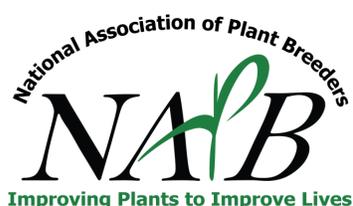

5th Annual Meeting: National Association of Plant Breeders
9th Annual Meeting: Plant Breeding Coordinating Committee

“Identifying and utilizing genetic diversity”

Hosted by Washington State University
Compton Union Building
Pullman, WA July 28-30, 2015



College of
Agricultural, Human, and
Natural Resource Sciences
WASHINGTON STATE UNIVERSITY

*Plant Breeding
Coordinating
Committee*



Local Organizing Committee

Arron Carter
Kate Evans*
Roger Freeman
Jim McFerson*
Rebecca McGee*
Nnadozie Oraguzie
* Executive Committee

NAPB Meeting Planning Committee

Don Jones
Heather Merk
Leah Ruff
Barry Tillman

Graduate Student Committee

Julia Harshman
Kelsey Hight
Emily Klarquist
Ericka Kruse
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Monday, July 27

Informal welcome reception 6:30-9:00pm *Senior Ballroom*
Registration open

Tuesday, July 28

Four mile fun run 6:00am *Depart from Marriott lobby*

Registration desk open 7:00am-12noon

Poster installation 7:00-10:00am

NAPB and PBCC Business meetings 8:00-10:00am

General Session *Barry Tillman (outgoing NAPB President) presiding*

8:00 **Housekeeping and announcements** Kate Evans, Washington State Univ

8:15 **NAPB General Session** Barry Tillman, Univ of Florida

8:40 **PBCC General Session** Jamie Sherman, Montana State Univ

8:55 **2016 meeting** Don Jones, Cotton Incorporated

Committee breakout sessions 9:00-9:40am (4 groups)

9:45 **Committee reports**

Break 10:00-10:30am

Welcome and Keynote (*Moderator: Kate Evans, WSU*)

- 10:30 **Housekeeping and announcements**
10:35 **Welcome to WSU** Bob Allan, WSU Emeritus
10:45 **Keynote presentation**
Philosophy and practice of utilizing genetic diversity in plant breeding
Rex Bernardo, Univ Minnesota

Poster mini-presentations #1 (*Moderator: Shelby Ellison, Univ Wisconsin*)

- 11:15 1-minute poster introductions (Acharya, Ames, Belcher, Bernau, Berry, Bhusal, Cobo, Cordero, Dohle, Dzievit, Falcon, Gilbert, Gizaw, Godoy, Harshman, Howell, Jimenez, Kruse, Levina, Lewien, Liabeuf)

Lunch 11:45am-12:15pm

Poster session #1 12:15-1:00pm (all presenters stand by posters)

Identifying and utilizing genetic diversity in plant breeding programs

1:00-3:30pm (*Moderator: Rebecca McGee, USDA-ARS Pullman*)

- 1:10 **Identification and conservation of apple genetic diversity**
Gayle Volk, USDA-ARS Ft Collins
- 1:30 **Sixty years of forest tree improvement in Oregon, Washington and British Columbia**
Keith Jayawickrama, NW Tree Improvement Cooperative
- 1:50 **Hazelnut breeding at Oregon State University**
Dave Smith, Oregon State Univ
- 2:10 **Identifying and exploiting genetic diversity in cherry to increase industry profitability**
Amy lezzoni, Michigan State Univ
- 2:30 **The USDA-ARS cool season food legume breeding programs**
Rebecca McGee, USDA-ARS Pullman
- 2:50 **Extreme makeover potato edition**
Shelley Jansky, USDA-ARS Madison
- 3:10 **Variation for epicuticular waxes and thrips resistance in onion**
Mike Havey, USDA-ARS Madison

Break 3:30-4:00pm

NAPB 2014 Awardees Presentation (*Moderator: Rita Mumm, Univ Illinois*)

4:00 **Lifetime Achievement**
Ted Crosbie, Monsanto (ret.)

Poster mini-presentations #2 (*Moderator: Arron Carter, Washington State Univ*)

4:15 1-minute poster introductions (Liu, Ma, Masor, Moreno, Muleta, Nankar, Niroula, Roberts, Rodriguez-Armenta, Ruff, Singh, Snodgrass, Spurlock, Stettler, Sykes, Tiede, Tomar, Tseng, Turner, Varella, Wahl, Xiong)

Poster session #2 4:45pm (all presenters stand by posters)

Mixer

6:15pm onwards at the Lewis Alumni Center, live music provided by **Train of Thought**
Informal dinner featuring regional, identity-preserved products. First-come, first-served
photo session for professional head shots available until 8:30pm

6:30 **Welcome and housekeeping**
Jim Moyer, Assoc Dean, WSU Ag Research Center
Kate Evans, WSU

Wednesday, July 29

Field trip to local WSU & ARS sites

8:00 **Depart Residence Inn**
'Lunch to go' at tour site
12:45 **Load buses & return to CUB**

Graduate student presentations (*Moderator: Shelby Ellison, Univ Wisconsin*)

1:30 **Greenhouse assays predict field performance of dry bean with regard to yield and symbiotic nitrogen fixation**
James A. Heilig, Michigan State Univ
1:45 **Field screening for selection to tolerance of heat stress in soft red winter wheat using an artificially warmed environment**
Kathleen Russell, Univ Kentucky
2:00 **Pedigree-based QTL mapping of resistance to two crown rot pathogens in allo-octoploid strawberry**
Jozer Mangandi, Univ Florida

Poster session #3 and refreshment break 2:15-3:00pm

NAPB 2014 Awardees Presentation *(Moderator: Rita Mumm, Univ Illinois)*

- 3:00 **Early Career**
Maria Salas Fernandez, Iowa State Univ

Plant breeding organization, policy, and funding *(Moderator: Jim McFerson, WTFRC)*

- 3:15 **Introduction**
Jim McFerson, WTFRC
- 3:25 **NAPB Strategic Plan**
Barry Tillman, Univ Florida
- 3:45 **Sustaining the future of plant breeding**
Mike Gore, Cornell Univ
- 4:00 **Amer Soc Plant Biologists Decadal Vision**
Bill Tracy, Univ Wisconsin
- 4:15 **USDA REE Plant Breeding Roadmap**
Jose Costa, ARS Beltsville
Ann Marie Thro, NIFA
- 4:45 **National and International Human Capacity Resources for Plant Breeding**
Fred Bliss, UC Davis & Seminis (ret.)
- 5:00 **New DNA-Editing Approaches: Policy Implications**
Don Blackburn, ASTA
- 5:30 **PBCC State representatives work session**
Pat Byrne, Colorado State Univ
Location: CUB rm 204 Senate meeting room

First chance for poster removal 5:15pm

Banquet/2015 research awards *(MC: John Clark, Univ Arkansas)*

- 6:30 **Pre-banquet networking**
- 7:30 **Dinner**
Welcome to Pullman
Fred Muehlbauer, USDA-ARS (ret)

2015 Research Awards *(Moderator: Rita Mumm, Univ Illinois)*

Lifetime Achievement: Stephen Baenziger, Univ Nebraska-Lincoln
Plant Breeding Impact: Rex Bernardo, Univ Minnesota
Early Career Scientist: Jennifer Yates, Monsanto

2015 Grad student poster awards *(Moderator: Loren Trimble, Monsanto)*

Thursday, July 30

Workshop 1

Breeding for consumer product quality: successes and challenges

(Moderators: Roger Freeman, Bayer CropScience & John Clark, Univ Arkansas)

8:30-10:00am

Panel A

Roger Freeman, Bayer CropScience

Bill Tracy, Univ Wisconsin

Erin Silva, Univ Wisconsin

Rich Novy, USDA-ARS Aberdeen

Panel B

John Clark, Univ Arkansas

Jim Olmstead, Univ Florida

Jim Luby, Univ Minnesota

Laurie McKenzie, Organic Seed Alliance

Break 10:00-10:30am

Workshop 2

Essential career skills for plant breeders

(Moderator: Kim Kidwell, WSU)

10:30-11:30am

10:30 **Welcome and session overview**

Kim Kidwell, WSU

10:40 **Co-evolution of plant breeding and breeders: Implications for breeder education and career development**

Fred Bliss, UCD & Seminis (ret)

11:00 **Career development, training, and mentoring panel**

Klaus Koehler, Dow AgroSciences

Kristin Schneider, Monsanto

Phil Simon, USDA-ARS Madison

Maria Salas Fernandez, Iowa State Univ

David Francis, Ohio State Univ

Jennifer Yates, Monsanto

Lunch & Facilitated Roundtable Discussion

Sponsored by Monsanto

12:00 noon

Breakout into tables each with a facilitator for informal lunch and discussion around a particular table topic.

Workshop 2 De-brief

1:30pm

Adjourn & remove all posters

2:00pm

Speaker Bios (alphabetical order)

ROBERT E. ALLAN, Washington State University, Pullman, WA

Robert E. Allan is an Emeritus Professor of Crops and Soil Sciences at Washington State University and a former Research Geneticist of USDA-ARS. He spent his entire career at Pullman and retired in 1996. He was the Research Leader of the Pullman wheat research unit for 22 years and Coordinator of Western USA regional wheat testing programs for 16 years. His personal research included a broad range of wheat genetic studies and development of wheat varieties and genetic stocks. Most notably he identified and isolated the Rht_1 and Rht_2 semidwarf genes used in the Green Revolution of Wheat. He developed nine winter wheat varieties and numerous genetic stocks. The varieties have been grown on over 18 million total acres. They included the first US varieties with highly stable resistance to eyespot foot rot and club wheat multilines that provided durable resistance to stripe rust. The genetic stocks included euplasmic-alloplasmic lines, cytoplasmic sterility-fertility restorer lines and near-isolines for several morpho-physiological traits. He served on several important international and national assignments including those sponsored by OICD, CIMMYT, USAID, and the National Research Council. He authored or co-authored over 200 publications including book chapters on wheat breeding methodology, soft wheat breeding in the USA and wheat hybridization procedures. He recently wrote a book entitled "Club Wheat". Recognitions included Fellow in both Crop Science Society of America and American Society of Agronomy, USDA-ARS Technology Transfer Award, Genetics and Plant Breeding Award from the National Council of Commercial Plant Breeders and Distinguished Service Award in Agriculture from Kansas State University. He continues to make crosses and conduct wheat genetic studies on his farm near Pullman.



STEPHEN BAENZIGER, University of Nebraska, Lincoln, NE

P. (Peter) Stephen Baenziger is the Nebraska Wheat Growers Presidential Chair and Professor in the Department of Agronomy and Horticulture at the University of Nebraska. He earned degrees from Harvard University (B.A.) in biochemical sciences and from Purdue University (M.S., Ph.D.) in plant breeding and genetics. Before joining the faculty at the University of Nebraska, he worked eight years on wheat and barley germplasm enhancement for the USDA-ARS at Beltsville, MD, and three years with Monsanto Corporation on wheat plant growth regulators and biotechnology. His research focuses on improving the agronomic performance and winterhardiness of winter wheat, barley, and triticale, and on developing new breeding methods. He has co-released 46 cultivars and 36 germplasm lines or populations. His teaching and service activities emphasize graduate education and outreach in plant breeding and genetics. Dr. Baenziger is active in Crop Science Society of America and has been a Division Chair and President, as well as an Associate Editor, Editor, and Editor-in-Chief of Crop Science (their flagship journal). He is also active in the American Association for the Advancement of Science where he was elected Chair of Section O (Agriculture, Food, and Renewable Resources). He is the past Chair of the National Wheat Genomics Committee, and the past Chair of the Plant Breeding Coordinating Committee. He is currently on the Board of Trustees for the International Rice Research Institute, on the Scientific Advisory Boards of BREADWHEAT, and is the Chair of the Hard Winter Wheat Improvement Committee and a member of the National Wheat Improvement Committee. He is an honorary professor of the Ningxia Academy of Agriculture and Forestry Sciences and a Fellow of American Society of Agronomy, Crop Science Society of



America, and the American Association for the Advancement of Science. In 2013, he received the Genetics and Plant Breeding Award from the National Council of Commercial Plant Breeders. He has co-released 46 cultivars and 36 germplasm lines or populations. He has over 250 publications and has received millions of dollars in grants to support his research.

REX BERNARDO, University of Minnesota, St Paul, MN

Dr. Rex Bernardo is Professor and Endowed Chair in Corn Breeding and Genetics at the University of Minnesota, where he conducts research on new ways of breeding maize and breeding maize for new uses. Most of his current work focuses on marker-assisted breeding. Dr. Bernardo obtained his B.S. degree in agriculture in the Philippines in 1984 and Ph.D. degree in plant breeding at the University of Illinois in 1988. He was formerly a research scientist with Limagrain Genetics and a professor at Purdue University. At Minnesota, Dr. Bernardo teaches graduate courses and short courses in plant breeding and in scientific writing. He has written two textbooks, entitled *Breeding for Quantitative Traits in Plants* and *Essentials of Plant Breeding*.



DONALD BLACKBURN, Dow AgroSciences, Indianapolis, IN

Don Blackburn is the Global leader for Seeds & Traits R&D with responsibilities for global field and lab breeding activities critical for germplasm improvement and final seed product launches. Prior to this role, Don had experience in Seeds Operations as the Seeds Technology Center Director and 24 years of experience in Dow AgroSciences R&D in a variety of roles including R&D Field Station Leader, Germplasm IP and Elite Genetics Leader, Traits & Germplasm Development Leader, and NA Seeds Field Breeding & Product Development Leader. Don joined Dow AgroSciences in 1989 as a Corn Breeder with a Ph.D. and M.S. in Plant Breeding & Cytogenetics and a B.S. in Crop and Soil Sciences. Don also serves on the Board of Directors for the Agronomy Society of America (ASA), the Board of Directors for the American Seed Research Foundation (ASRF), and is American Seed Trade Association's (ASTA) Liaison to the North American Plant Breeders Association (NAPB). Don has served on numerous boards including the National Council of Commercial Plant Breeders (NCCPB) from 2008-2014 (President, 2011) and ACS Membership and Society Identity Committee from 2006-2011 (Chair 2011). He has been a member of ASTA since 1989 and has been a member of ASA and Crop Science Society of America (CSSA) for 28 years. Don was the organizer of the 2012 Annual Meetings for NAPB and PBCC held in Indianapolis.



FRED BLISS, U C Davis & Seminis (retired)

Fred Bliss is Professor Emeritus in the Dept. of Plant Sciences at the University of California, Davis and retired from the Vegetable Division of Monsanto. A plant breeder, he has led improvement programs for cowpea, common bean, tomato, stone fruits and tree fruit rootstocks. He is author or co-author of articles and book chapters on topics that include genetic analysis and expression of bean seed protein; breeding dry and snap beans for improved performance; domestication and evolution of common bean; breeding legumes for increased fixation of atmospheric nitrogen; molecular genetic maps for *Prunus* (stone fruits); breeding improved rootstocks for peach and sweet cherry and education of plant breeding students. Fred was a faculty member of the Dept.



of Horticulture at UW - Madison from 1966 through 1988, when he accepted the Lester Endowed Chair in the Pomology Dept. at UC Davis. In 1998, he became Director of Worldwide Breeding, Seminis Vegetable Seeds. He held management positions at Seminis (now Monsanto) until retiring in 2010. Recent activities include work with the FAO on the Global Initiative for Plant Breeding, consulting to the Washington Tree Fruit Research Commission and a Delphi study at UC Davis to survey information about education and preparation of future plant breeders. He has participated in research and development projects in Nigeria, Somalia, Honduras and Brazil and as a consultant for numerous international studies. He is a member of the Scientific Advisory Panel for the RosBREED2 program and the Scientific Advisory Council at Driscoll's. Fred holds a B.S. Degree in Agronomy from the Univ. of Nebraska Lincoln and the Ph.D. Degree in Horticulture and Genetics from the University of Wisconsin-Madison followed by post doctoral study at the Univ. of Minnesota.

JOHN R. CLARK, University of Arkansas, AK

John R. Clark is a university professor of horticulture at the University of Arkansas. His research responsibilities are his primary appointment, where he directs the University's Division of Agriculture fruit breeding program. Crops he works with include blackberries, table grapes, muscadine grapes, blueberries, and peaches/nectarines. He also teaches in the areas of plant breeding and fruit production and advises graduate and undergraduate students. He has developed more than 50 varieties of various fruits and has cooperative breeding activities at several locations in the United States in addition to Europe, Mexico, South America, and Australia. He has worked in fruit breeding since joining the University of Arkansas in 1980.



JOSÉ M. COSTA, USDA, ARS, Beltsville, MD

José M. Costa is presently National Program Leader for Plant Genetics and Grain Crops at USDA-ARS. He oversees ARS research projects on genetics and breeding of wheat, barley, oats, switchgrass, corn and sorghum as well as the USDA-ARS-led US Wheat and Barley Scab Initiative. He led the University of Maryland small grains breeding program until 2013. He has extensive experience in plant breeding and started his plant breeding career at the National Institute of Agricultural Technology (INTA) in Argentina. Currently serves on the Executive board of the Borlaug Rust Initiative, the International Wheat Initiative and the International Wheat Yield Partnership.



THEODORE M. CROSBIE, Chief Technology Officer, State of Iowa

Dr. Ted Crosbie retired in March 2014 as the R&D Lead for the Integrated Farming Systems (IFS) platform, which he started as a member of Monsanto's Global Strategy Group in January of 2010. In this role, he pioneered the effort to develop and implement Monsanto's agronomic solutions and precision agriculture programs for farmers. Dr. Crosbie previously served as Vice President of Global Plant Breeding of the Monsanto Agricultural Sector, from 1998-2010, where he was responsible for seven crops worldwide. Monsanto's Plant Breeding organization is one of the largest breeding efforts in the world with more than 2,000 employees and over 125 sites worldwide in 20 countries. In January 2002, Dr. Crosbie was named a Distinguished Fellow in Science in recognition of his broad strategic impact in Monsanto through scientific leadership. He was a member of the Monsanto Advisory Committee, the Technology



Leadership Team, and the Global Strategy Group Leadership team. Dr. Crosbie joined Monsanto in 1996 as the Director of Global Wheat Breeding. In 1997, he joined the Seeds Business Team in the Ag Sector of Monsanto. He, along with Jim Tobin and Mike Morgan, coordinated, integrated and managed Monsanto's seed businesses through the acquisition strategy. Prior to joining Monsanto, Dr. Crosbie was the President and Chief Executive Officer of ICI Seeds, USA from 1990-95 after spending most of his career in plant breeding research beginning as a Graduate Faculty member of the Agronomy Department at Iowa State University from 1979-82. Dr. Crosbie earned a B.S. in Agricultural Education from Iowa State University in 1973. He earned a M.S. in Plant Breeding and Cytogenetics from Iowa State University in 1976 and his Ph.D. also in Plant Breeding and Cytogenetics from Iowa State University in 1978. In November of 2005, Iowa Governor Tom Vilsack named Dr. Crosbie to the position of Chief Technology Officer for the State of Iowa and he has served three Governors of Iowa in that position. In September of 2007, Iowa Governor Chet Culver named Dr. Crosbie to the Power Fund Due Diligence Committee, a group tasked with reviewing recommendations that came before the Power Fund Board for expenditures from a \$100,000,000 annual budget, to be utilized for enhanced energy conservation and biorenewable energy production in Iowa. In February 2011, he was re-appointed as Chief Technology Officer and named the Chair of the Iowa Innovation Council by Governor Terry Branstad. In 2013, Governor Branstad and the Iowa Innovation Corporation recognized him with a Lifetime Achievement Award for his contributions to economic development in the State of Iowa. Dr. Crosbie serves on the following boards. Iowa Economic Development Authority, Kemin Industries Board of Advisors, The Nelson Family Trust, Titan Machinery (TITN), Renewable Energy Group (REGI), Kaiima Bio-Agritech, Inocacor Technologies, and Blue River Technologies.

