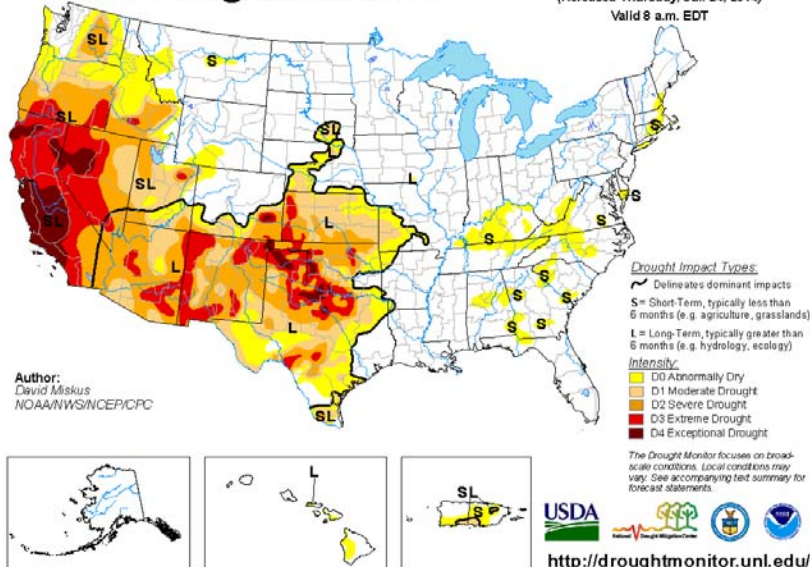


**4<sup>th</sup> Annual Meeting of the National Association of Plant  
 Breeders**  
**8<sup>th</sup> Annual Meeting of the Plant Breeding Coordinating  
 Committee**  
**“Breeding for Tolerance to Water Stress”**  
*Minneapolis, MN August 5-8, 2014*



**U.S. Drought Monitor**

**July 22, 2014**  
 (Released Thursday, Jul. 24, 2014)  
 Valid 8 a.m. EDT



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## Diamond Sponsor



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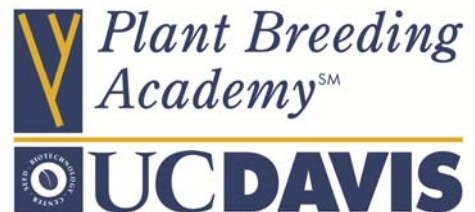
UNIVERSITY OF MINNESOTA

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## Bronze Sponsors



IOWA STATE UNIVERSITY  
Master of Science in Plant Breeding - Online Option



## TUESDAY, AUGUST 5

**Mixer** featuring **Par 4 Jazz Quartet** - 7:00-9:00 pm *Dublin/Belfast*

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## WEDNESDAY, AUGUST 6

**NAPB and PBCC "BUSINESS" MEETINGS** 8:00 - noon

**GENERAL SESSION** *Elizabeth Lee (NAPB President), and Pat Byrne (PBCC Chair)*  
*presiding - Salons A-D*

- 8:00 **Opening remarks** (E. Lee, P. Byrne)
- 8:05 **Welcome** (Michael A. Schmitt, Ph.D., Associate Dean, College of Food, Agricultural and Natural Resource Sciences. University of Minnesota)
- 8:10 **Election of officers** —(L. Lee)
- 8:25 **NAPB General Session** (L. Lee)
- 8:45 **PBCC General Session** (P. Byrne)
- 9:05 **Instruction for Committee sessions** (L. Lee)

**COMMITTEE BREAKOUT SESSIONS.** 9:10. London, Edinburgh, Oxford, Bristol

**BREAK & Exhibits and Poster set up.** 10:05-10:25 am- Dublin/Belfast

10:25 **Committee reports** - *Barry Tillman and Jamie Sherman presiding*

- Advocacy (Bill Tracy)
- Communications (Wayne Smith)
- Education (David Francis)
- Graduate Students (Duke Pauli)
- Membership (Don Cummings)

11:15 **Election Results** (B. Tillman and J. Sherman)

11:20 **Plant breeding working group and NIFA update** (Ann Marie Thro, USDA)

11:35 **Industry update** (Andy Lavigne, American Seed Trade Association)

11:50 **2015 Meeting** (Jim McFerson)

**LUNCH** 12:00 - Grand Courtyard

**RESEARCH PRESENTATIONS- AWARDEES.** David Francis (Salons A-D)

- 1:00 **From Depression Era Mules to the Moon and Back: My Lifetime with Cotton.** Lifetime Awardee- Johnie Jenkins, USDA/ARS, Genetics and Precision Agriculture
- 1:25 **Ten Things a Successful Plant Breeder Understands.** Impact Awardee- Roger Boerma, Georgia Seed Development, Athens, GA
- 1:50 **Plant Breeding Approaches and Technologies for Challenges in Agriculture: A View from a Texas Maize Breeding Program.** Early Career Awardee- Seth Murray, Texas A & M

**MINI-PRESENTATIONS: POSTERS AND SPONSORS** (David Stelly)

- 2:15 **1-minute poster** introductions Even posters (Al-Jaser, Boontung, Campbell, Fakthongphan, Gifford, Guerrero-Chavez, Latshaw, Li, Mahan, Masor, McLoud, Moore, Niroula, Ortiz, Pauli, Rasul, Sallam, Singh, Smallwood, Sykes Yesudasan)

- 2:40    **1.5 minute introductions from Platinum and Gold Sponsors** (AgReliant, Bayer, Douglas Scientific, Dow AgroSciences, SeedWorld, LGC, Monsanto, Pioneer hi-Bred, TCAP ,)

**POSTER AND SPONSOR SESSION - 3:00 evens - Dublin/Belfast**

- 4:30    **1-minute poster introductions** Odd posters (Anderson, Bian, Bubert, DeSantis, Falcon, Gilbert, Levina, Liabeuf, May, Nasseer, Park, Ramírez-Madera, Sater, Smeda, Tiede, Tseng, Xiong)

**BREEDING FOR TOLERANCE TO WATER STRESS (Celeste Falcon)**

- 4:55    **Flood Tolerant in Rice.** David J. Mackill, Mars, Incorporated; UC Davis; International Rice Research Center
- 5:20    **Drought tolerant tropical maize development and delivery in sub-Saharan Africa: CIMMYT's experience and perspective.** BW Prasanna, CIMMYT (International Maize and Wheat Improvement Center), Nairobi, Kenya
- 5:45    **Enhancing alfalfa forage productivity during drought.** Ian Ray, New Mexico State University

**ADJOURN FOR DINNER 6:10 (on your own)**

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**THURSDAY, AUGUST 7TH**

**VISIT/TOUR SYNGENTA STANTON, MN STATION**

- 6:30    Grab and Go Breakfast. Grand Foyer
- 7:00    Depart hotel to Syngenta

**"LUNCH TO GO" 12:00 - bus back to hotel**

**GRADUATE STUDENT TALKS (Leah Ruff)**

- 1:15    **Phenotypic evaluations of heat tolerance and fruit quality traits in segregating black raspberry (*Rubus occidentalis* L.) populations in North Carolina.** Christine Bradish, North Carolina State University
- 1:35    **Multi-environment analyses of winter wheat heading date across the US. Great Plains: Can we better optimize genotypes for specific environments?** Sarah Grogan, Colorado, State University
- 1:55    **General combining ability model for genome-wide selection in a biparental cross.** Amy Jacobson, University of Minnesota

**POSTER AND SPONSOR SESSION II- 2:15 odds Dublin/Belfast**

**CONTROLLING GENOTYPE X ENVIRONMENT INTERACTIONS (Tyler Tiede)**

- 3:25    **A Practical Approach for Understanding Genotype by Environment Interactions.** Chad Geater, Syngenta Seeds, Slater IA
- 3:50    **Potential to using remote sensing tools to screen germplasm.** Jerry Hatfield, National Laboratory for Agriculture and the Environment, USDA/ARS, Ames, IA
- 4:15    **Genomic Selection: Training Populations and GxE.** Mark Sorrells , Cornell University

## **PHENOTYPING AND PHYSIOLOGICAL RESPONSES TO WATER STRESS**

(Araby Belcher)

- 4:40 **Taking advantage of physiological priming in crops: breeding for greater acclimation to drought.** Diane Rowland, University of Florida
- 5:05 **The stress-induced synthesis of cytokinin regulates the coordination of C and N metabolism resulting in enhanced drought tolerance in rice transgenic plants.** Maria Reguera, University of California, Davis
- 5:30 **Improving drought tolerance of hard winter wheat through the Triticeae Coordinated Agricultural Project (T-CAP).** Pat Byrne, Colorado State University

**ADJOURN 5:55**

## **BANQUET / 2014 AWARDS / PLENARY LECTURE (Barry Tillman)**

- 6:30 **Cash Bar.** Grand Foyer
  - 7:00 **Dinner.** Grand Ball Room
  - 8:00 **2014 NAPB and PBCC Awards** (Phil Simon)
  - 8:20 **Recent Lessons in Drought Risk Management.** Michael Hayes, University of Nebraska-Lincoln
- 

## **FRIDAY MORNING, AUGUST 8TH**

### **UNIVERSITY OF MINNESOTA FIELD DAY**

- 6:30 **Grab and Go Breakfast.** Grand Foyer
- 7:00 **Depart**

**“LUNCH TO GO”** 12:00 - bus back to hotel

**CLOSING SESSION/LAST MINUTE BUSINESS.** 1:00 - Barry Tillman, Jamie Sherman.  
Salons A-D

### **CONCURRENT WORKSHOPS**

- 1:40 **Private Breeding Perspective Workshop** – (Duke Pauli) Salons AB
  - Rita Mumm, University of Illinois
  - Ron Ferris, Syngenta Seeds, Stanton, MN
  - Jane Dever, Texas A & M
  - Elliot Heffner, Pioneer Hi-Bred, Des Moines, IA
  - Chad Geater, Syngenta Seeds, Slater IA
- 1:40 **Tools to model and optimize Plant Breeding.** William Beavis, Iowa State University  
(Michael Gore) Salons CD

**CLOSE OF MEETING 4:00**

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## **SPEAKER BIOS**

**WILLIAM D. BEAVIS**, Iowa State University, Ames, IA

Bill's research interests include development of accurate predictive models and optimization of breeding processes for purposes of genetic improvement. Most often cited for his discovery of bias in estimates of genetic effects in statistical analyses (the "Beavis Effect"), Bill developed and applied novel statistical genetic methods at Pioneer Hi-Bred from 1986-1998. As CSO at the National Center for Genome Resources in Santa Fe, New Mexico, Bill provided scientific leadership in building a sustainable non-profit Bioinformatics research institute. In the fall semester of 2007, Bill joined the faculty at Iowa State University as the G.F. Sprague Chair for Population Genetics and served the university as Interim Director of the Plant Sciences Institute from 2009-2014. Currently, Bill collaborates with engineers and computer scientists in developing and evaluating predictive and optimization methods from systems and metabolic engineering to address limitations in genetic improvement. Bill's teaching interests are in assuring that the next generation of biologists will be prepared to address complex problems with mathematical and statistical skills, and his administrative interests are in developing entrepreneurial faculty interested in transforming biology from a descriptive to a predictive science.



**ROGER BOERMA**, Georgia Seed Development Commission, Athens, GA

Roger Boerma was born and raised on a grain and livestock farm in Logan County near Emden, Illinois. He received his B.S. in agricultural education from Illinois State University. He completed a M.S. and Ph.D. in plant breeding and genetics at the University of Illinois. He began his professional career after graduation at the University of Georgia as an assistant professor of agronomy where he spent the next 39 years. He and his wife, Cindy, have two daughters, Erica and LeeAnn, and a granddaughter, Anna. Prior to his retirement from the University of Georgia in 2011, he served as a Distinguished Research Professor and Director of the Center for Applied Genetic Technologies. His professional accomplishments include releasing 28 high yielding, multiple pest resistant soybean varieties for southeastern producers and publishing 175 scientific journal papers along with numerous book chapters and conference proceedings. His recent research focused on the development and integration of marker assisted selection in the soybean breeding pipeline. He was awarded six U.S. patents and a number of U.S. Plant Variety Protection Certificates. He was instrumental in the development of the University of Georgia's Center for Applied Genetic Technologies and was a founder of the Institute for Plant Breeding, Genetics, and Genomics. He directed 11 M.S. and 15 Ph.D. students and served as a mentor to 14 post-doctoral associates. In July of 2011 he was named Executive Director of Georgia Seed Development located in Athens GA where he is responsible for the providing direction and vision to the organization and administering the policies developed by the Board of Directors.



**CHRISTINE B. BRADISH**, North Carolina State University, Raleigh, NC

Christine M. Bradish is a PhD candidate in Horticultural Science at North Carolina State University, working under Dr. Gina Fernandez and Dr. Penelope Perkins-Veazie. Originally from Smithfield, VA, Christine has a B.S. in Biology from Old Dominion University and an M.S. in Horticultural Science from North Carolina State University. Her dissertation research on black raspberry is part of a larger project aimed at improving the commercial value and genomic tools for the crop. Specifically, she is looking at phenotyping and genotyping heat tolerance in two black raspberry mapping populations, in order to determine the best screening method and to find QTL regions associated with the trait. Upon finishing her degree, Christine hopes to pursue a career in public plant breeding, with the goal of continuing to work on fruit crop improvement in the South.



**PAT BYRNE**, Colorado State University, Fort Collins, CO

Patrick Byrne is a Professor in the Department of Soil and Crop Sciences at Colorado State University, where he teaches and conducts research in plant breeding, genetics, and biotechnology. His research focuses on applying quantitative and molecular genetics to crop improvement, with an emphasis on drought tolerance and bread making quality in wheat, disease resistance in dry beans, and seed yield in canola. He has been involved in a number of projects to evaluate the benefits and risks of genetically engineered crops. Prior to joining academia, Dr. Byrne spent 10 years with international agriculture development agencies in Nepal, the Cape Verde Islands, and Mexico.



**JANE DEVER**, Texas A & M, College Station, TX

Jane Dever is Professor and Cotton Breeder, Texas A&M AgriLife Research in Lubbock, and has a B.S. in Textile Engineering (1983), M.S. in Crop Science (1986), and Ph.D. in Agronomy (1989), all from Texas Tech University. Prior to her Texas A&M System appointment in 2008, she was Bayer CropScience Global Cotton Breeding and Development Manager for 10 years. Previous appointments include coordinator, Texas A&M AgriLife Extension Service AgriPartners program (25% appointment); Senior Research Scientist, BioTex; Textile Engineer, Plains Cotton Cooperative Association; and Head of Materials Evaluation, Fiber and Biopolymer Research Institute at Texas Tech University. Jane is Plains and Western chair of the National Cotton Variety Testing Committee, secretary of the CottonGEN steering committee and served as Associate Editor – Cotton, Journal of Plant Registrations. She was appointed a scientific member of the National Genetic Resources Advisory Council in 2011; has served on the Joint Cotton Breeding Policy Committee and had many project management and strategic review responsibilities at Bayer. Jane received the 2012 Cotton Genetics Research Award and the 2012 “Golden Hoe” award presented by Texas Organic Cotton Marketing Cooperative; as well as the 2007 Bayer CropScience Gold Laureate award.





**RON FERRIS**, Syngenta Seeds, Stanton, MN

After earning Ph.D. in Plant Breeding at University of Minnesota, began professional career in 1979 as a corn breeder for Northrup King. Held positions of Corn Breeding Regional Manager, then added Manager Seed Production and Agronomic Research, until becoming North America Corn Breeding Manager in 1987. Following the merger of Sandoz Seeds and Ciba Seeds in 1997, managed Global Corn Breeding, then Global Corn Genetic Development or early stage breeding. Following the formation of Syngenta in 2000, headed Global R&D Strategy Facilitation until joining Legal in 2006 as Head of Product Clearance and License Compliance. Current role in Syngenta is Global Lead for Germplasm Compliance, and North America Lead for the function of Germplasm Legal and IP.



**CHAD GEATER**, Syngenta Seeds, Slater, IA

Dr. Chad Geater received his Ph.D. in Plant Breeding from Iowa State University in 2000. He has worked for Syngenta since 2000 as a Product Evaluation and Advancement Scientist, Regional Corn Product Development Head, and Corn Product Evaluation Head for Seeds North America. He is currently the Senior Project Lead for the Syngenta Breeding Academy, a role in which he helps deploy leading edge tools and techniques to the global Syngenta breeding community. Dr. Geater works out of the Syngenta research station at Slater, Iowa.



**SARAH GROGAN**, Colorado, State University, Fort Collins, CO

Sarah Grogan is a Ph.D. candidate in Plant Breeding and Genetics and is advised by Dr. Patrick Byrne at Colorado State University. Her anticipated graduation is summer 2015, after which she is interested in a career in industry. She received her B.S. in Cellular and Molecular Biology from Beloit College in 2009, and afterwards spent several years conducting field research with the Bureau of Land Management in southern Idaho, and lab research at the Medical College of Wisconsin. Sarah's graduate research is part of the Triticeae Coordinated Agricultural Project (TCAP), within which she has taken on many active roles and countless opportunities to engage with other students and professionals. Her research focuses include evaluating agronomic differences contributing to water-use efficiency among winter wheat varieties through intensive field phenotyping; investigating the utility of high-throughput phenotyping using hand-held instruments to measure canopy spectral reflectance; and uniting genotype with phenotype through genome-wide association studies (GWAS).



**MICHAEL HAYES**, University of Nebraska-Lincoln

Dr. Michael Hayes is currently the Director for the National Drought Mitigation Center (NDMC) located within the School of Natural Resources at the University of Nebraska-Lincoln. He became the NDMC's Director in August 2007 and has worked at the NDMC since it was founded in 1995. The NDMC now has 16 faculty and staff working on local, tribal, state, national, and international drought-, climate-, and water-related issues. Dr. Hayes' main interests focus on drought risk management strategies. Dr. Hayes received his academic degrees from the University of Wisconsin-Madison and the University of Missouri-Columbia.



**JERRY L. HATFIELD**, Ph.D. USDA/ARS, Ames, IA

Dr. Jerry L. Hatfield is the Laboratory Director of the USDA-ARS National Laboratory for Agriculture and the Environment and Director of the Midwest Climate Hub in Ames, Iowa. His personal research focuses on quantifying the interactions among the components of the soil-plant-atmosphere system to quantify resilience of cropping systems to climate change and development of techniques to quantify plant response to the environment. He has served in numerous roles representing agriculture on the National Climate Assessment, member of the IPCC process that received the 2007 Nobel Peace Prize, and Lead Author on an IPCC Special report on the Effects of Climate Extremes. He is a Fellow of the American Society of Agronomy, Crop Science Society of America, and Soil Science Society of America and Past-President of the American Society of Agronomy and member of the American Meteorological Society, American Geophysical Union and Soil and Water Conservation Society. He is the recipient of numerous awards including the USDA Superior Service Award in 1997, the Arthur S. Flemming award for Outstanding Service to the Federal Government in 1997 along with the Distinguished Service Award, Kansas State University in 2002, Distinguished Alumni Award from Kansas State University in 2011, 2011 Conservation Research Award from the Soil and Water Conservation Society, and 2014 Soil and Water Conservation Award for Research Paper with Impact and Quality. He is the author or co-author of 408 refereed publications and the editor of 15 monographs.



**ELLIOT HEFFNER**, Pioneer Hi-Bred, Des Moines, IA

Dr. Elliot Heffner received his BS degree in Agroecology at Penn State University and his PhD in Plant Breeding and Genetics at Cornell University. During graduate school, Elliot investigated marker-based selection methods for crop improvement, with a particular focus on applying genomic selection in plant breeding programs. In 2010, he joined DuPont Pioneer as a Research Scientist and currently leads a commercial maize breeding program based in Dallas Center, Iowa. In his breeding program, he focuses on leveraging the latest breeding technologies to develop elite maize hybrids for North American farmers.



**AMY JACOBSON**, University of Minnesota, Minneapolis, MN

Amy Jacobson is a PhD student at the University of Minnesota advised by Dr. Rex Bernardo. Amy received her bachelor's degree in plant science from Cornell University in 2011. Her research focuses on utilizing genome-wide selection in a maize breeding program. Current research projects include marker imputation and improving training population design for genome-wide selection.



**JOHNIE N. JENKINS**, USDA/ARS, Mississippi State, MS

Dr. Johnie N. Jenkins received his BS degree from University of Arkansas in 1956, his MS and PhD degrees from Purdue University in 1958 and 1960. He spent one year as a Postdoc at University of Illinois and then was employed by ARS in 1961 where he has remained as a Research Scientist. Dr. Jenkins has participated in biological research for 58 years, 4 in corn genetics as a graduate student, 1 in corn genetics in a post-doctoral position, and 53 as a research geneticist with USDA in cotton host plant resistance research. He is recognized as a Plant Geneticist and Agronomist with particular emphasis on host plant resistance in cotton. He has also served as Major Professor for numerous graduate students who have earned the M.S. or Ph.D. degree. He has published 533 research papers. He is a Fellow in ASA, CSSA, and AAAS. He was inducted into the ARS Science Hall of Fame in 2007. He is currently the Director of the Crop Science Research Lab and Research Leader for the Genetics and Precision Agriculture Research Unit of ARS located at Mississippi State, MS.



**ANDREW W. LAVIGNE**, President and CEO, American Seed Trade Association

Andrew LaVigne joined the American Seed Trade Association in February 2006 as the president and chief executive officer. With a 17-year career in government relations, industry representation, public affairs advocacy and management, LaVigne is an expert in the areas of agriculture, food policy and international trade. During his time with ASTA, he has led the expansion of the association's domestic grassroots program and the reorganization of the international cooperator program. He also pushed to coordinate regional and international phytosanitary standards to facilitate the movement of seed globally. Prior to joining ASTA, the Florida native was executive vice president/ CEO of Florida Citrus Mutual, representing citrus growers on issues affecting their businesses. Prior to that, LaVigne spent four years as president/executive director for Florida Fertilizer and Agrichemical Association. He also worked in the U.S. Congress and the U.S. Department of Agriculture, serving as a Legislative Director and as an Agriculture Committee staffer. In both positions, he handled agricultural, environmental, immigration and trade issues. He currently serves on the board of directors for the National Friends of the Arboretum and is a member of the Agricultural Policy Advisory Committee for Trade.



**DAVID MACKILL**, Mars, Incorporated, UC Davis, International Rice Research Institute

David J. Mackill is a plant science manager with Mars Inc. and an adjunct professor in plant sciences at UC Davis. He has developed over 25 rice varieties and published research on the genetics of resistance to rice blast disease and submergence and drought tolerance. He and his colleagues identified a gene from traditional rice varieties that conferred tolerance to 2 weeks or more submergence. Over 3 million farmers have adopted the improved tolerant varieties since 2009. In addition to his leadership and research work, he has supervised the thesis research of 22 graduate students.



**RITA MUMM**, University of Illinois, Urbana, IL

Dr. Rita Mumm brings over 18 years' experience in the plant breeding industry. Dr. Mumm was a pioneer in developing and releasing some of the first transgenic traits in crops with Dekalb Genetics Corp. Her current research focuses on maize quantitative genetics, applications of genomic information to the development of improved hybrids, and deployment of traits created through genetic engineering, including efficient breeding strategies, and stewardship of governmentally regulated materials. Dr. Mumm was the founding director of the Illinois Plant Breeding Center at the University of Illinois, now one of the most prominent educational centers for crop genetic improvement in the USA. Dr. Mumm is UC Davis African Plant Breeding Academy. In addition to faculty at the University of Illinois, Dr. Mumm is principal at GeneMax Services, a consulting firm to the seed industry. She is past president of the National Association of Plant Breeders.



