAIR: ED CAHOON, University of Nebraska-Lincoln

12:50 - 2:45 P.M.

Advanced fuels from advanced plants

JAY KEASLING, University of California, Berkeley

12:55 – 1:35 P.M.

ABSTRACT: Today, carbon-rich fossil fuels provide 85% of the energy consumed in the United States: depleting oil reserves and raising CO_2 emissions plus global warming risks. Liquid hydrocarbon fuels' high-energy content may be a preferred energy source for transportation—which in the US consumes around 13.8 million barrels of oil per day and generates over 0.5 gigatons of carbon per year. Research into alternative, non-fossil energy sources shows biomass--a renewable resource--can be converted into carbon-neutral transportation fuels.

Currently, biofuels such as ethanol are produced largely from grains, but plant biomass is a large, untapped resource (estimated at more than a billion tons per year): a renewable, domestic source of liquid fuels via converting the starch content of the grain into sugars that can be fermented to ethanol. We use the latest advances in synthetic biology to engineer plants, enzymes, and microorganisms to more efficiently produce fuels from plant biomass--reducing cost and improving sustainability by altering biomass composition including lignin length and content, cellulose and hemicellulose content, and functionalization of hemicellulose. In biomass deconstruction, we developed methods to cleanly and efficiently extract sugars from plant material. We engineered the metabolism of platform hosts (Escherichia coli and Saccharomyces cerevisiae) for production of advanced biofuels--hydrocarbons that can directly replace gasoline, diesel, and jet fuel. Large-scale production of these fuels will reduce our dependence on petroleum and carbon dioxide emissions, while allowing us to take advantage of our current transportation infrastructure.

BIO: Jay Keasling is the Hubbard Howe Jr. Distinguished Professor of Biochemical Engineering at the University of California, Berkeley in the Departments of Bioengineering and Chemical and Biomolecular Engineering; senior faculty scientist and Associate Laboratory Director for Biosciences at Lawrence Berkeley National Laboratory; and Chief Executive Officer of the Joint BioEnergy Institute (JBEI). Dr. Keasling's research focuses on metabolic engineering of microorganisms for degradation of environmental contaminants or for environmentally friendly synthesis of drugs, chemicals, and fuels. His B.S. in Chemistry and Biology is from the University of Nebraska, and his M.S. and Ph.D. in Chemical Engineering are from the University of Michigan; he did post-doctoral research in biochemistry at Stanford University. He is a member of the American Academy of Arts and Sciences, the National Academy of Engineering and the National Academy of Inventors, and earned numerous awards. He is also the founder of Amyris, LS9, and Lygos.

PREDICTIVE CROP DESIGN: GENOME TO PHENOME

Application of high-resolution, functional genomic methods to study soybean root traits

GARY STACEY, University of Missouri

1:40 - 2:10 P.M.

ABSTRACT: "Systems biology is a comprehensive, quantitative analysis of the manner in which all the components of a biological system interact functionally over time." Twentieth century biology focused primarily on single molecules (e.g., DNA structure) while 21st century biology seeks to understand the function of biological systems as a whole. The ultimate goal is a predictive view of biology, supplanting the older descriptive understanding. However, the promise of this new 'predictive' science has yet to be realized. For example, integration of dissimilar data such as proteomics, metabolomics, and transcriptomics, remains a formidable challenge. A major issue that compounds the problems of data integration is "signal dilution," where studies average the response of whole tissues, obscuring cell-specific responses. While plant genomes may encode over 50,000 genes, many genes are expressed in only a few organs, tissues or cell types. However, it can be technically challenging to measure gene, protein or metabolite levels in a specific cell type. In order to respond to these challenges, we have applied methods to study soybean root function at a single cell level, which increases the sensitivity of our analysis and avoids signal dilution. We have applied these methods primarily to the study of the nitrogen-fixing soybean symbiosis but the approaches are generic and could be applied to any plant process.

BIO: Gary Stacey is Curators' Professor and MSMC Endowed Professor of Plant Sciences and Biochemistry at the University of Missouri-Columbia. His research focuses generally on molecular aspects of plant-microbe interactions, including studies of the beneficial legume-rhizobium symbiosis and plant-fungal pathogen interactions. He has also been instrumental in the development of genomic resources for soybean study. He has authored or co-authored more than 240 peer-reviewed research articles, 78 book chapters, and 13 patents. Two of his patents support the product OptimizeTM sold by Novozymes, Inc., to enhance rhizobial inoculant performance on soybean. He has also edited or co-edited 16 books/reports. Six of these volumes were part of the Plant-Microbe Interactions book series that he co-founded. In 2008, he was elected a Fellow of the American Association for the Advancement of Science (AAAS). In 2010, he was elected a Fellow in the American Academy of Microbiology and, in the same year, Fellow of the American Society for Plant Biology.

Developing integrated products to improve crop performance, efficacy, and durability

WENDY PLINE-SRNIC, Dupont Pioneer

2:15 – 2:45 P.M.

ABSTRACT: Reliable crop performance depends on a crop's ability to produce under a myriad of both abiotic and biotic stresses throughout the growing season. Crops resistant to biotic stresses and pests, via breeding, or biotechnology, can still be overcome by pest adaptation or resistance, especially when single modes of action are deployed. Integrated product concepts explore the entire tool kit of options (genetics, biotechnology, seed treatment, biologicals, crop protection chemistry, and management) to design and develop products with multiple modes of action against stress. Combining multiple independent mechanisms against individual or multiple pests can improve reliability of crop performance, efficacy of control, and improve product durability by slowing resistance development. Both growers and companies have interest in developing these products as novel solutions to combat pests, however the complexity of these products, in terms of design, efficacy, and deployment offer unique challenges.

BIO: Wendy Pline-Srnic is the director of Integrated Product Characterization and Development (IPCD) at DuPont Pioneer. The IPCD group focuses on designing, validating, assembling and evaluating Integrated Product Offerings to the business and our customers. Integrated products include evaluating and combining a wider range of available technologies to solve the challenges our growers are facing. These technologies include our current core of genetics and traits, but also seed treatments, biologicals, crop protection chemistries, and management practices. She joined DuPont Pioneer as a Research Scientist in Maize Product Development, following five years of agricultural biotechnology experience within the corporate ag industry in the United Kingdom and Italy. Since joining Pioneer, she has served in various research positions, most recently as director of Global Trait Integration. She leads the Pioneer Women's Network and chairs the CAST (Council for Agricultural Science and Technology) Plants Work Group. Wendy earned her Bachelor of Science degree in Crop and Soil Science from Michigan State University, a Master of Science degree in Weed Science from Virginia Tech University and Ph.D. in Crop Science from North Carolina State University.

PREDICTIVE CROP DESIGN: GENOME TO PHENOME

Panel Discussion: Future of biotechnology for crop improvement

CHAIR: JIM ALFANO, University of Nebraska-Lincoln

3:00 – 4:00 P.M.

Plenary Talk: What can plant metabolic engineering do for human health?

CATHIE MARTIN, University of East Anglia (England)

4:05 – 4:45 P.M.

ABSTRACT: Phenylpropanoid metabolism is the best understood pathway of specialised metabolism in plants, probably because the core pathways are widely distributed; for example, monolignol biosynthesis in ferns, gymnosperms and angiosperms, flavonoid metabolism in bryophytes, ferns, gymnosperms and angiosperms. Some specialised polyphenols have therapeutic properties and preparations of plants that produce them have been used widely as traditional medicines. Foods, particularly fruit and vegetables, are important sources of polyphenol phytonutrients that promote health. Because these compounds are not essential for life, they have been disregarded by many nutritional and biofortification programmes. However, the recognition of their importance in the diet is essential to meeting the objectives of food and nutritional security as defined by the FAO. By engineering phenylpropanoid metabolism we have been able to enrich tomato fruit with different phenylpropanoid compounds allowing us to compare the relative effects of different polyphenols on cardiovascular disease.

BIO: Cathie Martin is a group leader at the John Innes Centre and Professor at the University of East Anglia. Her interests span from fundamental to applied plant science. She researches into the relationship between diet and health and how crops can be fortified to improve diets and address the global challenge of escalating chronic disease. This work has involved linking leading clinical and epidemiological researchers with plant breeders and metabolic engineers to develop scientific understanding of how diet can help to maintain health, promote healthy aging and reduce the risk of chronic disease. She is also involved in genetic screens to identify crops which lack toxins that cause nutritional diseases, and has recently initiated a collaborative project with China to research on Chinese Medicinal Plants.

Wrap-up; Departure for optional tour of phenotyping greenhouses at Nebraska Innovation Campus

ED CAHOON, University of Nebraska-Lincoln

4:45 P.M.