DAVID FRANCIS, The Ohio State University, Wooster, OH.

David Francis is Professor of Horticulture and Crop Sciences at The Ohio State University. He received his early training in Biology at Pomona College and his PhD in Genetics from UC Davis. He is located on the Wooster campus of the Ohio Agricultural Research and Development Center where he leads the processing tomato breeding and genetics program. He and his students emphasize solving problems caused by bacterial diseases of tomato and the development of genetic resources for studying the effects of carotenoids on human health and nutrition. An expected application of his team's research discovery is the development of germplasm and varieties for commercial use. His varieties and parent lines have accounted for over 1M in seed sales. As part of the Solanaceae Coordinated Agricultural Project (SolCAP), he led development of the tomato SNP resources and has used these as a tool to facilitate practical breeding and to understand the effects of human selection within the context of plant breeding programs. Dr. Francis teaches advanced plant breeding and methods courses related to bioinformatics, data analysis, and genome assisted selection. He has been recognized by the Ohio Agricultural Research and Development Center for "Distinguished Research" and as the "Innovator of the Year"; by the Midwest food processing industry as the "H. D. Brown Food Processing Person of the Year"; and by the United States Department of Agriculture as a recipient of the Honor Award for Excellence.



ROGER E. FREEMAN, Bayer CropScience – Vegetable Seeds, Brooks, OR

Roger started his current job as carrot breeder in August 1982, working in this role at Brooks Oregon for now 33 years. He received his BS (77) in Horticulture from Texas A&M University and his MS (79) in Horticulture from



the University of Arkansas, Fayetteville. Roger received his Ph.D. (82) in Plant Breeding and Genetics from the University of Wisconsin, Madison. While at UW, Roger spent three years working within the new USDA Carrot Quality Lab, under the direction of Phil Simon and CE Peterson. Roger's main breeding focus is developing carrot hybrids for all North American markets which include whole root cello packaging, baby cuts, juice, bunching, and processing. The baby cut carrot market has been a major market segment for 20 years and efforts are being made to expand this globally. Roger's breeding efforts also target carrot markets around the world including Brazil, China and Europe. A significant effort over the last several years has been on colored carrots, bringing yellow, red, purple and white commercial high quality carrots to market. These are starting to show up in mixed color packs, and hopefully will become a mainstream snack product within the next 5-10 years. Thus far, Roger has released over 50 commercial carrot hybrids which have been used to produce several billion dollars in commercial carrot crop value for the carrot industry around the world. Bayer CS Vegetable Seeds (previously Nunhems/Sunseeds) has been a major supplier of hybrid carrot seed for USA/Canada agriculture for over 25 years. Roger looks forward to more years of carrot breeding. He loves living in the Pacific Northwest and enjoys time with his family, friends and spending time outdoors.

MICHAEL GORE, Cornell University, NY

Michael Gore is an associate professor of molecular breeding and genetics for nutritional quality and international professor of plant breeding and genetics at Cornell University, where he is a member of the faculty in the Plant Breeding and Genetics Section in the School of Integrative Plant Science. Mike is also a faculty fellow in the Atkinson Center for a Sustainable Future and Cornell Institute for Food Systems. He holds a BS and MS from Virginia Tech in Blacksburg, Virginia, and a PhD from Cornell University. Before joining the faculty at Cornell, he worked as a Research Geneticist with the USDA-ARS at the Arid-Land Agricultural Research Center in Maricopa, Arizona. His expertise is in the field of quantitative genetics and genomics, especially the genetic dissection of metabolic seed traits related to nutritional quality. He also contributes to the development and application of field-based, high-throughput phenotyping tools for plant breeding and genetics research. Mike teaches two short courses at the Tucson Plant Breeding Institute in Tucson, Arizona, serves on the editorial boards of Crop Science, Theoretical and Applied Genetics, and Plant Breeding and Biotechnology, and serves as the Vice-Chair for the Plant Breeding Coordinating Committee (SCC080)—the USDA-sponsored advisory group of representatives from land grant universities. His career accomplishments in plant breeding and genetics earned him the National Association of Plant Breeders Early Career Scientist Award in 2012 and the American Society of Plant Biologists Early Career Award in 2013.



MICHAEL J.HAVEY, USDA-ARS University of Wisconsin, Madison, WI

Dr. Havey is a USDA Research Geneticist and Professor in the Dept. of Horticulture at the University of Wisconsin-Madison (UW). He received his B.S degree in Plant Pathology from Iowa State University, M.S. degree in Plant Pathology from UW, and Ph.D. degree with a double major in Plant Pathology and Plant Breeding & Plant Genetics from UW. He completed post-doctoral research positions in Brazil and at Washington State University, before joining the USDA and UW faculty in 1988. Dr. Havey's research program focuses on the breeding, genetics, and genomics of the Alliums (onion and garlic) and cucurbits (cucumber, melon, and watermelon), and has published over 100 peer-reviewed papers. He has been chair of the



graduate program in Plant Breeding and Plant Genetics (PBPG) at UW-Madison for over 10 years, and served as major professor of 20 PhD and 7 Master's students all in PBPG. Dr. Havey also serves on the editorial boards of the journals Theoretical and Applied Genetics and Plant Breeding.

JAMES A. HEILIG, Michigan State University, East Lansing, MI.

Jim is a Ph.D. candidate in Plant Breeding, Genetics, and Biotechnology at Michigan State University in the Plant, Soil, and Microbial Sciences Department. He works in Dr. James D. Kelly's lab and anticipates graduating in summer 2015. Born and raised in Michigan, Jim received his B.S. degree in Horticulture from MSU. After working as a state agriculture inspector, he returned to MSU to pursue his M.S. in Plant Breeding, Genetics, and Biotechnology. Jim's graduate work has focused on symbiotic nitrogen fixation (SNF) in common bean (*Phaseolus vulgaris*). He is working with a RIL population derived from the black beans 'Puebla 152' and 'Zorro' to find QTLs associated with SNF traits to find markers useful for selection of advanced breeding lines with enhanced SNF characteristics. The population has been phenotyped in both the greenhouse and in the field in Michigan and Puerto Rico. Additionally, Jim has conducted on farm trials to evaluate dry beans grown under organic production systems and investigate the impact of SNF on productivity.



AMY IEZZONI, Michigan State University, East Lansing, MI

Amy Iezzoni is a University Distinguished Professor in the Department of Horticulture at Michigan State University where she directs the Michigan State University tart cherry scion and cherry rootstock breeding programs, has an active program in cherry genetics, and co-teaches two graduate courses in plant breeding and genetics. Dr. Iezzoni was the Project Director of the USDA- Specialty Crop Research Initiative (SCRI) coordinated agricultural project entitled "RosBREED: Enabling marker-assisted breeding in Rosaceae", an international collaborative project designed to increase breeding efficiency and the success of new cultivar adoption for apple, cherry, peach and strawberry. She is currently the Project Director of a second coordinated agricultural project, also funded by the USDA-SCRI program, entitled "RosBREED: Combining disease resistance with horticultural quality in new rosaceous cultivars" that seeks to extend the benefits of DNA informed breeding to more rosaceous crops and traits using expanded genomics information.



SHELLEY JANSKY, USDA-ARS, University of Wisconsin-Madison, WI

Shelley Jansky is a Research Geneticist with the USDA-ARS and an associate professor in the Department of Horticulture at the University of Wisconsin-Madison. Her research program focuses on potato germplasm enhancement, with the goal of developing genetics resources and parents for use by breeders in cultivar development. Currently, her program is developing recombinant inbred line populations in interspecific diploid potato populations and self-pollinating cultivated potato to create inbred lines for breeding and genetics analyses. Shelley received her B.S. in Biology at the University of Wisconsin-Stevens Point and M.S. and Ph.D. degrees in Plant Breeding and Plant Genetics at the University of Wisconsin-Madison.



KEITH JAYAWICKRAMA, Oregon State University, Corvallis, OR.

Keith Jayawickrama is Director of the Northwest Tree Improvement Cooperative (NWTIC) at Oregon State University (OSU), where he has served since 2000. His expertise is in forest tree breeding and tree improvement, and he currently assists the tree improvement programs of most of the significant forest growers in western Oregon and western Washington through the NWTIC. Dr. Jayawickrama's work and research for the past 27 years has focused on breeding, testing, selection, and deployment of commercially important conifer timber species (Douglas-fir, western hemlock, radiata pine and loblolly pine) through field-based breeding approaches. His research publications include work on realized genetic gain, inheritance of various traits, improvement of wood quality and breeding strategy. Prior to joining OSU, he worked in applied tree improvement programs at the Universidad Austral de Chile and the New Zealand Forest Research Institute. Keith earned a B.Sc. Special degree in Botany from the University of Colombo in 1986, and M.S. and Ph.D. degrees in Forest Tree Improvement from the North Carolina State University in 1990 and 1996.



KLAUS KOEHLER, Dow AgroSciences, Indianapolis, IN

After earning a PhD at the University of Hohenheim, Germany in 1986, Klaus Koehler began his professional career at KWS Saat AG, Germany as a Corn Breeder. In 1988 he moved to Champaign, IL to establish a proprietary KWS corn breeding program in the US Corn Belt. He became the NA Director of Corn Research in 1992 and added several breeding stations in the corn belt and a winter nursery site in Puerto Rico. In 1999 he became Head of Global Corn Breeding for AgrEvo with a strong emphasis on development of tropical corn breeding programs in South American and Asia. He maintained that position during the Aventis merger and the acquisition of that company by Bayer Crop Science. During this time period he established a site for event selection and trait QC for corn and soybeans in Champaign, IL. In 2004 he became Global Head of Product Development for MTI GmbH. In 2006 he joined Dow AgroSciences first as the NA Northern Corn Breeding Leader, responsible for northern breeding sites and early corn breeding strategy, then became Global Temperate Corn Breeding Leader in 2009. In this role, he developed the corn breeding strategy to adopt di-haploid technology, marker-assisted breeding and novel decision making tools. Since January 2014 he became the NA Breeding and Product Development Leader, responsible for all DAS breeding stations and all crops in the lower 48 states, Ontario and Puerto Rico. He is the current secretary of NAPB.



JIM LUBY, University of Minnesota, MN

Jim Luby is a Professor in the Department of Horticultural Science at the University of Minnesota where he has directed the fruit crops breeding program since 1982. The emphasis of this program has been to develop cultivars that combine high quality with cold hardiness and disease resistance. His research aims to determine the inheritance of these traits and identify important loci and markers for use in marker-assisted breeding. Luby's education includes a B.S. degree in Crop Science from Purdue University and a Ph.D. in Plant Breeding from the University of Minnesota. Under his direction, the University of Minnesota fruit crops breeding program at the has introduced 26 cultivars of apples, blueberries, strawberries, wine grapes, apples and other fruits including the Honeycrisp



apple which has become a favorite of North American consumers. Luby teaches and advises students in plant breeding and fruit production. He is Director of Graduate Studies for the Applied Plant Sciences program, which includes plant breeding and genetics. He is also a member of Driscoll's Scientific Advisory Council.

JOZER MANGANDI, University of Florida, Gainesville, FL

Jozer Mangandi is a PhD candidate in Horticultural Sciences at the University of Florida, advised by Drs. Vance Whitaker and Natalia Peres. He is originally from El Salvador, earning his B.S. in Agricultural Science and Production from the Pan-American Agricultural University "Zamorano", Honduras in 2005. He joined the University of Florida's Gulf Coast Research and Education Center in 2006, pursuing research on disease resistance on strawberries and ornamentals. He earned an M.S in Horticultural Sciences from University of Florida in 2010 and expects to complete his Ph.D. in December, 2015. His dissertation research is part of a concerted breeding effort to increase disease resistance in UF strawberry cultivars. Specifically, he is uncovering the inheritance of resistance to two strawberry crown rot pathogens (*Phytophthora cactorum* and *Colletotrichum gloeosporioides*), identifying and validating QTL associated with high levels of resistance. After graduation he will pursue his goal of a career in the plant breeding industry, with a strong focus on disease resistance traits.



REBECCA MCGEE, USDA-ARS, Washington State University, Pullman, WA

Dr. Rebecca McGee is a USDA-ARS Research Geneticist located at WSU in Pullman, Washington. She received a B.S. from the University of Washington, an M.S. from the University of Alaska and a Ph.D. from Oregon State University. Prior to joining the ARS, she was a Principal Scientist at General Mills, Inc. and directed the vegetable legume breeding programs. Currently, her research focuses on breeding cool season food legumes, primarily spring- and autumn-sown peas and lentils. The priorities of her breeding program include breeding for resistance to biotic and abiotic stresses and mineral biofortification. During her career in both the private and public sectors, she has contributed to the release of more than 35 varieties of peas and lentils. She is a member of the Executive Committee of the North American Pulse Improvement Association, the Chair of the Pisum Crop Germplasm Committee, and serves on the editorial board of the Journal of Plant Registrations.



LAURIE MCKENZIE, Organic Seed Alliance, WA

Laurie McKenzie is the Research and Education Associate for the Pacific Northwest region and a vegetable breeder with Organic Seed Alliance (OSA). She manages the OSA research farm in Chimacum, WA where she conducts breeding projects, vegetable variety trials, and seed production on a variety of crops. At OSA Laurie has authored and co-authored several publications and taught many classes and workshops on seed production and plant breeding. She received her M.S. in Horticulture and Plant Breeding from Oregon State University in 2012. In her breeding career Laurie has focused on breeding for organic production systems utilizing participatory and collaborative strategies. She is currently working on several collaborative breeding projects involving cabbage, kale, purple sprouting broccoli, carrots, and Swiss Chard. In her spare time Laurie enjoys creating her budding homestead, planting fruit trees, playing with her ducks, and growing flowers in the garden.



RICH NOVY, USDA-ARS, Aberdeen, ID

Rich Novy is a potato breeder/geneticist with the USDA-ARS at Aberdeen, Idaho and has been in this position since 1999. Prior to accepting his current position he was the potato breeder/geneticist at North Dakota State University, Fargo, ND. He attended Washington State University and obtained his B.S. in Horticulture and his M.S. and Ph.D. in Plant Breeding and Genetics at the University of Wisconsin-Madison. He is a member of the Northwest (Tri-State) Potato Variety Development team comprised of state and federal researchers in the states of Idaho, Oregon, and Washington and during his career has contributed to the release of 37 potato varieties. His contribution to potato variety development has been recognized with two ARS technology transfer awards, a Federal Laboratory Consortium for Technology Transfer Award from the Far West region, a USDA-NIFA Partnership Award for a SCRI grant in controlling zebra chip disease, and an Outstanding Extension Award for the storage management of new potato cultivars from the Potato Association of America. In addition, he has authored or co-authored 59 breeding and genetics publications in peer-reviewed journals.



JAMES OLMSTEAD, University of Florida, Gainesville, FL

Dr. James W. Olmstead is an Associate Professor in the Horticultural Sciences Department at the University of Florida, where he leads the blueberry breeding and genetics program. His breeding program focuses on development of low-chill requirement southern highbush blueberries that are adapted to subtropical climates. Improving fruit quality characteristics and developing wider adaptation in blueberry cultivars are focus areas in for research and breeding efforts. His research program covers a broad range of topics ranging from understanding consumer preferences to implementing genomic selection in autopolyploid crop species. Dr. Olmstead received his B.S. (1997) and M.S. (1999) degrees in Horticulture from Washington State University where he worked at the Irrigated Agriculture Research and Extension Center in Prosser, WA studying disease resistance in sweet cherry. He received his Ph.D. at Michigan State University (2006) in Plant Breeding and Genetics, where he identified QTL associated with fruit quality traits in sweet and sour cherry. Prior to his position at the University of Florida, he was a county extension agent in Yakima, WA. Since starting at UF in 2009, Dr. Olmstead has released six blueberry cultivars, and has served as a committee member for 26 graduate students including 7 as chair or co-chair. He teaches a graduate level course in Marker-Assisted Plant Breeding and co-teaches Advanced Genetics, and is a member of the UF Genetics Institute and the UF Plant Innovation Center.



KATHLEEN RUSSELL, University of Kentucky

Kathleen Russell is a Ph.D. candidate in Integrated Plant and Soil Sciences with a focus on Plant Breeding and is advised by Dr. David Van Sanford at the University of Kentucky. Her anticipated graduation is May 2016. She received her B.S. in Natural Resource Management (2004) and M.S. in Entomology (2007) from the University of Kentucky and afterwards spent some time doing field research with a private environmental consulting firm. Kathleen's graduate research is focused on understanding the effects of heat stress on nitrogen use efficiency in soft red winter wheat varieties adapted to the Southeastern United States and how to better screen for tolerance in the field for improved breeding strategies.



MARIA SALAS FERNANDEZ, Iowa State University, Ames, IA

Maria Salas Fernandez is an Assistant Professor in the Department of Agronomy at Iowa State University. Previous to her appointment in the academia, she worked in the private sector in Argentina, at the R&D Department of American Cyanamid Company and as a sorghum breeder at Nidera S.A. She received a B.S. in Agricultural Production from the Argentine Catholic University, M.S. in Plant Physiology from Texas A&M University, and Ph.D. in Plant Breeding and Genetics from Cornell University. She initiated and leads a sorghum field breeding program at ISU to develop germplasm for forage and biofuel production adapted to the Midwest. Her research program is also focused on the use of high-throughput genotyping and phenotyping technology to identify genetic mechanisms controlling traits such as plant architecture, photosynthesis, photoprotection and cold tolerance at germination. In 2012, Dr. Salas Fernandez was granted the prestigious NSF CAREER award for her novel research in photosynthesis and photoprotection. She was also recognized as the 2013 American Society of Agronomy (ASA) Early Career Professional Award and the 2014 NAPB Early Career Award. Her appointment at ISU also includes responsibilities as the instructor of an undergraduate course in Genetics, Agriculture and Biotechnology and as an advisor of 20 undergraduate students in Agronomy



KRISTIN SCHNEIDER, Monsanto

Kristin Schneider, Monsanto's Global Wheat Breeding Lead is responsible for managing the global breeding research program focused on improved wheat variety development. Trained as a plant breeder at Michigan State University, she started at Monsanto in 1999 as a corn breeder responsible for developing enhanced grain quality corn genetics. Navigating Monsanto's broad research and development pipeline, Kristin shepherded projects like INTACTA RR2 PRO™ soybeans, Genuity® Roundup Ready® 2 Xtend soybeans and corn high-yield concepts through early phases of development. Since 2011, Kristin has been leading the wheat breeding organization focused on applying Monsanto's pioneering expertise in advanced breeding and genomics technology to the improvement of wheat varieties for all market classes grown in the US. Kristin shares her time living in St Louis, MO and Twin Falls, ID where she and her team are executing novel wheat breeding strategies at the new Monsanto Wheat Technology Center.



ERIN SILVA, University of Wisconsin-Madison, WI

Erin Silva received her PhD in Horticulture from Washington State University in 2002, working in the area of onion seed production and pollination. Subsequently, she spent time as a postdoctoral researcher with Dr. Philipp Simon with the USDA-ARS carrot breeding program and then as an Assistant Professor at New Mexico State University. She is currently an Assistant Professor and Extension Specialist in Organic and Sustainable Cropping Systems at UW-Madison, working on several national projects to develop and identify vegetable cultivars with traits advantageous for organic production systems, including the Northern Organic Vegetable Improvement Collaborative and Carrot Improvement for Organic Agriculture.