**SETH MURRAY**, Texas A & M, College Station, TX

Dr. Seth C. Murray joined Texas A&M University in 2008 as an Assistant Professor in the Department of Soil and Crop Sciences where he directs a program focused on both quantitative genetic discovery and applied maize breeding. Important traits in his program include improved aflatoxin resistance, drought tolerance, nutrient use efficiency in yellow corn for Texas and the Southern US and the incorporation of novel genetic diversity for perennial, blue and QPM maize. He has developed statistical techniques for improved genetic mapping of natural variation and to increase understanding of crop improvement processes. Dr. Murray received a BS in Crop and Soil Sciences at Michigan State University in 2001 where he worked in a sugar-beet genetics lab and co-founded a student organic farm. He received his PhD at Cornell University in 2008 in Plant Breeding and Genetics where he identified regions of the genome (QTL) conditioning energy accumulation and carbohydrate partitioning in sweet and grain sorghums. Currently he is an Associate Editor for Crop Science, Associate Editor for the Journal of Plant Registrations (maize), a Web Editor for the National Association of Plant Breeders, and served as chair or vice-chair for regional and national scientific meetings. He has been / is a committee member for 37 graduate students including 17 as a chair/ co-chair, teaches a graduate level class in "Molecular Quantitative Genetics in Plant Breeding" to PhD students and teaches additional classes at the graduate and undergraduate level. Dr. Murray has been an



author or co-author on 29 refereed journal articles, four book chapters, three released germplasm lines and is the PI/co-PI of numerous federal, state, and commodity research grants.

**BM PRASSANNA**, CIMMYT (International Maize and Wheat Improvement Center), Nairobi, Kenya



BM Prasanna is Director of the Global Maize Program of CIMMYT (International Maize and Wheat Improvement Center) with its headquarters at Mexico. Prasanna is based at Nairobi, Kenya, and is leading a strong multi-disciplinary team of 45+ internationally recruited scientists located in sub-Saharan Africa, Latin America and Asia. The major focus of his team is on developing and delivering stress resilient and nutritious maize for the tropics, besides application of novel tools and technologies for increasing genetic gains and efficiency of maize breeding programs in the developing world. He had his MSc (1985-1987) and PhD (1987-1991) in Genetics from the Indian Agricultural Research Institute (IARI), New Delhi, and served as a faculty member and maize geneticist at the Division of Genetics, IARI, for two decades (1991-2010). Prasanna had the distinction of serving as Team Leader for India under the CIMMYT-led Asian Maize Biotechnology Network (AMBIONET) during 1998-2005, and as ICAR National Fellow (2005-2010) at IARI, New Delhi. He successfully developed and led several multi-institutional projects on maize genetics, diversity analysis, breeding and biotechnology. He received several awards for his maize research and post-graduate teaching contributions, and has nearly 100 peer-reviewed research publications and 45 book chapters to his credit.

**IAN RAY**, New Mexico State University, Los Cruces, NM



Ian Ray is a Professor of Agronomy at New Mexico State University (NMSU), where he has served since 1994. His expertise is in alfalfa and forage grass breeding and genetics. Dr. Ray's research for the past 20 years has focused on genetic characterization and improvement of drought tolerance in alfalfa through molecular techniques and conventional breeding approaches. His program has developed several alfalfa germplasms, including the cultivar 'NuMex Bill Melton', which has demonstrated high yield performance under variable soil moisture conditions in New Mexico. Prior to joining New Mexico State University, he served as a research geneticist (forage grass breeding and genetics) with USDA-ARS and North Dakota State University during 1989-1993. Ian received a B.S. degree in Agriculture from New Mexico State University in 1985, and M.S. and Ph.D. degrees in Plant Breeding and Genetics from the University of Wisconsin-Madison in 1987 and 1989.



**MARIA REGUERA**, Univeristy of California, Davis

As a Plant Biologist, the recent focus of my scientific career has centered on investigating the cellular and molecular mechanisms mediating the responses of plants to abiotic stress and on the analysis of the cellular and molecular mechanisms that regulate ion homeostasis in plants. My work has always maintained an applied agricultural perspective and focused on uncovering basic mechanisms involved in plant stress responses, especially those related to drought, salt and mineral nutrition. During my PhD research at the University Autonomous of Madrid (Spain), I contributed to a better understanding of how the symbiotic nitrogen fixation in legumes is compromised under boron defficiency by studying the molecular mechanisms which underlie the regulation of the interaction of boron (B) with plant glycoconjugates. Currently, I hold a Postdocotral position at the University of California at Davis where I am working in different research projects. i) I am using a multidisciplinary approach (combining biochemistry, molecular biology and whole plant physiology) to gain a better understanding of how stress tolerant genetically engineered crops adapt their N and C metabolisms to improve C and N assimilation during drought; ii) I am participating in the characterization of the cellular, biochemical and physiological roles of two intracelullar  $\text{Na}^+/\text{H}^+$  (NHX) antiporters, NHX5 and NHX6, which regulate ion and pH homeostasis of cellular compartments along the endomembrane system. The integrated nature of my research has allowed me to think creatively across different levels in biology and to use a systems biology approach to develop strategies to improve plant performance and yields. See more at: <http://blumwald.ucdavis.edu/Members/members.htm>



**DIANE ROWLAND**, University of Florida, Gainesville, FL

Diane Rowland is an Associate Professor at the University of Florida in the Agronomy Department where her research program is focused on sustainable and water-use efficient crop production. She has a particular emphasis on the whole plant physiological processes that can be manipulated through management and that lead to improved drought tolerance. Her focus in graduate education has been as the co-founder and –coordinator of the joint graduate concentration in Agroecology between the Agronomy and Soil and Water Science departments at UF.





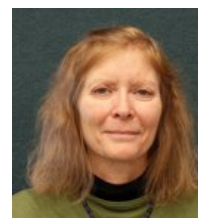
**MARK E. SORRELLS**, Cornell University, Ithaca, NY

Mark E. Sorrells received his PhD in Plant Breeding and Genetics from the University of Wisconsin – Madison in 1978 and then joined the faculty at Cornell University in the Department of Plant Breeding & Biometry. Since 1991 he has been Professor of Plant Breeding and since 2006 he has been Chair of the Department of Plant Breeding & Genetics. The primary focus of Dr. Sorrells' research program is on breeding methodologies and the development of small grains varieties. His breeding program has released 16 small grains varieties. Currently the focus of his research is optimizing genomic selection strategies. He has published 260 papers in peer-reviewed journals and is a fellow of the American Association for the Advancement of Science, the Crop Science Society of America, and the American Society of Agronomy. Dr. Sorrells has served as major advisor to 37 PhD students, 9 M.S. graduate students and minor advisor to 22 students.



**ANN MARIE THRO**, USDA, NIFA, Washington, DC.

Ann Marie Thro is presently National Program Leader (NPL) for plant breeding and genetic resources in the Institute for Food Production and Sustainability in USDA's National Institute for Food and Agriculture (NIFA). Dr. Thro provided leadership in the formation of the Plant Breeding Coordinating Committee (PBCC), a multi-state committee within the federal-state land-grant university partnership, and the multi-agency internal USDA Plant Breeding Working Group. Both entities work to identify priorities and opportunities for plant breeding in support of national strategic goals. During 2011/12, Dr. Thro served as a USDA Sr. Agricultural Representative in Afghanistan (northern region). Previous experience includes service as Commissioner of the USDA Plant Variety Protection Office (PVPO) (1999-2001); Coordinator, Cassava Biotechnology Network, International Center for Tropical Agriculture (CIAT), Cali, Colombia; Technical Advisor, National Grain Legume Program, Gandajika, Zaire (now D.R. Congo) (1991-92), and Associate Professor of Agronomy, Louisiana State University (1982-1992). Dr. Thro's advanced degrees are in Plant Breeding and Genetics from Iowa State University; with undergraduate degrees in Agronomy from Virginia Polytechnic Institute, and History and Languages from Bryn Mawr College.



## **SPEAKER ABSTRACTS**

### **FROM DEPRESSION ERA MULES TO THE MOON AND BACK: MY LIFETIME WITH COTTON**

Johnie N. Jenkins, ARS, USDA, Mississippi State, MS 39762

The twentieth and current century have been amazing times to be alive and involved in agriculture. This presentation will cover some of the discoveries and accomplishments that have made major changes in cotton production. Essentially all the progress in cotton production that has occurred since cotton cultivation began over 5,000 years ago have been made during my lifetime, except for the cotton gin and some early breeding efforts including the domestication of cotton production in the U. S. from wild relatives imported from Mexico and Central America. The effects that relative simple changes have made in cotton production will be highlighted. I will also discuss some of the more intractable problems and how they have been solved and will show how molecular biology is now making breeding improvements possible that had not previously been solved through conventional breeding. Public and Private research has made it all possible. Plant Breeders have been a critical part of the progress made in cotton production and some current approaches in cotton breeding that should be useful for the next 50 or more year will be discussed.

### **TEN THINGS A SUCCESSFUL PLANT BREEDER UNDERSTANDS**

H. Roger Boerma, Georgia Seed Development, Athens, GA

## PLANT BREEDING APPROACHES AND TECHNOLOGIES FOR CHALLENGES IN AGRICULTURE: A VIEW FROM A TEXAS MAIZE BREEDING PROGRAM

Seth Murray, Texas A & M, College Station, TX

Over the last century, plant breeding and agronomic technologies have vastly improve yield and reduced the amount of land needed to produce a unit of grain for many crops, with maize (*Zea mays* L.) as a prime example. Agriculture will be challenged in the future with decreasing availability of inputs, an increasing need for food safety and security, and increasing needs in the provision of ecosystem services, all under a changing climate. While the yield of maize continues to increase in the Midwest it has remained stagnant under the more stressful (hotter, drier) conditions in Texas over the last 15 years. These conditions exacerbate *Aspergillus flavus* / aflatoxin contamination and drought stress, which are predicted to become more frequent even in the Midwest Corn Belt. In the TAMU maize breeding program and in our molecular quantitative genetic studies (linkage and association mapping) we have identified exotic diversity useful for improvement of yield, yield under dryland conditions and for reducing aflatoxin. Yet a number of challenges remain in how we confirm these lines and alleles, incorporate them and get them adapted by industry and growers. More broadly, current limiting factors to improve the speed and efficiency in exotic germplasm introgression, phenotypic plant breeding and molecular genetic discovery can be improved. Increasing the number of effective recombination events through traditional methods and the cycling of gametes in vitro (COGIV), both appear promising with recent improvements in genomics technologies. To meet increasing demands on sustainable agricultural production, applying these and other technology's will allow breeding of perennial maize and sorghum, long-lived perennial crops, and even algae.

## FLOOD TOLERANT RICE

David J. Mackill, Mars Inc.; University of California, Davis; and International Rice Research Institute, Philippines

Rice is a major staple, and demand is expected to increase over the next several decades, but rice yields have been stagnating in recent years. New varieties that are tolerant to abiotic stresses are needed to reduce yield gaps in farmers' fields. Rice is well adapted to wet, monsoon climates and allows farmers to produce food in flooded landscapes. However, excessive rainfall often leads to inundation of the plants, resulting in yield loss and crop destruction. This problem afflicts over 20 million ha of rice production in South and Southeast Asia alone. Most rice varieties can tolerate only a few days of submergence, but a handful of farmers' traditional varieties were discovered that could tolerate two or more weeks of submergence. In all of the highly tolerant cultivars, submergence tolerance is conferred by the *SUB1A* gene that codes for an ethylene response factor. A marker assisted backcrossing (MABC) approach was used to transfer *SUB1A* from tolerant cultivars into the widely grown mega varieties of Asia. The first variety selected was Swarna, grown on approximately 6 million ha in India and Bangladesh. The MABC-derived version, named Swarna-Sub1, was over 99% genetically identical with Swarna except for the introgression of the *SUB1* locus. National governments officially approved the variety in 2009 and promoted its widespread distribution to farmers in submergence-prone areas. The variety was estimated to cover over 1.7 million ha in 2013. *SUB1* was similarly introduced into seven other mega varieties through MABC; national programs already officially released four of them and the rest are in the release pipeline. Under non-submerged conditions these tolerant cultivars have an average yield equal to the parent cultivars, generally 6 t/ha in the wet season. Under submerged conditions of 7-14 days they have an average yield advantage of 1.5 t/ha over intolerant cultivars in farmers' fields. The gene is also being combined with tolerance to drought and salinity stresses. Due to the increasing prevalence of submergence in lowland rice environments, *SUB1* is gradually being incorporated into all varieties developed for lowland ecosystems by IRRI.

## DROUGHT TOLERANT TROPICAL MAIZE DEVELOPMENT AND DELIVERY IN SUB-SAHARAN AFRICA: CIMMYT'S EXPERIENCE AND PERSPECTIVE

BM Prasanna, Director, Global Maize Program, CIMMYT (International Maize and Wheat Improvement Center), Nairobi, Kenya; Email: [b.m.prasanna@cgiar.org](mailto:b.m.prasanna@cgiar.org)

Maize is the key crop for food security and income generation for smallholder farmers in sub-Saharan Africa (SSA). More than 33 million ha of the sub-region's nearly 200 million ha of cultivated area under all crops is planted to maize, and the area is still expanding. The current average yield for SSA is below 1.8 t/ha, owing to several factors, including frequent droughts, poor soil fertility, yield losses due to pre- and post-harvest pathogens and insect-pests, weeds, poor agronomic management, lack of access to quality seed, and other constraints.

Under the Drought Tolerant Maize for Africa (DTMA) Project, jointly implemented by CIMMYT and IITA, in close collaboration with NARS and private sector institutions in 13 countries in SSA, a total of 149 drought-tolerant maize varieties have been released during 2007-2013, with close to 60% of them being hybrids. These varieties perform as well as or better than the commercial varieties currently available on the market under optimum (no water deficit stress) conditions and out-perform the best commercial checks by at least 25-30% under drought stress and low-input conditions. DTMA has also facilitated production and delivery of about 20,000 tonnes of seed in 2013 in partnerships with nearly 110 private and public seed companies, NGOs, and farmer organizations, benefiting an estimated 2 million African households. The Water Efficient Maize for Africa (WEMA) Project is another important public-private partnership, that is intensively engaged in developing and deploying drought-tolerant and insect-resistant white maize varieties in five target countries in sub-Saharan Africa (Kenya, Tanzania, Uganda, Mozambique, and South Africa), through a combination of conventional breeding, marker-assisted breeding and transgenes.

Climate projections suggest that elevated temperatures, especially in the drought-prone areas of sub-Saharan Africa, are likely to result in significant yield losses. Recent studies by CIMMYT in collaboration with partners in SSA indicated that current tropical/subtropical maize germplasm developed for drought tolerance may not perform well under drought stress at elevated temperatures. However, tropical maize germplasm of CIMMYT does offer some promising inbred lines with good levels of tolerance to combined drought and heat stress, and are being utilized in breeding strategies. Innovative approaches as well as partnerships are required to develop, test and deliver stress resilient improved maize varieties in SSA. The recent establishment of a Maize Doubled Haploid Facility for Africa (at Kiboko, Kenya), initiation of DH development service to NARS and SME seed companies in Africa and Latin America using tropicalized haploid inducers, and provision of phenotypic service to important abiotic and biotic stresses, including the maize lethal necrosis (MLN) in east Africa, are a few important steps in this direction. CIMMYT has also made significant progress in identifying, validating and deploying breeder-ready markers for some important traits – for example, resistance to maize streak virus (MSV) and MLN.

Experiences of CIMMYT also strongly indicate that besides strengthening the seed sector (especially the SME seed companies), appropriate government policies and adoption of progressive seed laws and regulations, are vital for improving smallholder farmers' access to improved seed, and for overcoming key bottlenecks affecting maize seed value chain, particularly in the area of policy, credit availability, seed production, germplasm and marketing.

## ENHANCING ALFALFA FORAGE PRODUCTIVITY DURING DROUGHT

Ian Ray\*, Gina Babb, New Mexico State University Department of Plant and Environmental Sciences; Nicholas Santantonio, Cornell University Department of Plant Breeding and Genetics

Large portions of Great Plains and the western United States are regularly plagued by drought and diminishing water resources for irrigation. Alfalfa cultivars adapted to these regions, and that can remain productive when soil water availability is limited, are clearly needed. This paper summarizes some of the work that has been conducted to develop alfalfa germplasms that are less sensitive to drought stress in the southwest United States. Such efforts have included field evaluation of several hundred elite populations and National Plant Germplasm System accessions for their ability to remain productive under reduced flood irrigation allotments (i.e. 50% of normal). Characterization of morphological and physiological traits in some of these populations suggested that higher yielding germplasms may possess one or more of the following features: reduced leafiness, greater carbon isotope discrimination (CID), or more extensive root systems. Subsequent DNA marker and field evaluation research in two experimental alfalfa mapping populations (n=185) identified several QTL that influenced alfalfa forage and root biomass production during water-stress. A follow-up modified selective phenotyping pilot study, that evaluated a subset of individuals (n=29) from one of the above mapping populations, identified nine putative QTL that influenced CID. Four of the CID QTL colocalized with either forage or root biomass QTL. In each of these four cases, the direction of the CID effect was positively correlated with shoot or root biomass effects. These results agreed with previous reports of positive genetic correlations between CID and forage yield in alfalfa, and suggest that in many cases, CID and shoot or root biomass production may be influenced by the same genetic factors. Several single dose alleles of the putative forage and root biomass QTL were subsequently transferred into different alfalfa cultivar backgrounds over two generations using DNA marker assisted selection (MAS). Forage yield of 32 MAS-derived populations were evaluated over six harvests in each of three years under reduced flood irrigation allotments. In the first-generation MAS populations (50% elite cultivar background), selection for high shoot and high root biomass markers, and selection against low shoot and low root biomass markers, benefited forage yield by 1 to 19%. To produce second-generation MAS accessions with a 75% elite genetic background, six of the first-generation MAS populations were each mated to three alfalfa cultivars which possessed varying degrees of drought tolerance. Significant ( $P < 0.10$ ) forage yield differences, ranging from 19 to 27%, were detected among the six MAS-derived synthetics within each cultivar group suggesting that MAS impacted alfalfa productivity in all three cultivar backgrounds. Phenotypic effects of the DNA markers appeared to be influenced by the cultivar genetic background in which they resided. Some second-generation MAS populations outperformed their original cultivar parent by 3 to 14%, with the greatest improvement occurring in the two cultivars that had not previously experienced selection for drought tolerance. Marker assisted selection did not benefit drought productivity of second-generation MAS populations derived from the cultivar which had previously experienced strong selection pressure for drought tolerance. Given that 50% of the plants in the second-generation MAS populations possessed any given marker allele, additional selection within these populations to increase marker frequencies may provide additional forage yield improvement. Collectively, the results suggest that the transfer of some biomass QTL into drought sensitive alfalfa cultivars via MAS may improve their forage productivity in water-limited environments.



## PHENOTYPIC EVALUATIONS OF HEAT TOLERANCE AND FRUIT QUALITY TRAITS IN SEGREGATING BLACK RASPBERRY (*RUBUS OCCIDENTALIS* L. ) POPULATIONS IN NORTH CAROLINA.

\*Christine M. Bradish, Gina E. Fernandez, North Carolina State University – Department of Horticulture; Jill M. Bushakra, Nahla V. Bassil, USDA-ARS National Clonal Germplasm Repository, Corvallis, OR; Penelope Perkins-Veazie, NC State University Plants for Human Health Institute; Michael Dossett, Agriculture and Agri-Food Canada - Pacific Agri-Food Research Centre; Chad E. Finn, USDA-ARS-Horticultural Crops Research Unit, Corvallis, OR

In recent years there has been a significant expansion in both the production and consumption of many small fruit crops, yet the black raspberry industry has not expanded beyond a limited commercial acreage in Oregon and a scattered small scale acreage across the country. Over the last 75 years, black raspberry breeding has been hindered due to a lack of elite germplasm and a lack of adapted, disease resistant cultivars. Despite this, recent research focused on the health benefits of a diet rich in polyphenolics, and black raspberries in particular, has led to a resurgence of interest in this fruit and a renewal of breeding efforts. In North Carolina, this study seeks to standardize phenotyping procedure and calculate yield parameters for black raspberry, and to define both the best phenotyping method and screening procedure to assess heat tolerance. Two half-sib populations, designated ORUS 4304 (192 progeny) and ORUS 4305 (115 progeny), were planted in 2012 at the Sandhills Research Station in Jackson Springs, North Carolina and evaluated for over two harvest seasons in 2013-2014 for fruit traits, yield, and heat tolerance. In 2013, average fruit size ranged from 0.17 – 3.12 g/berry, with highest fruit weight found in ‘Jewel’ elite checks and two progeny in ORUS 4304. Average yields were 1.4kg (3 lb) per plant, with no difference between populations. Yield was normally distributed, and positively correlated at  $p < 0.0001$  with 11 plant and fruit traits. Heat tolerance was measured by chlorophyll fluorescence, and ranged from 0.015 – 0.940, where 0.7 – 0.8 is normal and  $> 0.8$  is heat tolerant, by convention. Several progeny had higher fluorescence scores than parents, indicating transgressive segregation for the trait. Our results showed that fluorescence was negatively correlated with florican vigor and lateral length at  $p < 0.0001$ . Further, fluorescence was normally distributed and these results were consistent with previous research done on red raspberry in the same location. Proposed work includes examining additional methods for phenotyping heat tolerance and calculations of genotype x location x year interactions. Linkage map assembly of 4304 is underway in order to identify QTL for traits of interest. Validation with 4305 and comparative mapping between red and black raspberry will be used to further develop genetic tools for breeding black raspberry in the future.

# MULTI-ENVIRONMENT ANALYSES OF WINTER WHEAT HEADING DATE ACROSS THE U.S. GREAT PLAINS: CAN WE BETTER OPTIMIZE GENOTYPES FOR SPECIFIC ENVIRONMENTS?

\*Sarah Grogan, Scott Reid, Scott Haley, and Patrick Byrne, Colorado State University  
Department of Soil and Crop Sciences; and Gregory McMaster, USDA-ARS  
Fort Collins, CO

In wheat, heading describes the emergence of the inflorescence and indicates reproductive development and genotypic ‘earliness’. Variation in heading date among wheat varieties reflects adaptation to specific environmental conditions, such as differences in temperature and day length. Fine-tuning the timing of growth and development can reduce the occurrence of flowering and seed set during periods of cold, heat, or water stress. The objectives of this study were to 1) evaluate the extent of variation or plasticity in heading date when the same wheat varieties are grown in multiple environments; 2) assess genotypic variation for key developmental genes known to affect flowering time; 3) investigate the extent of genotype-by-environment interaction and whether particular multi-locus genotypes are better suited for certain regions or environments; and 4) predict heading date using a multiple linear regression that includes major developmental genes and several environmental variables.