POSTERS

SESSION BEGINS AT 5 P.M. ON THURSDAY, APRIL 6

POSTER #1 | Joshua Herr | SURVEYING THE PLANT MICROBIOME THROUGH PLANT GENOME SEQUENCING PROJECT DATA MINING | Currently more than 100 plant genomes with data in public repositories have been initiated for both species and cultivars. Utilizing this raw public sequencing data and existing plant genome assemblies, I conducted a multi-step process to remove, assemble, and annotate microbial reads from these sequencing projects. Both species and cultivar specific microbial strains can be identified from this sequencing data.

#2 | Lauren Segal, R.A. Wilson | THE MAGNAPORTHE ORYZAE RSR1 GENE REGULATES FUNGAL ANTIOXIDATION AND IS ESSENTIAL FOR HOST ROS NEUTRALIZATION DURING RICE CELL INVASION | Magnaporthe oryzae causes rice blast disease and must neutralize host reactive oxygen species (ROS) bursts to survive and proliferate in rice cells. We sought to identify components of the M. oryzae oxidative defense pathway that are under the control of glucose-sensing trehalose-6-phosphate synthase 1 (Tps1) protein. RSR1 is a novel regulator of Tps1-dependent antioxidation pathway. Î"rsr1 mutant strains have altered antioxidation gene expression and reduced pathogenicity compared to wild type. They are unable to proliferate or detoxify in planta ROS bursts. This work enhances our understanding of the crucial importance of fungal redox homeostasis and antioxidation signaling during plant infection.

#3 | Daniel Schachtman, Rebecca Bart, Thomas Brutnell, Daniel Chitwood, Asaph Cousins, Jeffrey Dangl, Ismail Dweikat, Andrea Eveland, Maria Harrison, Stephen Kresovich, Peng Liu, Todd Mockler, Jessica Prenni, Balasaheb Sonawane, Susannah Tringe, Arthur Zygielbaum | SYSTEMS ANALYSIS OF THE PHYSIOLOGICAL AND MOLECULAR MECHANISMS OF SORGHUM NITROGEN USE EFFICIENCY, WATER USE EFFICIENCY AND INTERACTIONS WITH THE SOIL MICROBIOME | The overall project goal is to establish a foundational, systems-level understanding of plant, microbial, and environmental interactions that will lead to strategies for enhancing growth and sustainability of sorghum through genetic and microbial adaptations to water and nitrogen limited environments. In 2016 the team conducted large field experiments on 30 sorghum varieties with several aims including: finding the most water and nitrogen use efficient germplasm, studying how the genotype of sorghum alters the microbiome, how low nitrogen and water deficit alters the microbiome, how transcript and metabolite profiles are influenced by abiotic stress and genotype. This poster will contain a description of the field trials, the biomass and height data as well as stable isotope data and plant nitrogen content. This research was supported by the Office of Science (BER), U.S. Department of Energy, Grant no DE-SC0014395.

#4 | Margarita Marroquin-Guzman, Richard A Wilson | THE FUNGAL NITROOXIDATIVE STRESS RESPONSE SUPPRESSES RICE INNATE IMMUNITY DURING BLAST | Understanding how microbes manipulate plant innate immunity and colonize host cells is a major but incomplete goal of plant pathology. Here, we report that the nitrooxidative stress response of the important rice pathogen Magnaporthe oryzae suppresses host defenses to facilitate fungal growth and development in rice leaf cells. We show that the M. oryzae nitronate monooxygenase NMO2 gene is required for mitigating nitrooxidative cellular damage and, in rice cells, maintaining redox balance to avoid triggering plant defenses that impact M. oryzae growth and blast interfacial complex (BIC) development.

#5 | Laura White, Karuppaiyan Jothibasu, R. Neil Reese, Xijin Ge, Volker S. Brozel, Senthil Subramanian | SOYBEAN RHIZOSPHERE BACTERIAL COMMUNITY STRUCTURE AS INFLUENCED BY ROOT ISOFLAVANOIDS | Soybean root isoflavonoids aid in plant defense and enable nodulation, but their influence on the rhizosphere microbiome is not known. We evaluated rhizosphere bacterial communities of soybean composite plants where isoflavonoid biosynthesis was silenced. PCR amplicons from variable regions V1-V3 and V3-V5 of 16S rRNA genes were sequenced and the resulting data resolved using MOTHUR and vegan packages. Isoflavonoids had a small effect on the bacteriome, particularly on Xanthomonads and Comamonads. Hairy root transformation notably influenced Sphingomonads and Acidobacteria, but large similarity between bacterial communities of untransformed and hairy roots suggested that hairy root transformation is a useful tool to evaluate rhizosphere microbiomes.

#6 | Peng Wang, Ellen L. Marsh, Greg Kruger, Aaron Lorenz, Daniel P. Schachtman | SHIFT OF BELOWGROUND MICROBIAL STRUCTURE IN RESPONSE TO THE WATER DEFICIT AND MAIZE GENOTYPES | Plant-associated microbiota have been reported to provide many types of benefits to plant growth. However belowground shifts in microbial community composition in response to water deficit and host genotype under water deficit are poorly understood. Here we analyzed the soil and root microbiomes at two stages of maize development under water-limited conditions in older and modern hybrids developed from 1950 to 2010. Water deficit caused a dramatic shift in microbial communities. Notably, certain phyla such as Actinobacteria and Firmicutes were significantly more abundant in the rhizosphere of the newer maize hybrids. These results suggested that plant host is important for bacterial community composition in response to water deficit which decreases soil water and nutrient availability. Microbial populations around roots of modern hybrids may shift to more oligotrophic microbes because the newer hybrids are able to compete more effectively for nutrients and water.

POSTERS

#7 | Erin Carr, Steve Harris | YOU'RE ONLY AS GOOD AS YOUR PARTNER: EXTREMOTOLERANT FUNGI SURVIVABILITY VIA SYMBIOSIS | The black yeasts are a group of fungi from the subdivision Pezizomycotina that are known for their extremotolerance. Some of the conditions they can withstand are heat, freezing, desiccation, osmolarity, UV, heavy metals, and in some cases radiation. Unique features of these organisms make them intriguing to study alone, but may also provide insight into the phylogenetically related lichen-forming fungi. Since lichens and these polyextremotolerant fungi share similar resistance features, the black yeasts may enable study of the lichen lifestyle without the challenges of directly working with lichens. In addition to sharing similar traits, black yeasts are also almost always found in the same location as algae, even in desert and polar ecosystems. This raises the intriguing possibility that these organisms interact in a lichen-like manner. We propose that black yeasts and algae indeed interact in a mutualistic fashion that resembles lichens, and that observing these interactions will reveal clues about the nature of the fungal-algal communication that underlies lichen formation. To test our hypothesis we have isolated black yeasts and algae from biological soil crusts and rock surfaces, identified isolates using their ITS sequences, subjected isolates to multiple stressors and nutritional conditions to investigate their phenotypic diversity, and co-cultured the fungi and algae together in a pair-wise manner. Isolates that were taken from a biological soil crust in one location resulted in 24 black yeasts and 43 algal isolates. These have been extensively phenotyped for carbon utilization, nitrogen utilization, temperature resistance, UV resistance, and metal resistance allowing us to observe a moderate range of diversity. Current efforts are underway to integrate the phylogeny and phenotype data, as well as co-culturing the black yeasts with the algal isolates to observe symbiotic tendencies and any phenotypes associated with symbiosis.

#8 | Bangjun Zhou, Ravi V. Mural, Xuanyang Chen, Matt E. Oates, Richard A. Connor, Gregory B. Martin, Julian Gough, Lirong Zeng | GENOME ANALYSIS AND FUNCTIONAL CHARACTERIZATION IDENTIFY A SUBSET OF TOMATO UBIQUITIN-CONJUGATING ENZYMES ESSENTIAL FOR PLANT IMMUNITY | Of the three classes of enzymes involved in ubiquitination, ubiquitin-conjugating enzymes (E2) have been often incorrectly considered to play merely an auxiliary role in the process and few E2 enzymes have been investigated in plants. To reveal the role of E2 in plant innate immunity we identified and cloned forty tomato genes encoding E2 proteins. Thioester assays indicated the majority of the genes encode enzymatically active E2. Phylogenetic analysis classified the forty tomato E2 into thirteen groups, of which members of group III were found to interact and act specifically with AvrPtoB, a Pseudomonas syringae pv. tomato (Pst) effector that uses its ubiquitin ligase (E3) activity to suppress host immunity. Knocking-down the expression of group III E2 genes in Nicotiana benthamiana diminished AvrPtoB-promoted degradation of the Fen kinase and AvrPtoB suppression of host immunity-associated PCD. Importantly, silencing group III E2 genes also resulted in reduced pattern-triggered immunity (PTI). By contrast, PCD induced by several ETI elicitors was not affected on group-III-silenced plants. Functional characterization suggested redundancy among group III members for their role in the suppression of plant immunity by AvrPtoB and in PTI and identified UBC11, 28, 29, 39 and 40 as playing a more significant role in PTI than other group III members. Our work builds a foundation for further characterization of E2s in plant immunity and reveals that AvrPtoB has evolved a strategy for suppressing host immunity that is difficult for the plant.