PHILIPP SIMON, USDA-ARS, University of Wisconsin – Madison, WI

Dr. Phil Simon is a USDA, ARS Research Geneticist and Professor of Horticulture at the University of Wisconsin, Madison. His research in vegetable genetics and breeding has focused on carrot improvement, targeting improved flavor and nutritional quality, nematode, disease and abiotic stress resistance. He led the development of widely used carrot germplasm with high carotene content, sweet, mild flavor, purple color, and root-knot nematode resistance. To complement his breeding effort, along with students and collaborators, he has developed breeding tools, including the sequencing of the carrot genome, and he has collected carrot, Allium, and other vegetable germplasm in nine collecting expeditions. He has undertaken related plant breeding research including the first production of true seed in garlic, and the development of cucumber and melon germplasm with orange color and elevated carotene content. He has supervised the training of 30 graduate students, is a Fellow of the American Society for Horticultural Science, recipient of the ASHS Vegetable Breeding Award, and of an Honorary Doctorate from the Agricultural University of Krakow, Poland. He is a past chair of the Plant Breeding Coordinating Committee.



DAVID SMITH, Oregon State University, Corvallis, OR

David Smith is a Senior Faculty Research Assistant in the Horticulture Department at Oregon State University, where he manages the greenhouse and field operations of the Hazelnut Breeding Program for Dr. Shawn Mehlenbacher. He received his B.S. in Horticulture at Oregon State in 1982 and began working with the breeding program shortly thereafter, where he is in charge of pollinations, propagation by seed and scion, disease screening inoculation, plot establishment, and keeping Shawn's chainsaws sharp. He is a co-developer, along with Shawn and Becky McCluskey, of 10 main crop, 11 pollinizer, and 3 ornamental cultivars of hazelnut, 4 of which are accounting for 3000+ acres of new orchard plantings annually in Oregon's Willamette Valley.



ANN MARIE THRO, USDA, Washington DC

Ann Marie Thro is 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). Through early 2015, she is serving as Sr. Agricultural Advisor for Plant Sciences in the Office of the Chief Scientist, USDA. 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. 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 (1992-1998); 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.



BILL TRACY, University of Wisconsin-Madison, WI

Bill Tracy is professor and chair of the dept. of agronomy, UW-Madison. He served as interim dean of the College of Agricultural and Life Sciences. As a sweet corn breeder, Bill works closely with commercial sweet corn breeders and has developed sweet corn inbreds grown commercially on every continent (with arable land). He has also developed sweet corn cultivars for organic cropping systems. Bill has had the pleasure of mentoring more than 40 graduate students most of whom work in commercial plant breeding. His research areas include the genetics, genomics, and biochemistry of endosperm carbohydrate synthesis, the relationship between plant development and pest resistance, and the origin and phylogeny of sweet corn. He serves the plant breeding community in a number of roles. He is the current chair of the Maize Crop Germplasm Committee, the CIMMYT Maize Germplasm Committee, and the International Sweet Corn Development Association, the corn breeding executive committee and the NAPB advocacy committee.



GAYLE M. VOLK, USDA-ARS National Center for Genetic Resources Preservation, Fort Collins, CO

Gayle Volk specializes in the conservation of vegetatively propagated crops and crop wild relatives (primarily fruits and ornamentals) in the U.S. National Plant Germplasm System. She has a B.S. in Biochemistry from Colorado State University, an M.S. in Horticulture from Purdue University, and Ph.D. in Plant Physiology from Cornell University. She is based at the National Center for Genetic Resources Preservation, one of the largest seed banks in the world. Her research focuses on identifying strategies to capture and maintain genetic resources in diverse clonal collections and on providing decision-support tools to evaluate the breadth and depth of genetic diversity in their collections. She also develops widely applicable and cost-effective methods to cryopreserve clonally-derived germplasm and seeks to better understand the physiological processes that occur during the cryopreservation process. She is currently the Chair of the U.S. Apple Crop Germplasm Committee as well as the U.S. Rosaceae Executive Committee, and is coordinating the development of the Global Conservation Strategy for Apple.



JENNIFER YATES, Monsanto

Interested in the field of genetics at an early age, Jennifer Yates pursued that interest to a B.S. degree in genetics at the University of Georgia, and, while there, refined that interest to the field of plant genetics. She attended the University of California-Davis for her M.S., originally intending to continue the crop genetic transformation research she had done at Georgia, but decided to switch to the field of plant breeding after taking a plant breeding course. Jennifer returned to the University of Georgia to obtain her PhD in Agronomy, specifically focusing on soybean breeding. Upon completing her degree, she joined Monsanto in 2006 as a soybean breeder in Galena, MD. She was a soybean breeder during Monsanto's transition from RR1 to RR2Y, and became an inventor and co-inventor on the many varieties that helped enable this full portfolio of RR2Y products. In late 2011, Jennifer accepted the position of Agronomic traits lead and relocated to St. Louis. In this role, Jennifer's team supports soybean breeders in North and South America, providing disease and abiotic stress characterization, as well as such discovery projects as yield loss assessments from disease and enabling rapid pathogen identification methods in the field. Jennifer was a recipient of a National Science Foundation



pre-doctoral fellowship and a participant in a 10-week study abroad session in S. Korea funded by NSF. Since joining Monsanto, Jennifer has been inducted in the Monsanto Fellows program, is an inventor on several marker and variety patents, has received a Global Breeding excellence award, and has pursued outreach activities such as volunteering to teach science experiments in classrooms and starting a mentoring program for women in plant breeding.

Speaker Abstracts (in order of presentations)

**PHILOSOPHY AND PRACTICE OF UTILIZING GENETIC DIVERSITY
IN PLANT BREEDING**

Rex Bernardo, University of Minnesota, Saint Paul, MN

The theme of the 2015 NAPB meeting is *Identifying and utilizing genetic diversity*. We as plant breeders have always said that we value plant genetic diversity in our breeding programs. But we often, if not usually or almost always for some species, fall short in effectively utilizing genetic diversity in cultivar development. In this presentation I will focus on critical questions, practical problems, possible solutions, and persistent issues in bridging the gap between the philosophy and practice of exploiting genetic diversity in plant improvement. From a breeding standpoint, what exactly is genetic diversity? Doesn't a plant breeder actually want to come up with the single, perfect cultivar that combines all of the best genes and, in so doing, actually exhaust the genetic diversity? Should genetic diversity be viewed in terms of genes, combinations of genes, germplasm, or something in between? Should we view genetic diversity primarily as a means of increasing long-term genetic gains, or as a means of mitigating risks due to abiotic and biotic stresses? What types of diverse germplasm might be the most promising? Can we effectively use molecular markers to selectively incorporate only the diversity that is good? Can we effectively select for both high performance and genetic diversity? Does selection based on genomewide markers hasten the depletion of genetic diversity? I do not promise profound answers to these questions, but I hope you come to this talk anyway.

IDENTIFICATION AND CONSERVATION OF APPLE GENETIC DIVERSITY

Gayle M. Volk, USDA-ARS National Center for Genetic Resources Preservation, 1111 S. Mason St., Fort Collins, CO 80521

The USDA-ARS National Plant Germplasm System (NPGS) maintains a vast collection of plant genetic resources that includes over 570,000 accessions representing nearly 15,000 species. This collection is dispersed amongst 17 active sites throughout the United States. The NPGS base collection at the National Center for Genetic Resources Preservation is among the largest gene banks in the world. We have focused on documenting the diversity of the NPGS Apple Collection maintained in Geneva, NY, and on proposing methods to capture genetic diversity that is not yet represented. We have sought to make the collection more useful to breeding programs by identifying core subsets and as well as relationships among domesticated apples and their progenitor species. Recently, we reviewed historical documentation of apple varieties in the US and determined the availability of key historical cultivars in US and English apple collections. In the process of developing a Global Conservation Strategy for Apple, we surveyed international apple collections and summarized key features such as species inventories and accessibility. These efforts to understand the diversity of global apple genetic resources will help ensure access to germplasm for breeding and research programs.

SIXTY YEARS OF FOREST TREE IMPROVEMENT IN OREGON, WASHINGTON AND BRITISH COLUMBIA

*Keith JS Jayawickrama¹

¹Oregon State University, Northwest Tree Improvement Cooperative, Department of Forest Ecosystems and Society, Corvallis, OR, U.S.

The first significant tree improvement trial in the Pacific Northwest was the Douglas-fir heredity study established in 1912. In the mid-1950s genetics programs were started at what became two leading institutions of applied tree improvement on the west coast (the US Forest Service PNW Research Station and the British Columbia Forest Service), and plus-tree selection and grafted clonal orchards were emphasized. The IFA-PNW "Progressive Tree Improvement System" was launched in 1966, emphasizing forming local cooperatives to share costs, on progeny testing large numbers of trees using wind-pollinated seed in small testing zones, and delivering improved seed from seed orchards established using full-sib crosses made on the parent trees.

Species emphasized in tree improvement, all conifers, include coastal Douglas-fir, western hemlock and Noble Fir (western OR and Washington), interior Douglas-fir (Inland Empire), and coastal and interior Douglas-fir, lodgepole pine, interior spruce, western red cedar and Sitka spruce (BC). Intensive disease resistance breeding work is done for western white pine, sugar pine and Port-Orford-Cedar. Douglas-fir breeding programs have dwarfed all the other programs on the west coast, with over 34,000 first-generation parents selected from the wild and tested. Tests were typically measured till they were 12 to 15 years from seed. Height was usually measured each time, and stem diameter at 1.4 meters from the ground at least once. The incidence of stem defects such as ramicorn branches, forks and stem sinuosity was often assessed. Indirect selection for wood quality (especially stiffness and strength) can be exerted by measurement of wood specific gravity or acoustic velocity.

Increased production of merchantable roundwood/hectare/year is the key breeding goal of forest tree improvement programs. This is achieved by: selecting for several traits (total height, diameter at breast height, low incidence of stem defect, tree health, lack of damage, and the ability to withstand disease in the case of resistance breeding programs) and by evaluating progenies over about ¼ of total rotation length in conditions comparable to those encountered in operational plantations. Abiotic challenges in the PNW include summer drought and high temperatures (sometimes over many months), sudden frosts in the spring and fall, low temperatures in winter, and heavy wet snow. The western red cedar program has emphasized developing trees unpalatable to deer and other herbivores, while the Sitka spruce program focused on resistance to the white pine weevil. Improved genetic material is generally delivered to forest growers in the form of wind-pollinated seed from grafted clonal seed orchards; those seed are germinated to grow one- or two-year-old seedlings which are hand planted in tree farms.

A subset of species (coastal Douglas-fir, western hemlock, western red cedar, Port Orford Cedar, western white pine) have been progressed to a second- or even third-cycle of testing. Second- and third-cycle breeding populations are typically smaller than the first-generation, but still number in the hundreds or thousands of individuals. Breeding strategies usually center on advancing a fairly large and genetically diverse breeding population through recurrent selection for general combining ability, with little or no emphasis on development of inbred lines, hybrids, cultivars, clones, or genetically modified organisms.

HAZELNUT BREEDING AT OREGON STATE UNIVERSITY

Shawn Mehlenbacher and *David Smith, Oregon State University Horticulture Department

Commercial production of European hazelnut, *Corylus avellana*, is based on genotypes that were selected from local populations of wild seedlings. Because hazelnut is an obligate out-croser, these elite selections were clonally propagated from basal shoots and became the named cultivars that now account for the majority of hazelnut plantings. The hazelnut industry in Oregon has been focused on the in-shell market, which prefers large-sized whole nuts, for most of the last century. However, the majority of hazelnuts worldwide are marketed as kernels for industrial use in the baking and confectionary trades and the requirements for the kernel market are quite different from the in-shell market. Superior kernel varieties are small, thin-shelled, with a pellicle that is easily removed, and have pronounced flavor and aroma after roasting. The development of new cultivars with these traits, which are also high-yielding and adapted to Oregon's Willamette Valley, has been the main goal of the breeding program at Oregon State University (OSU) since the inception of the breeding effort in 1969.

Eastern filbert blight (EFB), a fungal disease that is endemic on *Corylus americana*, the species native to the eastern U.S., made its way to Clark County, in SW Washington, and began infecting commercial orchards around 1960. EFB causes perennial cankers and is ultimately a tree-killing disease. It slowly spread southward and was discovered in Oregon's Willamette Valley in 1986. Most European cultivars are susceptible to EFB to varying degrees, but the obscure pollinizer 'Gasaway' was discovered to be completely free of disease symptoms and was used in the first crosses made by Dr. Maxine Thompson in 1976 to incorporate resistance to EFB. 'Gasaway' had no other redeeming qualities, but it transmitted EFB resistance as a single dominant gene, so improvement in productivity and nut qualities was relatively quick. It takes at least 17 years to release a new hazelnut cultivar, from the time that a controlled pollination is made to the time the data has been gathered from yield trials. Six cultivars with resistance to EFB from 'Gasaway' have been released since 2005 and the hazelnut acreage has doubled since 2009, to approximately 50,000 acres, with strong continued growth expected into the foreseeable future. Concern about the long-term durability of a single source of EFB resistance spurred the search for additional sources in European hazelnut and other *Corylus* species. The OSU and USDA hazelnut collections inherited by Dr. Shawn Mehlenbacher were mostly German, English, Spanish and Italian cultivars. Mehlenbacher travelled to Turkey, the Republic of Georgia, Azerbaijan, Iran, Ukraine and southern Russia and collected seeds and scions to increase representation from these areas. Some 60 accessions of diverse origins have now been identified with resistance to EFB. Several new incompatibility alleles have also been discovered. Molecular genetic tools are used for screening seedlings for EFB resistance, and an SSR marker-based dendrogram is used when designing crosses to maximize genetic diversity.

IDENTIFYING AND EXPLOITING GENETIC DIVERSITY IN CHERRY TO INCREASE INDUSTRY PROFITABILITY

*Amy Iezzoni, Michigan State University Department of Horticulture

The tart cherry (*Prunus cerasus* L.) industry in the U.S. is an example of an agricultural crop with extreme genetic vulnerability to disasters caused by pests, diseases, and unfavorable weather conditions. The entire U.S. tart cherry industry is based on one cultivar 'Montmorency' and Michigan and the Great Lake's Region produces 80% of the nation's tart cherries. This

monoculture proves an ideal environment for crop losses due to unfavorable weather or to disease and pest epidemics. Unfortunately, the vulnerability of this monoculture was realized in 2002 as spring freeze damage reduced tart cherry production to the lowest level recorded since 1945 (i.e. 2% of a normal crop) with a devastating effect on the industry and economy of the fruit growing regions. Would cultivar diversification have prevented this dramatic crop loss? An evaluation of pistil freeze damage from 21 other tart cherry selections planted along side Montmorency indicated that the nearly complete crop loss experienced in 2002 would have been greatly reduced if the industry had been growing an array of genotypes. This is just one of many examples that will be showcased of the need and potential for the utilization of a wider range of genetic diversity in tart cherry cultivars and rootstocks.

THE USDA-ARS COOL SEASON FOOD LEGUME BREEDING PROGRAMS

Rebecca McGee, USDA-ARS and WSU-Pullman

The cool season food legumes – peas (*Pisum sativum* L.), lentils (*Lens culinaris* Medik.) and chickpeas (*Cicer arietinum* L.) are grown in most temperate regions of the world and are some of the most ancient domesticated crops. In 2013, nearly 11 million tonnes of dry pea were harvested from 6.4 million ha, 5 million tonnes of lentils from 4.3 million ha and 13 million tonnes of chickpeas from 13.5 million ha. The CSFL are important rotational crops in predominantly cereal-based cropping systems as they help break disease and weed cycles and, through the symbiotic association with rhizobia bacteria, add nitrogen to the soil. Pea, lentil and chickpea seeds are high in protein, low in fat, have a low glycemic index and are important sources of mineral nutrients. The end uses of CSFL include food, feed, forage and cover crop. Although peas were the model crop for the genetic studies of Gregor Mendel, until recently the CSFL have been the ‘orphans’ in the adoption of molecular-genetic and genomic resources that have directly contributed to the significant and rapid expansion of gene discovery, knowledge of gene function (including tolerance to biotic and abiotic stresses) and genetic improvement of many crop species. This has been due in large part to the limited availability of genetic and genomic information. Peas and lentils have extremely large (>4Gb) and complex genomes characterized by highly repetitive sequences and retrotransposons that comprise 75-97% of the nuclear DNA.

The USDA-ARS spring pea and lentil breeding programs at WSU were established in 1964. The chickpea breeding program was initiated in 1987 in an effort to develop chickpea varieties with resistance to *Aschochyta* blight. The winter legume (peas and lentils) program was started in 1988. The breeding programs use pedigree, single seed descent and F2-derived family methods. Future challenges include yield improvements to maintain competitiveness as rotational crop, breeding for improved resistance to abiotic and biotic stresses, biofortification, and breeding for improved utilization as flour or fractions for new food applications. This presentation will highlight three projects - biofortification of peas, development of autumn-sown peas, and breeding for tolerance to *Aphanomyces* root rot - of the USDA-ARS CSFL breeding program.

EXTREME MAKEOVER POTATO EDITION

Shelley Jansky, USDA-ARS and UW-Madison

Despite tremendous advances in crop breeding and genetic methodologies in the past century, techniques for creating new tetraploid potato cultivars have not changed. Genetic complications arising from heterozygosity and tetraploidy limit gain from selection. Genetic gain for high-value traits such as yield, quality, and disease resistance has been dismal in potato compared to other staple crops. Furthermore, the methods currently used by potato breeders are inefficient and do not fully maximize the power of new genomics resources. It is time for a major makeover of the potato crop. We are converting potato into a diploid inbreeding crop, using wild species germplasm to accomplish this goal. But isn't the optimum ploidy level of potato tetraploid? Perhaps not. Some diploid hybrids between wild and cultivated potato produce tuber yields equivalent to major cultivars. Diploid cultivated inbreds, recombinant inbred lines, and other inbred germplasm resources hold promise for a new and improved way of breeding potatoes.

VARIATION FOR EPICUTICULAR WAXES AND THRIPS RESISTANCE IN ONION

Steven Damon, Dep. of Horticulture; Russell Groves, Dep. of Entomology; and *Michael Havey, USDA-ARS and Dep. of Horticulture, University of Wisconsin-Madison

Onion thrips (*Thrips tabaci*) and thrips-vectored *Iris Yellow Spot Virus* (IYSV) routinely cause significant losses to the bulb and seed crops of onion. Both pests have become more problematic as global temperatures rise. Natural variation exists in onion for amounts and types of epicuticular waxes on foliage, and plants with lower amounts of these waxes have been observed in the field to suffer less damage from thrips and IYSV. Epicuticular waxes on the leaves of onion accessions were evaluated for appearance using SEM and amounts and types determined using GC/MS. Specific ketones and fatty alcohols are the most prevalent waxes on leaves of onion and accessions were identified with significantly ($P < 0.01$) less of these waxes. In field and greenhouse experiments, numbers of adult and immature thrips were significantly reduced ($P < 0.05$) on accessions with less total wax relative to wild-type onions. Genetic mapping revealed that amounts of the primary ketone are controlled by a region on chromosome 5 and fatty alcohols on chromosome 2, indicating that onions can be developed with different compositions and amounts of epicuticular waxes. Intermediate amounts of epicuticular waxes should protect leaves from diseases and environmental stresses, while suffering less damage from thrips and IYSV, in an integrated program to manage these important onion pests.