We evaluated variation in heading date of 299 wheat varieties belonging to the Triticeae Coordinated Agricultural Project (TCAP) hard winter wheat association mapping panel, at 11 different environments in 2012 and 2013. Each environment is a unique combination of moisture treatment, location, and year. Trial locations include Fort Collins, CO; Mead, NE; Hays, KS; Greeley, CO; Manhattan, KS; Bushland, TX; and Ardmore, OK. Heading date was scored for each variety at all locations by the authors or collaborators, and ranged from an average of 108 days after January 1 in Ardmore to 150 days in Fort Collins.

The flowering pathway integrates cues from both vernalization (*Vrn*) and photoperiod (*Ppd*) genes. Additionally, dwarfing (*Rht*) genes and quantitative earliness per se (*Eps*) genes also affect timing of reproductive development. Most of these developmental genes have been selected indirectly while selecting for agronomic traits, leading to geographic variation of some alleles. Optimizing the multi-locus genotype could increase yield and yield stability. We genotyped the germplasm for several of these key developmental genes, and major effects and interactions are presented for each environment. The largest single gene effect on heading date was for *Ppd-D1*, where presence of the early allele explained an average of 14.8% of variation in heading, with an average effect of 3.7 days.

## GENERAL COMBINING ABILITY MODEL FOR GENOMEWIDE SELECTION IN A BIPARENTAL CROSS

\*Amy Jacobson, Lian Lian, Rex Bernardo, University of Minnesota Department of Agronomy and Plant Genetics; and Shengqiang Zhong, Monsanto Company

Genome-wide selection within an A/B biparental cross is most advantageous if it could be effectively done before the cross is phenotyped. Our objectives were to determine if a general combining ability (GCA) model is useful for genome-wide selection in an A/B cross, and to assess the influence of training population size ( $N_{GCA}$ ), number of crosses pooled into the training population ( $N_X$ ), linkage disequilibrium ( $r^2$ ), and heritability ( $h^2$ ) on the prediction accuracy with the GCA model. The GCA model involved pooling 4–38 maize (*Zea mays* L.) crosses with A and B as one of the parents into the training population for an A/B cross, whereas the same background (SB) model involved pooling crosses between random inbreds. Across 30 A/B test populations, the mean response to selection (R) with the GCA model was 0.19 Mg ha<sup>-1</sup> for testcross grain yield, -6 g kg<sup>-1</sup> for moisture, and 0.38 kg hl<sup>-1</sup> for test weight. These R values with the GCA model were 68–76% of the corresponding R values with phenotypic selection. The R values with the SB model were only 15–28% of the R values with phenotypic selection. Increasing the size of the training population with random crosses from the same heterotic group was less important than including crosses with A and B as one of the parents. The progeny in the populations were genotyped at low marker density, 49–100 polymorphic markers, and the parents were genotyped at a high density of 2911 markers. Marker imputation of the progeny improved R of the GCA model by 0.06 Mg ha<sup>-1</sup> for testcross grain yield, -1 g kg<sup>-1</sup> for moisture, and 0.05 kg hl<sup>-1</sup> for test weight. Our results indicated that the GCA model is routinely effective for genome-wide selection within A/B crosses, prior to phenotyping the progeny in the cross.

## A PRACTICAL APPROACH FOR UNDERSTANDING GENOTYPE BY ENVIRONMENT INTERACTIONS

Chad Geater, Ph.D., Syngenta Seeds, Inc.

Controlling genotype by environment interactions in field research can be a challenge, but steps can be taken to understand observed interactions more completely. Breeders can gain a practical understanding of genotype by environment interactions by accurately measuring cultivar performance, appropriately characterizing testing environments, segmenting environments into logical environmental types, analyzing cultivar performance within each segment, and comparing performance of cultivars across environmental types. A practical understanding of genotype by environment interactions allows breeders to make more appropriate selections in their breeding programs and provide better management recommendations to growers.

## POTENTIAL TO USING REMOTE SENSING TOOLS TO SCREEN GERMPLASM

Jerry L. Hatfield, Laboratory Director and Supervisory Plant Physiologist, National Laboratory for Agriculture and the Environment, Ames, Iowa 50011, [jerry.hatfield@ars.usda.gov](mailto:jerry.hatfield@ars.usda.gov)

Remote sensing allows for a non-destructive and repeatable measurement of the same area throughout a growing season. The wavelengths with documented use to observe vegetation extend from the visible through the thermal wavelengths and there have been a continual progression in the development of combinations of different wavelengths to estimate a number of different plant characteristics. These vegetative indices have been related to various plant parameters, e.g., leaf chlorophyll, leaf area index, biomass, light interception, ground cover, net primary productivity, nutrient stress, water stress, and phenotypic characteristics. The combinations of different wavebands into different vegetative indices, e.g., normalized difference vegetative index (canopy light interception), plant senescence reflectance index (rate of plant senescence), greenness index (leaf chlorophyll), red/near-infrared ratios (biomass) offers the potential for screening germplasm for a number of different characteristics. The advantage of using these techniques is that the small plants can be observed and the seasonal change in the vegetative index recorded throughout the growing season. Screening of wheat germplasm has been conducted with reflectance ratios to determine the rate of canopy development, brassica species have been screened for their growth rates, and cotton has been screened for water use efficiency. Combinations of wavebands can be used to estimate growth analysis parameters to provide a quantitative measurement of the growth rate which would provide a new detail to compare germplasm in different trials. Remote sensing tools are becoming easier to use in field experiments and applying this technology to genetic studies would provide a quantitative and nondestructive method for gathering data across multiple locations and entries.

## GENOMIC SELECTION: TRAINING POPULATIONS AND GXE

Mark E. Sorrells, Department of Plant Breeding & Genetics, Cornell University, Ithaca, NY;  
Jean-Luc Jannink, USDA-ARS, Cornell University, Ithaca, NY; Nicolas Heslot, Department of  
Plant Breeding & Genetics, Cornell University, Ithaca, NY

Genomic selection (GS) is the simultaneous use of genome-wide markers to increase accuracy of performance prediction for both phenotyped and unphenotyped individuals. In GS, a training population related to the breeding germplasm is genotyped with genome-wide markers and phenotyped in the target set of environments. That data is used in a prediction model to estimate breeding values of unphenotyped candidates. Design of the training population is critical to the accuracy of prediction models. Prediction models can incorporate performance over multiple environments and assess GxE effects to identify a highly predictive subset of environments. We have developed a methodology for unbalanced datasets using genome-wide marker effects to group environments and identify outlier environments. In addition, environmental covariates can be generated using a crop model and used in a GS model to predict GxE in unobserved environments and to predict performance in climate change scenarios. Current research is focused on optimizing the training population to improve efficiency and increase prediction accuracy in terms of genotypes, experimental design and environment sampling.



## TAKING ADVANTAGE OF PHYSIOLOGICAL PRIMING IN CROPS: BREEDING FOR GREATER ACCLIMATION TO DROUGHT

Diane Rowland<sup>1</sup>, Barry Tillman<sup>1</sup>, Paxton Payton<sup>2</sup>, Bertha Nguku<sup>1</sup>, Christopher Vincent<sup>1,3</sup>,  
Brendan Zurweller<sup>1</sup>, Bruce Schaffer<sup>3</sup>, And Seth Byrd<sup>4</sup>

<sup>1</sup>*University of Florida, Agronomy Department, Gainesville, FL, U.S.*

<sup>2</sup>*USDA-ARS, Cropping System Research Lab, Lubbock, TX, U.S.*

<sup>3</sup>*University of Florida, Tropical Research and Education Center, Homestead, FL, U.S.*

<sup>4</sup>*University of Georgia, Tifton Campus, Tifton, GA, U.S.*

Maintaining sustainable crop production under limited water resources has become the single most important challenge in the U.S. agricultural industry and worldwide. To find solutions to this challenge, we aim to take a top-down approach, integrating crop management, physiological screening, and genetic expression evaluation of diverse crop cultivars in both southwest and southeast U.S. environments. For this top-down approach, we have developed a water conservation management system (known as primed acclimation, PA) that takes advantage of the physiological process known as priming. Priming involves exposure to initial, often mild levels of stress that prepare the plant to better tolerate subsequent stresses which may occur during critical reproductive stages. This priming exposure has the potential to bring about an acclimated state so that the crop is better able to withstand ensuing drought stress and maintain yield. Common mechanisms among crops in response to PA include: deeper and more extensive rooting architecture, up-regulation of gas exchange responses, and indications that gene expression is altered during the initial priming response. We are now focused on screening genotypes for their priming capacity, particularly identifying and quantifying physiological responses that can be used as screening tools for the selection of priming potential. Current research activities have focused on: expanding the PA concept to diverse crops; the direct sensing of stress levels appropriate for successful priming; and the application of “cross priming” or the use of different types of priming stress to enhance drought tolerance. In this work, we aim to: 1) investigate the physiological and molecular basis of crop response to abiotic stress that occurs in limited water production systems, and the role that priming plays in this response, 2) develop straightforward crop management protocols that maximize plant acclimation capacity and effective water use while maintaining economic and environmental sustainability, and 3) use physiological and molecular methods to assist in selection and development of abiotic stress-tolerant crop cultivars. This top-down approach has the advantage of delivering a conservative water management system along with cultivars that have been developed for optimal production under the system, thus maximizing the benefit to growers.

## THE STRESS-INDUCED SYNTHESIS OF CYTOKININ REGULATES THE COORDINATION OF C AND N METABOLISM RESULTING IN ENHANCED DROUGHT TOLERANCE IN RICE TRANSGENIC PLANTS.

Reguera M. & Blumwald E., Department of Plant Sciences, University of California, Davis, CA 95616.

The development of high yielding cultivars with improved stress tolerance is a major challenge in agriculture. Among the abiotic stresses, drought is the main limiting factor affecting plant growth and productivity, reducing grain yield and compromising food-security worldwide. Drought accelerates plant senescence, reducing the ability of the plant to maintain proper sink/source relationships which is associated with carbon and nitrogen starvation. We investigate the hypothesis of increasing drought tolerance by delaying drought-induced leaf senescence of rice transgenic plants expressing the IPT gene (encoding isopentenyl transferase, a key enzyme in the synthesis of cytokinins) under the control of a maturation- and stress- inducible promoter (SARK, senescence-associated receptor kinase). The regulated expression of IPT under the control of PSARK significantly improved drought tolerance. Rice PSARK::IPT transgenic plants produced higher grain yield under water stress with an enhanced nutritional value. Using a multidisciplinary approach that combined genomics, proteomics, metabolomics and enzyme activity analysis we identify and characterize cellular/biochemical components that regulate Carbon and Nitrogen metabolism in wild-type and transgenic PSARK::IPT rice plants grown under water deficient conditions. Our results showed that the stress-induced cytokinin synthesis resulted in improvements of primary N assimilation, enhancement of biochemical properties of photosynthesis and the maintenance of protein synthesis that lead to the strengthening of sink capacity of the rice transgenic plants. This work contributes to a better understanding of the mechanisms that regulate stress tolerance in plants, indicating the great potential for crop improvement in water-limited areas of the world.

## IMPROVING DROUGHT TOLERANCE OF HARD WINTER WHEAT THROUGH THE TRITICEAE COORDINATED AGRICULTURAL PROJECT (T-CAP)

Patrick F. Byrne, Scott Reid, Sarah Grogan, Wahid Awad, and Scott Haley. Colorado State University, Fort Collins, CO.

Drought stress is a chronic problem for wheat in the U.S. Great Plains, with average wheat yields in Colorado just 2 tons/hectare due largely to moisture deficits. The frequency and severity of these drought episodes are expected to increase according to most climate models. Breeding for this variable climate requires a sound understanding of the target environments and of drought-adaptive traits that provide benefits in drought years without penalties in favorable years. However, attempts to identify secondary traits for improvement of drought tolerance have generally not been successful, probably due to the multiple mechanisms wheat plants use to adapt to low moisture and to confounding effects from other stresses. The USDA-funded Triticeae Coordinated Agricultural Project (TCAP) has now provided opportunities to associate dense marker arrays with yield-related traits across a range of soil moisture availability, and to evaluate the usefulness of canopy spectral reflectance and root traits as indicators of drought tolerance. Gene discovery for drought adaptation in hard winter wheat focuses on a 300-member association mapping panel grown in multiple environments, and preliminary results of genome-wide association analysis will be presented. Other notable components of the TCAP project are development of a comprehensive database for storage of genotype and phenotype data, training of 25 Ph.D. students in plant breeding and genetics, and research opportunities for students at minority-serving colleges. Selection for drought tolerance in winter wheat will remain challenging, but new tools and germplasm should advance progress in the coming decades.

## RECENT LESSONS IN DROUGHT RISK MANAGEMENT

Michael Hayes, NDMC, University of Nebraska-Lincoln

A recent 2013 United Nations report estimates that the direct losses from natural disasters globally since 2000 have been approximately \$2.5 trillion. This stunning estimate is significantly larger than any previous estimate, and it illustrates that natural disasters will be significant issues for all societies in the future. The report argued that the “economic losses from disasters are out of control” and that these losses will continue to “escalate” unless action is taken to reduce disaster risks in the future. With that context, and the estimate that the 2012 drought in the central United States cost at least \$30 billion in losses, drought risk management has recently become a relevant topic for policy discussions and the “action” that needs to take place if future drought losses are to be reduced. This presentation will focus on the recent lessons droughts have prompted across the U.S., as well as highlight the activities and drought risk management strategies, particularly in the area of drought planning and comprehensive water planning, taking place as a result.

## THE GOOD FORTUNE OF THREE YEARS OF DROUGHT ON A RESEARCH COLLABORATIVE

William Beavis, Iowa State University

The Soybean Nested Association Mapping (SoyNAM) project consists of 40 families, each consisting of 140 Recombinant Inbred Lines (RILs) adapted to maturity zones 2.8 – 3.8. All 5600 RILs and their parental inbreds were assayed at 5300 SNP loci designed for this project. The RILs were grown in 20 environments from Nebraska to Ohio during 2011 – 2013. Seven of the 20 environments experienced midseason droughts. In several of the environments droughty conditions lasted until after harvest. Analyses of data combined across all environments exhibited very low levels of repeatability among the entries due to the large impact of GxE on yield, maturity and grain quality traits. Significant heterogeneity and cross-over forms of GxE were expressed among the RILs, their parents and adapted check cultivars. Analyses of subsets of environments based on clustering of GxE responses provided much more repeatable results within the subsets. Mapping results using these subsets, revealed both consistent and unique genomic regions associated with expression of the traits. Many of the unique genomic regions associated with expression of the traits include genes known to participate in the Ureide biosynthetic pathway. Breeding strategies that take advantage of this information are suggested to produce stable high yielding lines.

## POSTER ABSTRACTS

### POSTER 1

#### IMPROVING DROUGHT TOLERANCE IN SOYBEAN

\*Hussein Abdel-Haleem, Roger Boerma, and Zenglu Li, University of Georgia Department of Crop and Soil Sciences; Tommy Carter, USDA-ARS Soybean and Nitrogen Fixation Unit

Seed yield is an ultimate goal of soybean production. Drought is the major factor that reduces crop productivity worldwide. Drought tolerance is a complex trait and the stressed plants often simultaneously utilize more than one mechanism at a time to mitigate drought. Two plant introductions (PIs) PI 471938 and PI 416937 were discovered to possess slow canopy wilting traits. In addition, PI 416937 was observed to possess a fibrous rooting trait. Using two RIL populations, Hutcheson x PI 471938 and Benning x PI 416937, which were tested in irrigated and rain-fed environments across the Southeast and mid-South regions, we have discovered quantitative trait loci (QTL) for yield and drought tolerance related traits. Three QTL on Lg-D2, F, and K inherited their slow canopy wilting alleles from PI 471938. Four QTL on Lg-A2, C1, D1a, and I, and five QTL on Lg-A1, A2, C1, H, and L inherited their alleles for increased fibrous roots and slower canopy wilting from PI 416937, respectively. To evaluate the impact of slow canopy wilting QTL on yield under drought conditions, the slow canopy wilting alleles are being backcrossed into two high yielding breeding lines developed in the University of Georgia (UGA) breeding program using a marker-assisted backcrossing approach. Some of QTL derived from PI 471938 and PI 416947 will be stacked in these two elite lines. The near-isogenic lines containing a combination of these QTL will be tested for yield under drought stress conditions.



## POSTER 2

### EVALUATE CHILI PEPPER YIELD UNDER WATER STRESS

\*Jaser Al-Jaser, Eduardo Blumwald, and Allen Van Deynze, University of California Davis  
Department of Plant Sciences

Water is the main limiting abiotic factor in agricultural globally. California's Mediterranean climate provides low rainfall level thus farmers tend to use irrigation water more efficiently. However, crops such as pepper have moderate demands of water; lowering irrigation level may impact yield and quality in pepper fruit and be less marketable. In this study we aim study the effect of different water treatment on biomass, height, number of fruit, size and weight and number of seeds. Pepper plants are grown from seed into flowering stage, and then grouped into four irrigation treatments: 100% (control), 80%, 60% and 40%. Height and fresh weight measurement are done weekly up until breaker stage during fruit ripening where irrigation stops and measurement of yield is calculated. In each treatment number of fruits is counted, size and fresh weight, then dry weight of the whole plant, fruit, and lastly number of seeds. The result has shown effects on biomass with different water treatments. Our hypothesis is that biomass is reduced with less irrigation as water plays a major role in photosynthesis and ultimately affects carbon distribution across the whole plant. Effects on fruit yield and quality will be presented.

## POSTER 3

### INDUCED STRUCTURAL VARIATION IN THE SOYBEAN GENOME

\*Justin Anderson and Robert Stupar, University of Minnesota  
Department of Agronomy and Plant Genetics

Modern soybean researchers and breeders are limited by the crop's overall lack of diversity. Attempts to introduce novel traits through mutagenesis and transformation have each resulted in unique and valuable changes. While the benefit from valuable changes is clear, off target modifications are often ignored. In this study a comparative genome hybridization array was used to compare the levels of standing variation to that induced through fast neutron mutagenesis and transformation. Fast neutron lines with no observable novel phenotype were shown to have structural variation commonly induced. Transformed lines had very little induced structural variation. While both methods are capable of creating desired novel phenotypes, these results show that off target effects are much higher in mutagenesis than in transformation.

## POSTER 4

### NESTED ASSOCIATION MAPPING OF STEM RUST RESISTANCE IN WHEAT USING GENOTYPING BY SEQUENCING

\*Prabin Bajgain, James A Anderson, University of Minnesota Department of Agronomy;  
Matthew N Rouse, Yue Jin, USDA-ARS Cereal Disease Laboratory; Godwin Macharia, Kenya  
Agricultural Research Institute; and Toi J Tsilo, South Africa Agricultural Research Council

Nested association mapping (NAM) is an approach to map trait loci in a specially designed mapping population where families within populations are interconnected by a common parent. By implementing joint-linkage association analysis, this approach is able to map causative loci with higher power and resolution compared to existing methods. The recently developed genotyping by sequencing (GBS) approach is a relatively fast, efficient and cost-effective method of genotyping large number of individuals. Additionally, the GBS method allows for discovery of *de novo* markers that are specific to the individuals or populations under study. We combined the NAM approach of mapping with high-throughput genotyping of the population to dissect and understand the genetic architecture controlling stem rust resistance in wheat. Ten resistant wheat varieties were crossed to the susceptible line LMPG-6 to generate F<sub>6</sub> recombinant inbred lines (RILs). The RIL populations were phenotyped at four environments in Kenya, South Africa, and St Paul, Minnesota. We identified several minor-effect QTL contributing towards adult plant resistance (APR) to N. American stem rust races as well as to the Ug99 group of races. The detected QTL can provide a much-needed resistance in Ug99-hotspot areas such as East Africa, and can help fight off the disease upon its arrival in other wheat growing areas of the world. Validation of markers that are significantly associated with the QTL is an important task that needs to be done in order to generate diagnostic markers for marker assisted resistance breeding. The usefulness of GBS-derived *de novo* SNPs in mapping APR to stem rust shown in this study could be used as a model to conduct similar marker-trait association studies in other crop or non-crop species.

## POSTER 5

### GWAS FOR QUANTITATIVE AND QUALITATIVE DISEASE RESISTANCE LOCI IN BARLEY (*HORDEUM VULGARE*)

\*Araby Belcher, Alfonso Cuesta-Marcos, Oregon State University Crop Science; Xianming Chen, Washington State University Plant Pathology; and Patrick Hayes, Oregon State University Crop Science

Replacing pesticides with plant disease control by resistant varieties is a key strategy of sustainable agriculture. Quantitative resistance is predicted to be more durable than qualitative resistance. Important diseases of barley are stripe rust, leaf rust, and scald (incited by *Puccinia striiformis* f. sp. *hordei*, *Puccinia hordei*, and *Rhynchosporium commune*, respectively). We used genome-wide association studies (GWAS) in a 300-line elite barley facultative/winter six-rowed panel to map quantitative trait loci (QTLs) for adult plant field resistance to the three diseases. We also mapped qualitative race-specific disease resistance loci to four barley stripe rust races. Stripe rust and scald were assessed in two field trials and leaf rust in one field trial. We identified 12 apparent maturity-independent disease resistance QTLs - three stripe rust, three scald, and six leaf rust – along with seven race-specific stripe rust QTLs. All GWAS used a P+K model and a trial-by-trait-wide false discovery rate of  $q^*=0.05$ . Our breeding program will use these results to develop disease-resistant barley varieties. That use will include approaches that are both indirect and direct. An example of the former is validating co-localizing QTLs mapped in other germplasm pools, and examples of the latter are release as cultivars and use as parents in marker-assisted selection programs.

## POSTER 6

### USE OF SHUTTLE BREEDING FOR RAPID IMPROVEMENT OF RICE BREEDING POPULATIONS

\*Gregory Berger, K.A.K Moldenhauer, Xueyan Sha, Debra Ahrent, Garrett Lee, and Charles Wilson Jr., University of Arkansas Rice Research and Extension Center; Anthony Rivera Vega, Universidad de Puerto Rico Recinto Universitario de Mayaguez.

Use of shuttle breeding nurseries allows rice (*Oryza sativa* L.) breeders to grow multiple generations of rice per year. The University of Arkansas rice breeding program is located at the Rice Research and Extension Center in Stuttgart, AR (34°28'32.38" N, 91°25'7.21"W). The general growing season for rice in Arkansas is April through late September which allows for the advancement of one generation per year. Use of a winter breeding nursery located at the University of Puerto Rico at Mayaguez Agriculture Experiment Station in Lajas, PR (18° 1'58.82"N, 67° 4'26.53"W) allows for advancement of two to three additional cycles per year. Beginning in August, breeding populations are planted at the Lajas, PR experiment station with the latest material being planted in late December through early January. Breeding material harvested from the winter nursery is then planted in Stuttgart, AR the following season. Use of the winter nursery has not been solely limited to generation advancement, but also isolated seed increases and hybrid seed production.