#9 | Guangchao Sun, Richard A. Wilson | A NOVEL INTEGRAL MEMBRANE PROTEIN (IMP1) MEDIATES TOR SIGNALING IN MAGNAPORTHE ORYZAE AND IS REQUIRED FOR DETERMINISTIC (NON-RANDOM) APPRESSORIUM FORMATION AND BIOTROPHIC GROWTH IN RICE CELLS | The Target of Rapamycin (TOR), a conserved regulator of cell growth in response to nutrient availability, drives appressorium formation when inactivated on the nutrient-free leaf surface and, when activated, promotes biotrophic growth in rice cells following host penetration. Here we report that an integral membrane protein, Imp1, mediates TOR signaling to ensure normal appressoria formation and in planta development by M. oryzae. 80% of the germinating spores of imp1 deletants formed undifferentiated swellings at germ tube tips demonstrating increased mitosis and loss of autophagy and those spores that formed appressoria could penetrate leaf cuticles but elaborated morphologically abnormal invasive hyphae that failed to conduct cell-to-cell movement in rice cells. Imp1 localized to vacuoles and mediated autophagosome-vacuole fusion and vacuolar functions in response to TOR activity status. We thus propose that Imp1 is a downstream component of TOR such that in response to TOR inactivation, Imp1 mediates autophagosome-vacuole fusion resulting in autophagy necessary for in planta development and, in germinating spores, mitotic arrest and deterministic appressorium development.

#10 | Suresh Damodaran, Senthil Subramanian | GmCYP83B1 MEDIATED AUXIN FLUX REGULATION IS CRUCIAL FOR SOYBEAN NODULE DEVELOPMENT | Nodules are organs that develop in legumes like soybean through a symbiotic association with nitrogen-fixing rhizobia bacteria. While auxin activity is present during soybean nodule organogenesis, it is unclear what mechanism dictate auxin accumulation. We evaluated the expression of genes associated with auxin metabolism in a global gene expression dataset from soybean nodules at early and mature stages. The results indicated that local auxin biosynthesis and catabolism might be active and contribute to auxin accumulation during nodule development. Results from functional analysis indicated that GmCYP83B1 plays a key role in dictating auxin metabolism and nodule development in soybean.

POSTERS

#11 | Thais Egreja, Joshua R. Herr | PHYLOGENETIC DIVERSITY, MICROBIAL ECOLOGY, AND BIOGEOGRAPHY OF THE MICROBACTERIACEAE, A KEY FAMILY OF PLANT-ASSOCIATED BACTERIA | Species from the family Microbacteriaceae are diverse in various ecosystems and some of them have been reported as plant pathogens. Clavibacter michiganensis subsp. nebraskensis is the causal agent of Goss's bacterial wilt and leaf blight in corn. Leifsonia xyli subsp. xyli, causal agent of ratoon stunting disease (RSD) in sugarcane, has been reported as the most economically important pathogen of sugarcane worldwide. This study seeks to provide clarity on the environmental diversity of this important family noted for devastating plant pathogens. To understand the biodiversity and geographic range of this group, we mined public 16S sequences, which clustered into 53,696,442 sample-specific operational taxonomic units. A consensus phylogeny consisted of four major sub-familiar lineages not conforming to previously described subfamilies. Pathogenic & non-pathogenic members of the family were found in sister clades which suggest pathogenicity in this family is regulated by the presence of mobile elements conferring toxicity.

#12 | Spencer Schreier, Tao Lin, Suvo Chakravarty, Sen Subramanian | IDENTIFYING HOW MIR160 INFLUENCES SOYBEAN ROOT NODULE DEVELOPMENT | As demand for both yield and sustainable agriculture increase, symbiotic root nodules offer an attractive alternative to environmentally harmful fertilizers. Understanding root nodule formation may generate insights for optimizing nodule performance. A major candidate in soybean nodule formation is miR160, which targets repressor auxin response factor transcription factors (ARFs) such as ARF 16-2. However, the effectors of this interaction remain unknown. Currently, reporter constructs show ARF16-2 is transcriptionally active throughout nodule development but its expression is post-transcriptionally regulated, likely by miR160. DNA interaction investigations show the ARF16-2 DNA-binding domain does not bind the classical AuxRE motif, suggesting alternative functionality.

#13 | Karen Da Silva, Joe Louis, James C. Schnable, Joshua R. Herr | BASELINE REGULATION OF KEY GENES IN HERBIVORE DEFENSE IN MAIZE AND THE ROLE OF MICROBES IN DEFENSE GENE INDUCTION | Plants defend themselves against herbivores by inducing defenses in response to herbivory that simultaneously confer resistance and tolerance. Studies have shown that microbes may induce a priming effect by upregulating key genes involved in defense-related biochemical pathways, such as the Jasmonic Acid and Phenylpropanoid pathway. Focusing on Maize for its importance both globally and to the state of Nebraska, we have characterized a baseline response utilizing public data sets of key genes recognized in herbivore defense. This information will be used to investigate the role of endophytes and arbuscular mycorrhizal fungi in initiating defense responses against insect herbivores in corn.

#14 | Sunita Pathak, Senthil Subramanian | DIFFERENTIAL GENE EXPRESSION IN TWO NODULE ZONES OF SOYBEAN | Leguminous plants and rhizobia establish symbiotic relationships, forming root nodules. Nodule development starts with cortical cell division forming infection and parenchyma zones which house N-fixing bacteria and nodule vasculature, respectively. Molecular mechanisms that direct the distinct differentiation of these zones during nodule development are not known. We generated nuclear envelope biotin tagging constructs driven by ENOD2 (nodule parenchyma) and ENOD40 (infection zone) promoters, to obtain cell type specific nuclei with >90% purity and >50% efficiency. Global gene expression profiles (using RNAseq) are expected to identify infection zone and parenchyma-enriched genes, and help determine key signaling pathways associated with nodule zone differentiation and function.

#15 | Ashley Stengel, Rhae A. Drijber, Joshua R. Herr | THE MAIZE-ASSOCIATED SOIL MICROBIOME: A META-ANALYSIS | The importance of robust and resilient microbial communities has been demonstrated across disciplines in recent years. However, a clear understanding of the diversity and variation in soil microbiomes is still lacking. This project seeks to explore bacterial community diversity across geographic locations and to investigate how field-level management practices may influence this diversity. Drawing on bioinformatics tools, such as the genomic analysis package QIIME, we present an overview of bacterial 16S rRNA sequences, looking at how geological conditions and human-mediated management practices act as drivers for microbial community composition. Understanding this layer of diversity in the soil microbiome is an important first step for future work into microbe-microbe and microbe-plant interactions that hold promise for informing management practices in agroecosystems.

#16 | Manny Saluja, Harkamal Walia, Scott E. Sattler | EFFECT OF LIGNIN MODIFICATION ON SORGHUM ROOT SYSTEM | Sorghum bicolor, a heat and drought tolerant cereal crop is an important source of animal feedstock and bioenergy. Modifying lignin content without affecting plant fitness is the major target for improving sorghum as forage and bio-energy crop. Present study aims to understand the implications of modifying lignin content on Sorghum root system. In the present study, roots traits of Sorghum brown mid rib mutants characterized for mutation in one of the steps in monolignol biosynthetic pathway that leads to decreased lignin content were studied under well watered and water limited conditions.

POSTERS

#17 Mohammad Mazharul Islam, Jaspreet Sandhu, Harkamal Walia, Rajib Saha | THERMAL STRESS ON PLANTS: INSIGHTS ABOUT GLOBAL REGULATIONS AND METABOLIC MODEL DEVELOPMENT | Increased global temperatures are detrimental to plant growth and development and lead to significant reduction in crop yields. In rice, heat stress during early seed development adversely affects the seed size and quality at maturity. Plants use a suite of strategies to respond to abiotic stresses, including changing the abundance of stress responsive genes, proteins, and metabolites. Complex gene-protein-reaction associations as well as regulatory mechanisms constitute a challenge to elucidate stress response mechanisms in plants. This research aims to understand the stress response mechanisms in developing rice seed using spatiotemporal transcriptomic analyses in control (28C) and stress (35C) conditions and in silico metabolic studies. The data was leveraged to identify global regulator(s) and will be used as regulatory information for developing next-generation tissue-specific and whole-plant metabolic models. This systems level study will identify bottlenecks in the metabolic pathways and subsequently propose genetic intervention strategies for developing stress tolerant rice.