GREENHOUSE ASSAYS PREDICT FIELD PERFORMANCE OF DRY BEAN WITH REGARD TO YIELD AND SYMBIOTIC NITROGEN FIXATION.

(Graduate student abstract winner)

*James A. Heilig and James D. Kelly, Michigan State University Department of Plant Soil and Microbial Sciences.

Worldwide, dry bean (*Phaseolus vulgaris* L.) is an important crop providing nearly one third of dietary protein. While able to fix N through the association with *Rhizobia* spp., dry bean is often considered a poor fixer. Variability in symbiotic nitrogen fixation (SNF) ability has been identified in dry bean; however SNF is not commonly selected for in breeding programs. Access to labs or

equipment needed to measure N content of plant tissue along with costs are prohibitive to measuring N and percent N derived from the atmosphere (%ndfa). The objective of this study was to identify methods to measure N and determine %ndfa, which would be useful in a breeding program to quickly and efficiently select genotypes with enhanced SNF ability. Seventy-nine black and navy dry bean advanced breeding lines, along with several commercial checks and one non-nodulating reference line, 'R99,' were grown on certified organic fields at two locations in Michigan in field seasons 2011, 2012, and 2013. Seeds were inoculated with *Rhizobia etli* strain CIAT899 prior to planting. The peat based inoculant was added to the seed, moistened with distilled water and mixed to adhere the inoculant to the seed. The plots were managed using approved organic production methods. Traits measured included days to flower, height, maturity, seed yield, and seed N content. The same lines were grown in the greenhouse in N free conditions. Seeds were surface sterilized and planted in 5.7 l plastic nursery pots filled with a perlite and vermiculite potting mixture (2:1, v/v). Pots were inoculated with 250 ml of a dilution made by mixing 500 ml of a 3 d old *Rhizobia etli* strain CIAT899 liquid yeast mannitol culture in 20 l water which had been adjusted to pH 6.5 resulting in approximately 10^3 cells ml⁻¹. Pots were inoculated at planting and at ten d following emergence. Plants were harvested at first flowering by cutting stems at the soil line. Roots were rated (0 to 6) for nodule development and shoot samples were dried, weighed, ground, and total N was measured. The non-nodulating check 'R99' was used as a reference to calculate %ndfa using the difference method for both the field and greenhouse studies.

Variability was seen in the SNF ability of the checks and advanced breeding lines under both field and greenhouse conditions. In the field, %ndfa ranged from 9.8 % in the lowest fixing advanced breeding line in 2012 to 71.7% in 2011 for the highest fixing breeding line. N yield ranged from 16 kg N ha⁻¹ in 2013 for the lowest performing breeding line to 94 kg N ha⁻¹ in 2012. Under N free conditions in the greenhouse, shoot biomass ranged from 0.75 g plant⁻¹ to 13.4 g plant⁻¹ for the breeding lines. Nodule scores ranged from 0.0 (no nodules present) to 6.0 (well developed nodules placed throughout the root system). Biomass difference was calculated by the equation (Biomass Difference=(Biomass fixer (g)-Biomass non-fixer(g))/Biomass fixer (g)). Greenhouse traits did correlate with field traits when characteristics measured in the greenhouse were compared to those in the field. The shoot biomass difference value was correlated with seed yield, %ndfa, and N yield. The highest Pearson correlation for shoot biomass difference and seed yield was $r=0.56$ ($p=0.0003$), for %ndfa was $r=0.73$ ($p\leq 0.0001$), and for N yield was $r=0.48$ ($p=0.0032$). Determination of biomass difference does not require the measurement of N and may serve as a suitable proxy for estimating SNF characteristics in the field negating the need to analyze samples for N content.

FIELD SCREENING FOR SELECTION TO TOLERANCE OF HEAT STRESS IN SOFT RED WINTER WHEAT
USING AN ARTIFICIALLY WARMED ENVIRONMENT
(Graduate student abstract winner)

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Temperature increases for the southeastern United States are projected to range from 1-3°C by 2050. High temperatures are known to affect crop development and breeding for tolerance to heat stress is difficult to achieve in field environments. A multi-year study investigating the effects of heat stress on soft red winter wheat (*Triticum aestivum* L.) varieties was conducted during the 2013-2015 growing seasons at the University of Kentucky Spindletop Research Farm

in Lexington, KY. Forty genotypes were chosen based on the combination of traits for vernalization and photoperiod sensitivity determined using marker analysis. These genotypes were planted in randomized headrows replicated twice across two environments, ambient and artificially warmed. To create a warmed environment, heating cables were buried 2.5 cm below the soil surface and connected to a datalogger programmed to maintain a 1-3°C increase in soil temperature based on replicated thermocouple temperature sensors. Heading date, averaged across genotypes, shifted 5.25 days earlier in the warmed environment compared to the ambient environment across both years ($p < 0.05$). Grain yield, averaged across genotypes, was significantly increased in the warmed environment by 157.2 kg/ha ($p < 0.05$) however yield response to environment varied among genotypes with several genotypes displaying a lower yield in the warmed environment. Based on these results, selection for tolerance to heat stress has the potential to increase yield due to increased early season tillering but shifts in phenology will increase the risk for late season freeze damage. Additionally, this field screening method shows potential for selecting genotypes that are well adapted to shifts in temperature regionally for incorporation into breeding programs.

PEDIGREE-BASED QTL MAPPING OF RESISTANCE TO TWO CROWN ROT PATHOGENS IN ALLO-OCTOPLOID STRAWBERRY

(Graduate student abstract winner)

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Crown rot epidemics in Florida's strawberry production are caused by several pathogens and can destroy entire fields. Chemical control is limited; and even proper disease diagnosis and timely applications are not necessarily curative. The species *Phytophthora cactorum* and *Colletotrichum gloeosporioides* are the most common crown rot pathogens in Florida, both causing economic losses due to plant collapse and subsequent yield loss. The strawberry breeding program at University of Florida (UF) develops cultivars that are widely used in Florida and other parts of the world. Deployment of cultivars with resistance to these two pathogens through traditional selection is a resource-consuming task, and very few cultivars are resistant to both diseases; however, genetic gain for resistance may be accelerated with the adoption of molecular tools. Toward this purpose, a pedigree-based QTL analysis was conducted in commercially relevant breeding germplasm. Approximately 600 seedlings from 52 full-sib families were obtained from crosses among 19 parents in an incomplete circular diallel mating design, with 10 families from crosses among additional parents of interest. A total of 23 direct parents from the UF elite breeding population were represented. Clonal replicates of each seedling were inoculated in separate, replicated field trials for each pathogen and evaluated during the 2013-14 season. Plant collapse was recorded weekly as an indication of crown infection. All parents and progeny were genotyped for 3,430 mapped single nucleotide polymorphism (SNP) loci spanning 37 linkage groups in allo-octoploid strawberry ($2n=8x=56$) using the Affymetrix Axiom[®]iStraw90[®] array. The selected loci were polymorphic in the germplasm tested, had highly reproducible scoring and were sub-genome-specific. The QTL analyses were performed using FlexQTL[™] software, allowing simultaneous QTL detection in all full-sib families based on their known pedigree connections. Broad variation was observed for resistance to both pathogens. Mortality ranged from 0 to 100% for both diseases; area under the disease progress curve (AUDPC) values for crown rot caused by *Phytophthora cactorum* (PhCR) ranged from 0 to 130.8 whereas those for crown rot caused by *Colletotrichum*

gloeosporioides (CCR) ranged from 0 to 110.8. Major QTL were detected, one for resistance to PhCR on LG 7D (Bayes Factor=30) and one for resistance to CCR on LG 6B (BF=26). Estimated phenotypic variation explained in the breeding germplasm by these QTL were ~13% and ~62% for resistance to PhCR and CCR respectively. Estimates of QTL narrow-sense heritabilities were ~0.35 for PhCR and ~0.30 for CCR. Analysis of SNP marker haplotypes associated with these major QTL regions and determination of allele effects should allow the development of DNA-based markers for enhanced parent and seedling selection.

CO-EVOLUTION OF PLANT BREEDING AND PLANT BREEDERS: IMPLICATIONS FOR BREEDER EDUCATION AND CAREER DEVELOPMENT

Fred Bliss, University of California Davis Department of Plant Sciences

Plant breeding is evolving steadfastly into the genomics era while maintaining important elements from previous eras defined by biometrics and individual plant performance. So too there have been changes in breeding methods driven by human creativity and new technology. Accompanying and/or leading these changes have been evolution of plant breeders from crop domesticators to specialized breeders, with more changes on the horizon. Concurrently, each plant breeder must be cognizant of his/her need to grow professionally in order to remain relevant and provide value as a professional. A career often spans several decades from new breeder to retirement, with evolving new innovations, technology, breeding methods and career paths offering challenges and opportunities. Programs, curricula and courses of study must be updated continually to provide relevant, cutting edge knowledge, experience and skills to prepare new breeders. Regardless of the quality and scope of graduate studies, there also must be a diverse array of continuing educational opportunities for all levels of breeders and technical support personnel to extend and upgrade their knowledge and skills of plant breeding for them to succeed personally and for the profession to remain relevant and fulfill expectations of society.

Poster Abstracts

POSTER 1

IDENTIFICATION OF QTLS FOR RESISTANCE TO TERMINAL DROUGHT

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Global cereal production is challenged by climate change for a variety of reasons, especially insufficient moisture. Cereals often respond to insufficient moisture late in the growing season by early senescence which ultimately reduces yield by decreased grain filling duration reducing the deposition of photosynthetic assimilates into seed. Therefore, in response investigators have identified a number of traits including functional stay-green and solid stems (Thomas and Howarth 2000, Lopes and Reynolds 2012). Since terminal drought is often an issue in Montana, we used an RIL population derived from a cross between Vida and MTHW0202 that varies in heading, maturity, and stem solidness to study the genetic basis of abiotic stress tolerance. The phenotypic data were collected from two years yield with 5 total environments each with a different level of water stress. Some traits such as days to heading, days to maturity, grain fill duration, canopy temperature depression at grain-fill, seed protein, seed size, seed weight, yield which may have direct relationship to terminal drought stress were measured. Likewise, we also measured plant height, number of tillers, stem solidness, test weight, seeds per head and seed hardness. Canopy spectral reflectance at grain filling stage was also used to calculate Normalized Difference Vegetative Index (NDVI) and Water Index (WI) as a proxy to measure chlorophyll content and plant canopy water status which showed strong correlation with yield, days to maturity and some other traits. Genotyping was performed using 90K Illumina SNP chips. Among them 5635 markers were found polymorphic and used in linkage map construction where 731 markers formed the skeleton map covering a total of 3149 cM. QTLs were identified using Genome Studio for clustering, Multipoint ver 3.3 (for linkage map construction) and MultiQTL ver 2.6 (for QTL analysis). We were able to identify large number of QTLs associated with all these traits mentioned above. Here, we will report the QTLs associated with grain-fill duration and stem solidness that also maintained yield stability under terminal drought. Some of the QTLs were found very interesting and were confirmed in a multi-location association mapping trial.

POSTER 2

DEVELOPING GENOMIC RESOURCES FOR PECAN IMPROVEMENT

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Pecan [*Carya illinoensis* (Wangenh.) K. Koch] is an economically important nut tree with an approximate \$500 million annual market value in the United States. Pecans are perennial trees native to the Mississippi River Valley and most commercial cultivars are diploid ($2n=2x=32$). Pecans are outcrossing and therefore cultivars are clonally propagated. Pecan scab (*Fusicladium effusum*) is a fungal disease that causes a reduction in the nut size and quality and may ultimately cause yield losses. Despite their significant agricultural value, genomic resources in pecans are lacking. The aim of this project is to develop genomic resources for pecan that could be used to understand the genetic basis for resistance to pecan scab. RNA-Seq from orchard-grown trees of the cultivars Pawnee and Kanza (contrasting for their response to pecan scab) was performed. Sequences were analyzed and using the black walnut as a reference for gene annotation, resulted in the identification of 43,417 SNPs between the two cultivars. The SNPs were classified into three different categories depending on whether they were homozygous for both cultivars or heterozygous for at least one of the two cultivars. High-resolution melting (HRM) analysis was used to validate a subset of the predicted SNPs identified from the RNA-Seq data. A total of the 59.37% of the sampled SNPs evaluated so far resulted in distinct melting curve profiles that could be used for genotyping a population segregating for scab resistance generated from a cross between these two cultivars. Overall, thousands of SNPs were identified in an important horticultural species currently lacking genomic resources. The discovered SNPs represent useful tools to evaluate the genetic diversity of pecan cultivars and to identify genetic determinants underlying variation for pecan scab resistance.

POSTER 3

IDENTIFICATION AND CHARACTERIZATION OF RESISTANCE TO HESSIAN FLY IN PACIFIC NORTHWEST SPRING WHEAT GERMPLASM

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Hessian fly, *Mayetiola destructor* (Say) is an important pest of spring wheat in the Pacific Northwest (PNW). Breeding for resistance is the most effective and economical control strategy to reduce yield losses. The objective of this research is to identify DNA markers for selection of the Hessian fly resistance gene in Washington breeding line WA8076, which may be used for routine breeding efforts. A doubled haploid population was developed with WA8076 as the resistant parent, with 300 progeny produced. Hessian fly phenotyping of the population indicates single gene Hessian fly resistance from WA8076, where 50% of the progeny were resistant or susceptible. A genetic map with 3218 co-dominant markers was constructed using genotyping by sequencing. Twenty-five linkage groups were obtained representing all the 21 chromosomes. Additional SNPs markers will be integrated into the genetic map in an attempt to obtain higher marker coverage and maximize the likelihood of identifying a diagnostic haplotype for the resistance gene. These diagnostic molecular markers will facilitate marker-assisted selection and assist identifying Hessian fly resistance genes in PNW spring wheat cultivars.

POSTER 4

REDUCING ENVIRONMENTAL EVALUATIONS IN GENOMEWIDE SELECTION

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Genomewide selection allows a breeder to circumvent the phenotyping of candidate lines or hybrids, or reduce the extent of phenotyping of the candidates. Our objectives were to (1) determine whether disregarding environments subject to large genome by environment interaction variance (V_{GE}) increases the accuracy of genomewide predictions, and (2) assess the equivalency between genomewide predictions and number of environments used in phenotyping the candidates. We predicted the performance of maize (*Zea mays* L.) lines in a A/B biparental cross, with the training population being all prior crosses with either A as a parent or with B as a parent. Phenotypic and marker data were provided by Monsanto for 969 biparental populations evaluated in multienvironment trials from 2001 to 2008. Deleting the environments associated with the largest V_{GE} did not improve prediction accuracy for grain yield, moisture, and test weight. However, prediction accuracy was maintained even when the mean numbers of environments were reduced from 7.3 (all environments used) to 5.4 for yield, 6.0 for moisture, and 5.1 for test weight. Shukla's method for calculating the V_{GE} associated with an environment was useful for identifying locations to avoid in future phenotyping. We found that if genomewide predictions from prior data are available, the number of locations in first-year phenotyping of testcrosses could be reduced by 1.4 to 1.9 locations. Overall, our results indicated that fewer environments could be used for the training populations without compromising accuracy, and that genomewide predictions could supplement phenotypic selection without compromising overall selection accuracy.

POSTER 5

NOVEL STEM RUST RESISTANCE GENE TRANSFER FROM *DASYPYRUM VILLOSA* VIA
WHEAT-ALIEN AMPHIPLOID AND ADDITION LINES

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Race TTKSK (Ug99) of stem rust, caused by *Puccinia graminis* f. sp. *tritici*, rendered many available resistance genes ineffective. Genetic resistance is the best approach to control the disease, and having as many and diverse resistance genes as possible is desirable. *Dasyphyrum villosa*, wild diploid relative of wheat, exhibits stem rust resistance to all races of wheat stem rust tested to date. We crossed highly susceptible durum wheat cv. "Rusty" to 10 accessions of *D. villosa* as a bridge to make amphi-hexaploids. These amphiploids were screened with Ug99 and phenotypes ranged from 0; to 3+. Highly resistant lines were crossed with common wheat cv. "Chinese Spring" (CS), then followed by series of back crossing to CS until a complete set of seven *D. villosa* single chromosome addition lines were recovered. These addition lines will be used to identify chromosomes which carry the new novel resistance genes, subsequently diagnostic markers will be developed using SNPs which were generated by genotyping CS-*D. villosa* addition lines via a Genotyping-by-Sequencing method.

POSTER 6

GENETIC VARIATION OF ROOT TRAITS IN TURKISH WHEAT GERmplasm

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Wheat landraces are locally adapted traditional varieties from active populations with ongoing evolution resulting in valuable genetic diversity for plant breeders. Six Turkish wheat landraces, along with fourteen bread and durum wheat cultivars were investigated for root characteristics over two consecutive seasons. Root and shoot traits were measured for plants grown until maturity in 1m PVC tubes in glasshouse conditions. Significant phenotypic and genotypic differences were found within and between groups. Landraces had the highest average root biomass in both seasons, 8.7g and 9.5g respectively, and cultivars had 4.85g and 6.04g respectively. There was an 8 fold increase of root biomass between the control 'Pavon-76', a CIMMYT bread wheat, and a Turkish wheat landrace. All of the 20 Turkish wheat accessions had a minimum of two fold increase in root biomass over Pavon 76. Shoot biomass, root biomass, number of tillers, deep root biomass, shallow root biomass, root to shoot ratio and plant height were significantly higher in landraces ($P < 0.01$). Climate change, water deficit and many other factors are making irrigated agriculture a less feasible farming practice, and there is a need for new drought tolerant wheat cultivars. Results of this experiment and other studies suggest that landraces, when compared with alien translocations or wild gene pools, may be a most valuable and useful resource for transferring genetic diversity to modern breeding programs.

POSTER 7

YIELD, YIELD COMPONENT, AND AGRONOMIC QUALITY GWAS IN ELITE FACULTATIVE/WINTER 6- ROWED BARLEY (*HORDEUM VULGARE*)

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Barley (*Hordeum vulgare*) is an attractive crop for sustainable food systems. It is input efficient and a FDA-certified heart healthy food. However, climate change brings new sustainability challenges. To this end, the Triticeae Coordinated Agricultural Project (TCAP) was created to develop wheat and barley varieties adapted to more variable temperatures and reduced inputs. As part of the TCAP, this project focuses on identifying alleles for nitrogen use efficiency (NUE) and agronomic quality in facultative/winter 6-rowed barley. To identify NUE loci, we tested a GWAS panel of 300 elite lines for performance under standard nitrogen (N) and reduced N (70% of standard) treatments, in two years and two locations (Corvallis, OR and Logan, UT), all fall-planted, with the Logan, UT site irrigated. In total, we rated 7 agronomic traits and 4 yield component traits. Genotypic data for GWAS were obtained by a 9,000 marker SNP assay. NUE QTLs were successfully identified and reported elsewhere; here we will focus on QTLs for simple agronomic traits. Preliminary analysis showed 105 genomic regions with maturity-independent significance for agronomic traits (FDR of 5%), 45 of which were identified in multiple years or locations. A thorough comparison of QTL results across trials and with previously reported QTLs will be provided.