## POSTER 7

### SENSITIVITY OF JOINT LINKAGE AND GENOME-WIDE ASSOCIATION ANALYSES OF MAIZE SOUTHERN LEAF BLIGHT RESISTANCE TO DATA INPUTS

\*Yang Bian, North Carolina State University Department of Crop Science; Qin Yang, North Carolina State University Department of Plant Pathology; Peter Balint-Kurti, USDA Agricultural Research Service Plant Science Research Unit and North Carolina State University Department of Plant Pathology; Randall J. Wisser, University of Delaware Department of Plant and Soil Sciences; and James B. Holland, USDA Agricultural Research Service Plant Science Research Unit and North Carolina State University Department of Crop Science

A previous study reported a comprehensive joint linkage (JL) quantitative trait locus (QTL) and genome wide association study (GWAS) of southern leaf blight (SLB) resistance in the maize Nested Association Mapping (NAM) panel. Since that time, the genomic resources available for such analyses have improved substantially. An updated NAM genetic linkage map has a nearly six-fold greater marker density than the previous map and the maize HapMap 2 provided 26.5 M SNPs for association analysis, 16 fold more than HapMap 1. In addition, phenotypic values of the NAM RILs were re-estimated to account for environment-specific flowering time covariates and a small proportion of lines were dropped due to genotypic data quality problems. We compared analysis results using these updated data inputs to the previously published analyses and evaluated the effects of changing linkage map density, population sample size, and phenotype estimates on results. Map density caused the largest changes in both JL models and GWAS. The updated QTL model has better cross-validation prediction accuracy and better consistency with other fine mapping results than the previous model. Whereas joint linkage QTL were relatively stable to input changes, the residual values from those QTL models (which are used as inputs to GWAS) were more sensitive, resulting in substantial differences between GWAS results of the studies. The highly polygenic nature of resistance to southern corn leaf blight complicates the identification of causal genes. Joint linkage QTL are relatively stable to perturbations of data inputs, but their resolution is generally on the order of tens or more Mbp. GWAS associations have higher resolution, but lower power due to stringent thresholds designed to minimize false positive associations, resulting in variability of detection across studies. The updated higher density linkage map improves QTL estimation and, along with a much denser SNP HapMap, greatly increases the likelihood of detecting SNPs in linkage with causal variants. We recommend use of the updated genetic resources and results.

## POSTER 8

### CONVERTING WINTER WHEAT GENOTYPES INTO RAPID CYCLING SPRING WHEAT GENOTYPES FOR EFFICIENT BACKCROSS BREEDING

\*Rungravee Boontung and P. Stephen Baenziger, University of Nebraska-Lincoln  
Department of Agronomy and Horticulture

Breeding winter wheat (*Triticum aestivum* L.) by backcrossing is used to add a desirable gene into an elite winter wheat genotype. However, the time of each backcross generation of winter wheat is four months or longer depending upon the genotype because winter wheat requires a period of vernalization. Therefore, decreasing the generation time would be very useful for a backcrossing winter wheat scheme. This research was conducted to determine the genetics of rapid cycling spring wheat genotypes (two months from sowing to harvest) and to add genes removing the vernalization requirement and adding the earliness per se genes of spring wheat type into 'winter' wheat background for accelerated backcrossing cycles. Three winter wheat cultivars, 'Overland', 'Goodstreak' and 'NW07505' were crossed with super dwarf and early heading spring wheat 'Apogee'. The F<sub>2</sub> population of 'Goodstreak x Apogee' and the F<sub>3</sub> population of 'Overland x Apogee' and 'NW07505 x Apogee' were planted and measured for anthesis date and height. Segregation analysis of F<sub>2</sub> between 'Goodstreak x Apogee' indicated that early anthesis/late anthesis fit the ratio of 63:1 or 255:1 ratio at  $P \geq 0.75$  with  $\chi^2 = 0.95$ . The F<sub>3</sub> population of 'Overland x Apogee' and 'NW07505 x Apogee' fit the ratio of 4015:81 (four dominant genes) at  $P \geq 0.05$  ( $\chi^2 = 3.38$ ) and  $P \geq 0.50$  ( $\chi^2 = 0.15$ ), respectively. We suggest at least three genes for spring growth habit (lack of vernalization requiring alleles) or earliness per se were transferred to the early progenies of these populations. The earliest progenies of the three populations after additional backcrossing to the recurrent winter wheat parent can be used for rapid backcrossing programs to greatly reduce backcross breeding cycle time. To recover the winter wheat genotype, the last backcross(es) will be made to the winter wheat genotype so that the all the vernalization and later heading genes are available for selection and recovery of the adapted winter genotype.

## POSTER 9

### EXPANSION OF MAKER STANDARD GENE SETS OF CEREAL GENOMES THROUGH PROTEIN HOMOLOGY AND NUCLEOTIDE CONTENT

\*Megan J. Bowman and Kevin L. Childs, Michigan State University  
Department of Plant Biology

The applicability of whole genome sequencing in laboratory research and plant breeding efforts depends on accurate gene prediction and annotation. Structural annotation of genomes is more accurate with the use of transcript or protein alignment evidence. The MAKER annotation pipeline assists de novo prediction programs by providing alignment evidence and selecting gene models that are the most concurrent with available protein and transcript alignments. The output of this pipeline is a set of predicted gene models, either with or without transcript or protein evidence. Of these gene models, those with or without transcript or protein alignment support but with Pfam domains are called the MAKER-Standard gene set. These gene models represent a highly confident set of structural gene annotations that can be used downstream in further analyses. While this gene set contains most predicted genes within a genome, it is possible that some true genes do not have the necessary evidence alignment needed to be promoted to a MAKER gene model due to errors in evidence alignment and ab initio prediction. Additional criteria may be helpful in expanding the number of genes within the MAKER-Standard gene set. In this study, we used a protein homology approach to identify gene models with no evidence alignment but that have high protein sequence similarity to other gene predictions within the same genome. We have tested this approach in maize, sorghum and brachypodium. Additionally, we examined the possible role of GC content in the creation of hidden markov models during the training of ab initio gene predictors. As whole genome sequencing continues to impact molecular breeding efforts, it is important to apply different bioinformatics approaches to ensure the most complete and accurate gene sets are used in downstream applications.



## POSTER 10

### FINE-MAPPING AND TESTING OF A FIBER LENGTH QTL IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM*, L.) ON CHR. 25 ORIGINALLY IDENTIFIED IN SEALAND 883

\*Nino Brown, Pawan Kumar, Peng Chee, and Andy Paterson, University of Georgia  
Department of Crop and Soil Science

Limited genetic diversity in the Upland cotton (*Gossypium hirsutum*, L.) germplasm base has limited the long-term genetic gain of cotton fiber quality. Germplasm enhancement by incorporation of beneficial alleles from diverse sources has generally been undertaken by breeders within the public sector; however, few of these germplasm lines have been utilized in the development of commercially available cultivars. It is believed that this is largely due to linkage drag associated with fiber quality trait introgression. To improve genetic diversity in Upland cotton and minimize the effect of negative linkage, we are identifying tightly linked molecular markers to create germplasm with excellent fiber quality and yield. A fiber length quantitative trait locus (QTL) was identified previously that explained 10 to 60% of the total phenotypic variation for UHML in the QTL mapping populations derived from crosses of the donor, Sealand 883 (SL 883), with 4 commercial cultivars, Acala SJ-4 (SJ-4), Paymaster HS-26 (HS-26), Deltapine 50 (DP 50), and an unreleased germplasm line, GA 89. Previous work identified *G. barbadense* introgression within the SL 883 genome. One of these introgressed segments, on chromosome 25 (Chr.25) harbors the fiber length QTL and has substantial effect on phenotype. The purpose of this project is to further validate the effect of this QTL and to fine-map its location. To accomplish this we have tested the QTL in 4 genetic backgrounds in the adaptation zones for which they are suited. In 2013 we selected individuals from segregating F<sub>4:6</sub> lines to serve as near-isogenic lines (NILs) for further testing and validation. A group of recombinant inbred lines with overlapping recombination events are currently being evaluated and analyzed to further fine-map the location of this fiber length QTL.

## POSTER 11

### USING QTL ENRICHMENT TO IMPROVE MAIZE NITROGEN UTILIZATION

\*Jessica Bubert, Jay Boddu, Yuhe Liu, and Stephen Moose, University of Illinois at Urbana-Champaign Department of Crop Sciences.

Increased nitrogen use efficiency (NUE) is an important target for future maize improvement. Essential to the design of an effective breeding program to select maize hybrids with enhanced NUE is an understanding of past progress, variation among maize germplasm for NUE and its component traits, and identification of phenotyping approaches to optimize genetic gain. We documented genetic variation for NUE and its component agronomic traits among a diverse collection of historical and recent elite maize inbreds and hybrids grown in field trials with different levels of soil N supply. Many of the genotypes evaluated also represent important resources for maize functional genomics. The results confirm previously reported trends for modern elite compared to historical hybrids, where grain yields have increased as a result of superior tolerance to higher plant densities, greater harvest index, and reductions in grain protein concentration. In addition, we demonstrate that past breeding has likely optimized N uptake for high grain yields, but that significant opportunities exist to further improve how maize plants utilize acquired N. We developed a phenotyping approach that estimates N utilization as the ratio of total biomass relative to total plant N, which effectively controls for the significant impacts of N-level, relative maturity, and heterosis on this trait. Using this measure of total N utilization, we identified the allelic genotypes associated with enhanced N utilization in the IBM population at nine previously identified potential NUE Quantitative Trait Loci (QTL). Selection of IBM lines showing maximum enrichment of high NUE associated alleles at the potential QTLs shifted the population mean for NUE in some environments. Coupled with lines selected for minimum enrichment at the same locations, these enriched lines capture the diversity in the original population with minimal field space and phenotyping providing a new strategy for future trait assessment.

## POSTER 12

### QUANTITATIVE TRAIT LOCUS (QTL) MAPPING OF HEAT STRESS TOLERANCE AND YIELD COMPONENTS IN *CAMELINA SATIVA*

\*Brian Campbell, Pat Byrne, Jerry Johnson, Arathi Seshadri, and Scott Reid, Colorado State University Department of Soil and Crop Sciences

*Camelina* (*Camelina sativa*) is a promising bioenergy crop that is low-input and drought resistant, with the potential to fill a unique niche in fallow periods of winter wheat-based cropping systems. A major barrier to ensuring consistently acceptable yields of camelina in Colorado is susceptibility to reproductive failure when high temperatures coincide with flowering or grain-fill periods of its life cycle. The primary goal of this study is the identification of novel heat stress tolerance alleles in a camelina recombinant inbred lines (RIL) population, comprised of 188 lines. Alleles will be identified using a quantitative trait locus (QTL) study, across multiple environments. These environments include a Conviron E15 growth chamber where heat stress is induced during flowering, as well as replicated field trials at two locations in Colorado (Fort Collins and Greeley). Both field trials were planted approximately four weeks later than a typical planting date to increase the chance of significant heat stress during flowering. The field trials also utilize irrigated and dryland treatments to separate the effects of drought stress from heat stress. Analysis of phenotypic data will identify heat tolerant and susceptible lines within the population, as well as significant correlations among traits. QTL for heat stress tolerance and yield/yield components will be identified and mapped using RQTL and WinQTL Cartographer to compare phenotypic data to genotypic data from a single nucleotide polymorphism (SNP) marker generated genetic map. This genetic map is a significant improvement over the original map for this population and was recently completed (2014) by Agriculture and Agri-Food Canada (AAFC) scientist, Dr. Isobel Parkin. Preliminary results from the growth chamber experiment have been promising, with the population exhibiting a range of responses to the heat stress treatment. The field trials will be completed by the end of August 2014 and will provide more comprehensive data for QTL discovery. The phenotypic analysis of this experiment will identify lines with potential for immediate production in Colorado, while the genotypic analysis will serve as a broader resource for improvement of camelina cultivars via molecular marker-assisted selection. In addition, this research will help to elucidate the genetic mechanisms responsible for heat tolerance/susceptibility in camelina.

## POSTER 13

### CLONING OF SOYBEAN CHLOROPHYLL DEFICIENT MUTANTS REVEALS IDENTICAL SUBSTITUTIONS IN UNLINKED MAGNESIUM CHELATASE PARALOGS

\*Benjamin W. Campbell, Dhananjay Mani, Shaun J. Curtin, Phil Schaus, Jean-Michel Michno, James H. Orf, and Robert M. Stupar, University of Minnesota Department of Agronomy and Plant Genetics; Rebecca Slattery, University of Illinois Department of Plant Biology; Donald R. Ort, Photosynthesis Research Unit U.S. Department of Agriculture/Agricultural Research Service at the University of Illinois; and Reid G. Palmer, Iowa State University Department of Agronomy

The soybean (*Glycine max* (L.) Merr.) chlorophyll deficient line MinnGold is a spontaneous mutant characterized by yellow foliage. Two populations were developed to fine map the causative mutation to a 165.3-kb interval on chromosome 13. Sequencing of a Mg-chelatase subunit candidate gene (ChlI1a) identified a non-synonymous single nucleotide polymorphism (SNP) in the third exon. Mapping of the chlorophyll deficient mutation T219H (*YIIyII*) to chromosome 13 suggested that the mutants could be allelic, though the phenotypes of the MinnGold and T219H (*YIIyII*) are clearly distinct. Sequencing of ChlI1a in *yII* identified a different non-synonymous mutation in the third exon. Whole plant transformation of MinnGold with a genomic clone of the wild-type allele fully rescued the wild-type phenotype. The genetic position of CD-5, another chlorophyll deficient mutant, was previously mapped to chromosome 15, where a ChlI1a paralog resides. Sequencing of this paralog, ChlI1b, identified a non-synonymous SNP in the third exon. Analysis of progeny segregating for the MinnGold, T219H, and CD-5 phenotypes confirmed perfect co-segregation of the chlorophyll deficiency phenotypes and their respective candidate SNPs. Protein sequence alignments of the two Mg-chelatase subunits indicated that the sites of amino acid modification in MinnGold, T219H, and CD-5 are highly conserved among photosynthetic species. Collectively, these findings indicate that the MinnGold, T219H, and CD-5 phenotypes are caused by spontaneous non-synonymous mutations in the coding regions of the Mg-chelatase subunit genes ChlI1a and ChlI1b. The negative interactions between the mutant and wild-type ChlI1a and ChlI1b proteins provide evidence for constrained sequence evolution in soybean paralogs. To our knowledge, this is the first study to report the cloning and validation of chlorophyll deficiency loci in soybean.

## POSTER 14

### ESTABLISHING GENOME-WIDE SELECTION FOR *VACCINIUM CORYBOSUM*

\*Catherine Cellon, James Olmstead, University of Florida Department of Horticultural Sciences; Rodrigo Amadeu, Patricio Munoz, University of Florida Department of Agronomy

Blueberry consumption has dramatically increased over the past decade. With the growth of this industry there is a need to effectively select for varieties to meet this rising demand and expand available production areas. Florida has a niche market for fresh berries due to the ability to produce fruit in March and April. The current breeding program at the University of Florida is based on phenotypic recurrent selection, which is a lengthy process and typically takes about 10 to 15 years to produce a new cultivar. Genome-wide selection (GWS) has been used with great success in animal and crop breeding to shorten the selection time. GWS is typically accomplished using BLUP models to predict breeding values for parent and individuals. However these models assume disomic inheritance, while cultivated blueberry species are autopolyploid. These species experience the phenomena of double reduction, which distorts allele segregation and leads to an inaccurate calculation of the BLUP models. The objective of this study is to estimate the proportion of double reduction that occurs in *V. corybosum* by collecting phenotypic information for eight key selection traits, estimate heritability for these traits, and obtain accurate BLUP models for breeding values. A training population consisting of 2,000 pedigree-linked seedlings was established in 2012. A phenotyping pipeline was developed to efficiently analyze the eight selection traits (yield, stem scar area and diameter, and the fruit characteristics of weight, diameter, firmness, color, and sugar content). Because the amount of double reduction is unknown, values from 0 to 0.25 will be used to fit the model to compare maximum likelihood for each trait. The heritability and breeding values obtained from this study will allow for genome-wide prediction to be used in the blueberry breeding program to accelerate genetic gain and shorten the selection cycle.

## POSTER 15

### MAPPING DROUGHT AND HEAT ADAPTATION QTL ANALYSIS USING NEXT-GENERATION GENOTYPING AND PHENOTYPING

\*Jared Crain, Kansas State University Interdepartmental Genetics Program;  
Matthew Reynolds, International Maize and Wheat Improvement Center (CIMMYT);  
and Jesse Poland, Kansas State University Wheat Genetics Resource Center  
Department of Plant Pathology

Nearly 30% of the world's wheat producing areas are subject to drought and heat stress. With compounding effect of climate change, new cultivars that can withstand higher temperatures and drought are needed. We investigated two RIL populations that were developed from contrasting parents for heat and drought tolerance physiology. Selection resulted in RIL's that did not have more than a 10 day range in anthesis, showed no GxE interaction in flowering time under different environments, and were not contrasting for known *Ppd* or *Vrn* markers. During the 2013 and 2014 crop cycle, the populations were planted with two replications in both heat and drought stressed environments at the International Maize and Wheat Improvement Center, Ciudad Obregon, Mexico. Plot yield, heading, flowering time were recorded during the season. Additionally, high-throughput phenotyping was completed with a sensor, which integrated normalized difference vegetative index, canopy temperature, and geo-referenced location. We collected these parameters because of their known relationship to crop yield. Phenotypic measurements using the integrated sensor were taken throughout the growing season with each measurement day corresponding to more than 10,000 data points per population. DNA was extracted from the RIL's, and genotyping-by-sequencing was used for single nucleotide polymorphism discovery and QTL mapping.

## POSTER 16

### VALIDATION OF QUANTITATIVE TRAIT LOCI FOR QUALITY TRAITS IN WHEAT

\*Hung Dao, Scott Reid, and Patrick Byrne, Colorado State University  
Department of Soil and Crop Science

Wheat end use quality can be characterized by several quality parameters, including grain protein content, grain ash content, test weight, flour color, and kernel diameter, hardness, and weight. A previous QTL study the Byrne lab for wheat quality traits in the Platte x CO940610 doubled haploid population detected many QTL for quality traits (Crop Science 2013, 53:1953-1967). Among these, three QTL of interest were located on chromosomes 1B, 6B, and 7B. Each of these three chromosomal regions showed a cluster of co-located QTL for various quality traits. Thus, the objective of my research was to validate the selected QTL of interest, based on the same parental lines (Platte and CO940610), but in recombinant inbred line (RIL) and backcross (BC) populations. The population of 186 F<sub>5</sub>-derived RILs was grown in Akron, CO rainfed environment and Greeley, CO irrigated environment. Thirty-seven backcross populations were grown in three environments: Fort Collins fully irrigated, Greeley fully irrigated, and Greeley dry. The quality traits were measured using near-infrared spectroscopy and the Single Kernel Characterization System. The study's results showed that some of the significant marker-trait associations were consistent with the results of the doubled haploid population study. Surprisingly, however, the markers associated with grain protein content were unstable across environments. These results partially confirm the previously detected QTL and provide clues for finding candidate gene(s) underlying the QTL regions associated with wheat end use quality traits.

POSTER 17  
DIALLEL ANALYSIS OF BIOMASS YIELD IN LEAVES VERSUS STEMS OF LOWLAND  
SWITCHGRASS

\*Alexandria DeSantis, Virginia Sykes, and Fred Allen, University of Tennessee  
Department of Plant Sciences

Switchgrass (*Panicum virgatum* L.) is an important forage crop and potentially a biofuel crop. Breeding for certain traits is important to optimize ethanol production for use in biofuel. Examining the biomass yield from the stems versus leaves may help with breeding selection. The objectives of this research are i) Obtain the biomass yield from leaves vs. stem in a 5x5 parent diallel, and ii) determine general specific combining ability (GCA) and specific combining ability (SCA) for leaf:stem ratio in a 5x5 parent diallel. 'Alamo' selections (A1 and T1), Kanlow selections (K2 and K3), and Miami (M) were crossed in a complete diallel. Progeny of these crosses were clonally divided and planted (1m centers) in space planted nurseries in Knoxville, TN and Crossville, TN. Nurseries were planted in randomized complete block design with twenty replications of each cross and eight clonal replications of each parent. In fall, heights of individual plants were recorded and the plants were harvested for biomass yield. Subsamples of plants from each plot were separated into leaves and stems, ground, and analyzed using NIRS to predict ethanol yield from leaves vs. stems. At both locations the cross 'T1 x K3' had the highest overall biomass yield (160g in Crossville and 222g in Knoxville). In Crossville, cross 'M x K3' had the largest leaf:stem ratio (3.86). In Knoxville, 'M x A1' had the largest leaf:stem ratio (5.28). Crosses differed in biomass yield, but did not differ in leaf:stem ratio. Location had an effect on the performance of crosses for leaf to plant ratio ( $p < 0.05$ ). However, block by location showed no effect on the performance of crosses for leaf to plant ratio ( $p > 0.05$ ). The highest GCA value obtained for the parents was M, Miami, (0.06410), and the lowest was T1, an Alamo selection (-0.006). The highest SCA value for leaf to plant ratio in crosses was 'M x K3' (0.049), and the lowest SCA value was for 'K3 x K2' (-0.008). Data will be collected on the 3 year old plants at both locations in 2014.



## POSTER 18

### GENOME-WIDE CHARACTERIZATION OF EXOTIC ALLELES FOR INCREASED YIELD FROM PRIMARY SYNTHETICS

\*Sandra M. Dunckel, Kansas State University Interdepartmental Genetics; David G. Bonnett, CIMMYT; and Jesse A. Poland, Kansas State University Department of Plant Pathology

To address the loss of genetic diversity due to domestication and breeding, exotic alleles from bread wheat progenitors *Triticum dicoccum* and *Aegilops tauschii* have been captured in primary synthetic bread wheat lines developed by CIMMYT. The primary synthetics carry resistance and tolerance to a range of biotic and abiotic stresses. Selected lines from double haploid (DH) and recombinant inbred line (RIL) populations between the elite CIMMYT cultivar Opata and six different primary synthetics were evaluated for grain yield, agronomic, and physiological measurements. Field trials were conducted at CIMMYT, Cd. Obregon, Mexico over several years in full-irrigation, heat, and drought stress environments. Several synthetic derived lines outperformed the elite parent Opata under irrigated, heat and drought-stressed conditions. This indicates that the primary synthetics contribute alleles increasing yield. Whole genome profiles were generated using genotyping-by-sequencing (GBS) to identify yield promoting genomic regions inherited from the primary synthetics. Applying genomic selection (GS), valuable alleles are rapidly introgressed and high-yielding breeding lines developed. Testing of multiple types of synthetic derivatives will provide rigorous validation of identified alleles and predictive power of our GS models. This pioneering study takes a whole-genome approach to characterize, improve and utilize exotic germplasm to increase yield.