#18 Yeongho Kim, Ee Leng Terng, Wayne Riekhof, Edgar Cahoon, Heriberto Cerutti | A PROKARYOTIC-LIKE 1-ACYLGLYCEROL-3-PHOSPHATE ACYLTRANSFERASE IS REQUIRED FOR TRIACYLGLYCEROL SYNTHESIS IN CHLAMYDOMONAS | Microalgae accumulate triacylglycerols (TAGs) under nutrient deprivation. Transcriptome analyses of C. reinhardtii in nitrogen-depleted medium revealed up-regulation of a gene encoding a 1-acylglycerol-3-phosphate acyltransferase (CrAGPAT/CrLPAAT2). Suppression of CrAGPAT expression by RNA interference (RNAi) indicated that the enzyme is required for TAG synthesis in Chlamydomonas. Interestingly, in vitro and in vivo assays using recombinant CrAGPAT preferred C16:0-CoA over C18:1-CoA. Despite these prokaryotic features, CrAGPAT appears to localize to the endoplasmic reticulum (ER) in Chlamydomonas. This observation suggests that the FA bias in Chlamydomonas TAGs is partly determined by the acyl-CoA preference of the unique ER-localized CrAGPAT.

#19 Tara Nazarenus, Tadele T. Kumssa, Patrick Rädler, Sandra Erdozain Salón, Edgar B. Cahoon | COMPLEX METABOLIC ENGINEERING OF CAMELINA FOR ADVANCED BIOFUELS AND INDUSTRIAL FEEDSTOCKS | Camelina sativa (camelina or false flax) is an emerging Brassicaceae oilseed crop in the North American Great Plains and US Pacific Northwest. Growing interest in camelina is largely due to its potential for biodiesel production in geographic areas with sub-optimal rainfall and soil fertility. Camelina has emerged as an especially attractive platform because it can be rapidly transformed by Agrobacterium with technical ease. This capability has enabled complex metabolic engineering of novel oil-related traits. Progress to date from greenhouse and multi-year field trials of genetically enhanced camelina lines will be presented.

#20 Hannah Tetreault, Erin D. Scully, Thomas E. Clemente, Scott E. Sattler | MODIFYING LIGNIN COMPOSITION AND CONTENT OF SORGHUM BIOMASS FOR IMPROVED BIOENERGY CONVERSION | Sorghum (Sorghum bicolor) is an opportune crop for bioenergy due to its high yield potential, and lower nitrogen and water requirements. Transgenic constructs expressing monolignol biosynthetic genes under control of 35S promoter have been developed and used for sorghum transformation to examine the consequences to biomass composition and energy content. Ectopic expression of caffeoyl CoA O-methyltransferase (SbCCoAOMT), an enzyme in the monolignol pathway, resulted in an increase in total energy content and modifications to cell wall composition that were detectable through histochemical staining and GC-MS analysis. 35S::SbCCoAOMT induced changes may improve sorghum biomass for a range of conversion technologies.

#21 Xiangjun Li, Alicen M. Teitgen, Wei Zhang, Chunyu Zhang, Martha D. Morton, Robert E. Minto, Edgar B. Cahoon | DISCOVERY OF TWO NOVEL DIHYDROXY FATTY ACIDS AS MAJOR COMPONENTS OF THE SEED OIL OF THE BRASSICACEAE ORYCHOPHRAGMUS VIOLACEUS | The Brassicaceae Orychophragmus violaceus (Chinese violet cress, February orchid) is native to China and has been used in intergenic crosses with Brassica napus to study genome stability. Previously published analyses have indicated that the seed oil of this plant is enriched in linoleic acid (18:2) and has low very long-chain fatty acid content. Re-evaluation of O. violaceus oil by thin layer chromatographic analysis serendipitously revealed the presence of a highly polar oil composition. Consistent with this, two fatty acids with extended retention times accounting for 40% to 50% of the seed oil were identified in gas chromatographic analysis of silylated fatty acid methyl esters from O. violaceus seed oil. Data from GC-MS and NMR analyses were consistent with the identity of these fatty acids as the C24 dihydroxy fatty acids 7,18-OH-24:1Δ15 and 7,18-OH-24:2Δ15,21. In addition to these fatty acids, small amounts of C18-C24 monohydroxy fatty acids were detected in O. violaceous seed oil. Co-expression of cDNAs for an oleic acid 12-hydroxylase and a variant 3-keto-acyl-CoA synthase found in the O. violaceus seed transcriptome was sufficient to confer nebraskanic acid synthesis in Arabidopsis seeds, without the need for a second fatty acid hydroxylase. These data together with the detection of C20¬ 3-OH and C22 5-OH dihydroxy intermediates in fatty acid and acyl-CoA pools of O. violaceus seed indicated a novel route for hydroxy fatty acid synthesis involving premature or discontinuous elongation of the 3-OH intermediate during a carbon chain extension cycle.

POSTERS

#22 **Haejin Kim, Thomas E. Clemente, Edgar B. Cahoon | IMPLEMENTATION OF SYNTHETIC BIOLOGY FOR INDUSTRIAL AND NEXT-GENERATION BIOFUEL CROP IMPROVEMENT |** Conventional plant breeding and biotechnology approaches for crop improvement approaches typically target only one or a small number of traits at a time. In contrast, the emerging discipline of synthetic biology offers tools for making step changes in crop improvement by enabling integration of many trait genes into the host crop genome in a single genetic transformation event. We have constructed ten modules with different trait genes for heat tolerance, seed size, oil content, oil quality, and protein quality using GoldenBraid technology to improve sustainability and biofuel and industrial quality traits and to evaluate the upper limit of transgene numbers into camelina from one construct.

#23 **Haejin Kim, John B. Ohlrogge, Edgar Cahoon | IDENTIFICATION OF ACYL-ACP THIOESTERASES FROM CORIANDER DEVELOPING ENDOSPERM FOR ENHANCED PETROSELINIC ACID PRODUCTION |** Petroselinic acid is the major fatty acid of the seed oil of most Apiaceae and Araliaceae species and has potential industrial significance because of its unique unsaturation at carbon 6 (18:1Δ6cis). This biosynthetic pathway has been previously shown to require a specialized Δ4-palmitoyl-ACP (PAD) desaturase, a specialized KASI for elongation of 16:1Δ4-ACP to 18:1Δ6-ACP, and a specialized acyl-ACP thioesterase for release of 18:1Δ6 from ACP. To date, cDNAs for Δ4 PADs have been isolated from the Apiaceae coriander (Coriandrum sativa) and the Araliaceae English ivy (Hedera helix) gene, and a putative petroselinic-acid specialized KASI cDNA has been identified in coriander. Still missing in our understanding of petroselinic acid synthesis is the specialized petroselinoyl-ACP thioesterase and its cDNA. To identify this cDNA, 454 transcript sequencing was performed from developing coriander endosperm. Three genes encoding acyl-ACP thioesterases, CsFatA, CsFatB1, and CsFatB2, were found in this transcriptome. Co-expression of these thioesterases with the coriander Δ4-PAD is being conducted to define the biosynthetic pathway of petroselinic acid using camelina and tobacco callus. We are also pursuing transcriptomic studies with developing carrot and English ivy seeds to gain additional insights into the specialization of fatty acid biosynthesis and metabolism that is necessary to achieve high levels of petroselinic acid synthesis and accumulation.

#24 **Umidjon Iskandarov, Hae Jin Kim, Jillian E. Silva, Rebecca E. Cahoon, Edgar B. Cahoon | METABOLIC ENGINEERING FOR REDESIGN OF FATTY ACID CARBON CHAIN-LENGTHS FOR ADVANCED BIOFUELS IN CAMELINA |** A potential renewable source of hydrocarbons of chain-lengths similar to those found in jet fuels are vegetable oils that contain short- and medium-chain fatty acids. Cuphea pulcherrima and Cuphea viscosissima seeds contain over 90% of 8:0 and 70% of 10:0 fatty acids, respectively, indicating the existence of specialized enzymes thioesterases and acyltransferases accumulating short chain fatty acid rich TAG in seeds. Genes from these species can be used to engineer short- and medium-chain fatty acid biosynthetic pathways into seeds of an oilseed crop such as Camelina (Camelina sativa (L.) Crantz) that can be produced in the United States.