POSTER 8

POTENTIAL EVAPOTRANSPIRATION (PET) ESTIMATORS AS A TOOL FOR INDICATING DROUGHT TOLERANCE IN CHILE PEPPERS OF SOUTHERN MEXICO

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Identifying stress tolerance in both wild and domesticated plants through environmental manipulation experiments can be challenging and time consuming. Increasingly, global datasets are being used to gain a better understanding of an accession's native environment. Since we might expect traits expressed by accessions to have evolved in response to these native environments, climate data may be able to predict adaptations to environmental stress. Thus, habitat drought stress indices based on potential evapotranspiration (PET) estimators were calculated for locations in two states of Mexico (Oaxaca and Yucatan) where chile pepper (*Capsicum* spp.) accessions were collected. In doing so, accessions could be identified with a high likelihood of drought stress avoidance and/or tolerance. PET estimators use temperature, precipitation and atmospheric data to approximate the amount of evaporation that would occur if sufficient water were available. Monthly PET values were paired with monthly precipitation averages to calculate a monthly drought index (DI) for each estimator. These DIs provide insight into the water balance and the seasonality of available water throughout the year. A cluster analysis of max and mean DIs and drought-related bioclimatic variables was used to further explore the DIs, and accessions from 28 collection sites appear to divide into distinct ecological niches. It is expected that sites with a high DI for a given month will correspond to an accession with potential for short-term drought stress avoidance. Alternatively, a site with a high average monthly DI will correspond to an accession with a potential for long-term drought tolerance. Future work on this project will include environmental manipulation experiments to test these hypotheses.

POSTER 9

NESTED BACKCROSSED RECOMBINANT INBRED POPULATIONS FOR UNRAVELING THE POTENTIAL OF WILD COMMON BEANS

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Wild common beans (*Phaseolus vulgaris* L.) still thrive in highly variable ecosystems, but as result of genetic bottlenecks during domestication, the variation within the wild germplasm remains untapped. The evaluation of wild beans under modern agricultural conditions is impractical because of wild beans's photoperiod sensitivity, extended growth cycle, pod shattering, and vigorous climbing growth habit. Therefore, systematic evaluation of the genetic variation of wild beans necessarily involves the recombination of wild beans with a domesticated genetic background for practical phenotyping under agricultural conditions. Furthermore, the beneficial wild alleles might interact differently under a domesticated genetic background. In a modified scheme of the Nested Association Mapping in maize, we developed three RIL populations resulting from the cross between a domesticated elite breeding line (SEA 5) to three wild accessions (PI 319441, PI 417653 and PI 343950) that originate from areas with the most extreme and also an intermediate level of rainfall in their Mesoamerican distribution. SEA 5 was developed at CIAT using the Mesoamerican domesticated gene pool and was selected for its drought tolerance; it has an indeterminate prostrate growth habit III, photoperiod neutrality, cream-colored seeds and is resistant to *Fusarium* root rot, ashy stem blight and BCMV. Our RIL populations were developed with a single backcross to SEA 5 and four subsequent generations of selfing before the genetic and phenotypic evaluations. There was no selection in the process except against photoperiod sensitivity in the S_2 generation. At least 240 BC_1S_4 individuals of each domesticate x wild backcross population were recovered and the $BC_1S_{4,5}$ families were planted in the field in Davis in 2014 in a partially replicated design for field evaluation and seed increase. High and low transgressive segregation was found in days to germination and flowering, seed size, and especially yield. There were lines within each population that produced 40% more grain yield than the recurrent domesticated parent, suggesting the potential of wild beans to increase the productivity. A subset of these populations of the $BC_1S_{4,6}$ will be evaluated in 2015 under control and drought conditions. These lines are being genotyped with BARCBEAN6K_3 the Illumina Infinium Genechip. Having the same SEA 5 genotype nested in all three populations will allow joint mapping, increasing the power and mapping resolution, and a direct comparison of QTL allele effects between the genotypes.

POSTER 10

BREEDING FOR A FAST COOKING BEAN: STUDY OF GENOTYPES ACROSS ENVIRONMENTS TO DETERMINE PHENOTYPIC STABILITY IN *PHASEOLUS VULGARIS*

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Dry beans (*Phaseolus vulgaris*) are one of the most nutritious and low cost vegetables available. However, beans are not as highly consumed in the U.S., possibly because of the longer cooking time required to prepare beans for consumption. Considerable variation in cook time exists in dry beans, post-harvest, ranging from 20 to 90 minutes with an average cook time around 40 minutes, whereas after a year or more of storage, cooking time increases further. Little is known about the genetic basis for these differences in cook time. Development of fast cooking bean varieties would mean that less energy is required to prepare beans for consumption. These benefits would be magnified on a commercial production level, as well as in developing countries where firewood is the main fuel source for cooking.

This study was conducted to determine the stability of the cook time phenotype in dry beans across different environments. By understanding the phenotype in more detail, genetic analyses can be performed to determine areas of the genome associated with fast cook time. Areas of the genome discovered can then be used as a screen in breeding populations. Also, these areas could be introgressed into commercially popular bean varieties. This study was also performed to observe if previously identified fast and slow cooking genotypes maintained their cooking time difference across different environments.

TZ-27 and TZ-37 were chosen for the study since they have similar seed weight and color but different cooking times. Average cook time for TZ-27 is 64 minutes, while TZ-37 requires an average of 36 minutes to cook. These two genotypes were grown in 12 different environments: three in Washington and two in Michigan, USA; two in Puerto Rico; two in South Africa; and three in Tanzania. Cooking time was measured with a pin drop cooker on unsoaked and soaked (12 hr) seed.

When beans were soaked prior to cooking, genotype ($p < .0001$) and environment ($p < .0001$) had a significant effect on cook time. Compared to the other 9 environments, beans grown in Cedara, Puerto Rico, and SUA locations required longer to cook than seed grown at the other field sites. A genetic by environmental influence on cook time was also observed ($p = .0066$) as cook time varied by environment, but also by genotype. In contrast, when comparing unsoaked seeds, environmental effects are still observed ($p = .0185$), but genotype is no longer significant ($p = .2398$).

TZ-27 and TZ-37 cook similarly across most of the environments tested; a result typically seen when a trait has a strong genetic component. Cook time results from these lines represent early work into elucidating what areas of the genome are responsible for cook time.

POSTER 11

NEW SOURCES OF EASTERN FILBERT BLIGHT RESISTANCE IN HAZELNUT

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Eastern filbert blight (EFB), caused by the pyrenomycete *Anisogramma anomala* (Peck) E. Müller, is a serious threat to the hazelnut industry in the Pacific Northwest. EFB, which is an endemic disease in the eastern US, occasionally produces small cankers on American hazelnut (*C. americana* Marsh.). Cultural practices including scouting, pruning out infected branches and fungicide applications are recommended to slow disease spread but are expensive and are not completely effective. Utilization of resistant cultivars is both ecologically and economically sound approach, and is the main focus of the hazelnut breeding program at OSU. 'Gasaway' resistance, which is governed by a dominant allele at a single locus, has been extensively used in the OSU hazelnut breeding program. 'Gasaway' and some of its offspring have been infected by EFB isolates from New Jersey, Minnesota, and Michigan. Even in Oregon, small cankers have been observed on 'Jefferson' and 'McDonald' under high disease pressure. Finding, studying, and utilizing new sources of resistance are crucial to sustain hazelnut industry in Oregon. In this study, 12 new sources of resistance were investigated. Structure inoculated progenies of 'Grand Traverse', *C. heterophylla* 'Ogyoo', 'Yoder #5' and *C. americana* 'Rush' segregated in 1:1 ratio, and seedlings were scored with previously mapped SSR markers. Resistance from 'Grand Traverse' and *C. heterophylla* 'Ogyoo' were assigned to LG6, while resistance from 'Yoder #5' was assigned to LG7 and resistance from *C. americana* 'Rush' is unlinked to LG6 markers. Based on grafted trees of 'Uebov' seedlings inoculated in the greenhouse, 'Uebov' resistance was also assigned to LG6 based on correlation with mapped SSR markers (LG682: $|r| = 0.72$). Resistance from Moscow N23, Moscow N26, Moscow N27 and Moscow N37 segregated in a 1:1 ratio indicating control by a dominant allele at a single locus. Moscow N26 appears to be on LG6, while resistance from other Moscow selections has not yet been assigned to a LG. When the LG is identified, all available SSR markers on that LG will be scored and a precise map will be created for each resistance sources. Identification of tightly linked, robust DNA markers will enable pyramiding of several resistant sources and the development of cultivars with durable EFB resistance.

POSTER 12

MOLECULAR MAPPING OF SOYBEAN APHID RESISTANCE IN PI 603712

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Soybean aphid, (*Aphis glycines* Matsumura), a native pest of soybean in Asia, has become one of the major pests of soybean in the northern United States and southeastern Canada. In the United States, at least four biotypes of soybean aphid have been confirmed, which can defeat one or more known genes or loci of soybean aphid resistance in soybean. Evolution of soybean aphid biotypes justifies the need of broadening genetic diversity of soybean aphid resistance. Genetic characterization of new sources of soybean aphid resistance will facilitate to expand the gene pool of soybean aphid resistance and thus will help to develop soybean aphid resistant cultivars. To characterize the genetic basis of soybean aphid resistance in PI 603712, a newly identified resistant germplasm accession, two F₂ populations derived from the crosses between PI 603712 and susceptible cultivars 'Roberts' and 'Brookings' were developed and evaluated for the soybean aphid resistance both in the greenhouse and field. For the cross Roberts x PI 603712, 142 F₂ lines along with their parents were genotyped with the BARCSoySNP6K Illumina Infinium II BeadChip. A genome-wide molecular linkage map was constructed with 1495 polymorphic SNP markers by using JoinMap 4.0. QTL analysis revealed that PI 603712 possessed two major loci of soybean aphid resistance on chromosome 7 and 16, respectively. The resistance locus on chromosome 7 was dominantly expressed and positioned about one Mega-base-pair (Mb) far from the previously identified resistance locus *Rag1*. The locus on chromosome 16 was recessively expressed and positioned about one Mb far from the previously identified resistance locus *rag3*. Interestingly, PI 603712 also carried a minor locus for susceptibility to soybean aphid on chromosome 13, which was positioned at least 15 – 20 Mb far from previously identified soybean aphid resistance locus *Rag2*. The epistasis interactions indicated that the effect of the dominant resistance locus on chromosome 7 was decreased by the homozygous alleles of the susceptible loci either on chromosome 16 or 13. The recessive resistance locus on chromosome 16 exhibited small numbers of aphids per plant in all the cases. However, the dominant resistance locus on chromosome 7 exhibited significantly higher resistance against soybean aphid when the interacting alleles were absent. In the marker-assisted selection (MAS) for soybean aphid resistance using PI 607312 as a donor parent, therefore, inclusion of the resistance loci on chromosomes 7 and 16 and exclusion of the susceptible locus on chromosome 13 would be the optimal choice for developing soybean aphid resistant cultivars.

POSTER 13

CONTROLLING WATER LOSS BY MULTILAYERED MEDIA IN SMALL CONES TO SIMULATE PROLONGED DROUGHT PROGRESSION IN TALL FESCUE UNDER GREEN HOUSE CONDITION

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Conducting drought experiment under in-vitro condition is highly critical. Most of the drought study is done following a short term drought exposure of plants followed by re-watering. Researchers always struggle to devise appropriate re-watering technique for plants survival under artificially induced water stress condition. Two pilot experiments were conducted to study drought tolerance in tall fescue. First experiment was done following two factors CRD using five replications. Clones of six tall fescue genotypes were planted in specially filled 14" cones and allowed for establishment with full irrigation for three weeks. At three weeks of the establishment, irrigation was stopped till 80% plants were completely senesced. Among the measured trait, osmotic potential was significantly higher in B400 (942 mmol/kg, Molal concentration) followed by B348 (920 mmol/kg, Molal concentration) while the lowest OP was found with W279 (628 mmol/kg, Molal concentration). Similarly, B400 had the best performance for chlorophyll content and stay green trait. Penetration ability of roots was also measured in the same experiment. We found a significant variability of root penetration ability among the genotypes. B400 plants were found to survive till 55th day of no irrigation. This result was completely in agreement with a previous study where B400 and B348 were reported to have the best drought tolerance ability. Second experiment was done using same genotypes following the similar experimental design, where drought was created using 20% PEG in hydroponics. GK45115 (38) was found to be the best for higher chlorophyll content followed by B400 at sixth day of PEG exposure. Stay green trait and root traits were not meaningful in this experiment. Comparing between the two experiments, first experiment with specifically designed pot filling can impose a prolonged drought progression which can be used for drought tolerance screening of large breeding population.

POSTER 14

STACKING RESISTANCE ALLELES FROM THREE SOURCES TO INCREASE RESISTANCE TO SOYBEAN CYST NEMATODE (SCN)

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Soybean cyst nematode (SCN), *Heterodera glycines* (Hg) Ichinohe, is the largest economic threat to soybean [*Glycine max* (L.) Merrill] yields in the United States causing over a billion dollars a year in losses. The best method to manage SCN is through the use of resistant varieties. Genetic resistance to SCN is controlled by several genes known as quantitative trait loci (QTL). Over 118 soybean accessions have been identified as possible sources of resistance to SCN; however, only seven resistant sources are commonly used by breeders. The most widely used resistance source is PI88788. With the ability of some field SCN populations to overcome these resistance sources, it is important to continue to evaluate novel resistance sources. A genetic region from PI567516C on chromosome (chr) 10 (formerly linkage group (LG) O) has been identified and confirmed to confer resistance to several Hg types. Additionally, two resistance QTL from wild soybean (*Glycine soja* Siebold & Zucc.) accession PI468916 have been mapped to regions on chr 15 (LG E) and 18 (LG G). The two QTL have been confirmed and designated as cqSCN-006 and cqSCN-007, respectively. In this study, a population segregating for resistance from PI567516C, PI468916, and PI88788 was evaluated with two nematode isolates. In these stacks of resistance genes, the SCN resistance alleles from each source significantly increased SCN resistance compared to the alternative alleles. Lines homozygous for the four resistance alleles had a lower SCN female index (FI) than those homozygous for the susceptible alleles. These results indicate that combining multiple sources of resistance can be an effective means to increase SCN resistance.

POSTER 15

EVALUTION OF PHYTOPHTHORA CAPSICI RESISTANCE IN RECOMBINANT INBRED LINE BELL PEPPER POPULATION

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Phytophthora capsici is one of the major pathogens affecting bell pepper (*Capsicum annuum*) production. This soilborne pathogen causes root rot, crown rot and leaf blight. Even with good management practices, all commercial varieties lose the majority of their yield due to cultivar susceptibility and high pathogen variation. There are several sources of *P.capsici* resistances from landrace accessions. The Mexican landrace 'Criollo de Morelos 334' or CM334 is known for having a very high level of resistance towards many aggressive *P.capsici* isolates. To understand the genetic basis of *Phytophthora* resistance in bell pepper, phenotypic evaluation in a population segregating for resistance is needed. We have developed a recombinant inbred line (RIL) population between the resistant (CM334) and a susceptible cultivated bell pepper variety (Maor) to evaluate the segregation of resistance in the population. 650 RILs with parent controls were tested for *Phytophthora* resistance with 3 replications and 6 subsamples. Three *P.capsici* isolates with high and moderate virulence were chosen for the inoculation. Seedlings were inoculated at 2-4 leaf stage and evaluated for root rot disease levels. Data were calculated by the area under the disease progress curve (AUDPC) method to determine the resistance level. Segregation in resistant levels among lines was observed. Some resistant RILs had higher resistant levels than CM334 across all isolates. Genetic and environmental variance in AUDPC was determined.

POSTER 16

MAPPING AND VALIDATION OF A QTL CONFERRING PARTIAL RESISTANCE TO STRIPE RUST IN HEXAPLOID WHEAT.

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A mapping population of 96 recombinant inbred lines (RIL) was developed from a cross of Argentine varieties Klein Proteo and Klein Chajá. Using the iSelect Illumina platform for 9,000 wheat SNP, a map was built including 2,698 SNP and 108 SSR markers. The population was evaluated for stripe rust response in replicated field experiments at Davis, CA in 2012, 2013 and 2014. Stripe rust response was measured by infection type (IT, 0-9 scale) and disease severity (S, 0-100%). Both parental lines showed moderate levels of resistance to local PST races. Independent QTL analyses were performed for each year using composite interval mapping. A partial resistance QTL (*QYr.ucw-1BL*) conferred by Klein Chajá was identified on the distal region of chromosome 1BL in all three years ($P < 0.001$, 22% IT and 23% S explained variation). A validation population for *QYr.ucw-1BL* was generated by crossing one of the original RILs carrying only the *QYr.ucw-1BL* resistant locus, with a RIL carrying susceptible alleles for all other QTL. In 2015, 1,300 segregating $F_{2:3}$ plants from the validation population were evaluated for rust resistance in the field to refine the mapping. Fingerprinting of the parental lines with the 90,000 iSelect SNP marker platform was used to develop eight new markers in the QTL region. To test if *QYr.ucw-1BL* was a different gene than *Yr29/Lr46*, we evaluated 759 F_2 plants segregating for both genes in the field in 2014. We identified 15 fully susceptible plants suggesting that *QYr.ucw-1BL* is different from *Yr29/Lr46* and that the two genes are approximately 5cM apart. Lower levels of resistance were observed for *Yr29/Lr46* than *QYr.ucw-1BL* under field conditions, but the combination of both genes resulted in the best resistance. Germplasm combining these two resistance genes will be publicly available.

POSTER 17

DISSECTION OF REPRODUCTIVE COLD TOLERANCE IN RICE: INVESTIGATING ANTHOR LENGTH AND STERILITY RESPONSE IN CALIFORNIA AND CHILEAN GERMPLASM

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Exposure to low temperatures ($\leq 20^{\circ}\text{C}$) during the reproductive stage of rice plants causes sterility resulting in lower yields. This is a major problem in temperate and high altitude regions where rice is cultivated and is primarily due to prolonged periods of low air temperatures. In the U.S. and Chile, a considerable amount of water may be used to insulate developing panicles which extend from the base of the rice plants during the reproductive growth stage. This can limit the production area. Breeding for reproductive cold tolerance is an important objective to increase the stability of production and reduce the economic and environmental costs of excessive water use. One promising area of investigation involves the role of anther length on cold tolerance. Therefore we investigated the phenotypic variation in anther length and sterility in rice germplasm previously classified as cold tolerant and susceptible under cold stress and normal temperature conditions. Also we developed genetic mapping populations (RILs) for future QTL analysis of reproductive cold tolerance.

POSTER 18

LIMA BEAN RESEARCH TO SUPPORT BREEDING FOR LYGUS TOLERANCE

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California is the leading producer of dry Lima beans (*Phaseolus lunatus*) in the United States. California growers are largely concerned with economic loss due to yield reduction and seed damage from lygus bug (*Lygus hesperus*) which cause flower and young pod abortion as well as seed damage. Fields under high lygus pressure, not treated with insecticides may result in 80% yield reduction. The purpose of this research is to increase understanding of mechanisms involved in lygus tolerance in lima beans while simultaneously developing improved lygus tolerant cultivars and genetic tools for a crop which historically has had relatively little research investment. To do this UC-Davis is developing a genetic population and maps using agronomically valuable cultivars of Lima bean with different genetic and phenotypic profiles. A population of 230 Recombinant Inbred Lines (RILs) has been made from reciprocal crosses between a lygus tolerant (UC Haskell) and susceptible (UC 92) parent. The lygus tolerant parent is a vine type, baby Lima bean from the Mesoamerican genepool and the susceptible parent is a bush large Lima from the Andean genepool. The RILs in this population segregated for many traits including development, growth habit, seed size and pest resistance. Using next-generation DNA sequencing we developed a physical Single Nucleotide Polymorphism (SNP) map for Lima bean based on the two parents which currently has ~50,000 putative SNPs spread across all 11 chromosomes with at least 5x coverage. UC-Davis researchers will take advantage of the large amount of genetic variation from the two parents combined with the segregating phenotypes in the RIL population to do QTL mapping for lygus resistance in lima beans. RILs are being evaluated in the field under lygus pressure, with and without insecticide treatment for two seasons (currently in second season). An increase in lygus damage on seeds has been correlated with reduced yield within genotype. We anticipate lygus tolerance to be highly complex and involve multiple plant traits such as flowering time, plant architecture and secondary metabolite defense compounds.