## POSTER 19

### GENETIC ANALYSIS AND MOLECULAR MAPPING OF PIGMENT ACCUMULATION IN CARROT (*DAUCUS CAROTA* L.)

\*Shelby Ellison, Massimo Iorizzo University of Wisconsin-Madison Department of Horticulture;  
Philipp Simon, Douglas Senalik USDA Vegetable Crops Research Unit

Carotenoids are pigments ranging from yellow (lutein) to orange (alpha- and beta-carotene) to red (lycopene) that absorb short-wavelength visible light. In the plant, carotenoid pigments support light collection, photoprotection, strigolactone production and lead to the biosynthesis of abscisic acid. Humans utilize carotenoids, particularly beta-carotene, as a provitamin A precursor that is critical to eye health and also to regulate the immune system by helping white blood cells fight infections. Further, lycopene has been associated with a lowered risk of prostate cancer in men and a reduction of heart disease, while lutein can cause a significant reduction in the risk for cataract and age-related macular degeneration. Orange carrot (*Daucus carota* L.) is one of the richest sources of naturally occurring beta-carotene while red and yellow carrot varieties contain large quantities of lycopene and lutein, respectively. Until recently, understanding the regulation and accumulation of carotenoids in carrot was limited by the amount of genomic resources available. We have taken advantage of the carrot genome draft assembly and Genotyping-by-Sequencing (GBS) to develop genome-wide markers in various carrot mapping populations that segregate for beta-carotene, lycopene, and lutein accumulation. Phenotypic data for each pigment was collected using High Performance Liquid Chromatography (HPLC). GBS SNPs were identified and used in an association analysis (MLM) in the TASSEL application. We have identified well-defined genomic regions on Chromosome 1 (lycopene), 3 (lycopene), 5 (lutein) and 7 (beta-carotene) that are significantly associated with carotenoid accumulation. Fine-mapping, expression analysis, and functional assays are currently underway to further characterize and verify the genetic control of carotenoids in carrot. Increased understanding of the genetic regulation of carotenoids will help breeders improve existing carrot varieties by enhancing their health promoting properties.

## POSTER 20

### SUPPRESSION OF DIVERSE RYE SECALINS BY RNA INTERFERENCE IN WHEAT GENETIC BACKGROUNDS

\*Juthamas Fakthongphan, P. Stephen Baenziger, University of Nebraska Department of Agronomy and Horticulture; Robert Graybosch, USDA-ARS Lincoln NE; and Ann Blechl, USDA-ARS Albany CA

RNA interference (RNAi) allows targeted silencing of genes of interest for both basic and practical purposes. In primary transgenic lines, an RNAi construct was used to silence genes encoding rye (*Secale cereale* L.) seed storage proteins, secalins, present in wheat genetic backgrounds. Genes encoding secalins found on the long and short arms of rye chromosome 1R have been transferred by breeders to wheat cultivars to exploit favorable genes for disease and abiotic stress tolerance. Breeding programs world-wide have developed cultivars carrying rye chromatin, most often in the forms of wheat-rye 1AL.1RS or 1BL.1RS chromosomal translocations. Unfortunately, the presence of secalin-encoding genes on these same chromosome arms may contribute to negative bread-making and other end-use quality defects of 1RS wheats. To determine whether RNAi induced silencing would be useful in silencing secalins in diverse genetic backgrounds, inheritance studies were conducted. A primary transformant of the 1BL.1RS cultivar 'Bobwhite', designated L26-20 was previously found to have drastically reduced secalin production in the endosperm. This line was crossed to: 1) the 1R(1B) substitution line, PI 598314; 2) a 1BL.1RS translocation line, SD05W030; 3) a 1AL.1RS translocation line, 'TAM-107'; 4) a non-rye containing wheat control, 'Wesley'. Effects on secalin production were observed via SDS-PAGE separation of 70% ethanol soluble flour proteins, with a system optimized to detect the  $\omega$ -secalins arising from the *Sec-1* locus on 1RS. In the F<sub>1</sub> seed examined, secalins were either absent or dramatically reduced. In the F<sub>2</sub> generation of all crosses, three secalin phenotypes were observed: present, absent, and reduced. Results demonstrated that RNAi can suppress secalin synthesis in primary transformed lines, that the transgene can suppress secalins arising from different translocation lines, and that effective RNAi constructs, once stabilized, may be transferred to subsequent generations via traditional crossing and selfing approaches.

## POSTER 21

### HAPLOTYPE ANALYSIS OF NITROGEN USE EFFICIENCY IN ELITE BARLEY GERMPLASM

\*Celeste Falcon and Kevin Smith, University of Minnesota

Many genome-wide association studies have utilized single nucleotide polymorphism (SNP) markers for identifying genotype-phenotype associations. However, another approach is to group SNP markers into haplotype blocks and then test these for associations with phenotypes. Depending on the population, marker density, and phenotypic trait at hand, haplotype analyses provide various advantages that may improve the power and accuracy of association mapping (AM). We evaluated nitrogen use efficiency related traits in an AM panel consisting of 256 spring six-row barley (*Hordeum vulgare*) lines representing five breeding programs. Nitrogen use efficiency is an important trait in small grain production which is particularly constrained by nitrogen availability. The panel was genotyped with 3,072 SNP markers and grown under nitrogen-limiting and non-limiting treatments in three experiments Minnesota and North Dakota in 2011 and 2012. Our objectives were to 1) compare different methods of haplotype analysis with single SNP marker analysis and 2) identify haplotype classes which differ in their trait means. Association mapping using single markers was compared with AM using two different kinds of haplotypes: 1) haplotypes created in Haploview based on recombination and 2) haplotypes created by a sliding window approach. Results of these analyses will be presented.

## POSTER 22

### EVALUATION OF EARLY SELECTION ON PERENNIAL TROPICAL FORAGES

\*Ulisses Jose De Figueiredo, Jose Ailton Rodrigues Nunes, Federal University of Lavras  
Department of Biology; Cacilda Borges Do Valle, Embrapa Beef Cattle; and Patricio Munoz,  
University of Florida Department of Agronomy

Brazilian livestock production relies almost completely on tropical pasture systems. The perennial grass of the genus *Brachiaria* is one of the most prevalent in these systems. Currently, new cultivars of these grasses are evaluated for at least two years over multiple harvests before selection, an expensive and time consuming process. Nevertheless, early selection has the potential to accelerate this process and make it more efficient. The objective of this study was to evaluate early selection of cultivars in early evaluation (screening) and advanced evaluation (elite) stage on the breeding process. Data from a screening evaluation stage (Trial 1) and from two elite evaluation stages (Trial 2 and 3) were used to evaluate early selection. Trial 1, had 52 genotypes of *Brachiaria humidicola*, located in Campo Grande in a randomized complete block design (RCBD) with eight blocks and a plot size of 2 m<sup>2</sup>. Trial 1 was harvest five times during the first year and four times during the second year. Trials 2 and 3, both contained the same eight elite genotypes of *Brachiaria* ssp., in RCBDs with four blocks each and plots of 4.0 m<sup>2</sup>. Trial 2 was located in Campo Grande and Trial 3 in Terenos. Plots in these trials were harvested eight times each of the two years evaluated. Traits measured in all experiments were total dry matter (TDM), percentage of leaf blades (%L), leaf dry matter (LDM) and regrowth capacity (RC). A linear mixed model was fitted for pairs of harvests in the software ASReml and used to estimate genotype by harvest (GxH) interaction. Likelihood ratio test (LRT) was used to test the significance of GxH in each pair combination. A mixed model considering the cumulative harvests was fitted for harvests 2 through 9 for Trial 1, and 2 through 16 for Trials 2 and 3. Repeatability was estimated using the replicate by genotype as the permanent effect. The GxH interaction effect was significant for almost all analysis combinations for all traits evaluated (LRT at P<0.01). The significant interaction of genotype-by-harvest indicated that significant changes in genotype ranking occurs between harvests and that cumulative analyses that consider more than one harvest are needed to reach high accuracy of selection. The coefficient of repeatability varied depending on the number of harvests considered and the trait being analyzed. However, for Trial 1 the repeatability analysis indicates that TDM, LDM and %L can be selected as early as seven harvests, while eight are needed for RC. In the case of the elite trials the repeatability analysis indicates that TDM, LDM and RC can be selected as early as eight harvests, while seven are needed for %L. For the screening trial, our results indicate that the shortest reliable selection period is 1.5 years. However, our results support that a reliable early selection (1 year) is possible for elite variety trials. This difference in potential early selection may be due to the large number of genotypes with high variability in the screening trial. These results indicate that for evaluation of elite cultivars a second year of harvesting does not contribute to define the top selections for the next cycle. We are compiling more experiments using these and other species to confirm the current results. As the number of varieties decrease with the process of selection of a cultivar, early selection in each stage after screening can save considerable time, effort, and resources.

## POSTER 23

## MUTATION BREEDING IN HOP

B. Getty, \*A. Fricker, S. Townsend, B. Reed, and J. Henning, Oregon State University Department of Crop and Soil Sciences and USDA-ARS Corvallis Oregon

Hop is a perennial herbaceous plant in which the female inflorescence (cone) is used by brewers to impart bitterness, flavor, and aroma to beer. The chemical profile of a hop cone is quite complex, and the mechanisms by which hops impart flavor and aroma to beer are not fully understood.

Furthermore, hop production is a relatively expensive endeavor due to the considerable infrastructure and hand-labor involved. For these reasons, aroma hop variety development is quite challenging and partially explains the continued popularity of several aroma hop cultivars that are more than 60 years old. Mutation breeding offers the potential to introduce subtle but meaningful changes to the chemical profile or agronomic properties of currently accepted cultivars. The objective of this work was to evaluate hop survival to various amounts of gamma radiation. Nodal sections and shoot tips were excised from micropropagated 'Cascade' hops and placed onto sterile MS media in 20 cm plastic petri dishes. Dishes containing plant material were irradiated at 0.5, 1.0, 2.0, 3.0, 4.0 and 5.0 Krad doses of gamma radiation, placed in a low light room, and evaluated 1 month later for survival. Surviving plant sections were rooted, transferred to greenhouse media for establishment, and planted in a field nursery for phenotypic observation. No shoot tip or nodal sections survived the 2.0, 3.0, 4.0, or 5.0 Krad treatments. Three plants were regenerated from the 1.0 Krad treatment while 59 plants were recovered from the 0.5 treatment (25% survival).

Surviving plants are establishing in a field nursery near Corvallis, Oregon for phenotyping and DNA sequencing. Results from this work suggest that 0.5 Krad of gamma radiation or less may be optimum for inducing random genetic variation in Cascade hop. Additional work is planned to establish the optimum gamma radiation dose on a number of hop cultivars.

## POSTER 24

### FINE MAPPING OF ONE SELF-INCOMPATIBILITY LOCUS IN *MISCANTHUS SINENSIS*

\*Justin M. Gifford and John A. Juvik, University of Illinois at Urbana-Champaign  
Department of Crop Sciences

Despite the worldwide importance of the grass family, little is known about the self-incompatibility mechanisms operating within many of the grass species. Researchers have identified two unlinked loci, S and Z, controlling the phenomenon, but the genes underlying these loci have remained elusive. With the recent emphasis on bioenergy crops, many perennial grass species have been evaluated as biofeedstock candidates, and interest in identifying the genes responsible for self-incompatibility has been renewed. One such genus of grasses that has shown promise as a potential biofeedstock is *Miscanthus*, a native of southeastern Asia. The genus is of particular interest as an energy crop due to its high yields and longevity, C<sub>4</sub> photosynthetic pathway, and its adaptation to temperate environments. *Miscanthus* is an obligate outcrossing genus that recently underwent a whole genome duplication event. Both of these factors complicate the genetic dissection of traits pertinent to biomass production and a breeder's ability to maximize heterosis. Attempts to create double haploids within the *Miscanthus* genus have been met with very limited success. An alternative to double haploids would be the creation of inbred materials through the manipulation of self-incompatibility loci. In order to do so, these loci must first be mapped. In this study, we utilized a pseudo F1 mapping population consisting of 221 individuals segregating for a single incompatibility locus. Individuals in the mapping population were placed into four incompatibility groups based on pollen tube growth. If none of the pollen from one individual was compatible with another plant's stigma, then the plants were classified into the same incompatibility group. The group number of each individual was then used as the phenotype for QTL mapping. A single peak was observed on chromosome 15. The synteny between *Miscanthus* and sorghum was then used to identify potential gene candidates.

## POSTER 25

### IDENTIFYING BLUEBERRY CONSUMER PREFERENCES

\*Jessica L. Gilbert, Thomas A. Colquhoun, Laura A. Levin, Howard R. Moskowitz,  
Eric Q. Dreyer, Charles A. Sims, David G. Clark, and James W. Olmstead,  
University of Florida Plant Innovation Program

Blueberries are high-value fruit that have experienced extraordinary growth in consumption in the past decade. Maintaining this growing market requires an understanding of the current market and its potential for expansion. In a psychophysical study conducted to identify consumer blueberry preferences, subjects responded with the most positive purchase interest to blueberries described as sweet and with intense blueberry flavor. Descriptors of negative texture attributes such as seediness were the most detrimental to interest. In an attempt to identify specific biochemical breeding targets to define the intangible “blueberry flavor,” the University of Florida southern highbush blueberry (SHB, *Vaccinium corymbosum* L. hybrids) breeding program has employed consumer-assisted selection by implementing the use of large consumer sensory panels in conjunction with biochemical profiling. Over the course of three years, nineteen SHB varieties were evaluated in thirty sensory panels (N=72 to 109, average=92). Panelists rated overall liking, texture, sweetness, sourness, and flavor intensity using hedonic general Labeled Magnitude Scales (gLMS) (-100 to +100; -100=worst sensation of any kind, +100=best sensation of any kind) and intensity gLMS (0,+100; 0=no sensation, 100=most intense sensation of any kind), which allow for improved comparison between panelists and between years. Panelists were also asked to rate the intensity of taste and flavor sensations of a hypothetical ideal blueberry. Perceived sensory parameters, texture ( $R^2=0.56$ ), sweetness intensity ( $R^2=0.49$ ), and blueberry flavor intensity ( $R^2=0.46$ ), had a significant positive relationship with the panelists’ overall liking a blueberry sample ( $P<0.001$ ). Panelists’ average ratings of actual sweetness and flavor intensity of all nineteen blueberry varieties sampled fell short of the averaged ideal values (23 vs. 42, 26 vs. 43, respectively). However, actual and ideal blueberry sourness were in agreement (16). When ideal berry sweetness, sourness, and flavor intensity were subjected to cluster analysis, four distinct preference profiles were discovered. These studies suggest that breeders and producers should exploit trait variation between cultivars to market different qualities to different groups of consumers.



## POSTER 26

### DOUBLE-CROSS BASED MAPPING TO DETECT QTLS FOR BACTERIAL LEAF STREAK RESISTANCE IN SPRING WHEAT

\*Rosa Guerrero-Chavez, Karl Glover, and Jose Gonzalez. South Dakota State University  
Plant Science Department

*Xanthomonas campestris* pv *translucens*, the causal agent of Bacterial Leaf Streak (BLS) in wheat produces yellow longitudinal leaf streaks which reduces photosynthesis and therefore grain yield. Seed treatment and chemical applications in field have not been effective in controlling the disease. Low test weight and yield losses of up to 35% have been reported. Deploying resistant varieties is considered the best approach in controlling BLS. Accordingly, the objective of this project was to use a double-cross mapping population to detect QTLs for BLS resistance. Doubled-haploid (DH) lines derived from a four-way cross were developed, their DNA was extracted, amplified, and subjected to a 9K SNP array. Doubled-haploid lines were evaluated for BLS resistance in two locations and three replications in summer 2013. Bacterial inoculation with isolate XctSD-17 at  $6 \times 10^8$  CFU ml<sup>-1</sup> was carried out at the tillering stage. Severity and height of disease on the canopy were rated four times at seven day intervals starting at heading. Percent Disease Severity (PDS) and Area Under Disease Progress Curve (AUDPC) were calculated. Effects of the DH lines and their interaction with locations were highly significant. Correlations between PDS and AUDPC as well as days to heading were highly significant. A linear regression of the disease severity over time explained 60% of the variation. Doubled-haploid lines with lower AUDPC than the resistant parent (SD4205) were observed. As part of the ongoing work, SNP data is being analyzed in order to detect the QTLs that confer resistance to BLS.

## POSTER 27

### MAPPING INCREASED YIELD AND IMPROVED CANOPY WATER STATUS TO A REGION OF A RYE CHROMOSOME ARM INTROGRESSION IN COMMON WHEAT

\*Tyson Howell, University of California Davis Department of Plant Sciences; Iago Hale, University of New Hampshire Durham Department of Biological Sciences; Ljupcho Jankuloski, Faculty of Agricultural Sciences and Food Skopje Macedonia Department of Genetics and Plant Breeding; Marco Bonafede, Instituto de Recursos Biológicos CIRN Instituto Nacional de Tecnología Agropecuaria (INTA); and Jorge Dubcovsky, University of California-Davis Department of Plant Sciences and Howard Hughes Medical Institute

Wheat is an important food staple, estimated to account for approximately 20% of all human food calories consumed worldwide. Increases in wheat yields are required to accommodate increasing food demand caused by the rapidly growing human population. One potential source for that improvement is the introgression of alien chromosomes, in particular the translocation of the short arm of rye (*Secale cereal* L.) chromosome one (1RS) into common wheat (*Triticum aestivum* L.) on chromosome 1B (1RS·1BL). The 1RS translocation is used in wheat breeding programs worldwide due to its positive effect on yield, particularly under abiotic stress, but is associated with negative bread making quality. To eliminate the negative effects of this translocation on bread making quality a derived 1RS line carrying proximal (<sup>P</sup>) and a distal (<sup>D</sup>) interstitial wheat segments (henceforth, 1RS<sup>WDP</sup>) was previously developed. In this study, we developed and evaluated two sets of 1RS/1RS<sup>WDP</sup> near isogenic lines (NILs). Field trials in multiple locations over multiple years showed that 1RS lines have significantly higher yield, better canopy water status, and higher carbon isotope discrimination (CID) than the 1RS<sup>WDP</sup> NIL in both well watered and water-stressed environments, indicating that one or both of the introgressed wheat regions are responsible for the difference in performance. We intercrossed the NILs from one of the genetic backgrounds and generated two additional NILs, carrying either the distal (1RS<sup>WD</sup>) or the proximal (1RS<sup>WP</sup>) wheat segment. Field trials showed significantly higher yields, better canopy water status and CID in the lines carrying the distal 1RS region (1RS and 1RS<sup>WP</sup>) than in the NILs carrying the distal wheat segment (1RS<sup>WPD</sup> and 1RS<sup>WD</sup>). We conclude that the distal 1RS region carries the beneficial allele(s) for wheat grain yield, canopy water status and CID.

## POSTER 28

### UNDERSTANDING RESISTANCE TO DOWNY MILDEW IN IMPATIENS

\*James Keach, Cornell University Department of Plant Breeding; Margery Daughtrey, Cornell University Department of Plant Pathology; and Mark P. Bridgen, Cornell University Department of Horticulture

Impatiens are one of the most popular annual bedding plants and have traditionally been an important source of early season income for many American greenhouse growers. Unfortunately, in 2004 impatiens downy mildew *Plasmopara obducens* started interfering with U.S. greenhouse production of the most common impatiens species: *Impatiens walleriana*. Since 2011 the pathogen has been disseminated and become a significant problem in the landscape. This disease results in wilting, leaf and flower drop and ultimately death of this important bedding plant and other existing hybrids that include *I. walleriana*. As the genus contains over one thousand described species, an investigation has begun into how universal susceptibility to this disease is, and whether factors correlated to resistance can be identified. Reports on the disease have already recognized that New Guinea impatiens, *I. hawkeri*, exhibit a high degree of resistance. However previous research has also shown that *I. hawkeri* is cross-incompatible with *I. walleriana*, limiting its use in resistance introgression. Approximately one hundred impatiens species have been acquired and are being screened for resistance to the pathogen. In addition to field trials, an *in vitro* assay is being developed. The two methods will be analyzed to ensure that the *in vitro* results are predictive of infection in the landscape. The screening work is being complemented with explorations into factors that might contribute to resistance, including relatedness, geographical range, and biochemical differences. A range of plant breeding techniques are also being utilized in order to transfer resistance from identified putative resistant species into *I. walleriana*.

## POSTER 29

### DEVELOPMENT OF SCREENING METHODOLOGIES FOR COLD ACCLIMATION AND FREEZING TOLERANCE ASSESSMENT IN ST. AUGUSTINEGRASS

\*Jennifer A. Kimball, Susana R. Milla-Lewis, North Carolina State University Department of Crop Science; Tan D. Tuong, David P. Livingston III, USDA and North Carolina State University Department of Crop Science,

Winter survivability is a major limiting-factor in the production and widespread use of St. Augustinegrass (*Stenotaphrum secundatum* [Walt.] Kuntze) as turf in the transition zone of the United States. A freezing protocol that accurately depicts a large range of freezing tolerances found in St. Augustinegrass would be advantageous, especially for diversity assessments as well as for screening segregating populations and nurseries, and would offer an expedited, less expensive alternative to field evaluations. Therefore, the main objectives of this study were to i) evaluate the responses of nine St. Augustinegrass cultivars to four different freezing temperatures, ii) identify a reliable way to visually evaluate the survivability and recovery of St. Augustinegrass plants post freezing, and iii) validate our visual rating system using digital analysis and node counts. Four different freezing temperatures and two acclimation treatments were evaluated. Digital imaging, node counts, and visual ratings were used to evaluate stress and recovery of genotypes for six weeks after freezing. Freezing injury and recovery varied between temperatures. Genotypes 'Raleigh', and '106SVT3' survived the coldest temperatures at -5 and -6°C, while cold-susceptible genotypes 'Sunclipse', 'Captiva', 'Sapphire', and 'Floritam' still had low survival at the warmest temperature tested (-3°C). Genotypes killed at the lowest freezing test temperatures tended to not recover, while genotypes recovered more rapidly and to a greater extent at the highest freezing temperature tested. The results indicate that -3°C or -4°C would be the best temperature to evaluate a large range of freezing tolerances in St. Augustinegrass. Survivability in the genotypes tested agreed with previous field based studies as well as with digital analysis and node counts, indicating that our visual rating system was adequate for controlled freezing tests. Controlled freezing tests, using regrowth as a measure of hardiness, appear to be useful for evaluating freezing temperature tolerance of St. Augustinegrass.

## POSTER 30

### WHOLE GENOME PREDICTION OF GRAIN YIELD AND GRAIN PROTEIN CONCENTRATION IN HARD WINTER WHEAT

\*Susan Latshaw, Eric Storlie, Harish Manmathan, and Scott D. Haley, Colorado State University  
Soil and Crop Sciences Department

Wheat producers maximize net returns per acre with high yielding wheat varieties, while wheat end-use quality is conditioned by adequate grain protein concentration. These traits are commonly negatively related, confounding breeder selections to combine both high yields and high protein concentration. Phenotypic selection for either trait is resource intensive, requiring several years of data from multi-environment trials. Genomic selection may increase the rate of genetic gain for quantitative traits by enabling selection before obtaining phenotypes or by increasing the accuracy of selection. Genomic selection utilizes whole genome SNP marker data to generate marker effects estimates, relying on the assumption of all QTL being in linkage disequilibrium with markers. The goal of this study was to model genome wide SNP marker effects to enable genomic selection for grain yield (GY) and grain protein concentration (PROT). Additionally, marker effects were modeled for grain protein deviation (GPD), the squared deviations from the inverse relationship between yield and protein, in order to evaluate the efficacy of this trait for simultaneous selection for GY and PROT.