#25 **Lucas Busta, Evan LaBrant, Edgar Cahoon | STRUCTURE AND BIOSYNTHESIS OF BIOACTIVE POLYACETYLENES |** Antipathogenic lipids called polyacetylenes are produced in various Apiaceae (e.g. carrot) and Asteraceae species, and are thought to be potentially valuable resources for creating crops lines with improved pathogen resistance. The new high quality carrot genome has enabled functional genomics approaches to exploring polyacetylene biosynthesis and function. We have performed detailed chemical analyses of polyacetylenes in diverse carrot tissues and have identified 27 FAD2-like sequences in the carrot genome as candidates for catalyzing the first step in polyacetylene biosynthesis. We correlated polyacetylene abundance with acetylenase expression pre- and post-pathogen treatment using RNA-seq and are functionally testing acetylenases in tobacco.

#26 **Jose A. Aznar-Moreno, Timothy P. Durrett | USING GENOME EDITING TO ALTER OIL PRODUCTION IN CAMELINA SATIVA |** Camelina sativa possess an allohexaploid genome where up to three homologues of each gene might be expressed in seeds and therefore need to be silenced. The emergence of genome editing techniques such as CRISPR-Cas9 offer the ability to generate genetically stable Camelina lines where the activity of endogenous biosynthetic genes has been eliminated. We targeted two Camelina enzyme activities, diacylglycerol acyltransferase (DGAT) and phospholipid:diacylglycerol acyltransferase (PDAT) whose activities catalyze the last step for the synthesis of TAG. To determine whether all three DGAT1 or PDAT1 homologues could be simultaneously edited by Cas9, guide RNA sequences were designed to target sequences conserved across the three genes. Analysis of T2 seed revealed alterations in the fatty acid profile and reductions in seed oil content consistent with mutations in the target genes.

POSTERS

#27 Jithesh Vijayan, Maya Khasin, Paul Staswick, Kenneth W.Nickerson, Wayne Riekhof | AUXIN MEDIATED CELL-TO-CELL COMMUNICATION IN MICROALGAE, CHLORELLA SOROKINIANA | Auxin is a well studied phytohormone with a diverse set of functions in plant development and growth. Although auxin signaling has been studied for well over 50 years, very little is known about the evolution of this signaling system. In our work with Chlorella sorokiniana, a unicellular microalgae, we found that auxin is synthesized and secreted into the growth media. Genome of this organism also encodes for proteins that are involved in synthesis, secretion and perception of auxin. Taken together, we hypothesize that auxin is involved in cell-to-cell communication in this organism. This information is pivotal in the study of evolution of hormonal communication because it reveals the presence of auxin mediated communication in microalgae which is widely accepted as the predecessor of land plants. To further understand the role of this extracellular signaling system in miroalgae, we undertook a chemical genetics approach and identified three molecules from a chemical library screen, that inhibited the growth of C.sorokiniana while exogenous addition of auxin recovered the growth. We intend to study the mechanism of inhibition of growth by these molecules and how auxin recovers the growth. By this means we expect to understand the absolute necessity and role of auxin signaling in the of growth C.sorokiniana.

#28 Karanbir Aulakh, Timothy Durrett | IDENTIFICATION OF GENES ASSOCIATED WITH REDUCED OIL ACCUMULATION IN DGAT1 MUTANT | Triacylglycerols (TAG) are the major storage lipids found in the developing seeds of plants and serve as an important lipid and energy reservoirs. In Ara-bidopsis thaliana seeds, DGAT1 is the major en-zyme contributing to TAG biosynthesis. dgat1 mu-tants retain 60-80% seed TAG content due to in-volvement of PDAT1 in acyl-CoA independent TAG biosynthesis. RNA-Seq analysis of developing seeds identified differen-tially expressed genes in dgat1 relative to WT. Sig-nificant changes in gene expression profile were detected in lipid related genes such as lipases, de-saturases and elongases. Further, lipid profiling of T-DNA insertional mutants for some differentially expressed genes revealed significant changes in lipid content and composition. For example, mutations in a member of the α,β-hydrolase family, resulted in smaller seed and an al-tered seed oil phenotype. In addition, combining the dgat1 and abh gene re-sulted in lethal pheno-type, demonstrating the important role of this en-zyme in embryo devel-opment and TAG biosyn-thesis

#29 Jonathan Markham, Inga Krassovskaya | PLANT SPHINGOLIPIDS: NEW TARGETS FOR ENGINEERING COLD-TOLERANCE IN CROPS | Low temperature largely determines what crops can be grown in certain areas and defines the growing season for others. A single modification of membrane lipids in the otherwise cold-hardy plant Arabidopsis thaliana is sufficient to make that plant extremely sensitive to even a mild cooling. This modification, a desaturation of the very long-chain fatty acids in sphingolipids, is relatively uncommon in nature, being found only in a few cold-tolerant plant species. The hypothesis that sphingolipid desaturation is an adaptation to allow growth a cold-temperature is being tested by modification of sphingolipids in Camelina, barley, soybean and maize.

#30 L. Virlouvet, Q. Du, C. Zhang, N. Liu, T.J. Avenson, M. Fromm, Z. Avramova, S.E. Russo | DEHYDRATION STRESS MEMORY: GENE CO-EXPRESSION NETWORKS LINKED TO THE PHYSIOLOGICAL PHENOME DURING SUCCESSIVE DEHYDRATION STRESSES IN ZEA MAYS | How changes in gene expression in response to environmental variability translate into physiological responses dictating plant survival, growth, and reproduction is poorly understood. Dehydration stress response involves memory, in which an initial, sub-lethal stress alters responses to subsequent stresses. Using a whole-transcriptome approach, we identified expression changes correlated with leaf physiology involved in dehydration stress memory in maize. Our co-expression network analysis showed that transcriptional changes grouped into relatively few modules of stress memory genes with varying strengths of correlation with drought-tolerance parameters. A key challenge is to identify genes mediating stress memory to improve tolerance of dehydration in crops.

#31 Jennifer Myers, Allison C. Barnes, J. P. Mower, R. Roston | EVOLUTION OF THE ACTIVATION OF A KEY FREEZING TOLERANT PROTEIN IN PLANTS FREEZING RESISTANCE IN PLANTS IS A TRAIT THAT ALLOWS THEM TO SURVIVE BETTER IN COLDER TEMPERATURES | The Sensitive to Freezing (SFR2) protein in Arabidopsis thaliana is activated during freezing conditions to help plants be more freezing tolerant. Here, we are testing multiple plant species in normal and freezing conditions, then mapping the relationship of activation of SFR2 homologs to a phylogenetic tree. An oligogalactolipid product of SFR2 is being analyzed using thin-layer chromatography (TLC) to determine the relationship between SFR2 sequence and activation. Three categories of SFR2 activation were identified: always active, never active, and active in freezing conditions.

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#32 Daniel Carvalho, Yang Zhang, James C. Schnable | IDENTIFYING COMMON AND UNIQUE ENZYMATIC CHANGES ASSOCIATED WITH THREE C4 BIOCHEMICAL PATHWAYS IN RELATED GRASSES | Plants using C4 photosynthesis are more productive, particularly in hot and dry environments. Despite requiring complex morphological and biochemical changes, C4 photosynthesis has evolved multiple times, using three different biochemical pathways. Here we study a group of grasses containing all three observed biochemical subtypes of C4 photosynthesis, and use measurements of protein sequence change in shared and sub-type specific enzymes to determine whether all three lineages evolved from a common C4 ancestor and then diverged biochemically, or C4 photosynthesis originated independently in these lineages. Comparisons across multiple C4 lineages provides the opportunity to engineer a more efficient synthetic C4 pathway.

#33 Talukder Jubery, Baskar Ganapathysubramani,Matthew E. Gilbert, Daniel Attinger | IN SILICO DESIGN OF CROP IDEOTYPES UNDER A WIDE RANGE OF WATER AVAILABILITY | Given changing climate and increasing impact of agriculture on global resources, it is important to identify phenotypes which are global and sustainable optima. Here an in silico framework is constructed by coupling evolutionary optimization with thermodynamically sound crop physiology, and its ability to rationally design phenotypes with maximum productivity is demonstrated, within well-defined limits on water availability. Results reveal that in mesic environments such as the North American Midwest, phenotypes optimized for maximum productivity and for survival under drought are similar to those with maximum productivity under irrigated conditions. A similar result is obtained in humid continental environments like Iowa. In hot and dry environments like California, phenotypes adapted to drought produce 40% lower yields when irrigated compared to those optimized for irrigation. In all three representative environments, the tradeoff between productivity under drought versus that under irrigation was shallow, justifying a successful strategy of breeding crops combining best productivity under irrigation and close to best productivity under drought. Our results demonstrate that breeding in silico is a promising complement to conventional breeding.