POSTER 19

HIGH-THROUGHPUT PHENOTYPING AND GENOTYPING TO DISSECT CANOPY ARCHITECTURE IN MAIZE

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Improved canopy architecture is one of the ways maize hybrids have adapted to higher plant densities. Modern hybrids have been moving increasingly towards upright leaves, which assist in distributing light more effectively in the canopy. This study is being conducted to further the understanding of maize canopy architecture, specifically looking at how differences in LA affect yield and how light is distributed throughout the canopy. PHW30 was identified as having an upright leaf angle (LA) (75.9°), whereas B73 (63.1°) and Mo17 (55.7°) have a flatter LA. Four reciprocal bi-parental populations (upright x flat) were developed, and LAs for the F₂ progeny were measured. Subsets (flat, average, and upright) of F₂ lines for each population were selected for genotyping and creating double haploid lines (DHLs). Extensive genotyping and phenotyping with an unmanned aerial vehicle (UAV) and individual plant image analysis will be used to reclassify the DHLs into phenotypic groups and improve QTL mapping from the F_{2:3} data. Additionally, the identified LA QTL will be used to backcross the favorable QTL from PHW30 into B73 and Mo17. Four different hybrid combinations will be made with the modified and unmodified versions of B73 and Mo17, and extensively phenotyped with a UAV and tested for yield. Improving canopy architecture is one of many approaches necessary for yield improvements in maize. To accomplish this, a procedure was outlined that uses using high throughput genotyping and phenotyping across different types of mapping populations to obtain desirable homozygous lines for dissecting a quantitative trait.

POSTER 20

GENETICALLY AND AGRONOMICALLY CHARACTERIZING A CORE-SET OF INTERSPECIFIC BREEDING LINES

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Concern often arises within the soybean community over the lack of genetic diversity in the U.S. soybean breeding germplasm pool, specifically the southern breeding pool. Despite these concerns, there is an overwhelming amount of freely available breeding material housed within the USDA Germplasm Collection. As of May 2015, over 21,000 accessions exist within the germplasm collection. Of those 21,000 accessions, nearly 1,200 belong to the freely-crossing progenitor species, *Glycine soja* (wild soybean). A significant genetic bottleneck during the domestication of soybean allows for the possibility that useful genetic variation exists within the progenitor species that may aid in the improvement of soybean. Due to the unruly and undesirable agronomic characteristics of the wild soybean, previous efforts to incorporate it into breeding programs have focused on multiple rounds of backcrossing to develop a testable product. Unfortunately, with each round of backcrossing, a large percentage of the wild species genome is lost. Since there is no way to effectively model how novel genetic regions will affect soybean growth and development, it is of utmost importance that breeding efforts work to recover the most diversity, while still maintaining agronomic performance. As an alternative to backcrossing, a mega-population, bulk-breeding, pedigree approach was used to develop approximately 225 F₄-derived interspecific breeding lines. The breeding lines were yield tested for three years (2008-2010) and subjected to a 1,536 SNP marker analysis. After filtering for yield potential ($\geq 70\%$ of check), 17 lines were selected since they captured all of the genetic diversity within the wild species, as indicated by the marker analysis. The 17 breeding lines, alongside the appropriate checks, were further evaluated for yield, protein and oil content in 2013 and 2014. Five highly uniform single-plant selections were made from each breeding line and subjected to 6k SNP marker analysis to better estimate overall diversity present, as well as the size and distribution of linkage blocks across the genome. Finalized results, as well as information regarding the release of these materials, will be presented at the meeting.

POSTER 21

UNVEILING CARROT ROOT ARCHITECTURE USING 2D AND 3D IMAGE ANALYSIS

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Effective phenotyping in carrot is complicated by the fact that the agronomically valuable portion of the crop is underground. To better understand the genetics of carrot root architecture, novel approaches must be conceived and applied in the field of high resolution, high throughput phenotyping. One such approach is the use of microscale X-ray Computed Tomography (μ CT). This technique allows for the non-destructive imaging of roots in soil conditions similar to those found in the field. Optimizing μ CT for carrot will greatly increase the understanding of how storage root architecture develops across maturation. To better understand carrot root architecture we have used μ CT to image four carrot cultivars, exhibiting extreme growth types, across five developmental time points. Further, we have utilized the 2D image analysis software, RootNav and SmartRoot, to measure carrot root architecture traits in an F_2 mapping population between wild and cultivated carrot. Phenotypic measurements will be used in conjunction with genotypic information to further understand the genetic basis of lateral root formation and root shape in carrot. Establishing a protocol for μ CT and 2D image analysis in carrot, as model root crop, will facilitate the application of these technologies to other root and tuber crops such as sugar and table beet, potato, and cassava. Finally, increased knowledge pertaining to carrot root architecture can be used to design cultivars with better water and nutrient use efficiency.

POSTER 22

GENOME-WIDE ASSOCIATION MAPPING FOR NITROGEN USE EFFICIENCY IN SPRING TWO-ROW AND SIX-ROW ELITE BARLEY GERMPLASM

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Rising carbon dioxide concentrations in the atmosphere inhibit nitrate assimilation in plants, reducing their productivity and protein levels. Growing crop varieties with improved nitrogen use efficiency (NUE) could counteract this hindrance and decrease fertilizer input costs for producers. We evaluated NUE-related traits in two association mapping (AM) panels—one consisting of 250 spring two-row barley (*Hordeum vulgare*) lines and one consisting of 250 spring six-row barley lines. Each panel was genotyped with 3,072 single nucleotide polymorphism (SNP) markers and was grown under nitrogen-limiting and non-limiting treatments in four environments. Stress indices calculated for relevant traits can be used to compare lines' performance under stressed and non-stressed conditions. The objectives of this study were to: (1) determine the genetic variation in each AM panel for NUE as defined by relevant traits and stress indices; (2) define the trait's genetic architecture and identify alleles for improved NUE using genome-wide association mapping; and (3) compare the results of AM between the two-row barley and six-row barley panels. Both panels were assessed for six traits (grain yield, grain protein content, heading date, plant height, grain plumpness, and test weight), and the six-row panel was assessed for three additional traits (spikes per area, kernels per spike, and kernel weight). All traits plus two NUE indices of these traits—geometric mean and stress tolerance index—consistently showed significant genetic variation. Using AM with a K model to correct for relatedness among the lines in each panel, we identified markers associated with all the traits assessed in the two-row panel and with grain protein content, heading date, plant height, plump grain, and kernels per spike in the six-row panel. Additionally, we identified markers associated with the geometric mean and stress tolerance index for all traits in the two-row panel and for grain yield, grain protein content, heading date, and plant height in the six-row panel. Genetic variation for NUE and markers linked to loci for these traits should inform breeding efforts to improve spring two-row and six-row barley for NUE.

POSTER 23

LEVERAGING GENOMIC RESOURCES TO BREED A DIFFICULT PERENNIAL CROP: APPLE ROOTSTOCKS

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Rootstocks are the foundation of a healthy and productive orchard. As such, the choice of a rootstock can influence the productivity and profitability of an orchard in a very significant way. Rootstock performance is highly correlated with the genetic potential of such rootstock to provide anchorage, explore the soil profile, absorb and transfer nutrients to the scion, adapt to pedo-climatic conditions, tolerate extreme weather events, resist or cope with pathogens, propagate efficiently and impart positive architectural properties to the scion – like vigor control and precocity. The inheritance and control of all these desirable characters is quite complex making breeding (the action of combining high performance traits in same rootstock) quite challenging. Recent advances in genomic technologies are allowing more efficient, and informed way of selecting new rootstocks during the breeding process. Furthermore, breaking down complex traits like tree vigor into component traits (hormonal transport, nutrient uptake and transport, root architecture, water use efficiency) and further characterization of the inheritance these component traits can simplify the understanding of complex traits and improve the breeding process and outcome. In the Geneva® breeding program we have been studying root architecture, nutrient uptake and translocation, inheritance of gene expression to better characterize breeding populations and select parents and seedlings for the next generation of apple rootstocks. We present data relating to these traits and how they are associated to good performance of released and elite stage apple rootstocks.

POSTER 24
ALTERNATIVE APPROACHES TO BREEDING VALUE PREDICTIONS
WITHIN FAMILY

*Adam Festa and Ross Whetten, N.C. State University Department of Forestry

The goal of this study is to increase the selection intensity within Loblolly Pine breeding programs, by assessing the relationship between unique patterns of family gene expression and parental breeding values (BV). We hypothesize that selection intensity can be increased in pine breeding programs under two conditions -first, that there are genetic differences among families in gene regulatory networks, and second, that those differences are correlated with family mean performance in field tests of progeny. Currently, selections for advanced generations of Loblolly Pine are made on the basis of family mean phenotype, where phenotypically superior individuals are selected from top-performing families, and progeny tested to screen for those trees that have the best BVs. However, there is little confidence that phenotypically superior selections from a progeny test will carry forward the traits intended from the family, because many traits of interest to breeders have low individual-tree heritability. In order to estimate the BV of a tree, a BLUP (Best linear unbiased predictor) analysis is conducted where phenotypic/pedigree data are utilized to help define the genetic covariance among a set of families from a specified mating design. It is reasonable to suspect that portions of the differences we see in family mean phenotypes can be accounted by differences in gene structure, or gene regulation patterns. By utilizing RNA seq as a means to collect information on these types of differences, instead of progeny testing, we may be able to provide a more cost-effective way of screening future selections within Loblolly Pine families. Additionally, by using covariate structures in a BLUP analysis that are defined by differences in gene structure and expression patterns instead of, or in addition to, the standard numerator relationship matrix, we may be able to provide a higher prediction accuracy of BV's.

To test this hypothesis, we have chosen 43 different parents, from a wide geographic distribution, with pre-existing progeny phenotype data available from field tests across multiple sites. Seeds (open-pollinated or pollen-mix in 37 cases, controlled-cross in 6 cases) from each of these parents were grown in a greenhouse, and seedlings were harvested at 3 months for RNA extraction/sequencing, which is still underway. The RNA expression results from corresponding families will be used to create covariance matrices reflecting shared genetic variation in coding sequences on one hand, and shared variation in gene regulatory networks on the other. Cross-validation of BLUP models using these covariance matrices, as well as a standard numerator relationship matrix, will be used to test the hypothesis that phenotypic variation can be accurately modeled by covariance of these two classes of genetic variation. This resulting analysis should provide insight into the capability of using RNA expression patterns as another screening effort in selecting individuals as parents for future breeding populations.

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POSTER 25

EFFECTS OF SOIL ACIDIFICATION AND PINE BARK AMENDMENT ON SOUTHERN Highbush
BLUEBERRY FRUIT QUALITY

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Acidification and organic matter amendments are required to grow Southern highbush blueberries (*Vaccinium corymbosum* hyb.) in basic, sandy Florida soils. While soil acid and amendment treatments drastically affected plant vigor and yield, the effects of soil cultivation upon blueberry fruit quality have rarely been examined. Two widely planted Florida cultivars, 'Farthing' and 'Meadowlark,' were grown in subplots with and without sulfuric acid supplementation, and with and without pine-bark amendments. Over two seasons, fruit was harvested from all genotype-acid-amendment combinations for biochemical fruit quality analyses. Sugars, acids, and volatile compounds were measured and compared between treatments. No effects of soil treatment were found on sugars or acids in the first season, but fruit pH of both cultivars was higher in acidified subplots in the second year. For both years and cultivars, seven volatiles, including four aldehydes, were found to be highest in fruit harvested from subplots with the commercial amendment and acidification regime. Five volatiles were found to be highest in subplots that received no acid supplementation. These five volatiles have previously been implicated with biotic and abiotic plant stress responses. In conclusion, primary metabolites appear to be under more stringent genetic control than secondary metabolites when subjected to variations in soil pH and organic matter content.

POSTER 26

GENOME-WIDE ASSOCIATION STUDY OF REMOTELY SENSED STAY GREEN AND CANOPY TEMPERATURE IN WINTER WHEAT

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Soil moisture deficit is a major constraint for wheat production in the US Pacific Northwest. This experiment is part of a broader initiative to identify and utilize agronomic and physiological attributes of yield in wide range of soil moisture regimes. The main objectives of this study was to use spectral reflectance indices (SRIs) and canopy temperature (CT) as surrogate for phenotypic and genetic analysis of stay green, plant hydration status, and cooling efficiency. A total of 402 genotypes (87 hard and 315 soft) were evaluated for grain yield, phenology, spectral reflectance indices, and CT in moist-cool, irrigated, and dry conditions in 2012 and 2013. Genotype and environment had significant effect on grain yield, stay green, area under vegetation index curve (AUVIC) and CT ($p < 0.001$). Both CT and AUVIC showed moderate to strong correlations with flag-leaf senescence and grain yield ($p < 0.001$) indicating the possibility of using these approaches for canopy-level estimation of stay green and early prediction of agronomic performance. A genome-wide association study was conducted for these traits in mixed linear model that accounts for bi-allelic polymorphism of 3,526 SNP markers (from 9K iSelect assay), principal components ($Q=3$), and compressed relatedness matrix ($k=237$). We identified quantitative trait loci (QTL) in 1A, 1B, 1D, 3A, 4A, 7A, and 7B that were significantly associated with one or more of the studied traits (FDR =10%; $R^2 = 2-6\%$). Co-localized quantitative trait loci (QTL) for CT and stay green were identified in 1A and 1B. This presentation will focus on the QTL regions that have yield advantage in the study environments and no association with major developmental traits such as heading date and plant height.

POSTER 27

AN ELITE SPRING WHEAT PANEL FOR GENOMEWIDE ASSOCIATION MAPPING OF AGRONOMIC TRAITS

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Most association studies in wheat are implemented using a diverse global collection of genotypes with sufficient level of genetic variation for target traits. The effectiveness of these studies, however, are often affected by extensive population substructure and limited phenotypic performance of less adapted genotypes. Elite inbred varieties and advanced breeding lines are highly adapted and have been subjected to numerous recombination and strong allelic selection for desired traits. This is very practical since majority of the genetic variation manipulated by breeders is already contained in this elite gene pool. The main purpose of this study was to implement genome-wide association mapping for twenty agronomically important traits using elite inbred lines. A panel consisting of 250 elite spring wheat lines from different wheat breeding institutions in North America and CIMMYT were evaluated in eight locations for three years. A total of 16915 polymorphic SNP markers were used to characterize the panel for linkage disequilibrium (LD), population structure and kinship. The panel was also assayed with markers linked to major wheat genes (plant height, photoperiod sensitivity and vernalization). Phenotypic variation within the panel was reasonably large for all the traits. Genome-wide LD was observed to decay within a map distance of 5-7cM. Highly significant marker-traits associations were identified for all of the traits. Some of these are novel QTL while others co-localize with known wheat genes. Our results show the potential of an elite inbred panel in genome-wide association studies in targeting agronomic traits. Currently, this panel is used to map traits for disease resistance, grain, milling and baking qualities.

POSTER 28

USE OF THE SHUTTLE BREEDING METHOD IN THE NORTH CAROLINA STATE UNIVERSITY PEANUT BREEDING PROGRAM

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The main objective of the N.C. State Univ. peanut breeding program is to improve yield, quality, and disease resistance while meeting the needs of the shelling and processing industries. Four diseases that often reduce yield and quality in North Carolina are leaf spots caused by *Cercospora arachidicola* and *Cercosporidium personatum*, Cylindrocladium black rot (CBR) caused by *C. parasiticum*, Sclerotinia blight (SB) caused by *S. minor*, and tomato spotted wilt (TSWV) caused by *Tomato spotted wilt tospovirus*. Traditionally, the inbreeding and selection of disease resistant lines were divided into subprograms devoted to the four diseases separately, often resulting in lines with resistance to one disease that were highly susceptible to another. Single-plant selections were made in the target environments one time per year, requiring a significant amount of time. An alternative to accelerate this process is the use of the shuttle breeding method with simultaneous evaluation of lines for resistance to all four diseases. Through the use of a winter nursery, the shuttle breeding method results in two generations of inbreeding obtained per year, allowing for acceleration of the development of multiply disease resistant breeding lines. The objective of this research was to increase the genetic gain obtained on a yearly basis through the use of shuttle breeding while simultaneously selecting new high yielding lines with good resistance to the four major diseases. The shuttle breeding method consisted of a combination of single-plant selection and single-seed descent (SSD), with the F_1 , $F_{2:3}$, $F_{4:5}$ and $F_{6:7}$ generations grown during the winter in Puerto Rico, the $F_{2:3}$ and $F_{4:5}$ generations harvested first using SSD. The $F_{2:3}$, $F_{4:5}$, and $F_{6:7}$ generations then were harvested in bulk for disease evaluations of $F_{2:4}$, $F_{4:6}$ and $F_{6:8}$ families during the growing season in North Carolina. Single-plant selection was practiced in selected $F_{2:4}$ and $F_{4:6}$ families that were planted for the purpose using the seeds from SSD. For leaf spot evaluations, plots were grown without leaf spot fungicide and scored on a proportional scale of 1 (no defoliation) to 9 (complete defoliation). A decline in defoliation due to leaf spot ($b = -0.058 \text{ units yr}^{-1}$) and an increase in pod yield without fungicide ($b = 32 \text{ kg ha}^{-1} \text{ yr}^{-1}$) were observed for lines emerging from the shuttle breeding program. Incidence of CBR- or SB-symptomatic plants was measured separately on suitably infested soils with no application of fungicides. From the time the program was initiated, declines in the incidence of both CBR ($b = -0.020$) and SB ($b = -0.011$) were observed for the breeding lines from the program. Over the same time period, a decline was also found for TSWV incidence ($b = -0.009$) in plots with seeds planted 20 in (50 cm) apart and with no insecticide applied to control the tobacco thrips (*Frankliniella fusca*) that vector TSWV. There is no chemical control for TSWV. We demonstrate here that the use of the shuttle breeding method on average resulted in a three year reduction in the amount of time required to develop a high yielding multiple disease resistant peanut cultivar.

POSTER 29

COST AND ACCURACY CONSIDERATIONS FOR TRIAL DESIGN OF ADVANCED APPLE SELECTIONS

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Field evaluation of advanced apple selections is expensive and, with limited resources, the design of these trials is a trade-off between maximizing accuracy of identifying truly elite candidates and minimizing cost. Here we investigate the effect of alternative trial designs on the cost and accuracy of fruit quality assessment using instrumental and sensory traits in the Washington State University Apple Breeding Program as a model. Critical percentage difference, response to selection, and correlated response were used as measures of accuracy. The number of locations, years and harvests per year were decreased from the current design of three to either two or one. For most traits, the loss in accuracy from a reduced design was less than 5%. Reduction in the number of harvests resulted in the smallest loss in accuracy for all traits, but only a negligible decrease in program cost. Reducing both number of harvests and locations to two resulted in a greater loss in accuracy, but still relatively small, and would allow the program to evaluate twelve additional candidates per year for a similar total program cost. Overall, the total cost of the program could be reduced if the design is reduced, with minimal loss in accuracy and the additional capability to trial more selections. The methods employed in this analysis offer a framework for other tree fruit breeding programs to investigate their own trial design accuracy and efficiency questions.