We report on the accuracy of 10-fold cross validation for genomic estimated breeding value prediction within a genomic selection model training population (N=398) and for accuracy of prediction of a population of doubled haploid selection candidates (N=231). The model training population consists of hard winter wheat breeding lines from the CSU Hard Winter Wheat Breeding Program and 23 released varieties from CSU and other public and private programs. The validation population was composed of 231 doubled haploid breeding lines from 17 crosses. Trait values were computed as best linear unbiased predictors (BLUP) from the 2012 and the 2013 growing seasons. A genotyping-by-sequencing SNP marker matrix for the training population was applied to obtain marker effects estimates for each trait through a ridge regression linear model. Through applying a threshold of 50% missing marker data and the random forest method of imputation, 29,390 markers were retained in the matrix. Cross-validation (prediction) accuracies were 0.59 (0.32) for GY, 0.56 (0.48) for PROT, and 0.49 (0.42) for GPD. These accuracies are sufficient to warrant further optimization and eventual implementation of genomic selection in the breeding program.

## POSTER 31

### IDENTIFYING GENETIC MARKERS FOR NUTRIENT LEVELS IN POTATO

\*Anna Levina, Owen Hoekenga, and Walter De Jong, Cornell University Department of Plant Breeding and Genetics

The potato *Solanum tuberosum* is an important staple crop worldwide. Because of the significant role that potatoes play in the global diet, it is beneficial to focus potato breeding efforts on nutritional quality in addition to yield, disease resistance and agronomic traits. Potatoes can provide a wide range of nutrients such as vitamin C, folate, potassium, Vitamin B6, and selenium, as well as polyphenols, flavonoids, anthocyanins and carotenoids, all of which confer positive effects to human health. This project aims to facilitate the selection of potatoes with higher nutritional quality by developing genetic markers linked to individual, or groups of nutritionally important metabolites. To work towards this goal, this project makes use of a potato diversity panel – a collection of individuals representing a wide range of phenotypes and genotypes – containing 229 named cultivars and advanced breeding clones. This panel has previously been genotyped with 8303 SNP markers. Since potatoes are cooked before consumption, metabolite analysis will be performed on cooked samples of each clone through the use of Ultra Performance Liquid Chromatography coupled with Mass Spectrometry (UPLC-MS). Statistical analyses will then be performed, combining metabolite data with the SNP marker data, to identify genetic markers correlated with the levels of individual or correlated metabolites.

## POSTER 32

### GENOTYPE BY ENVIRONMENT INTERACTION AND EPISTASIS OF FLOWERING TIME

\*Xin Li, Jianming Yu, Iowa State University Department of Agronomy; and Tesfaye Tesso,  
Kansas State University Department of Agronomy

Flowering time is a complex trait involved in the adaptation of plants to their local environment. Flowering time in sorghum is controlled by multiple genes. To date, only three of these genes (*Ma1*, *Ma3*, and *Ma6*) have been identified. The objectives of this research are to investigate the genotype by environment ( $G \times E$ ) interaction of sorghum flowering time, and to identify the underlying genes. The experiment was carried out in three years (2011 to 2013) at three locations (Guayanilla Puerto Rico, Manhattan Kansas, and Ames Iowa). Flowering time was measured on a sorghum recombinant inbred line (RIL) population with 250 entries. This RIL population was genotyped using genotyping by sequencing (GBS). A total of 10,370 SNP markers were used for linkage map construction and QTL analysis. Genotypes of high photoperiod sensitivity flowered early in tropical region but significantly late in temperate region. Genotypes of low photoperiod sensitivity, however, flowered late in tropical region but early in temperate region. Two major QTL regulating flowering time were detected on chromosome 6 and 10 in this RIL population. The two QTL show QTL-by-QTL interaction (epistasis). The effect size and direction of each QTL depend on the status of the other QTL. A third QTL on chromosome 8 was only detected in tropical environment. This QTL likely controls flowering time by responding to the ambient temperature. This study shed light on how plants adapt to their local environments, and how epistasis plays an important role in regulating flowering time in plants.

## POSTER 33

### DISCOVERY AND ELUCIDATION OF RESISTANCE TO *XANTHOMONAS GARDNERI* IN THE *SOLANUM PIMPINELLIFOLIUM* ACCESSION LA2533

\*Debora Liabeuf, David Francis, The Ohio State University Ohio Agricultural Research and Development Center Department of Horticulture and Crop Science; Sung-Chur Sim, Sejong University Korea Department of Bioresources Engineering

Bacterial spot of tomato is caused by four *Xanthomonas* species. Recently, *X. gardneri* became a dominant component of epidemics in Brazil, the United States, and Canada. Damage in Ohio and Michigan processing tomato crop was estimated at \$7.8 M in 2009 and 2010. Few chemicals are effective against bacterial spot, thus the use of resistant varieties is an important component of the strategy to reduce disease. The objective of this study was to (1) identify sources of resistance to *X. gardneri*, (2) describe the genetic of this resistance. From a survey of 190 accessions, *Solanum pimpinellifolium* accession LA2533, was found to be resistant. It showed Hypersensitive Response (HR) and low levels of disease under field conditions. A backcross (BC) population was developed with LA2533 as donor parent and OH2641, an elite line from the Ohio breeding program, used as recurrent parent. The genetics was studied using a selective genotyping approach: The BC<sub>1</sub> generation was evaluated under inoculated field conditions and the seven most resistant and the eight most susceptible individuals were selected and self pollinated. BC<sub>1</sub>S<sub>1</sub> individuals were genotyped with 204 SNP markers, and BC<sub>1</sub>S<sub>2</sub> families were evaluated under field conditions in a randomized complete block design with two blocks. Three genomic regions were associated with resistance. Regions on chromosome 4 and 8 originated from the elite parent. Resistance on chromosome 11 originated from LA2533 and accounted for 38% of the phenotypic variation. These results are currently being used to develop breeding strategies for resistant varieties.



## POSTER 34

### COMPARISON OF MAPPING POPULATION DESIGN AND ANALYSIS OF BLUE ALEURONE IN A 4-WAY MAIZE CROSS

\*Adam L. Mahan, Seth C. Murray, Texas A&M University Department of Soil and Crop Sciences; Patricia Klein, Texas A&M University Department of Horticulture

Traditional mapping populations in maize involve the use of recombinant inbred lines (RILs) produced from a biparental cross. An increase in the number of parents, as well as the use of intermating can increase the overall recombination that occurs during the creation of the population, thus making it possible to map traits with increased resolution because markers are mapped closer to regions of interest. The use of exotic parents in combination with increased recombination will also be studied to determine if improved lines can be selected from the progeny due to the more frequent breakage of linkage blocks. To compare multiple mapping population designs, an unprecedented, 1246 line, 4-way maize population was developed. This population consists of  $F_5$  and  $F_6$  subpopulations representing biparental, and 4-way RILs, as well as 4-way RILs with 1, 2, or 3 generations of intermating. The population has been sequenced on an Illumina HiSeq platform yielding approximately 100,000 informative SNP markers. Association mapping completed thus far has accurately detected the *Y1* allele on chromosome 6 for yellow endosperm, confirming that our genotypic data is accurate and that association mapping is an effective method of analysis for populations with greater than two parents. Observed kernel colors across the population include 23% blue, 31% white, 33% yellow, and 13% segregating. The ~25% blue indicates two major genes are necessary for blue aleurone in this population and that both blue parents have both genes. Further work includes genetic map construction of the 4-way population, and genetic mapping of recombination modifiers in addition to the blue aleurone trait.

## POSTER 35

### TRITIPYRUM – A GENETIC RESOURCE FOR WATER-STRESSED ENVIRONMENTS?

\*Francois Marais, Mohamed Somo, and Seyed Mostafa Pirseyedi, North Dakota State University  
Department of Plant Sciences

First generation, hexaploid d-tritipyrums were established by combining the A- and B-genomes of tetraploid durum wheat (*Triticum turgidum* ssp durum) with a single, re-arranged J genome from the autotetraploid grass, *Thinopyrum distichum*. These hybrids ( $2n = 6x = AABBJJ$ ) have seven rearranged *Thinopyrum* chromosomes, with each individual chromosome originating from either the  $J_1^d$  or  $J_2^d$  genomes and altered through recombination with its homoeologue. First generation hybrids were crossed with a common wheat (*T. aestivum* L.)\*2/*Th. distichum* secondary amphiploid ( $2n = 8x = 56 = AABBDDJ_1^d J_2^d$ ) and the  $F_1$  backcrossed to tritipyrum so as to broaden J-genome variability. Second generation hexaploids and near-hexaploids exhibited a rich diversity of *Thinopyrum*-derived traits. Attempts are being made to characterize the material for salt tolerance, initiate mapping of the modified J-genome and improve productivity and thresh-ability. The ultimate aim is to establish an intermediate, well-adapted germplasm that can be compared more effectively to wheat for the analysis and utilization/ transfer of key physiological trait genes.

## POSTER 36

### MOLECULAR MAPPING OF DROUGHT TOLERANCE GENES IN COWPEA (*VIGNA UNGUICULATA* L. WALP)

\*Laura Masor, D. B. Hays, B.B. Singh, and H. Zhang, Texas A&M University

Cowpea (*Vigna unguiculata* L. Walp) is a leguminous crop that many people around the world rely on to meet their basic nutritional needs. Both humans and livestock consume the protein and fiber rich grain and vegetative matter of the cowpea plant. Water stress affects this crop like many other crops; by reducing total biomass and grain yields. Genotypes of cowpea have been identified that contain genes that confer tolerance to drought. In order to map the quantitative trait loci (QTL) associated with the drought tolerance traits, a recombinant inbred line population (RIL) was created from the parental genotypes IT98K-476-8 and 'Green Eye Cream' (GEC). This population was phenotypically analyzed for drought response. The genes conferring the drought tolerance are being mapped using restriction site-associated DNA sequencing (RAD-seq) and SNP markers closely linked to the genes of interest are being identified. With this knowledge of the underlying genetics regulating drought tolerance in cowpea, molecular tools can be created which will further help in the breeding of more drought tolerant species.

## POSTER 37

### BREEDING FOR ROOT LESION NEMATODE RESISTANCE IN MONTANA WINTER WHEAT

\*David May, Philip L. Bruckner, Alan T. Dyer, and James E. Berg, Montana State University-  
Bozeman Department of Plant Science and Plant Pathology; Deven R. See,  
USDA-ARS Pullman, WA

Root lesion nematodes (*Pratylenchus* spp.) present a serious challenge to dryland wheat production worldwide. Development of resistant cultivars would provide great economic benefit to growers. From 2012-2013, a set of backcross lines (MT08185//MT08184/Persia 20) was screened twice for resistance to *P. neglectus*. Progeny and parent lines were grown in infested soil for 16 weeks. Nematodes were then extracted from roots of individual plants and counted to obtain per plant final populations. ANOVA results from the 2013 screen showed significant differences in mean *P. neglectus* populations among lines ( $p < 0.01$ ). The median final population of susceptible parent MT08184 was an estimated 4.0 times greater than that of resistant parent Persia 20. A 2013 field trial in the absence of root lesion nematodes indicated reductions in grain yield, volume weight, and protein were not associated with resistance. Identification of QTL for resistance to root lesion nematodes will facilitate marker-assisted introgression of resistance genes in a backcross-breeding program. Single marker analysis of 104 genome-wide SNPs was performed to identify genomic regions associated with resistance to *P. neglectus*. The analysis identified putative marker-trait associations on chromosomes 1A, 1D, 2B, 5B, 5D, 7A and 7D (all  $p < 0.05$ ). These potential QTL regions will be tested in analysis of phenotypic and genomic data obtained from 200 BC<sub>1</sub>F<sub>3</sub> (MT08185//MT08184/Persia 20) progeny, and 228 F<sub>2</sub> progeny derived from a separate cross (Persia 20/McNeal).

## POSTER 38

### COTTON FLEAHOPPER (*PSEUDATOMOSCELIS SERIATUS*) (HEMIPTERA: MIRIDAE) DAMAGE IN *GOSSYPIMUM HIRSUTUM*: BREEDING EFFORTS TOWARDS INCREASED RESISTANCE

\*Laura Ann McLoud and Steve Hague, Texas A&M University

Cotton fleahopper (*Pseudatomoscelis seriatus*) (Hemiptera: Miridae) is a piercing-sucking insect that has emerged as a major pest in the Texas cotton industry over the past decade. Cotton fleahopper feeding results in square abscission and damage and subsequently, yield-loss. Previous studies in *Gossypium hirsutum* indicate that plant trichome density plays an important role in conferring resistance to cotton fleahopper, but the mechanism of resistance remains largely unknown. In this project, three families of lines proven to be resistant in non-choice laboratory studies and two high-yielding, but susceptible breeding lines, were evaluated for resistance to cotton fleahopper under controlled and field infestation conditions to determine gene expression and heritability of the resistance, respectively. RNA was isolated using a Spectrum™ Plant Total RNA Kit and analyzed with the Illumina Hi-Seq 2000 using 100-SE reads. The heritability of the resistance was measured with a diallel mating design. Genotypes within the three families exhibited pubescences ranging from smooth to pilose; of the high-yielding lines, one was smooth and the other hairy. Plants were screened in College Station and Corpus Christi, TX, and square-mapping was used as the primary tool by which to monitor the plants' responses to cotton fleahopper feeding pressure. Plants in the resistant families showed significantly less square loss than either of the non-resistant lines, and within those families. Our findings suggest this native trait is heritable with good efficacy versus this insect pest, with differential RNA expression when infested by the cotton fleahopper. This source of host plant resistance has the potential to replace insecticide control options and may improve resistance to other piercing-sucking insect pests.

## POSTER 39

### FLOW CYTOMETRY AND A THIOREDOXIN-LIKE GENE: USEFUL TOOLS TO IDENTIFY *POA ARACHNIFERA* X *POA PRATENSIS* INTERSPECIFIC HYBRIDS

\*Meghyn Meeks, Texas A&M University Department of Soil and Crop Sciences; and  
Ambika Chandra, Texas A&M AgriLife Research

Hybrid bluegrasses are growing in popularity in the southern United States for their visual appeal and competitive heat and drought tolerances to tall fescue. However, the phenotypic assessment of *Poa arachnifera* x *Poa pratensis* hybrids can be time consuming and sometimes unreliable. Here we demonstrate the utility of flow cytometry and the *trx* gene as useful tools in the identification of true hybrids. Replicated samples were taken from one gram of fresh plant tissue and analyzed using flow cytometry to determine diploid (2C) DNA content for each of 19 *P. arachnifera* and 4 *P. pratensis* genotypes, as well as 5 interspecific hybrids from two *P. arachnifera* x *P. pratensis* pedigrees. Flow cytometry results show that interspecific hybrids have an intermediate nuclear DNA content to each of their polyploid parents. Furthermore, we observed a wide range of nuclear DNA content within *P. arachnifera* suggesting a possible variation in the chromosome numbers in the species. Additionally, the *trx* gene was amplified through polymerase-chain-reaction in the *P. arachnifera*, *P. pratensis*, and hybrid genotypes. Sequencing and phylogenetic analyses of the *trx* alleles shows that *P. arachnifera* x *P. pratensis* hybrids inherit allele sequences from both parents. One unique 851bp allele was found to be uniformly present among 19 male and female *P. arachnifera* ecotypes as well as interspecific hybrids but completely absent in examined *P. pratensis*. Thus, the discovered 851bp allele can not only be used to prove *P. arachnifera* inheritance in hybrids, but also to distinguish *P. arachnifera* from *P. pratensis* genotypes. This allele is characterized by a 163 bp insertion within the intron region that folds to form a hairpin loop. Results of the miRBase search show sequence similarity of the hairpin loop stem structure with micro RNA from sorghum, wheat, rice, and barley, suggesting a potential role as a precursor to a micro RNA.

## POSTER 40

### ASSOCIATION ANALYSES OF LEAF RUST AND STRIPE RUST RESISTANCES IN A PANEL OF EASTERN U.S. WINTER WHEAT CULTIVARS, LANDRACES, AND BREEDING LINES

\*Keith R. Merrill, Criston T. Jarrell, J. Paul Murphy, and Jeffrey D. Prayer, North Carolina State University Department of Crop Science; Xianming Chen, Michael O. Pumphrey, Washington State University Department of Crop and Soil Sciences; Jerry W. Johnson, University of Georgia Department of Crop and Soil Sciences; James A. Kolmer, USDA-ARS Cereal Disease Laboratory; Richard E. Mason, N. Subramanian, University of Arkansas Department of Crop Soil and Environmental Sciences; and Gina L. Brown-Guedira, USDA-ARS Eastern Regional Small Grains Genotyping Lab

We report results from association analyses to discover new disease and insect resistance genes within a diverse panel of 424 eastern U.S. soft winter wheat lines. The panel comprises both landrace and elite cultivars of current or historic importance to eastern U.S. wheat breeding programs. Lines were submitted by eastern U.S. wheat breeders for inclusion in the panel. The population was evaluated for resistance to both stripe rust and leaf rust in eight or three environments (year x location combinations), respectively. These diseases can significantly decrease yields of susceptible varieties in the eastern U.S.A. This population was tested for resistance to leaf rust at one location in 2012 (North Carolina), and two locations in 2013 (North Carolina and Georgia). In addition, seedling tests were performed at the USDA-ARS Cereal Disease Laboratory using four *Puccinia triticina* races. During 2013, stripe rust tests were conducted at four locations in Washington State and one location in Arkansas. Phenotypic data were used in an association analysis with 5,169 polymorphic SNP loci, and obtained using the Illumina iSelect 9k Wheat Chip. Results for leaf rust indicate the existence of several major seedling resistance genes in this germplasm and further analysis is underway. Preliminary results for both stripe rust infection type and severity across the five locations indicate significant loci for resistance on chromosomes 1A, 2A, and 3B, as well as several unmapped loci. We discuss the use of our results in discovering new genes for resistance to these diseases and also in providing breeders with additional tools for marker-assisted selection.

## POSTER 41

### GENOME-WIDE PREDICTION OF GENETIC VARIANCE AND PROPERTIES OF RECOMBINANT INBRED LINES IN SELF-POLLINATED CROPS

\*Mohsen Mohammadi, Tyler Tiede, and Kevin P. Smith, University of Minnesota  
Department of Agronomy and Plant Genetics

Improving crop species, especially those grown as inbred cultivars, often involves a series of crosses, followed by an inbreeding process, and stages of field evaluation to identify superior progeny, which often are then “recycled” back into the crossing block. This style of breeding scheme naturally focuses on crosses between the most elite germplasm. While elite-by-elite crosses ensure a desired population mean, they do not guarantee any level of genetic variation ( $V_G$ ). Unlike population mean which is simply predicted by the mid-parent value, prediction of genetic variance relies on the knowledge of population parameters that are not readily known. The purpose of this research was to predict  $V_G$  of simulated RIL populations resulting from pairwise crosses among parent candidates using a procedure that combines genomic simulation and marker effect estimation commonly used in genomic prediction work. In our example, we use the procedure to evaluate the 435 possible crosses resulting from a half-diallel of 30 parents to identify a manageable number of crosses that could then be advanced to field-based trials. We show that the degree of transgressive segregation observed is highly correlated with the theoretical probability of observing transgressive segregants according to quantitative genetics theory. For illustration purposes, we chose to work with two traits that are unfavorably correlated - disease resistance and yield.



## POSTER 42

### PROXIMAL SENSING FOR FIELD PHENOTYPING OF SYNTHETIC-DERIVED BACKCROSS LINES OF WINTER WHEAT

\*Angela Moore, Judy Harrington, Scott Reid, and Patrick Byrne;  
Colorado State University Department of Soil and Crop Sciences

Proximal sensing techniques may be valuable in identifying useful, heritable traits for selection. Traditional field phenotyping methods often involve destructive sampling or employ expensive, labor-intensive techniques, limiting the amount of material from which breeders can evaluate detailed trait information. One of the most accessible of the current methods being used in efforts to develop field-based high-throughput phenotyping (HTP) programs involves the collection of canopy spectral reflectance data, which has the potential to aid breeders in screening traits related to growth parameters, water status, photochemistry and other physiological factors. However, deriving optimum metrics from reflectance data collected during HTP that are highly correlated with yield or accurately quantify target traits remains challenging. We are using spectrally-configurable active reflectance sensors and passive hyperspectral photometers to phenotype a winter wheat (*Triticum aestivum* L.) test population of 132 synthetic-derived backcross lines and cultivar checks under rainfed and irrigated conditions. We will compare a series of derived trait estimates against manually measured phenotypes and estimate the contributions of selected traits to yield.

## POSTER 43

### A TILLER GENE AFFECTS PHENOTYPIC PLASTICITY IN SPRING WHEAT

\*Afaf Nasseer, Jamie Sherman, HwaYoung Heo, John Martin, and Luther Talbert,  
Montana State University Plant Science and Plant Pathology Department; Yukiko Naruoka,  
Washington State University Department of Crop and Soil Sciences

Variability in productive tiller number (PTN) in wheat may provide phenotypic plasticity and allow plants to adapt to environmental variation. An important locus controlling productive tiller number recently identified in wheat is (*QTn.mst 6B*.) Our goal was to assess the impact of (*QTn.mst 6B*) under different competition levels and levels of available water. Five near-isogenic line (NIL) pairs were developed for high and low tiller number alleles at (*QTn.mst 6B*) in two genetic backgrounds (Reader/Choteau, Vida/McNeal). Three competition levels were imposed on the NIL pairs in replicated experiments. Competition levels were 1) bordered rows representing high competition and limited water, 2) non-bordered rows representing less competition and more available water, and 3) space-planted rows representing no competition and abundant water. The experiment was planted in three locations over 2012 and 2013 our results show that the high tiller allele (*QTn.mst 6B*) caused initiation of a high number of early tillers regardless of the locations. The early tillers more often developed into productive tillers in conditions with less competition (non-bordered rows and space-planted rows). Early tillers did not develop into productive tillers in conditions of high competition and low water. The high plasticity of PTN was associated with high plasticity in grain yield, seed number per spike, and low plasticity of seed weight. In conclusion, (*QTn.mst 6B*) leads to high early tiller initiation. These tillers translate into a high productive tiller number in favorable environments, and may result in higher yield potential.

## POSTER 44

### GENETIC BASIS OF MATERNAL ENVIRONMENT EFFECT ON LETTUCE SEED THERMOINHIBITION: QTL FOR PHENOTYPIC PLASTICITY

\*Mohan Niroula, Fei-Yian Yoong, and Kent J. Bradford, University of California Davis  
Department of Plant Sciences

Failure of seeds to germinate at high temperature (thermo-inhibition) reduces the overall crop stand establishment of cultivated lettuce (*Lactuca sativa* L.). Susceptibility to thermo-inhibition is often influenced by both genetics and maternal environment during seed maturation. The objective of this research is to find the genetic basis of phenotypic plasticity or the maternal environmental effect on the lettuce seed thermo-inhibition trait. Seeds of a *Lactuca sativa* wild accession PI251246 x *Lactuca sativa* cv. Salinas recombinant inbred line (RIL) populations of 122 F8 families were produced in four different location-year combinations with differing ambient temperatures. Germination phenotypes of seeds produced in multiple production environments were evaluated at 25, 30, 32, and 35°C. Mean germination percentages and standard deviations of RILs across environments were calculated, and treated as main trait phenotype and plastic trait phenotype respectively during quantitative trait loci (QTL) analysis. QTL analysis for the main trait phenotype consistently detected a QTL on chromosome 9 (qHTG9.1) contributed by the PI251246 parent that explained up to 47% of the phenotypic variances across all environments. QTL analysis on the plastic trait phenotype revealed a second significant QTL on chromosome 9 (qPHTG9.2) contributed by the Salinas parent, which explained 20% of the variance of the standard deviation of germination by RILs across production environments. QTL analysis on the germination differences between environment pairs as the plastic trait supported the identification of qPHTG9.2 with differing magnitudes across different environment comparisons. QTL by environment interaction analyses on the germination means of RILs across different environments also showed a significant QTL that collocated with the qPHTG9.2. Distinct genetic loci for main trait QTL (qHTG9.1) and plastic trait QTL (qPHTG9.2) suggests the possibility of a regulatory action of the plastic QTL on the main trait QTL. The estimate of broad-sense heritability ( $h^2$ ) for the main trait QTL (qHTG9.1) was ~0.4, indicating that *L. sativa* PI251246 could be a potential source of seed thermotolerance for introgression into lettuce. Informed deployment of these QTL could result in improved temperature tolerance of lettuce seed germination and reduced variability in seed lot performance across production environments.