#34 Jaspreet Sandhu, Kan Liu , Jinyu Li, Qi Zhang , Chi Zhang, Harkamal Walia | IMPACT OF HEAT STRESS ON EARLY SEED DEVELOPMENT IN RICE | Cereals are main source of calories consumed worldwide. Among cereals, rice is the major crop grown throughout world. Major traits which determine crop yield include seed size, seed weight and number of seeds per unit area. In rice, 70% of mature seed is contributed by endosperm and also endosperm serves as nourishing tissue for germinating seedlings. Endosperm development in cereals is characterized by different stages, syncytium formation, cellularization, differentiation, and maturation.The duration of the syncytial stage and the rate of mitotic divisions are important determinants of seed size at maturity. In Rice (Oryza sativa) var. Kitaake under control conditions cellularization is initiated between 48 and 72 hours after fertilization, and completed by 96 HAF. Any kind of environmental stress during early seed development has an adverse effect on seed size at maturity. In different sets of experiments,we observed that the syncytial stage is highly sensitive to heat stress. Therefore, it is critical to elucidate molecular mechanisms controlling this process, which would be helpful in improving thermal resilience of rice. Here, we explored the spatiotemporal transcriptome of developing seeds under control (28Â°C) and stress (35Â°C) conditions to identify potential genetic and epigenetic regulators of early seed development in rice.

#35 Atefeh Hosseini, Brent Ewers, Carmela Rosaria Guadagno | THE IMPACT OF GENOTYPIC VARIATION ON HYDRAULICS AND PHOTOSYNTHESIS OF DIVERSE CROP PLANT | During the last decades, water scarcity and rising temperatures have influenced crop management choices worldwide. These sudden changes in the environmental conditions necessitate the development of more comprehensive mechanistic models to predict final yield production. A model that incorporates both plant biophysical processes and morpho/phenological characteristics of above and below ground tissue can be used to predict yield in growth-limiting conditions. Due to the presence of complex interactions among different compartments of the hydraulic-growth model and other several unknown parameters, linking genotypic and phenotypic information are required to estimate the functional model parameters. It is the first step, we monitored photosynthetic characteristics (e.g. gas exchange and chlorophyll fluorescence), leaf morphology and anatomy, root morphology and above and below ground biomass of 7 crop accessions in growth chambers to evaluate water use and carbon allocation characteristics.

#36 Jyothi Kumar, Anthony Mosher and Steven D. Harris | ADAPTATIONS OF EXOPHIALA DERMATITIDIS IN STRESSFUL ENVIRONMENTS | Fungi are known to inhabit extreme environments that are constantly exposed to high salt, high temperature, cold and desiccation stress. A multitude of factors enable colonization of these environments, including melanization and UV resistance. Exophiala dermatitidis is a model black yeast extremophile that causes cutaneous and subcutaneous infections in humans. Studies indicate that it can produce carotenoids, melanins, and oxidative enzymes in response to stress and as a means to survive extreme environments. Our objectives are to investigate the mechanisms that underlie stress resistance in E. dermatitidis. In this study, we performed a transcriptomic analysis of E. dermatitidis using

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RNA sequencing to investigate the role of the conserved GTPases Cdc42 and Rac1 in stress tolerance Differential expression analyses revealed important genes / processes involved in light responses, carotenoid synthesis, oxidative stress, heat shock proteins and MAPK signaling pathways. Transcription factors like RLM1, SMP1, PHO2 involved in the regulation of melanin synthesis, the HOG1 pathway and phosphate synthesis were also modulated. E. dermatitidis requires photoinduction for carotenogenesis and has an intriguing set of light sensing genes. We studied the role of light in regulating pigmentation by phenotypic and expression profiling of genes involved. Our study provides important insight into the link between Cdc42 and light responses and also identifies probable pathways involved in the regulation of light, carotenoids and melanin sythnesis in Exophiala dermatitidis.

#37 | Dipak Kumar Sahoo, Chinmay Hegde and Madan K. Bhattacharyya | A HIGH THROUGHPUT PHENOTYPING SYSTEM FOR IDENTIFYING CANDIDATE ARABIDOPSIS GENES THAT REGULATE ADAPTATION TO EXTREME TEMPERATURE CONDITIONS | To uncover the genetic mechanisms regulating plant adaptation to extreme weather conditions, we have developed a phenotyping system by equipping Arabidopsis Percival growth chambers (AR22LC9) with digital cameras (CropScore, Tubingen, Germany) to study the natural variants. We have developed a method to batch process digital images of hundreds of Arabidopsis seedlings to numerical data in a spreadsheet-ready CSV file. We have phenotyped different Arabidopsis ecotypes in this newly developed system for abiotic stresses. By studying genome-wide association of responses of 437 Arabidopsis ecotypes to heat and cold stresses with the genotypes of individual ecotypes, we have identified 13 candidate genes under each of cold and heat stresses. Surprisingly, two of the cold stress-related genes encode NBS-LRR-type proteins. A Myb protein with high identity to a previously characterized rice regulator of stress tolerance was identified under cold stress. Among the heat stress-related genes, two encode putative LRR containing protein kinases.

#38 | Truc Doan, Tu Doan, Michael J. Kangas, Christina Wilson, Rachel Lukowicz, AdreAnna Ernest, Andrea E. Holmes, Erin L. Doyle, Tessa Durham Brooks | USING COLORIMETRIC DETECTION, NINHYDRIN, TO DETECT FREE-AMINE MOLECULES IN ROOT SURFACES | A colorimetric method was developed to detect spatial and temporal changes in the composition of nitrogen-containing exudates within the rhizosphere. A detection paper was developed by formulating ninhydrin into a print solution, uniformly deposited onto tissue paper with a commercial printer. The paper was gently pressed onto the seedling root. Images of seedlings and dried ninhydrin papers were captured and overlaid for analysis. The colorimetric method was found to be stable and still allow linear plant growth.This novel method allowed simultaneous collection of spatial and temporal data of the root surface molecules using a solid supported ninhydrin indicator.

#39 | Zhikai Liang, Geng Bai, Yufeng Ge, Oscar Rodriguez, James Schnable | FIELD PHENOTYPE PREDICTION ON MAIZE USING NOVEL PHENOMIC TOOLS AND ENVIRONMENTAL INFORMATION | Image-based phenotyping is creating new possibilities for the quantitative genetic study of crop plants. However, depending on the phenotype of interest, extracting numerical measurements from tens of thousands of plant images remains challenging, requiring the development and testing of new computer vision algorithms. Early efforts in this area have focused on replicating transitional phenotypes which have been manually measured under field conditions in the past. However, image-based phenotyping also creates the possibility to identify and study the genetic basis of variation novel phenotypes which would not be practical to measure manually, but which may be linked to agronomic performance under field conditions. In order to stimulate the development of new algorithms for extracting novel quantitative measurements of plant architectural and compositional phenotypes we have generated a set of controlled environment phenotypic data for maize lines where are also being grown and phenotyped at field locations across the US as part of the public-private Genomes to Fields (G2F) project. The first, already released dataset consists of RGB, thermal infrared, and hyperspectral data from each plant collected once per day during vegetative development. A second soon to be released dataset will include data from 139 maize hybrids and extend image capture through flowering. Currently we are able to extract only crude measurements from the resulting image datasets, but these data can already produce large numbers of synthetic and derived phenotypic traits, suggesting that dimensional reduction and trait selection will both be important initial steps in any attempt to identify meaningful correlations between architectural and compositional traits in the greenhouse and field performance under different environmental conditions.

#40 | Natasha Pavlovikj, Kevin Begcy, Sairam Behera, Malachy Campbell, Harkamal Walia, Jitender S. Deogun | COMPARING TRANSCRIPTOME ASSEMBLY PIPELINES FOR WHEAT | Transcriptome analysis is currently one of the main focuses of research for a great number of scientists. The assembly of raw sequence data to obtain a draft transcriptome is a complex multi-stage process including f pre-processing, assembling, and post-processing. In order to implement these stages, a great knowledge of different algorithms and tools is required. In this paper, we generate multiple transcriptome assembly pipelines with different tools and approaches. Analyzing these pipelines, we observe that the error correction method with Velvet Oases and merging the individual k-mer assemblies with highest N50 produce the most stable base for further downstream analysis.

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#41 **Adam Voshall, Sairam Behera, Jitender S. Deogun, Edgar B. Cahoon, Etsuko N. Moriyama | ENSEMBLE DE NOVO TRANSCRIPTOME ASSEMBLIES IMPROVE SEQUENCE AND GENE COUNT PREDICTIONS FOR NON-MODEL PLANTS |** Using simulated benchmark data from the No-0 strain of Arabidopsis thaliana, of the 15,539 transcripts expressed in the simulation, the number of transcripts correctly assembled by each tool ranged from 10,710 to 11,766, while the number of incorrect predictions ranged from 46,831 to 99,877, (3-6 times the number of expressed transcripts). In contrast, using an ensemble assembly, 11,502 of the correctly assembled transcripts were preserved, while the number of incorrectly assembled transcripts was reduced to 3,725. Further, the total number of predicted genes (15,227) closely matches the number of transcripts expressed in the simulation.