POSTER 30

MAPPING OF QTL FOR TOLERANCE TO CEREAL YELLOW DWARF VIRUS IN TWO-ROWED SPRING MALTING BARLEY

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Cereal yellow dwarf virus (CYDV-RPV) causes a serious viral disease affecting small grain crops around the world. In the US, it frequently is present in California where it causes significant reduction in yield and has been a major impediment to the release of an adapted two row malting barley variety. To identify genetic locations associated with tolerance to CYDV, a segregating population of 184 recombinant inbred lines (RIL) from a cross of the California adapted malting barley line Butta 12 and the CYDV tolerant Madre Selva was used to construct a genetic map including 180 polymorphic markers mapping to 163 unique loci. Tolerance to CYDV was evaluated in replicated experiments where the population was challenged by aphid mediated inoculation with the isolate CYDV-RPV. Quantitative trait loci (QTL) analysis revealed the presence of two major QTL for CYDV tolerance from Madre Selva on chromosomes 2H (Qcyd.MaBu-1) and 7H (Qcyd.MaBu-2), and 4 QTL of less effect from Butta 12 on chromosomes 3H, 4H, and 2H. In addition, two of the lines from this mapping population containing all major QTL for CYDV tolerance and retained the agronomic performance and malting quality of Butta 12 are currently in state wide yield and quality trials as candidates for variety release.

POSTER 31

DEVELOPMENT AND CHARACTERIZATION OF THREE DOUBLED HAPLOID BREAD WHEAT MAPPING POPULATIONS

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Three related doubled haploid bread wheat mapping populations were developed and characterized as a resource for studying quantitative traits. Populations were designed with a built in system for verification of quantitative trait loci (QTL) across populations and genetic backgrounds. This was accomplished by including each parent in two of the three populations through a triangular crossing pattern. The three parents are landrace cultivars with contrasting phenotypes for traits like drought tolerance, plant height, heading date, awn type and root characteristics. Over 200 doubled haploids were created for each population and 150 individuals from each population were genotyped using the Illumina 90K iSelect High-density SNP Array. Phenotype data was collected in the field and greenhouse for traits such as plant height, heading date, yield, root biomass, seminal root angle, awn color, awn/awnless, and waxiness/pubescence. Linkage maps are being generated and phenotyped traits will be added to these maps. The populations will be available to those who are interested.

POSTER 32

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

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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 and a distal interstitial wheat segment (henceforth, 1RS^{WW}) was previously developed. In this study, we developed and evaluated 1RS/1RS^{WW} near isogenic lines (NILs) in two different genetic backgrounds. 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^{WW} 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^{RW}) or the proximal (1RS^{WR}) 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^{WR}) than in the NILs carrying the distal wheat segment (1RS^{WW} and 1RS^{RW}). We conclude that the distal 1RS region carries the beneficial allele(s) for wheat grain yield, canopy water status and CID.

POSTER 33

UTILIZING WILD *CAPSICUM ANNUUM* GERMPLASM FOR BREEDING *CURTOVIRUS* RESISTANCE IN CULTIVATED CHILE PEPPER

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Geminiviruses are the largest family of viruses threatening vegetable production globally, and *Beet curly top virus* (BCTV) is one of the most damaging Geminivirus of pepper (*Capsicum annuum*) in the United States, especially the Western US. The demand for pepper is significant, with the US Pepper industry valued at \$834 M grown on 74,000 acres in 2014. BCTV is a DNA virus that affects several economically important crops such as pepper, sugar beet, tomato and spinach, and it significantly impacted California vegetable production in 2013 due to unusually large vector populations. Curly top disease, which results from infection by viruses in the genus *Curtovirus* like BCTV (family *Geminiviridae*), affects >300 plant species from 44 different families and are transmitted by the beet leafhopper (*Circulifer tenellus*). Little is known about resistance to BCTV, and only a few sources of moderate resistance have been serendipitously identified with the most resistant sources being wild accessions. Over thirty pepper lines (nine reportedly resistant accessions, nineteen wild accessions, and two commercial lines) have been screened for *Curtovirus* resistance using an *Agrobacterium*-mediated screen. In the *Agrobacterium*-mediated screen, a clone of BCTV (strain - *Pepper curly top virus*) is introduced into the plant genome via *Agrobacterium*. As the genome is replicated, BCTV genomes are produced and cause a viral infection. Two of the reportedly resistant lines were shown to be susceptible to BCTV, as well as the commercial lines tested. Several wild accessions screened show resistance and are being re-screened with leafhoppers to confirm resistance. Those accessions showing resistance are being crossed to a cultivated hot pepper variety to introgress BCTV resistance from wild pepper germplasm into a cultivated background. Integrating BCTV resistance into a cultivated background will be useful for pepper production as well as understanding the genetic mechanism of BCTV resistance.

POSTER 34

USE OF TRITICUM DICCOCCOIDES AS A SOURCE OF GENETIC IMPROVEMENT FOR DURUM WHEAT

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Often, wild and progenitor plant species have been shown to be effective sources of simply inherited traits, such as disease resistance. More recently, it has been shown that quantitatively and more complexly inherited traits can be improved by the introgression of genes from wild ancestors, in tomato and rice yields, for example.

We have created three genetic mapping populations to investigate the ability of *Triticum dicoccoides* as a contributor of genetic variability in domestications and agronomic traits into *T. durum*. The first being a recombinant inbred line (RIL) population, consisting of 523 individuals, created by single seed descent. The subsequent two populations were backcross recombinant inbred line (BRIL) populations, created by backcrossing the F1 progeny to either the domesticated or wild parent for 3 or 4 generations, before selfing for another 2 or 3 generations, consisting of 365 BRILs. A genetic map was created independently for each type of population. The RIL and BRIL populations were evaluated for domestication and agronomic traits, while a selection of BRIL lines, which were selected against shattering, were also evaluated for yield.

We found that there were genes present in *T. dicoccoides* that increased yield and seed size in the background of *Triticum durum* cv. Langdon. Preliminary results show that, when comparing the ability to investigate the agronomic traits, we can see that with an increased number of affecting loci, there is an associated increase in the ability of a backcross population mapping approach to differentiate them, and thus the genes that control them.

POSTER 35

CANDIDATE GENE IDENTIFICATION WITH SNP MARKER-BASED FINE MAPPING OF ANTHRACNOSE RESISTANCE GENE *Co-4* IN COMMON BEAN

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Anthracnose, caused by *Colletotrichum lindemuthianum*, is an important fungal disease of common bean (*Phaseolus vulgaris*). Alleles at the *Co-4* locus confer resistance to a number of races of *C. lindemuthianum*. A population of 94 F_{4:5} recombinant inbred lines of a cross between resistant black bean genotype B09197 and susceptible navy bean cultivar Nautica was used to identify markers associated with resistance in bean chromosome 8 (Pv08) where *Co-4* is localized. Three SCAR markers with known linkage to *Co-4* and a panel of single nucleotide markers were used for genotyping. A refined physical region on Pv08 with significant association with anthracnose resistance identified by markers was used in BLAST searches with the genomic sequence of common bean accession G19833. Twenty three unique annotated candidate genes were identified that spanned a physical region of 936.46 kb. A majority of the annotated genes identified had functional similarity to leucine rich repeats/receptor like kinase domains. Two annotated genes had similarity to 1, 3- β -glucanase domains. There were sequence similarities between some of the annotated genes found in the study and the genes associated with phosphoinositide-specific phospholipases C associated with *Co-x* and the *COK-4* locus found in previous studies. It is possible that the *Co-4* locus is structured as a group of genes with functional domains such as leucine rich repeats/nucleotide binding site, kinases, phospholipases C as well as β -glucanases.

POSTER 36

FINDING NEW SOURCES OF EASTERN FILBERT BLIGHT IN HAZELNUT

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Hazelnuts have been grown commercially in Oregon since the early 1900s. Eastern filbert blight (EFB) caused by the pyrenomycete *Anisogramma anomala* (Peck) E. Müller was discovered in the Willamette Valley in 1986 and is an immediate and costly concern of the US hazelnut industry. Host genetic resistance is the most effective method of control. Complete resistance to EFB was first discovered in 'Gasaway', which is controlled by a dominant allele at a single locus. It has been extensively used in the hazelnut breeding program at Oregon State University. Resistance based on the single dominant gene from 'Gasaway' may not be durable, as new races of the fungus that can overcome this R-gene may arise or be introduced. If new hazelnut cultivars with "pyramids" of different R genes are developed, it is expected that the fungus will find it difficult to simultaneously overcome all genes. In spring 2013, 50-60 seedlings from each of progenies were inoculated by exposure of potted trees under a structure topped with diseased wood. Twelve progenies showed the 1:1 segregation ratio for resistance while some other progenies did not show a 1:1 segregation ratio. DNA extracted from fresh leaves will be used to screen with Simple Sequence Repeat SSR markers starting with those on linkage group 6 (LG6). Resistance from these new sources will be assigned to Linkage group based on correlation with SSR markers. If the correlation coefficient is less than 0.5, SSR markers from LG2 (Georgian resistance) and LG7 (Ratoli resistance) will be pursued. When the LG has been identified, all available SSR markers in that group will be used and the new R-genes will be mapped.

POSTER 37

QTL ANALYSIS OF SNOW MOLD RESISTANCE IN WINTER WHEAT

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Winter wheat accounts for 70-80% of wheat production in the United States and is prone to snow mold infection. Although snow mold is not a threat in all wheat-growing regions, it is serious enough in Washington that resistant cultivars are widely planted. Because snow mold infection depends on environmental conditions, it is inconsistent year to year and very difficult to phenotype, thus breeding for resistance is challenging. Our objective is to identify QTL and DNA markers for the resistance found in 'Eltan'. Four years of replicated field data have been collected from a population of 151 Finch x Eltan RILs planted in Washington and Idaho. The population was genotyped with 9,000 SNP and 200 SSR markers. Polymorphic markers were assigned to linkage groups using JoinMap. QTL Cartographer analysis identified three putative QTLs on chromosomes 5A, 3B, and 6B. The 5A QTL is located between 159 and 172 cM, has a LOD score ranging from 20 to 115, and accounts for approximately 49% of phenotypic variation. The 3B QTL is located between 6 and 33 cM, has a LOD score ranging from 14 to 63, and accounts for approximately 7% of phenotypic variation. The 6B locus is in a 34 cM interval, has a LOD score ranging from 13 to 67, and accounts for approximately 15% of phenotypic variation. Additional polymorphic SNP markers are being run in the population to better characterize and narrow these regions. The resulting QTL and associated markers will be applicable to marker assisted selection for snow mold resistance.

POSTER 38

MAPPING AND IDENTIFYING CANDIDATE GENES OF THE *MODIFIER OF AMYLOSE EXTENDER 1* (*MAE1*) MUTATION IN MAIZE (*ZEA MAYS* L.).

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Knowledge of the genes and proteins involved in starch synthesis has grown tremendously by the study of reverse genetics, however the complex process is still not fully understood. In maize (*Zea mays* L.), *amylose extender 1* (*ae1*) mutants are associated with an increase in amylose-like starch from 25 to 70%, affecting kernel hardness and levels of resistant starch. A novel maize phenotype of completely shrunken, collapsed kernels was observed when backcrossing two recessive *ae1* alleles into the white food-grade inbred line cgx333. This novel mutation appears to be recessive and due to the segregation of a single gene, which we have named *modifier of amylose extender 1* (*mae1*). The objectives of this research are to map the *mae1* mutation in a family of RILs segregating for *mae1* using GBS, to identify candidate genes for further analysis and to analyze the effect of *mae1* on kernel starch properties.

MASS SELECTION FOR FABA BEAN TOLERANT TO DROUGHT-LIKE CONDITIONS

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Faba bean (*Vicia faba* L.) is one of the most drought sensitive cool-season pulses contributing to unacceptable yield instability. However, water deficits during growth and development and terminal drought are common throughout much of its production range. Therefore, genotypes with heritable drought resistance or drought escape and avoidance mechanisms should exist. In the face of climate change there is a need to identify genotypes with yield stability under water-limiting conditions. To meet this challenge a bulk population composed of 466 USDA WRPIS accessions was spring-sown at the Central Ferry (CF) Research Farm in Central Ferry, WA for four consecutive years (2011-14) without irrigation. The CF location has a Chard silt loam soil, which is lighter than the soils typically found on the Palouse and the growing season is typically warmer and drier than much of southeastern Washington due to its low elevation. A block of winter-type faba bean was included as a check in 2014.

Mass selection was practiced each year selecting for early maturing individuals with above average pod set. The selection index was approximately 10%. Four rows spaced 35 cm apart were sown with a Hege 120 planter on 9 April 2011, 4 April 2012, 2 April 2013, and 1 April 2014. Planting density was low ($40 \text{ kg}\cdot\text{ha}^{-1}$) to maximize evapotranspiration, increase moisture stress, and to streamline single plant selections.

During the final cycle of selection in 2014 plants with no pods to over 20 pods were observed. Still yield was perceptibly lower than adjacent irrigated trials. Early flowering appeared to be related to pod set and single plant yield. The block of winter-type faba bean was later to flower and mature and was notably taller at maturity than the mass selected population. Consequently, fewer plants with more than 10 pods were found. Prior to flowering adjacent seedlings exhibited distinctive responses to drought stress. The most vigorous turgid seedlings were often the individuals selected at harvest.

Drought escape and dehydration avoidance traits appear to be present within the WRPIS faba bean germplasm. Plants with smaller, or lanceolate, leaves common of Mediterranean genotypes, appear to be more tolerant to water deficit than the larger oval leaves common of northern European cultivars. Early flowering, pod set, and maturity should be the main traits of interest when selecting for a terminal drought cropping system. While seedling selection appears promising it remains to be seen if the juvenile drought tolerance phenotype is heritable. Since drought tolerance in faba bean has been reported to respond to heterosis, additional cycles of mass selection and progeny testing will be necessary. If heritability is low however, dissemination of a mass-reservoir population could be one way to exploit heterosis for drought tolerance.

POSTER 40

IDENTIFYING GENETIC MARKERS FOR METABOLITE LEVELS IN POTATO

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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 improved composition by developing genetic markers linked to individual, or groups of, important metabolites. Methanol extracts of cooked tubers from 229 diverse potato cultivars and breeding clones were analyzed by Ultra Performance Liquid Chromatography coupled with Mass Spectrometry (UPLC-MS). The same potatoes were genotyped with an Infinium SNP chip (8303 SNP markers). Nine-hundred and eighty one metabolic “features” were detected. Weighted Gene Correlation Network Analysis (WGCNA) was used to cluster individual features into groups. Eleven groups were formed. Step-wise regression was done on potato chip color, and group eigenvalues; two groups were correlated with chip color at $p < 0.05$.

POSTER 41

EVALUATING THE POTENTIAL OF CHLOROPHYLL FLUORESCENCE IMAGING FOR IDENTIFICATION OF HEAT TOLERANT WHEAT GERMPLASM

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Precise, accurate and rapid measurement of traits plays an important role in the improvement of new plant varieties. Therefore, a considerable amount of research and development has taken place in the area of phenomics, the rapid collection of precision phenotypic data on an organism-wide scale. Chlorophyll fluorescence imaging (CFI) could potentially have a large impact on wheat breeding as it can be used to rapidly and non-invasively quantify overall photosynthetic performance and measure plant stress. Heat stress has become an increasingly important factor limiting wheat production throughout the world due in part to a reduction in photosynthetic capacity and the associated yield reduction. Therefore, a better understanding of techniques to accurately measure photosynthesis, such as CFI, is needed. The object of this study was to assess the feasibility of using CFI for early detection of heat stress on adult and juvenile wheat plants. At the Washington State University Phenomics facility twenty elite spring wheat lines from the Pacific Northwest varying from heat tolerant to highly heat susceptible were selected for screening. All experiments were arranged in a randomized complete block design, with three biological replicates, and two experimental replicates per treatment that included plant non-stressed, adult heat stressed, juvenile non-stressed and juvenile heat stressed. The CFI measurements were taken twice a day (day and night) for 10 days for all treatments. Results after four non-stressed and four heat-stressed trials showed that environmental variation (light, temperature irregularity, watering time) was too large to produce accurate and repeatable results, thereby limiting the utility of the data collected. The methods used in this study demonstrated no significant advantage over standard phenotypic evaluation of heat stress using methods such as chlorophyll concentration measurement. In fact, more money, energy and time were required for CFI. Although the results obtained had limited applicability, several changes in phenomics methods could lead to a reduction in experimental error and allow for CFI to be an accurate, precise and rapid tool for measuring heat stress. To test this hypothesis additional trials with alternative CFI methods have been initiated. These results and those of the current study will provide knowledge to wheat breeders around the world who are working to create heat tolerant wheat lines.

POSTER 42

EMPIRIC COMPARISON BETWEEN GENOMIC AND PHENOTYPIC SELECTION FOR RESISTANCE TO BACTERIAL SPOT OF TOMATO

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Genomic selection employs models which take into account genotypic and phenotypic data from a breeding population in order to predict performance of subsequent generations based solely on their genotypes. The potential of genomic selection in plant breeding has gained prominence with the increasing ease of detecting single nucleotide polymorphisms (SNPs) to be used as genetic markers. There remain practical issues in genomic selection that have not been investigated through empirical studies. The use of a large number of markers can lead to redundancy in the data due to low recombination frequencies in breeding populations. We used resistance to *Xanthomonas euvesicatoria*, a causal agent of bacterial spot of tomato to evaluate the effect of marker coverage for genomic selection. We compared a model with markers covering the whole tomato genome at low density and a model with markers targeting known QTLs. We also compared the efficiency of genomic selection to phenotypic selection. The population consisted of 109 lines of processing tomatoes directionally selected from a breeding population developed to combine resistances against several *Xanthomonas spp.* The 109 lines were observed under *X. euvesicatoria* inoculated conditions in the field in a randomized complete block design (RCBD) in one location. Best linear unbiased predictors (BLUPs) of the disease score were calculated for each line. The lines were genotyped using markers selected from the "SolCAP" Infinium SNP array. 397 markers were used for whole genome coverage, and 40 markers were used to target known QTLs. Genomic Estimated Breeding Values (GEBVs) were calculated using Bayesian linear regression with a Gibbs sampler algorithm based on an inverted chi-squared distribution. Selections were made for expected response to infection based on either their phenotypic BLUPs or their GEBVs for 397 and 40 markers. The selfed-seed from selections were tested as plots in RCBD evaluations in the field under inoculated conditions in two different locations. The adjusted R^2 for the correlation against BLUPs across both locations from the second year field trial was 0.24 for phenotypic data evaluated during the first year, 0.15 for GEBVs from whole genome coverage, and 0.16 for GEBVs estimated from targeted QTLs. The proportion of prediction accuracy for genotypic selection with whole genome coverage compared to the accuracy of phenotypic selection was 87% for one location, 31% for the other, and 61% across both environments. For genotypic selection targeting known QTLs, the proportions of accuracy compared to phenotypic selection were 84% and 41% in each location and 65% across locations. This empirical study demonstrates that genomic selection models, even with low marker coverage, offer the potential for genetic gain when advancing selections, but are not a replacement for phenotypic selection.