## POSTER 45

### NATURALLY OCCURRING VARIATION IN THE PROMOTER OF THE FRUIT-SPECIFIC *CYC-B* GENE IN TOMATO CAN BE USED TO MODULATE LEVELS OF $\beta$ -CAROTENE USING MARKER-ASSISTED BACKCROSS BREEDING

\*Caleb Orchard, Elisabet Gas, and David Francis, The Ohio State University Department of Horticulture and Crop Sciences, OARDC; Jessica Cooperstone, Steven Schwartz, The Ohio State University Department of Food Science and Technology

$\beta$ -carotene is an important carotenoid for human health due to its pro-vitamin A activity. We examined the carotenoid profiles of vintage and contemporary tomato (*S. lycopersicum*) varieties to identify sources of high  $\beta$ -carotene. Red tomatoes had a range from 0.2 – 0.97 mg/100 g fresh weight of  $\beta$ -carotene, while several orange fruited varieties had 1.67 – 4.0 mg/100 g. The *B* gene (*CYC-B*) encodes a fruit-specific lycopene- $\beta$ -cyclase that converts *trans*-lycopene to  $\beta$ -carotene. We used high-throughput genotyping to detect known genetic variation and *de novo* sequencing to discover new variation in *B*. The non-transcribed region 5' to the *B* gene (promoter) contains significant nucleotide variation, with nine unique haplotypes across 1850 bp of sequence. Seven unique alleles occurred in high  $\beta$ -carotene varieties. Association mapping and non-parametric statistical approaches suggest two single nucleotide changes (SNPs) as the most likely cause(s) of high  $\beta$ -carotene, presumably through their influence on transcription of the gene. Analysis of the sequence data using clustering techniques suggested that the *B* promoter found in vintage varieties, contemporary breeding lines, and hybrids was originally derived from wild tomato species. A marker-assisted backcross breeding scheme leveraging genome-wide SNPs was used to rapidly develop a series of genetic resources containing different alleles of *CYC-B* in a uniform genetic background. Replicated field trials demonstrated that distinct alleles can be used to modulate the levels of  $\beta$ -carotene in tomato. These genetic resources are available to develop  $\beta$ -carotene enriched food products or to study dietary adsorption and utilization of carotenoids in the food matrix.

## POSTER 46

### PHOTOSYNTHESIS AND CHLOROPHYLL FLUORESCENCE VARIATION IN SORGHUM UNDER DROUGHT

\*Diego Ortiz and Maria G. Salas Fernandez, Iowa State University

Sorghum (*Sorghum bicolor* (L) Moench) is a promising bioenergy crop for its high biomass production and its wide environmental adaptation. The large genetic diversity present in this crop can be exploited for obtaining genotypes with superior drought stress tolerance. For this, the selection for an improved capacity to deal with excessive energy conditions under stress could contribute to the enhancement of crop productivity. Photoprotection is a series of mechanisms triggered under stress conditions that prevent plants from the damage produced by reactive oxygen species (ROS) generated as a result of excessive light. The assessment of genetic diversity in photoprotection and carbon exchange can contribute to discovery of genes/markers associated with superior performance under stress conditions. For this, it is important to generate protocols to evaluate a large number of genotypes, i.e. for Linkage Disequilibrium mapping studies. The main objective of this research was to evaluate the variable response in chlorophyll fluorescence and photosynthesis of sorghum genotypes subjected to drought stress, and their subsequent recovery.

Two experiments were conducted in growth chambers with a 16 hour photoperiod, photosynthetically active radiation of  $1300 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ , and day and night temperatures of  $28^{\circ}\text{C}$  and  $24^{\circ}\text{C}$ , respectively. Carbon assimilation and fluorescence parameters were measured using a Li-6400 (Li-Cor Biosciences, Lincoln, NE). In both cases, nine sorghum genotypes were grown under full irrigation during 45 days, after which drought was imposed. In the first experiment, irrigation was stopped during 5 days and then plants were re-watered. In the second experiment, plants were differentially watered during 10 days to achieve two final water levels (5% and 15% volumetric water content), after which they were re-watered. In both abiotic stress experiments, a wide range of responses were obtained for fluorescence parameters (non-photochemical quenching,  $F_0$ ,  $F_{\text{max}}$ ,  $\Phi\text{PS2}$ ,  $F_v'/F_m'$ ) and photosynthesis (maximum delta photosynthesis, percent recovery). The knowledge generated in this study could be applied to develop accurate protocols for high throughput phenotyping of sorghum plants.

# QTL ANALYSIS OF TETRAPLOID POTATO FOR THREE POTATO AGRONOMIC TRAITS WITH SNP MARKERS

\*Jaebum Park and Walter De Jong, Cornell University Department of Plant Breeding and Genetics; Xiaohong Wang, Cornell University Department of Plant Pathology and Plant-Microbe Biology

QTL analyses are useful for identifying the regions of a genome responsible for variation in a trait of interest. However, QTL analyses with tetraploid potatoes (*Solanum tuberosum*) have not been pursued as extensively as with diploid potatoes, primarily because of the difficulty in generating sufficient numbers of informative markers. QTL mapping in 4x potato is nevertheless important, as commercial breeding is performed at the 4x level. The recent development of the SolCAP SNP chip, which simultaneously interrogates 8303 SNPs for polymorphism, makes QTL mapping possible in 4x potato. Furthermore, assistance of computer software, TetraploidMap improves visualization of QTL maps in 4x potatoes. The primary purpose of this research is to do QTL analysis of tetraploid potato for three potato agronomic traits. To map loci that influence chip color, specific gravity, and resistance to pathotype Ro2 of the golden cyst nematode, a cross was made between 4x clones NY121 (Ro2 resistant) and NY115 (Ro2 susceptible, excellent chip color from cold storage). The parents and 214 progeny with three replications were grown in a field and scored for chip color (scale: 1-10) and specific gravity ( $W \text{ in air} / [W \text{ in air} - W \text{ in H}_2\text{O}]$ ; W = weight) from two cropping seasons. For Ro2 resistance assay, the same potato clones with four replications were planted in a greenhouse maintaining 23 °C and 14 hours day length. Eight thousands of Ro2 eggs were inoculated into each plant and then the plants had been grown for 10 weeks with irrigation. When the plants were matured, the numbers of cysts obtained from each clone were counted under a compound microscope. Evaluation of Ro2 resistance is ongoing. Through scanning DNA samples of the plants mentioned above with the SolCAP SNP chip, genotype data could be achieved. When the genotype and phenotype data were imported into TetraploidMap, the software revealed significant QTL peaks for chipping color on chromosomes 2 and 10, and significant peaks for specific gravity on chromosomes 4 and 5. These QTL may prove useful for marker-assisted selection of chip color and specific gravity. In conclusion, this study showed strong potential for efficient QTL analysis in tetraploid level.

IDENTIFICATION OF NOVEL BARLEY ALLELES IMPACTING MALT QUALITY TRAITS

\*Duke Pauli and Thomas Blake, Montana State University  
Department of Plant Sciences and Plant Pathology

Malting quality has been one of the primary focuses in barley (*Hordeum vulgare* L.) breeding programs but has been difficult for breeders to manipulate due to the quantitative nature of the traits involved. To assist in breeding for malt quality traits, identifying and locating genomic regions that impact these traits is essential. Two populations were used to conduct genome-wide association studies in order to elucidate the alleles responsible for variation in key malting traits. The first population, composed of 332 lines genotyped with 3,072 SNP markers, represented the germplasm of the Montana State University barley breeding program, including feed, food, and malt lines. The second population, with 650 lines genotyped with 384 SNPs, consisted of eleven bi-parental families whose parents were lines developed strictly for malting purposes. All lines were phenotyped at the USDA-ARS Cereal Crops Research Unit in Madison, Wisconsin. Mixed linear models were applied to the data using a Q+K approach in order to find single marker-trait associations. The R package "GAPIT" (Lipka et al 2012) was used with the implementation of FDR p-values to identify significant associations. The result of this work gives a comprehensive overview of the salient regions of the barley genome impacting malting traits. These beneficial alleles will prove useful for development of superior malting cultivars for the Montana barley production region.

## POSTER 49

### QTL MAPPING AND GWAS FOR TRAITS UNDERLYING PLANT DENSITY TOLERANCE IN MAIZE

\*Sarah Potts, Dow AgroSciences; and Martin Bohn, University of Illinois Urbana-Champaign  
Department of Crop Sciences

In order to meet current food production demands grain yields will need to increase on a per unit area basis if global food security is to be realized. Achieving this goal can be accomplished by increasing the number of plants grown per unit area while maintaining individual plant yield. However, the increase in plant density will result in increased competition between plants for light, water, and nutrients. The ability of the plant to maintain per plant yield under this increase in plant density will be determined by the response to this increased competition. A connected population of 320 hybrids was derived from six off-patent inbreds (ex-PVP) exhibiting plant density tolerance in a previous study. This mapping population was used to identify quantitative trait loci (QTL) as well as candidate genes underlying plant density tolerance. The connected population was grown in five environments over 2012 and 2013, and was planted at a high plant density of 116,140 plants ha<sup>-1</sup> (47,000 plants per acre). Grain yield and 22 agronomic and morphological traits were evaluated. QTL mapping was executed and 246 QTL were identified in the nine subpopulations. Additionally, a genome wide association study (GWAS) revealed eight single nucleotide polymorphisms (SNPs) that were significantly associated with traits determining plant density tolerance.



DETERMINATION THE GENETIC RELATIONSHIP BETWEEN DROUGHT TOLERANCE  
AND CHARCOAL ROT RESISTANCE

\*Osman Radwan, University of Illinois at Urbana-Champaign Department of Natural Resources and Environmental Sciences; and Glen L. Hartman, USDA-ARS and University of Illinois at Urbana-Champaign Department of Crop Sciences

Other than irrigation, conditions of drought are difficult to rectify. In addition, certain diseases like charcoal rot of soybean increase under drought stress. For soybean growers, there are few if any options to manage either drought or charcoal rot unless irrigation is available. Genetic resources for drought tolerance and charcoal rot resistance have been found for some crops, including low to moderate levels in limited soybean accessions. However, soybean growers have no or limited options when wanting to grow soybean cultivars with enhanced drought tolerance or charcoal rot resistance because of the lack of availability. More research is needed to develop advanced elite breeding stock with enhanced drought tolerance and charcoal rot resistance and to understand the three-way interaction of drought, the fungus causing charcoal rot, and soybean. The goal of our research is to develop advanced breeding lines for release to breeding programs that enhanced drought tolerance and charcoal rot resistance. To begin this process, we evaluated soybean accessions for enhanced drought tolerance and charcoal rot resistance to determine if any accessions have positive attributes of both traits. Initially, we tested soybean accession for seedling drought tolerance using a set of accessions that were reported to have drought tolerance, charcoal rot resistance, or public advanced breeding lines. These tests showed that some soybean genotypes were superior to both traits. Additional research is planned to repeat the drought tolerance evaluations by using an *in vitro* method of polyethylene glycol (PEG) for assessing drought tolerance, repeat the charcoal rot evaluations, and develop an assay to evaluate both drought tolerance and charcoal rot resistance in one test. The identified genotypes from this project will aid molecular biologists and breeders in pursuing genetic improvement of soybean for resistance/tolerance to both stresses.

GENETIC AND ENVIRONMENTAL EFFECTS ON PRODUCTION OF SPONTANEOUS  
TETRAPLOIDS IN CUCUMBER (*CUCUMIS SATIVUS L.*)

\*Axel O. Ramírez-Madera, University of Wisconsin-Madison Department of Horticulture;  
Michael J. Havey, Yiqun Weng, USDA Vegetable Crops Research Unit and  
University of Wisconsin Madison

The appearance of spontaneous tetraploid (4x) plants is a serious problem for cucumber growers and the seed industry. These plants produce unacceptable fruits with poor quality that do not meet market standards, and result in substantial losses. A higher frequency of spontaneous 4x plants has been associated with the recessive locus (*zym*) conditioning resistance to Zucchini Yellow Mosaic Virus (ZYMV). To test the hypothesis that production of 4x plants is associated to the *zym* locus, three ZYMV-R (resistant) and one ZYMV-S (susceptible) inbred lines plus 49 recombinant inbred lines (RILs) segregating for *zym* will be field grown and evaluated for 4x plants, using visual characteristics (leaf, flower and fruit morphology) and flow cytometry. A second hypothesis to be tested is whether there is an environmental effect on spontaneous 4x production. Three ZYMV-R and two ZYMV-S lines were grown under different environments (one field and two greenhouses) in 2013 and 2014. Flow cytometry will be performed for 4x identification and ANOVAs will be used to test for the environmental effect on tetraploidy. If the frequency of 4x is similar across environments then the production of spontaneous tetraploid in cucumber is not significantly affected by the environment. Our results will provide valuable information towards the understanding of the genetic and environmental effects on spontaneous 4x cucumbers. If there is a genetic effect controlling this phenotype, cucumber industry would greatly benefit from molecular markers to: 1) make cheaper and more efficient the 4x identification process, 2) make more effective selection against 4x background in marker assisted backcrossing program, and 3) to select against the introgressed 4x trait present in current elite germplasm used in production of hybrid seed.

# ADDITIVE-DOMINANCE GENETIC MODEL ANALYSES FOR LATE-MATURITY ALPHA-AMYLASE ACTIVITY IN A BREAD WHEAT CROSSING POPULATION

\*Golam Rasul, Karl D. Glover, and Jixiang Wu, South Dakota State University Department of Plant Science; Padmanaban G. Krishnan, South Dakota State University Department of Health and Nutritional Sciences; and William A. Berzonsky, Bayer CropScience LP Lincoln Nebraska

Pre-harvest sprouting (PHS) in wheat is generally associated with high levels of late-maturity  $\alpha$ -amylase activity (LMAA), one of the four modes of  $\alpha$ -amylase enzyme accumulation.  $\alpha$ -Amylase is one of the enzymes that occurs naturally in all wheat and is found mainly in the aleurone layer. This enzyme is activated during the germination or sprouting process and its activity can quickly break down starch and convert it into free sugar molecules, resulting in a loss of flour viscosity. Elevated levels of  $\alpha$ -amylase are a concern in bread making because this enzyme breaks down starch granules in wheat flour when mixed with water causing the dough to become wet, sticky and difficult to handle. Late-maturity  $\alpha$ -amylase activity appears to be a genetic defect as it is limited to certain genotypes. Therefore, a bread wheat crossing population was developed by hybridization between parents with high- and parents with low- levels of LMAA. The parents and their hybrids in F<sub>2</sub> and in F<sub>3</sub> generations were evaluated for LMAA. The datasets were analysed to estimate genetic variance components and narrow-sense heritability for LMAA, and to predict favorable genetic effects; i.e. general combining ability or predicted additive effects for the parents, and specific combining ability or predicted dominance effects and heterosis for the hybrids in order to improve PHS resistance by reducing LMAA. Additive-dominance genetic model and a mixed linear model approach MINQUE (minimum norm quadratic unbiased estimation) were used to analyse the datasets using R software package 'qgtools\_1.0' (Wu et. al. 2013). Results showed that all variance components and their proportion to the phenotypic variance based on eight parents and their 22 F<sub>2</sub> hybrids were significant except dominance x environment variance, and the narrow-sense heritability for LMAA was 12% and significant. Significant negative additive effects for parents revealed that 'LoSprout', Lancer and Chester can be used as good general combiners. Significant negative dominance effects and best-parent heterosis for hybrids showed specific hybrid combinations, such as 'Larma52' x Lancer, 'Larma52' x 'LoSprout', Janz x 'Seri-82' and Chester x Kinsman could be used to reduce LMAA in spring wheat to develop PHS resistant bread wheat cultivars.

## POSTER 53

### UTILIZING HISTORICAL WHEAT GENOTYPES AND PHENOTYPES FOR MODERN PLANT BREEDING

\*Trevor W. Rife, Kansas State University Interdepartmental Genetics; Bob Graybosch,  
USDA Agricultural Research Service; and Jesse A. Poland,  
Kansas State University Department of Plant Pathology

Plant breeding programs exert considerable effort evaluating new breeding lines across many locations to identify superior performing candidates for release as new varieties. For this evaluation in wheat, regional testing networks have developed in the U.S. to provide additional information to breeders on the performance of their lines. Previously, the information collected in these trials, was only applicable on the line *per se*. With the development of inexpensive, high-density genetic markers, whole-genome profiles can be obtained for every experimental line and can transition to allele based breeding with genomic selection prediction models that take into account alleles common between lines. With this approach, models can then be used to predict phenotypes and pre-select new lines based on ideal allelic combinations. The Southern Regional Performance Nursery is an 81-year-old nursery established by the USDA-ARS to characterize performance and quality of near-release wheat varieties from breeding programs in the central plains at more than 30 locations each year. Entries are submitted annually and genetic gain is measured across years by including multiple long-term check cultivars for comparison. Whole genome profiles have been generated via genotyping-by-sequencing for 907 entries, dating back to 1992, and more than 110,000 phenotypic observations are available. Further work will determine the most suitable training population structure, establish the available prediction power, compare prediction models across the set, and derive a more accurate assessment on reported genetic gain of wheat across the Midwest. This research will refine GS models that have the ability to leverage preexisting regional testing networks for increased genetic gain.

## POSTER 54

### COMBINING MARKER AND PEDIGREE INFORMATION FOR GENOMIC PREDICTION IN BARLEY

\*Ahmad Sallam and Kevin Smith, University of Minnesota  
Department of Agronomy and Plant Genetics

There are several expected limitations for selection schemes based on phenotypes including: i) the phenotype might be an inaccurate predictor of individual breeding value, ii) some traits are difficult to measure due to the highly quantitative nature of these traits, iii) and some traits are expensive to evaluate. Pedigree predictions have been used in dairy cattle for a long time, but have recently been found to be less effective than genomic selection based on dense marker coverage. Several studies showed that genomic prediction based on G-BLUP can perform well even for traits with low heritability. A limitation of G-BLUP is that the (G) matrix may not be positive definite if lines have exactly the same genotype. A possible solution is the inclusion of pedigree relationship matrix (A) to be intermixed with the (G) matrix. Another advantage of combining pedigree and marker relationship information is the use of non-genotyped individuals. Increasing the size of the training population by including non-genotyped individuals may improve prediction accuracy. Five breeding cycles between 2006 and 2010 that include genotyped and non-genotyped individuals were evaluated for yield and plant height over multiple locations. Relationship matrices were calculated using marker and pedigree data. We performed genomic prediction using marker and pedigree information for yield and plant height by using all the available phenotypic, pedigree, and marker information to predict the following breeding year. We found that combining marker and pedigree information improved prediction accuracy in several cases which could be implemented in breeding programs to improve selection efficiency.

## POSTER 55

### EARLY SCREENING OF RECOMBINANT INBRED LINES FOR FISSURE RESISTANCE IN STANDARD HEIGHT RICE

\*Haley Sater, Karen Moldenhauer, and Virginia Boyett, University of Arkansas Rice Research and Extension Center; Shannon Pinson, Eric Grunden USDA Dale Bumpers National Rice Research Center; and Richard Esten Mason, University of Arkansas Crop Soil and Environmental Sciences Department

Rice (*Oryza sativa* L.) kernel fissuring poses a major problem for both rice farmers and millers. Fissures increase in the percentage of broken kernels, which decreased value of processed rice. This study employs the use of fine mapping to increase the genetic resolution of fissure resistance traits found in ‘Cybonnet’, a tropical *japonica* cultivar, as well as the transfer of these alleles into standard height rice. Early recombinant inbred lines (RILs) originate from a cross between a breeding line with low head rice yield, and fissure susceptibility with ‘Cybonnet’. Using putative QTLs identified in previous fissure resistance studies, three regions of the genome were selected for mapping using SSRs to identify recombination in the F<sub>2</sub> generation. Eleven individuals were selected to advance to F<sub>2:3</sub> based on the following criteria: 1) the individual maintained at least one standard height allele at the *sd-1* locus from the breeding line parent. 2) individual possessed recombination in the genomic region identified in previous studies 2013 labeled as *qFIS1-2* where a major fissure resistance QTL was detected. Homozygotes from each population were identified based on their recombinant genotype and will be subsequently phenotyped. Phenotypic data will be regressed with genotypic data. Thus, this study aims to quantify the linkage disequilibrium between *sd-1* and *qFIS1-2* as well as the effect of fissure resistance traits, mainly *qFIS1-2*, in standard height rice plants.

BROADENING GENETIC BASE OF HEXAPLOID WHEAT USING D-GENOME  
PROGENITOR, *AEGILOPS TAUSCHII*, FOR CLIMATE ADAPTABILITY

\*Narinder Singh, Kansas State University Interdepartmental Genetics Wheat Genetics Resource Center; Sunish K Sehgal, Duane Wilson, Jon Raupp, Bikram S Gill, and Jesse Poland, Kansas State University Wheat Genetics Resource Center  
Department of Plant Pathology

Wheat is an important cereal food crop around the world and its production is threatened by depleting resources and adverse climate. Two polyploidization events and early domestication of wheat have resulted in bottleneck for genetic diversity. *Aegilops tauschii*, the D-genome donor of bread wheat has remained genetically diverse and is thought to be an excellent source for broadening genetic base of wheat. With this vision, we assessed the genetic diversity in *Ae. tauschii* collections at Wheat Genetics Resource Center at Kansas State University, and developed a PowerCore and MiniCore sets. We genotyped 551 accessions of *Ae. tauschii* representing the world collection by genotyping-by-sequencing (GBS). More than 120K SNPs were discovered using TASSEL pipeline. SNPs with less than 50% missing data were filtered and a random subset of 15K SNPs was selected to identify a PowerCore consisting of 144 *Aegilops tauschii* accessions retaining most of the genetic diversity and maintaining frequency of alleles in core set similar to the entire collection. Further, the PowerCore was optimized based on genetic distance to represent the major clusters of phylogenetic tree. A MiniCore set of 52 accessions was selected from the PowerCore set to represent all the major clusters in of phylogenetic tree. The MiniCore set of 52 accessions will be crossed to elite wheat cultivars to produce wheat *Ae. tauschii* amphiploids. These amphiploids will be selfed and backcrossed to elite wheat lines to enhance the diversity of bread wheat for drought and heat tolerance.