#42 **Trevor Nolan, Sriram Chockalingam, Colton M. McNinch, Adedotun Akintayo, Soumik Sarkar, Maneesha Aluru, Patrick S. Schnable, Srinivas Aluru, and Yanhai Yin | NETWORK-BASED DISCOVERY OF BRASSINOSTEROID REGULATION OF PLANT GROWTH AND STRESS RESPONSES IN ARABIDOPSIS |** Understanding gene regulatory networks that control plant growth and stress responses is essential to optimize crop yield in an ever-changing environment. Plant steroid hormones, the Brassinosteroids (BRs) regulate plant growth and stress responses, including that of drought. BRs signal to regulate the activities of the BES1/BZR1 family transcription factors, which in turn mediate the expression of more than 5,000 BR-responsive genes. Recent studies identified several thousand BES1/BZR1 target genes and about 500 BR-related Transcription Factors (BR-TFs) that likely function along with BES1/BZR1 to regulate the large number of BR target genes. Although several families of BR-TFs have been functionally characterized, the networks through which BRs, BES1/BZR1 and BR-TFs function remain to be fully defined. We have used an integrated approach to address this challenge, which involves computational modeling, phenomics and functional genomics. We have built a comprehensive BR gene regulatory network (GRN) using more than 11,760 publicly available microarray datasets and prioritized BR-TFs for functional studies using NEST (Network Essentiality Scoring Tool). Further, our phenomics studies identified hundreds of BR-TF mutants that display altered BR responses. Clustering of BR-TFs based on their predicted target genes showed that the 5 top ranking TFs with strong BR phenotypes are distributed in 3 clusters that are enriched for BR and drought target genes and contain the majority of BR-TFs with BR response phenotypes. Genetic and genomic analysis of these clusters is being used reveal how BR-TFs regulate specific aspects of growth and stress response programs. This research is supported by grants from NSF (IOS1257631) and the Plant Science Institute at Iowa State University.

#43 **Wheaton Schroeder, Rajib Saha | K-ATHALIANA - TOWARDS A MULTI-TISSUE KINETIC MODEL OF ARABIDOPSIS THALIANA |** Computational modeling of metabolism is now an indispensable tool to drive the processes of understanding, discovering, and redesigning of biological systems. Although Flux Balance Analysis (FBA) is the primary tool used for this purpose, it has significant limitations due to the lack of reaction kinetics, chemical species concentration, and metabolic regulation. These are important to design engineering interventions directed to overproduction of a specific bioproduct or improvement of plant performance, particularly in the presence of feedback regulation. Arabidopsis thaliana has been a model system for modern plant science for the past three decades due to its small genome, short lifecycle, and ease of genetic manipulation. Several FBA models for A. thaliana already exist, and most regulatory interactions are well studied and documented. Hence, combining and advancing this knowledge in a kinetic model framework will allow us to answer important questions of regulation and tissue interaction in a model plant system.

#44 **Avimanyou Vatsa, Ann E. Stapleton, Toni Kazic | COMPUTATIONAL ISSUES IN GROUPING COMPLEX PHENOTYPES |** Discovering patterns in data is fundamental to solving the problem of providing the world's people with enough food now and in the future. A key part of ensuring food security is improving crops. Recognizing, measuring, grouping, and classifying features of crop growth, yield, and stress resistance --- some of many of the most agronomically important phenotypes---is the first and last task in crop improvement, and at many stages in between. Clustering is a well understood computational technique for grouping objects by a similarity criterion. So the quality of the groups constructed by clustering can only be as good as the wisdom of the computational geneticist in exploring and transforming the data, and in selecting clustering algorithms. Here, we examine the effects of common data treatments, standardization and clustering algorithms on an experimental phenotyping data set. The standardization method chosen should only minimally distort the natural clusters inherent in the data. We investigated the effects of sixteen different standardization methods on the clusters obtained by seven different clustering algorithms. We compared to a novel standardization method we call SDFS (Standardization for Distribution Free Statistics). Our results show that clusters or groups obtained by MODECLUS using SDFS are reasonable for the experimental, orthonormal and synthetic data.

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#45 | Ying Ren, Devin Rose,Oscar Rodriguez,Roch Gaussoin, David Holding | PROGRESS IN THE DEVELOPMENT OF QUALITY PROTEIN POPCORN(QPP) | Quality Protein Maize (QPM: modified opaque-2) has nearly double the amount of two essential amino acids (Lys and Trp) and is considered as a more balanced source of nutrition for humans and monogastric animals compared to normal dent corn. Availability of in-gene o2 SSR markers has facilitated the conversion of vitreous endosperm popcorn to QPM. We started introgression of the o2 allele into popcorn by making F1 crosses between several elite popcorn lines and QPM lines. After selfing with concurrent backcrossing of selected partially modified BC2F2 individuals (type II and type III opaques), we characterized o2 mutants with fully modified kernels in BC2F3, which were further self-pollinated for selection. With BC2F5 generation advancement underway, we aim to: (1) maximize recovery of popcorn genome; (2) carry out amino acid profiling and popping analysis; (3) assess agronomic traits of QPM conversion lines compared to popcorn lines. Recent progress and plans in this project will be presented.

#46 | Xianjun Lai, Lang Yan and James C. Schnable | SEARCHING FOR PARALLEL SIGNATURES OF SELECTION DURING DOMESTICATION IN MAIZE AND SORGHUM | Artificial selection to create crops from wild grass species have targeted many of the same phenotypes during the domestication of different crop species. For a few key single gene phenotypic changes, it has already been possible to test whether the same gene was the target of domestication efforts in related crops. Genes which have been targets of selection during domestication or crop improvement in one species, but not another, may be useful targets for future breeding efforts. Maize and sorghum are two closely related crop species which diverged from a common ancestor approximately 12 million years ago. Almost all maize genes cloned through forward genetics are conserved at syntenic orthologous locations in the genome of sorghum. In each species, previous resequencing has generated large sets of polymorphisms for wild relatives, landraces, and improved lines. Using syntenic orthologs identified between these two species, we have identified genes that show parallel or lineage specific patterns of selection during domestication and crop improvement in each species. The resolution of current population genetic tools is sufficiently high that it may also be possible to observe whether selection on the same gene in both lineages are consistently targeted in the same way (ie both changes in protein coding regions or both changes in associated noncoding sequence) or whether the function of same genes were changed through alteration of protein coding exons in one species and noncoding regulatory regions in another.

#47 | Lang Yan, Xianjun Lai, Oscar Rodriguez, James C. Schnable | DEVELOPING TRANSCRIPTOMIC RESOURCES FOR TRIPSACUM TO STUDY THE ADAPTATION OF A MAIZE RELATIVE TO TEMPERATE CLIMATES | As the sister genus of maize, Tripsacum have been widely used as outgroup in studies of maize origin, evolution and domestication. Intriguingly, unlike the direct progenitor of maize, teosinte, Tripsacum dactyloides is native temperate climates. These climates are far more similar to those in which most commercial maize production occurs today in the United States and China. The common ancestor of the Zea/Tripsacum lineage is predicted to be adapted to tropical latitudes, so studying tripsacum is an approach to understanding how a tropical grass adapted to temperate environments through natural selection, a parallel story to how maize adapted to temperate environments through artificial selection. However, genomic resources for tripsacum, which has a large, polyploid, and high repeat content genome have been difficult to develop. In order to improve genomic resources for tripsacum, we are conducting single-molecule sequencing of mRNAs isolated from wild Tripsacum dactyloides collected in eastern Nebraska. In addition to improving the utility of tripsacum as an outgroup for maize studies, this data will be used to identify genes experiencing accelerated evolution or positive in tripsacum, as well as conserved patterns of divergence in alternative splicing between homeologous genes following the whole genome duplication which is shared by both Zea and Tripsacum. Preliminary analysis with second generation sequencing data has already identified a number of genes experiencing accelerated rates of evolution in tripsacum relative to both maize and outgroup species. We hope this study can serve as a foundation for future studies aiming to take use of the wild relatives underlying the genetic basis of maize adaptation.

#48 | Shamseldeen Eltaher, Ahmed Sallam, Vikas Belamkar, Hamdy A. Emara, Ahmed A. Nower, Khaled F. M. Salem, Jesse Poland, P. Stephen Baenziger | GENOME WIDE ASSOCIATION MAPPING FOR DROUGHT TOLERANCE TRAITS AT SEEDLING STAGE USING NEBRASKA WINTER WHEAT | The detection of genotypes variation in drought tolerance at seedling stage could help in selection intensity in the wheat breeding program. Genome wide association study GWAS was performed using 9,765 SNPs marker in mixed liner model with 20% false discovery rate and identified ten SNPs associated with two drought traits i.e., days to wilting (DTW) and sum of wilting degree (SWD). In total, ten marker-trait associations MTAs were detected. Two SNPs in the 6B chromosome were associated with SWD. Also, eight SNPs were associated with DTW three in chromosome 6B and four in 2D and one in chromosome 5B.

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#49 Aixia Li, Shangang Jia, Shirley Sato, Thomas Clemente, Ismail Dweikat,Chi Zhang, David Holding | IMPROVING DIGESTIBILITY AND PROTEIN QUALITY IN SORGHUM BY KAFIRIN GENE EDITING | Kafirins, the major storage protein in the sorghum grain, specify poor protein quality and digestibility. Kafirins are classified as α, β, γ and δ subuits and the sorghum α-kafirins alone comprise about 80% of the total kafirins and are encoded by a family of highly similar genes. In this study, a CRISPR-CAS9 approach was used to target the α-kafirin family to create reduced kafirin mutants with improved protein quality and digestibility. A single sgRNA was designed to introduce mutations in a highly conserved region encoding the N-terminal ER signal peptide region. 27 T1 events were generated and kernels in some events show a desired partially opaque phenotype. Preliminary SDS-PAGE analysis of kafirin protein from T1 seeds reveals that some mutants with reduced kafirin accumulation were generated by gene editing. Sequecing analysis are ongoing to elucidate the scope and nature of kafirin gene mutations at the target site.

#50 Wei Zhang, Sheng Liu, Yuanwei Zhou, Edgar B. Cahoon ,Yongming Zhou and Chunyu Zhang | GENOME-WIDE ASSOCIATION STUDY ANALYSIS OF SEED TOCOPHEROL CONTENT AND COMPOSITION IN RAPESEED (Brassica Napus L.) | Tocopherols and tocotrienols,collectively known as toco-chromanols, are essential lipid-soluble antioxidants in human nutrition and health. Rapeseed (Brassica napus L, AACC, 2n = 38) is one of the most important oil crops and contains high amounts of tocopherols. Given that individual accessions differ in their degree of tocochromanols, variation for tocopherols composition and content in rapeseed among diverse inbred lines provide the opportunity for breeding high-tocopherol rapeseed varieties with superior tocopherol content. For enhancing the understanding the genetic basis of traits would be valuable to improve nutritional quality by breeding,we conducted a genome-wide association study of three tocopherols compounds and their sums, ratio with a 430 inbred association panel that was genotyped for 25,903 SNP markers.Six candidate genes were found across 2-year phenotypic data, among which gamma-tocopherol methyltransferase(Bn-γTMT) was identified as the major factor responsible for α-τ content, while 2-Methyl-6-prenylbenzoquinol methyltransferase (Bn-VTE3) and chlorophyll synthetase (Bn-CHLG) were identified as the major factor responsible for total content.This study will aid future efforts to better understand the role of genetic factors underlying α-τ content and total content variations, which will significantly contribute the research on biosynthesis mechanisms and tocopherols improvement of rapeseed.

#51 Lili Hou, Hanh Nguyen, Shirley Sato, Gina Mai, Deanna Mosley, Aaron Jensen, Phu Nguyen and Thomas Clemente | MONITORING DS TRANSPOSITION IN THE SOYBEAN GENOME | The maize Ac/Ds transposon system was introduced into soybean as a method to create random activation tags in the genome. Towards this goal, the T-DNA element (pPTN999) was designed which carries the cassava vein mosaic virus promoter (CaVMV), delineated by Ds. To estimate germinal transposition frequencies the transgenic allele in a set of pPTN999 events was mapped, and subsequently stacked with an Ac transposase cassette. Genotyping of derived F2 populations revealed a ~3% germinal transposition frequency and most residing in unlinked locations relative to the original locus. We found 277 germinal transpositions to date of which 142 have been mapped.

#52 Malachy Campbell, Nonoy Bandillo, Sandeep Sharma, Ben Fouad Al-Shiblawi, Kan Liu, Qian Du, Aaron Schmitz, Chi Zhang, Anne-Aliénor Véry, Aaron Lorenz, Harkamal Walia | ALLELIC VARIANTS OF OSHKT1;1 UNDERLIE THE DIVERGENCE BETWEEN INDICA AND JAPONICA SUBSPECIES OF RICE (ORYZA SATIVA) FOR ROOT SODIUM CONTENT | Genome wide association mapping using a rice diversity panel (RDP1) identified HKT1;1 as a factor involved root Na+ content. Within the rice diversity panel we observed higher Na+ levels in root tissue in the indica subpopulation compared to Japonica (temperate and tropical japonica) accessions. Here, we show that three non-synonymous variants within HKT1;1 alter Na+ transport properties and Na+ accumulation in root tissue. Introducing HKT1;1 from an indica accession into a Japonica background resulted in a phenotype similar to that exhibited by the indica subpopulation, indicating these variants are likely responsible for the higher root Na+ observed in indica accessions.

#53 Haozhe Zhang, Daniel Nettleton | PREDICTION-GUIDED STATISTICAL RANKING OF MAIZE SEED BRANDS | Although genomic selection has become an promising tool for agronomists in plant breeding, one of the most important problems for a growers is how to select seed brands. In this paper, we proposed a statistical framework of ranking maize seed brands. Based on the performance of prediction accuracy of phenotypes, three methods, including elastic net regression, generalized additive model and random forests, were compared through cross validation on stratified samples. Random forests were eventually selected to rank brands, utilizing brand-environment interaction and within-environment interaction.

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#54 Zuo Li, Wenfang Xiao, Heming Chen, Fubing Lu | **CORE COLLECTION CONSTRUCTION OF CULTIVATED PHALAENOPSIS** | Plenty of Phalaenopsis germplasm resources bring tremendous difficulties and energy loss to the variety identification and utilization and the production management. Core Collection could directly resolve the contradiction between the germplasm collection and effective utilization. This project were using SSR molecular data combined with ornamental and agronomic traits data to construct the Core Collection of 412 Phalaenopsis germplasm. After comparative analysis of genetic diversity and divergence, the 30% sampling proportions was the most suitable Core Collection, selected from five candidate Core Collections was eventually chosen.

#55 Fan Qiu, Kenneth Whitney, Eric Baack, Dan Bock, Loren Rieseberg, Mark Ungerer | **GENOME SIZE EVOLUTION IN THE WILD SUNFLOWER GENUS HELIANTHUS** | In this study, genome size estimates are determined for 49 sunflower species. Genome size variation among diploid species ranges from 2C=6.42 to 22.93 pg, variation among tetraploid species ranges from 2C=15.68 to 24.41 pg, and variation among hexaploid species ranges from 2C=19.69 to 23.41 pg. Clade-specific patterns show genome size increases, decreases and relative stasis when compared to an ancestrally reconstructed genome size estimate. A single annual diploid species, H. agrestis, has undergone a massive genome size increase, with a current genome size 2.60 fold higher than the ancestrally reconstructed estimate and 1.59-3.59 fold higher than any other diploid species.

#56 Sunil Kumar, Mon-Ray Shao, Sally Mackenzie | **EPIGENOMIC PLASTICITY OF ARABIDOPSIS MSH1 MUTANTS UNDER PROLONGED COLD STRESS** | We sequenced the methylome and transcriptome of msh1 T-DNA mutants under cold stress to understand their differential response and its potential in enhancing phenotypic and epigenetic plasticity. Our results suggest that chronic cold low light stress influences non-CG methylation in msh1 to a greater degree compared to wild-type Col-0. Furthermore, CHG changes are more closely pericentromeric, whereas CHH changes are located around the pericentromere, but generally more dispersed. Interestingly, this increased variation in methylome divergence does not seem to have any significant effect on the previously described msh1-derived enhanced growth after mutants are crossed with isogenic wild-type.The detection of genotypes variation in drought tolerance at seedling stage could help in selection intensity in the wheat breeding program. Genome wide association study GWAS was performed using 9,765 SNPs marker in mixed liner model with 20% false discovery rate and identified ten SNPs associated with two drought traits i.e., days to wilting (DTW) and sum of wilting degree (SWD). In total, ten marker-trait associations MTAs were detected. Two SNPs in the 6B chromosome were associated with SWD. Also, eight SNPs were associated with DTW three in chromosome 6B and four in 2D and one in chromosome 5B.

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