# DROUGHT AND HEAT RELATED RESPONSES IN PEANUT BREEDING LINES

\*Daljit Singh, Eva Collakova, Virginia Tech Department of Plant Pathology Physiology and Weed Science; Gregory Welbaum, Virginia Tech Department of Horticulture; Thomas Isleib, North Carolina State University Department of Crop Science; and Maria Balota, Virginia Tech Tidewater Agriculture Research and Extension Center

The Virginia-Carolina (VC) region including Virginia, North Carolina, and South Carolina, is the most important peanut production region for the large seeded, virginia-type peanut in the United States. In recent years an increased frequency of heat and drought episodes with significant effects on peanut yield was observed in the VC region. Because limited information is available on the mechanisms virginia-type peanut develops in response to heat and water stress, the present study evaluated several physiological and metabolic characteristics and their relationship with yield for eight cultivars and breeding lines. Experiments were conducted under rainfed and irrigated field trials in 2011 and 2012, and in a growth chamber under optimum (30/25 °C) and high temperature (40/35 °C) conditions. The long-term goal of this study is to help development of tolerant peanut cultivars to heat and drought in the VC region. Visible symptoms of water-deficit stress were observed in peanut during the field experiments in both years. Significant ( $p \leq 0.05$ ) variations for yield, membrane injury, chlorophyll fluorescence ( $F_v/F_m$  ratio), specific leaf area, SPAD chlorophyll content, and relative levels of polar and non-polar metabolites were observed in response to water regime, growth stage, and genotype in both years during the field studies. Similarly each year, the  $F_v/F_m$  ratio, organic acids, and saturated fatty acids decreased in rainfed vs. irrigated plants, while the sugars and sugar alcohols relative levels increased. Regardless the water regime, lower levels of saturated fatty acids and sugars, and higher levels of unsaturated fatty acids and sugar alcohols were associated ( $p < 0.05$ ) with higher pod yield in field conditions. Genotypes Phillips, SPT06-07, and N05006 showed potential tolerance and N04074FCT, CHAMPS, and Bailey susceptibility to water deficit in field studies. Significant physiological and metabolic changes were also observed in response to heat stress under controlled conditions in peanut seedlings. A general decrease in organic acid and saturated fatty acids levels, and increase in membrane injury, sugars, and unsaturated fatty acid levels was observed under both water deficit and heat stress conditions. Overall, results from both experiments were suggestive of natural stress response rather than adaptive mechanisms to water-deficit and heat stress of the virginia-type genotypes used in this study. Among all genotypes SPT 06-07 showed improved tolerance to both stresses. Our results encourage the application of chlorophyll fluorescence and metabolite profiling for improvement of water and heat stress tolerance of the virginia-type peanut.



## USING GENOMIC SELECTION FOR SOYBEAN YIELD IMPROVEMENT

\*Chris Smallwood and Vince Pantalone, University of Tennessee Department of Plant Sciences

Soybean yield improvement is a major goal for researchers seeking to meet the demands of a growing population. Marker-assisted breeding strategies are being pursued to improve soybean yield in a timely and resource efficient manner. Due to the quantitative inheritance of soybean yield, marker strategies which only focus on a few major loci often limit the possibility for gain. Additionally, phenotypic selection (PS) strategies for soybean yield using measured values or visual scores at the progeny row stage can be difficult for predicting broad performance due to the many sources of environmental variation which effect soybean yield. Genomic selection (GS) for soybean yield improvement offers promise for addressing these challenges. The purpose of this research was to compare GS with PS for yield improvement in a soybean population consisting of 282 F5 derived recombinant inbred lines (RIL). This population was genotyped with over 17,000 polymorphic SNP markers spread throughout the soybean genome. In order to simulate progeny rows, each RIL was grown in a single plot in 2010 in Knoxville, Tennessee. Measured yield values from the 2010 harvest were used to rank each RIL for PS, and genotypic and phenotypic data were combined to predict the rank of each RIL for GS. The 282 RIL were grown in 2013 in a replicated, multi-environment field trial. The RIL rankings using the 2013 yield data were correlated to the 2010 PS rankings ( $R=0.19$ ,  $P<0.05$ ) and the 2010 GS rankings ( $R=0.29$ ,  $P<0.05$ ). The rankings for GS and PS were compared to the 2013 rankings for 10%, 15%, and 20% selection intensity. Matches of RIL for PS were 17.9, 21.4, and 23.2%, respectively; while matches for GS were 14.3, 21.4, and 28.6%, respectively. Additionally, for the 10, 15, and 20% selection intensities, PS rankings yielded 88.2, 87.7, and 88.7% of the 2013 rankings, respectively; while GS rankings yielded 87.6, 89.2, and 90.4% of the 2013 rankings, respectively. While the differences were often slight between PS and GS for soybean yield at the progeny row stage, GS showed greater improvement overall. These findings demonstrate potential for GS for soybean yield. Further efforts seeking to refine GS for soybean yield and other quantitative traits will continue using this population.

## POSTER 59

### UTILIZING ACYLSUGAR CHEMISTRY TO PREBREED TOMATOES FOR OPTIMAL PEST CONTROL

\*John Smeda, Brian Leckie, and Martha Mutschler, Cornell University  
Department of Plant Breeding and Genetics

Tomatoes are attacked by many pests, causing losses directly through feeding damage and indirectly through virus transmission, resulting in reductions in quality and yield. Even with the use of integrated pest management, control of insects relies heavily on pesticides, a practice that is increasingly limited by development of pesticide-resistant insects, and increased health and environmental concerns; therefore, alternative means of insect control are necessary. Acylsugars, which are one of the most promising classes of plant-derived control agents, are exuded from trichomes of some wild *Solanum* species, and exhibit strong insect deterrence against a wide range of tomato pests. Acylsugars are composed of a sugar backbone, either sucrose or glucose, to which are esterified 3 or 4 fatty acids, which can be straight or branched, even or odd, short, medium or long. The sugar and fatty acid together is termed a chemotype. Using *S. pennellii* LA716, Mutschler's breeding program created the current benchmark acylsugar-producing tomato, CU071026, which demonstrated control of whiteflies in field tests under high natural infestation. While CU071026 and lines developed from it all produce the same chemotype of acylsugars, there is incredible diversity of acylsugar chemotypes among *S. pennellii* accessions. Capturing this diversity is integral to optimizing acylsugars as a successful defense strategy. There are two main objectives for this study. The first is to introgress previously identified QTL affecting acylsugar chemotype into a common background, CU071026, and characterize the resulting lines. The second objective is to evaluate the lines with unique acylsugar chemotypes in field trials to ascertain if some chemotypes have improved efficacy against insect pests of tomato. To create sister lines differing for addition of the chemotype QTL we utilized mono-introgression lines containing the pertinent QTL which were crossed and backcrossed to CU071026. A colorimetric invertase assay and gas chromatography were used to determine acylsugar level and chemotype. Field trials are being conducted in the summer of 2014 in North Carolina and California for thrips and in Florida for whiteflies. Acylsugar levels and chemotypes as well as insect feeding and oviposition are being determined for the genotypes included in these trials. The data from these locations will help elucidate the effect of the fatty acid QTL on insect feeding and oviposition which will facilitate the development of optimal acylsugar chemotype breeding lines that can be utilized in the development of insect resistant tomato cultivars.

## POSTER 60

### COMPARISON OF SPACE AND SWARD PLANTED SWITCHGRASS FOR ESTIMATES OF GENETIC PARAMETERS AND RANKING OF BIOMASS AND ETHANOL YIELD

\*Virginia Sykes, Fred Allen, and Alexandria DeSantis, University of Tennessee  
Department of Plant Sciences

Switchgrass (*Panicum virgatum* L.) is an important potential biofuel crop. Switchgrass breeding nurseries are typically space-planted; however, production is in dense swards. This disconnect may impact selection. The objectives of this research are to compare space- and sward-planted switchgrass biomass and ethanol yield for i.) correlations between morphological traits, ii.) estimates of general and specific combining ability (GCA, SCA) and heritability, and iii.) rankings among crosses. Eight parents selected from the varieties *Kanlow* (2 selections), *Alamo* (4 selections) and *Miami* (1 selection) were crossed in a complete diallel design. In 2012, progeny were divided into two clonal propagules and planted in adjacent nurseries in Knoxville, TN. Each nursery was arranged in a randomized complete block design containing twenty replications of each cross. The space-planted nursery (HSP) contained single-plant plots on 1 m centers. The sward-planted nursery (HSW) contained plots of 4x7 plants on .33 m centers with 1 m alleys. Spring evaluations (2013) included height, tiller number, tiller diameter, leaf diameter, leaf angle, and color. Fall evaluations (2012, 2013) included rust, height and biomass yield. Ethanol yield (2013) was evaluated using NIR. Data were analyzed in SAS. HSP and HSW were strongly correlated for rust (0.80), ethanol yield (0.71), and tiller diameter ( $r=0.71$ ) with moderate correlations for all remaining traits ( $r=0.39-0.68$ ). GCA direction was similar between nurseries with 93% agreement for biomass yield and 100% agreement for ethanol yield. SCA direction was similar between nurseries for biomass yield with 96% agreement; however, SCA direction for ethanol yield showed only 54% agreement between nurseries. Heritability estimates for biomass yield were similar between nurseries (HSP: $h^2=0.05$ ,  $H^2=0.19$ , HSW: $h^2=0.02$ ,  $H^2=0.20$ ). Heritability estimates for ethanol yield differed between nurseries (HSP: $h^2=0.23$ ,  $H^2=0.53$ , HSW: $h^2=0.12$ ,  $H^2=0.18$ ). Comparing cross rankings between nurseries, 2012 (yr-1) biomass yield disagreed for 53% of the top and 41% of the bottom 1/3. 2013 (yr-2) biomass yield disagreed for 88% of the top and 93% of the bottom 1/3. Rankings for ethanol yield disagreed for 40% of the top and 50% of the bottom 1/3. Results indicate selection in an evaluation environment different from the production environment may impact selection and rate of crop improvement. Data will be collected again in 2014 (yr-3).

## POSTER 61

### A PACKAGE FOR GENERATING FIELD-BASED TRIAL DESIGNS THAT ENABLE SPATIALLY-ADJUSTED AND RELATIONSHIP-ADJUSTED ENTRY EFFECT ESTIMATES/PREDICTIONS

\*Tyler Tiede, Mohsen Mohammadi, and Kevin P. Smith, University of Minnesota Department of Agronomy; Jean-Luc Jannink, USDA-ARS R.W. Holley Center for Agriculture and Health and Cornell University Department of Plant Breeding and Genetics; Aimin Yan, Cornell University Department of Plant Breeding and Genetics

Field-based trials in plant breeding and genetic research are crucial for evaluating the performance of entries, whether they are breeding lines or experimental entries in a genetic mapping experiment. Phenotypes, especially those of quantitative traits, are highly subject to micro-environmental (i.e. plot level) variation and thus may not be accurate estimates of the entry's true genetic value. Replication of entries within and across environments reduces the non-genetic influence on the effect estimate of an entry. However, breeding designs and large scale mapping studies often employ unreplicated designs to maximize the number of genotypes evaluated. Therefore, detecting and adjusting for spatial variation in field trials is particularly important to reduce non-genetic effects on entry values. A tool has been developed in the form of an R package (R Core Team, 2013) that will provide an incomplete block field design with augmented checks. The design function requires limited user input such as the number of experimental entries, the number of unique check entries, and the number of field rows (sometimes called beds or ranges) to be planted. Given the user-defined inputs the most efficient design possible will be generated. Once data is collected the user can estimate trial and macro-environmental (i.e. beds, planter passes, etc...) effects, as well as micro-environmental effects using moving mean and autoregressive procedures available via the trial analysis function. In addition, relationships among entries can be leveraged into the prediction of their genetic value. This flexible design and analysis tool allows researchers to generate efficient field designs and estimate genetic values while efficiently using available resources.

## POSTER 62

### ANALYSIS OF HISTORICAL HOP CHEMISTRY DATA USING BLUP ANALYSIS

\*Shaun Townsend, J. Kling, J. Henning, G. Nickerson, and A. Haunold, Oregon State University  
Department of Crop and Soil Sciences and USDA-ARS Corvallis Oregon

Hops are widely used in the brewing industry for providing bitterness, flavor, and aroma to beer. Although hop breeding programs have been active for more than 100 years, limited inheritance information has been published for principal agronomic and chemical traits. Hop breeding is expensive due to a significant combination of infrastructure and logistical problems associated with transporting the plants for harvest. Furthermore, estimation of breeding values for chemical traits in male genotypes would be especially useful since progeny testing in hop is expensive and time-consuming due to the time required for plant maturation. The USDA-ARS has maintained a hop breeding program in Corvallis, Oregon since the 1930s and has accumulated considerable data for a variety of chemical traits. These data are being mined and analyzed via BLUP so that appropriate selection strategies can be determined for target traits. Results from this work will be presented for a variety of agronomic and chemical traits in hop.

## POSTER 63

### IDENTIFYING SSR MARKERS LINKED TO TSWV RESISTANCE IN PEANUT CULTIVAR FLORIDA-EP<sup>TM</sup>113'

\*Yu-Chien Tseng, Barry L. Tillman, University of Florida Department of Agronomy North Florida REC; Jianping Wang, University of Florida Department of Agronomy

Spotted wilt caused by tomato spotted wilt virus (TSWV) is one of the major diseases affecting peanut (*Arachis hypogaea* L.) production in the Southeastern USA. Occurrence, severity, and symptoms of spotted wilt disease are highly variable from season to season making it difficult to efficiently evaluate breeding populations for resistance. Molecular markers linked to spotted wilt resistance could overcome this problem and allow selection of resistant lines regardless of seasonal conditions. The objective of this study is to identify the simple sequence repeat (SSR) markers linked to TSWV resistance in peanut through genetic mapping using a biparental segregating population.

A total of 199 F<sub>2</sub> progeny derived from a cross between Florida-EP<sup>TM</sup>113', a TSWV resistant cultivar and Georgia Valencia, a highly susceptible cultivar were evaluated by ELISA (enzyme-linked immunosorbent assay) for the presence of TSWV. The F<sub>2:3</sub> and F<sub>2:4</sub> populations were further phenotyped by two different methods: visual evaluation and immunostrip test.

The Immunostrip results confirmed that symptomatic plants were infected by TSWV and many asymptomatic plants exhibited a positive immunostrip reaction. This result indicates that immunostrip test is a more sensitive method for TSWV phenotyping since asymptomatic, but infected plants can be identified. For genotyping, a total of 60 SSR markers flanking a known QTL for TSWV resistance were screened using the two parental lines Florida-EP 113 and Georgia Valencia. Twelve markers are polymorphic. These markers were then used to genotype the whole F<sub>2</sub> population. The results showed that the same QTL for TSWV resistance exists in Florida-EP 113. Fine mapping will be conducted to identify markers closely linked to spotted wilt resistance conferred by Florida-EP<sup>TM</sup>113'.

## POSTER 64

### UTILIZING BIPARENTAL AND ASSOCIATION MAPPING TECHNIQUES TO IDENTIFY LEAF RUST RESISTANCE IN DIVERSE WHEAT ACCESSIONS

\*M. Kathryn Turner and Jim Anderson, University of Minnesota Department of Agronomy and Plant Genetics; Jim Kolmer, USDA-ARS Cereal Disease Lab

Leaf rust is common in wheat, consistently reducing yields by 5-15% with higher losses recorded. In hard red spring wheat growing regions of the U.S., farmers apply fungicides annually to mitigate crop losses, but genetic resistance can provide less expensive, effective control. Our objectives are to map leaf rust resistance genes and evaluate the utility of association and biparental mapping approaches. Six populations developed from selected diverse National Small Grains Collection lines were evaluated for seedling resistance, which has been mapped using bulk segregant analysis. Two populations were developed for adult plant resistance, which will be mapped using recombinant inbred lines. Association mapping will be used to identify loci contributing to resistance in the diverse NSGC lines. This project will identify new resistance loci and effective combinations of genes, contribute to characterization of leaf rust resistance genes in global germplasm, and compare biparental and association mapping approaches.

## POSTER 65

### MOLECULAR CHARACTERIZATION OF VERNALIZATION GENE VRN-B1 IN WINTER WHEAT AGS 2000, PIONEER 26R61, AND NC-NEUSE

\*Mai Xiong and Mohammed Guedira, North Carolina State University; Gina Brown-Guedira, USDA/ARS PSR

In many important agronomic crop species, flowering time has been continuously selected by breeders directly and indirectly to best adapt crops to different growing regions and agricultural practices. By assessing the genetic diversity of genes that modulate flowering, it is possible to define strategic breeding goals to adapt crops for cultivation in various geographical locations that will be impacted by climate change. In winter wheat, time from planting to ear emergence is influenced by variation for vernalization requirement duration. Analysis of mapping populations from the crosses between winter wheat cultivars AGS 2000, Pioneer 26R61, and NC-Neuse detected a major flowering QTL co-located with the *Vrn-B1* locus on chromosome 5B. The objectives of this study are to sequence and characterize the *vrn-B1* alleles present in winter wheat cultivars AGS 2000, Pioneer 26R61, and NC-Neuse to determine genetic polymorphisms that may result in vernalization requirement difference between cultivars. Genome specific primers were designed from cultivar Triple Dirk C (AY747604) *vrn-B1* sequences to PCR amplify the 13 kb gene by parts. Sequence analysis of the *vrn-B1* gene revealed no genetic polymorphism in exonic regions but considerable variations were detected in intronic regions. Although this study detected structural polymorphism in intronic regions, additional studies will need to be conducted to determine if these variances are responsible for flowering time differences. The molecular characterization of the *vrn-B1* genes in winter wheat cultivars AGS 2000, Pioneer 26R61, and NC-Neuse is useful for breeding adapted cultivars for different winter wheat growing regions.



## POSTER 66

### GENOME-WIDE ASSOCIATION STUDY OF DOMESTICATED TRAITS IN MAIZE

\*Shang Xue, North Carolina State University Bioinformatics

Maize (corn) was domesticated about 8000 years ago from a wild grass, teosinte. Numerous morphological traits have changed in maize compared to its wild ancestor, including the floral morphology. Teosinte produces flowers on many nodes along lateral branches, with each flower having female florets near the base and terminating in male tips. In contrast, maize normally has male flowers (tassels) only at the top of the main stem of the plant, and has usually only a single completely female ear at the end of a highly reduced lateral branch called a shank. Furthermore, teosinte flowers produce one row of seeds, whereas modern maize can produce ears with more than 20 rows of seeds. Several major QTL and specific genes controlling these differences between maize and teosinte have been identified. Despite the severe bottleneck that occurred during domestication and strong selection for the maize plant type, these traits still vary among different maize varieties. To uncover the underlying genetics basis for the phenotypic variation, genome-wide association has been conducted on 2480 maize inbred lines and reveals several significant association among the whole genome.

## POSTER 67

### GENOTYPE X ENVIRONMENT INTERACTION AND STABILITY ANALYSIS OF TEST WEIGHT IN WINTER WHEAT

\*Dalitso Noble Yabwalo and Bill Berzonsky, South Dakota State University

Market grades and subsequent grain price of wheat are primarily determined by grain quality; particularly, test weight (TW). Millers are interested in TW because several studies have shown that high TW is positively correlated to high flour yield and better overall end-use quality. However, TW measurements tend to fluctuate over space and time which are attributed to genotype x environment interaction (GEI). The purpose of this study was to assess GEI and performance stability associated with TW of 24 cultivars maintained in the state-wide crop performance trials (CPT) in South Dakota. The cultivars were tested in 16 environments, thus; 8 locations in 2012 and 2013 with four replications per location. Data was collected on TW and other morphological grain attributes. Additive-Main Effects and Multiplicative Interaction model (AMMI), Finlay-Wilkinson's regression and Shukla's stability variance were employed to partition the genotype and the GEI. Results indicated that some genotypes are stable with high TW while others are stable with low TW. The findings suggest that while GEI affects TW, there are genetic factors in certain genotypes that can be manipulated for higher and stable TW in winter wheat. Statistical tools that were primarily developed for yield stability assessment can be used successfully to evaluate and select for high and stable TW.

## POSTER 68

### UNDERSTANDING SUBSTRATE SPECIFICITY OF DIHYDROFLAVONOLREDUCTASE IN POTATO

\*Teddy Yesudasan and Walter De Jong, Cornell University Department of  
Plant Breeding and Genetics

Pigmented potatoes (*Solanum tuberosum* L.) are a rich source of anthocyanins. Pigments from potatoes can potentially be used as natural colorants and can meet the fleeting needs of the innovative potato industry. Dihydroflavonol-reductase is a rate limiting enzyme in the flavonoid pathway that catalyzes an essential reaction that gives rise to the anthocyanin pigments red pelargonidin, pink cyanidin and purple delphinidin by reducing dihydrokaempferol (DKH), dihydroquercetin (DHQ) and dihydromyricetin (DHM), respectively. The *df*r gene has been studied in detail in various species. It was previously reported that the potato *df*r allele corresponds to potato R locus and that the *df*r allele demonstrated significant differences in potato skin color. Several constructs of the *df*r allele were made using site-directed mutagenesis. The constructs were placed under the control of the CaMV 35S promoter and introduced into the potato cultivar Prince Hairy (genotype dddd rrrr P-), which has pale blue flowers. The phenotype of the flowers were analyzed for observed changes in color. Simultaneously, 3D protein models of the different potato DFR constructs were constructed using template based homology modelling to further study the enzyme-substrate complex. Docking was performed with Autodock to analyze enzyme-substrate interaction, multiple binding site interactions and to infer the biochemical basis of the substrate specificity.

GENOMIC SELECTION OF BIOMASS YIELD IN A GLOBAL COLLECTION OF  
ONE THOUSAND SORGHUM ACCESSIONS

\*Xiaoqing Yu, Xianran Li, and Jianming Yu, Iowa State University;  
Yuye Wu, Kraig L. Roozeboom, Donghai Wang, Tesfaye T. Tesso, Kansas State University;  
Sharon E. Mitchell, Cornell University; Rex Bernardo, University of Minnesota;  
and Mingli Wang, Gary A. Pederson, USDA-ARS

Substantial genetic diversity exists in sorghum (*Sorghum bicolor*), a key lignocellulosic biofuel species in the United States. The implementation of genomic, genetic tools to select and enhance current germplasm will greatly accelerate new variety development. Our objectives in this study are to address several key questions: 1) *How to tap into the vast plant germplasm collections for biomass crop improvement?* 2) *How to increase the information contained in genotypic and phenotypic data for the selected germplasm?* 3) *How to leverage a high-throughput phenotyping method such as Near Infrared (NIR) to facilitate plant biomass composition investigation?* 4) *How robust are the various genomic prediction models on biomass traits?* In this study, genotyping by sequencing (GBS) with the Illumina HiSeq platform was conducted for 1000 sorghum accessions sampled from germplasm bank and generated 125k SNPs after low quality ones have been filtered. A set of 300 accessions, selected to be most representative from this panel were extensively phenotyped for biomass yield, plant height, stem diameter, stalk number, stalk lodging, and root lodging at Kansas in 2013 and Taxes in 2012 and 2013. Cellulose and lignin content were investigated through both wet chemical and high throughput NIR methods. Bringing phenotype and genotype data together, genomewide prediction models were established with all common methods. Biomass traits of the 700 untested accessions were predicted by using the optimal genomic selection model and will be validated through phenotyping the accessions with extreme high and low biomass potential as well as a random 100 accessions from the untested panel.



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