POSTER 43

GENOME-WIDE ASSOCIATION MAPPING FOR STRIPE RUST RESISTANCE IN ELITE DURUM WHEAT

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Wheat stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*), is one of the most extensive diseases that affect the wheat production worldwide. Driven by the climate change toward higher temperatures and intense and variable rainfall, new aggressive strains are flourishing in wheat growing areas. Novel sources of resistance are therefore desirable to tackle this growing threat of stripe rust. Previous studies indicated durum wheat (*Triticum turgidum* ssp. *durum*) has good potential for improving stripe rust resistance of wheat, but few new genes have been identified so far. In this study, 260 durum elite accessions mainly from Mediterranean countries, North American and international agricultural research centers (CIMMYT and ICARDA) were used to identify new sources of resistances via genome wide association analysis (GWAS). The population was planted at three environments to evaluate stripe rust response at the adult stage in 2014. Seven stripe rust isolates collected in United States and Italy were inoculated at seedling stage under greenhouse conditions. The panel was genotyped with the 90,000 Illumina iSelect wheat single nucleotide polymorphism (SNP) chip, providing 12,143 polymorphic SNP markers for GWAS. Preliminary analyses identified 12 QTL on seven chromosomes (4A, 5A, 7A, 1B, 2B, 5B and 7B) that were associated with resistance to *Pst* at the seedling stage with marker-wise significant *P* value <0.001. A total of 8 QTL on five chromosomes (1A, 2A, 6A, 7A and 5B) were significantly associated with resistance at the adult stage in at least two environments. Now, we are in the process of collecting additional data in the summer of 2015 at four environments. After completion of these GWAS study, tagged resistance loci will be identified to diversify the stripe rust resistance gene pool and will facilitate incorporation of resistance loci into common wheat.

POSTER 44

GENOME-WIDE SNP IDENTIFICATION, LINKAGE MAP CONSTRUCTION AND QTL MAPPING FOR SEED WEIGHT IN PEA

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Pea (*Pisum sativum* L.) is one of the oldest domesticated crops in the world and is an important source of protein in human food and animal feed. It is rich in a variety of nutritional components, such as mineral nutrients, carbohydrates and several vitamins. While lagging behind other crops in genomic research, the advent of next generation sequencing technology is now enabling more widespread research in this area. The objectives of this project are to develop genome-wide single nucleotide polymorphism (SNP) markers using genotyping by sequencing (GBS), construct a high-density linkage map for pea and a comparative map with *Medicago truncatula*, and identify quantitative trait loci (QTL) associated with seed weight. A total of 359,724,355 high quality reads were obtained from GBS after filtering by FastQC. Using the UNEAK analysis pipeline, 2,292 SNP loci were shown to be polymorphic between Kiflica and Aragorn, two parents of an F₆-derived recombinant inbred line population. 1,683 markers including 75 previously published markers and 1,608 SNP markers developed from the GBS assay were mapped on a linkage map with a map size of 1328.1 cM. Using comparative mapping, a high degree of synteny was observed with the genome of *M. truncatula*. The population was planted in two environments in 2014. Three seed weight QTLs were detected using composite interval mapping. The QTLs for 100-seed weight were identified on linkage groups IV and V. This study will provide an important sets of tools to enable marker-assisted selection (MAS) in pea breeding programs.

POSTER 45

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

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Cowpea (*Vigna unguiculata* L. Walp) is a leguminous crop that many around the world rely on to meet their basic nutritional needs through the consumption of the protein and fiber rich grain and vegetative matter. 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 'Golden Eye Cream' (GEC). This population was phenotypically analyzed for drought response in the field and greenhouse. The genes conferring the drought tolerance were mapped using double digest restriction site-associated DNA sequencing (ddRAD-seq) and SNP markers closely linked to the genes of interest were identified. With this knowledge of the underlying genetics conferring drought tolerance in cowpea, molecular tools can be created which will further aid in the breeding of more drought tolerant species.

POSTER 46

A GENOME-WIDE ASSOCIATION STUDY REVEALS NOVEL STEM RUST RESISTANCE LOCI IN HEXAPLOID WINTER WHEAT

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Hexaploid bread wheat (*Triticum aestivum*) is a staple cereal crop that provides approximately 20% of calories for the global human population. Wheat stem rust (*Puccinia graminis* f. sp. *tritici*), especially the Ug99 race group which is prevalent in east Africa, threatens food security in many countries. The persistent arms race between plant pathogens and their hosts requires an ongoing effort to characterize new sources of genetic resistance. Here, we report a genome-wide association study (GWAS) which detected novel stem rust resistance loci in a worldwide collection of hexaploid winter wheat. Sixteen hundred accessions were obtained from the USDA-ARS National Small Grains Collection and genotyped with the Illumina Infinium Wheat SNP 9K assay. This yielded 5,362 markers suitable for association analysis. To identify genes conferring vertical resistance, accessions were screened at the seedling stage with stem rust races TTKSK (Ug99), TRTT, TTTTF, BCCBC, and a field bulk of six North American isolates. Association analysis with a mixed linear model revealed over one hundred markers significantly associated ($p < 0.001$) with resistance to at least one of the races tested. The resistance loci detected in this germplasm can be attributed to both novel and previously characterized alleles. In addition to identifying new sources of genetic resistance for future wheat improvement, the closely linked markers will serve as useful tools for breeders to carry out marker-assisted selection.

POSTER 47

IDENTIFYING NEW SOURCES OF PARTIAL RESISTANCE TO *ALTERNARIA DAUCI* IN THE U.S. PLANT INTRODUCTION *DAUCUS SSP.* (CARROT) GERMPLASM COLLECTION

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The US produces approximately one billion kilograms of carrots annually, which provides growers with an estimated value of 692.8 million dollars. *Alternaria* leaf blight (ALB) caused by *Alternaria dauci* (Kühn) is one of the most devastating fungal diseases of carrots and can cause losses from 40 up to 99%. In a 2015 survey of US growers, breeders, and processors, ALB was ranked as one of the top three most important diseases and pests. To date, there are no completely resistant cultivars, and some growers still need to spray between 10 and 30 applications of fungicide each season. Given the economic and environmental impact of ALB, this study has two objectives: first, to examine the USDA carrot germplasm collection for new sources of resistance to ALB and second, to examine the repeatability of the disease severity phenotype score among the accessions across years and locations. In total, 650 Plant Introduction accessions, including both cultivated and wild carrot, were grown and evaluated in three separate field experiments, one in 1992 in Sanford, FL and two in 2013 and 2014 in Hancock, WI. On a disease severity rating score between 0 and 5, where 0 is no visible disease damage and 5 is severe disease and defoliation, higher levels of resistance were not common, with only 27 accessions scoring a rating of 2.5 or less. Complete immunity to ALB was not found. Moreover, 45 accessions were grown in all three experiments and analyzed for their disease phenotype repeatability. It was found that 24% of the accessions had the same score in all three years, 40% had a max difference of 0.5, and 80% had a max difference of one on the disease scale between all of the years. Using nonparametric analysis of variance on the rank scores for each accession, it was found that regardless of growing locations or years, there was no significant difference in ALB scores. These results suggest a common genetic basis for the disease phenotypes. A closer examination of the most resistant accessions will be conducted to confirm the identity of the most resistant germplasm sources, determine ALB inheritance, and introgress resistance into breeding populations.

POSTER 48

PATTERNS OF GENETIC DIVERSITY, LINKAGE DISEQUILIBRIUM AND GENOME-WIDE ASSOCIATION STUDY OF RESISTANCE TO STRIPE RUST IN A GLOBAL COLLECTION OF SPRING WHEAT ACCESSIONS

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Stripe rust, caused by the fungus *Puccinia striiformis* f. sp. *tritici*, is a widespread and major threat to wheat production in the Pacific Northwest of the US and the world. Identifying new sources of resistance and incorporating multiple genes into elite cultivars is required to ensure durable protection against the dynamics of pathogen virulence. Wheat germplasm collections maintained in genebanks including landraces, cultivated lines, improved cultivars and breeding lines provide access to repertoires of useful sources of genetic resistance. Here, a total of 1163 spring wheat accessions originating from 91 countries were used to identify sources of stripe rust resistance through a genome wide-wide association study (GWAS). Adult plants and seedlings of the accessions were evaluated for stripe rust resistance under field conditions in six environments in Washington and greenhouse conditions, respectively. A genome-wide set of 5960 high quality single nucleotide polymorphism (SNP) markers generated through the Infinium wheat 9K-assay were used to investigate the genetic structure, patterns of linkage disequilibrium (LD) and GWAS of stripe rust resistance in the germplasm panel. The model-based clustering algorithm with correlated allele frequency analysis using STRUCTURE program revealed two genetically distinct sub-populations. Membership of individuals to the two clusters were consistent with the geographic origin as well as improvement status of the accessions. Average genetic differentiation between individuals within clusters were higher than the net nucleotide distance between the two populations. Genetic diversity analysis indicated significantly higher gene diversity and polymorphism information content in the landraces and cultivated lines compared to cultivars and breeding lines. However, average stripe rust resistance was significantly lower in cultivars and breeding lines than in landraces. Genome-wide LD was predicted to decay below the critical $r^2 = 0.23$ at an inter-marker distance of 2.5 cM. GWAS identified 9 genomic regions significant at false discovery rate (FDR)-adjusted probability < 0.10 for conferring adult plant stripe rust resistance. Similarly, GWAS of seedling resistance detected 6 genomic regions significant at FDR probability < 0.10 . The significant QTL were identified on chromosomes 1A, 1B, 2B, 3B, 4B, 4D, 5B, 5D, 6A, 6D and 7B. Four of the significant QTL on 1A, 5B, 6A and 6D appeared to be novel, while the remaining 11 QTL were mapped close to previously reported stripe rust resistant genes or QTL. The molecular markers of the genomic regions detected in this study for resistance to stripe rust should be useful in marker-assisted selection in wheat breeding after validation using proper germplasm and populations.

POSTER 49

COMPREHENSIVE ANALYSIS OF AGRONOMIC AND BIOCHEMICAL TRAITS OF BLUE CORN

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Borderland landraces of blue corn have been cultivated for centuries as part of the diet in native communities in the southwestern U.S. They are rich sources of genetic variation and display diverse kernel colors. Our objectives were to evaluate the grain yield performance, analyze the biochemical composition and investigate the phenotypic diversity of six landraces and two populations across different environments in New Mexico. All accessions were evaluated as field trials in 2012 and 2013. Near infrared spectroscopy was used to quantify the protein, oil, starch, kernel density and essential amino acids lysine, methionine and cysteine. Principal component analysis was used to evaluate the phenotypic diversity among the blue corn landraces. All landraces displayed considerable variation except Flor del Rio and Ohio Blue. Across all locations and years, grand mean of grain yield for all accessions was 2.27 Mg/ha; the highest average grain yield was at Farmington and the lowest at Las Cruces 2.45 and 2.20 Mg/ha, respectively. Borderland landraces of blue corn displayed higher protein and oil content than dent (Ohio Blue) and flint corn (Flor del Rio). Yields were low as anticipated; however, variation for elevated oil, protein and essential amino acids in future may make their variation in traditional diets advisable.

POSTER 50

PHENOTYPING STRATEGIES TO EVALUATE ROOT GROWTH OF ALFALFA CULTIVARS RANGING IN FALL DORMANCY

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Plant roots serve essential functions including the acquisition of water and nutrients, are the site of interaction with soil microbes and anchor the plant to the soil. Alfalfa (*Medicago sativa* L.) is an important perennial forage legume species worldwide due to its biomass yield, protein content, persistence, capacity for biological nitrogen fixation and reduction of soil erosion. The objective of this project was to develop root phenotyping systems and quantify differences in root growth of alfalfa cultivars ranging in fall dormancy. The root system of eight alfalfa cultivars was evaluated using multiple types of mesocosms ranging from 25.4 cm to 1 m and filled with various soil substrates. Clear mesocosms allowed visualization of alfalfa roots non-destructively in real time and these were used to determine the root length at different stages of plant growth and development within the mesocosm area. Shoots and roots from each individual were harvested from each mesocosm and root phenes including shoot biomass, biomass at different growing depths, total root biomass, and total root length were measured. Variation for root phenes was observed within the alfalfa cultivars evaluated and these differed in the different growth substrates used. The phenotyping methods developed here represent an initial framework for a root screening pipeline to evaluate alfalfa germplasm for variations in root system architecture and ultimately identify the root phenes that result in improved agronomic performance under abiotic and biotic stress conditions.

POSTER 51

GENETIC VARIATION FOR LETTUCE SEED THERMOINHIBITION PLASTICITY IS ASSOCIATED WITH TEMPERATURE-SENSITIVE EXPRESSION OF GIBBERELLIN, ETHYLENE AND ABSCISIC ACID BIOSYNTHESIS, METABOLISM AND RESPONSE GENES

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Failure of seeds to germinate at high temperature (thermo-inhibition) reduces overall crop stand establishment of cultivated lettuce (*Lactuca sativa* L.). Susceptibility to temperature induced seed dormancy in lettuce is influenced by seed's genotype 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 *Lactuca sativa* wild accession PI251246 (PI) produced at 35°C and 25°C greenhouses had germination threshold-temperature of 37° and 32°C respectively, whereas seeds of *Lactuca Sativa* L. Salinas (SAL) produced at same two environments had minor shift on the germination threshold-temperature. PI and SAL Seeds harvested from both 35°C and 25°C greenhouses (GH) were subjected to quantitative PCR of 27 known genes involved in GA, Ethylene and ABA biosynthesis and metabolic pathways. In addition, recombinant inbred line (RIL) population of 122 F8 families, derived from PI and SAL, were produced in 5 different location-year combinations with differing ambient temperatures. Additive Main Effect and Multiplicative Interactions (AMMI) statistics on the thermo-inhibition trait revealed significant genotype by environmental interaction. QTL studies on the thermo-inhibition trait identified a previously known major quantitative trait locus (qHTG9.1); however QTL effects varied significantly with production environments. In addition, the QTL for plasticity or variance in germination across production environments (GXE) collocated with the minor QTL on Chromosome 9 (qPHTG9.2), suggesting that different genes may be responsible for differential expression of the trait across multiple environments. Comparative gene expression analysis on phenotypic plasticity revealed differentially expressed genes linked to GA, ABA and Ethylene biosynthesis and metabolic pathways. Notable amongst them were LsGA3ox1, LsERS1, LsACS1, ABI3, AT5PTASE2, LsABA8ox4, LsNCED4, SnRK2.2, UDP-glucuronosyl, In general, GA and Ethylene-related genes were expressed highly in seeds produced at high temperature maternal environment, whereas ABA-related genes were expressed highly on seeds produced at low temperature maternal environment. In particular, LsGA3ox1, a gene encoding enzyme in the GA biosynthetic pathway, was upregulated (10X) in PI seeds produced at 35°C GH compared to seed produced at 25°C GH, when subjected to 12 hours of imbibition at 35°C germination temperature. The production temperature sensitivity of expression of LsGA3ox1 may determine the threshold temperature for lettuce seeds produced in multiple environments and may indirectly influence other regulatory pathway via interconnected pathways.

POSTER 52

AN EXTENSION-BASED APPROACH TO INTEGRATING DNA INFORMATION INTO ROSACEAE BREEDING PROGRAMS: THE IMPORTANCE OF PREACHING TO THE CHOIR.

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The development of trait-predictive DNA tests has been accelerating in rosaceous crops. These DNA-based assays can help increase the accuracy and efficiency of Rosaceae crop improvement and improve the competitiveness of commercial horticultural production in peach, apple, strawberry and cherry. Despite the availability of these advances, many Rosaceae breeding programs are not exploiting them. The breeders have indicated a lack of knowledge about the protocols, utility, and practical applications as a barrier to implementing DNA technologies in crop improvement decisions. In 2010 and 2014, plant breeders, geneticists and other supporting scientists were surveyed regarding their training needs and preferred formats for information delivery. Those results were used to formulate recommendations for training resources that will best address the training needs of these breeders and scientists. We have begun to assemble training materials to address breeder needs for routine use of DNA information in breeding decisions and operations. The targets for training include both current breeders and breeders-in-training. The education aims are similar for the two, but the approaches for these groups are different given the differing experience and available time for training. By providing breeders of peach, apple, strawberry and cherry with training resources on effective use of DNA-based genetic information in their crop improvement programs, those breeders will have greater opportunity to leverage the vast array of genomic information available. This information can enable breeders to develop innovative cultivars more efficiently, benefitting the fresh fruit industry.

INHERITANCE OF LEAF COLOR AND WEEPING ARCHITECTURE
IN EASTERN REDBUD

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Redbud (*Cercis canadensis* L.) is a small landscape tree that exhibits considerable morphological diversity, including variation in size, architecture, and flower and leaf color. The objectives of this study were to investigate the inheritance of purple and gold leaf color, and weeping architecture in *C. canadensis*. Inheritance of purple leaf color and weeping architecture was investigated in F₁, F₂ and BC₁P₁ and BC₁P₂ families derived from controlled hybridization of 'Covey' (green leaf, weeping architecture) and 'Forest Pansy' (purple leaf, non-weeping architecture). The F₁ family consisted of 23 plants, all showing green leaves and non-weeping architecture. Chi-square tests for heterogeneity among the four F₂ families for segregation of purple leaf color and weeping architecture were both non-significant ($P=0.09$ and 0.87 , respectively), so data was combined prior to analysis for both traits. Segregation for leaf color fit the expected test ratio of 3:1 (green leaf : purple leaf) at $P=0.02$. Slight underrepresentation of purple leaf progeny was observed in the F₂ family. The F₁ and F₂ data indicate that purple leaf is recessive to green leaf, and that purple leaf is controlled by a single recessive gene for which we propose the designation *pl*. Segregation for weeping architecture fit a 3:1 (non-weeping: weeping) test ratio ($P=0.26$). The F₁ and F₂ data indicate that weeping architecture is recessive to non-weeping, and weeping is controlled by a single recessive gene for which we propose the designation *wpl*. Combined co-segregation analysis for the purple leaf and weeping traits fit the expected 9:3:3:1 ratio ($P=0.05$) that would be predicted for a di-hybrid cross involving two recessive genes. This suggests lack of linkage between the purple leaf and weeping loci which was confirmed by a contingency test ($P=0.35$). Inheritance of gold leaf color was explored in F₁, F₂ and BC₁P₂ families derived from hybridization of 'Covey' (green leaf) x 'Hearts of Gold' (gold leaf). Since five different F₂ families were utilized in this study (each derived from a separate F₁ tree), a chi-square test for heterogeneity was conducted to ensure families could be combined for analysis ($P=0.55$). The F₁ family derived from 'Covey' x 'Hearts of Gold' consisted of 30 plants, all showing green leaves. We initially predicted that F₂ progeny would segregate into only green leaf and gold leaf categories. However some segregants demonstrated a leaf color phenotype unlike either parent, classified as bleached. F₂ plants were separated into one of three categories based on leaf color (green, gold and bleached). The segregation of green, gold and bleached progeny did not fit any known Mendelian segregation ratio, perhaps suggesting the interaction of more than one locus. However, when bleached and gold segregants were combined into a single category (gold + bleached), each F₂ family and the combined F₂ data fit a 3:1 ratio (green leaf: gold + bleached leaf) at $P = 0.06$ (combined data). We have demonstrated that both purple leaf color and weeping architecture in *C. canadensis* are controlled by single, recessive genes inherited in a simple Mendelian fashion. While inheritance of gold leaf color appears to be more complex, we have shown that inheritance is not cytoplasmic, and it can still be exploited in hybridization efforts with relative efficacy. Understanding how these morphological traits are inherited can lead to opportunities for genetic improvement and the development of new ornamental cultivars.

POSTER 54

CHROMOSOME PAIRING BEHAVIOR BETWEEN *VACCINIUM CORYMBOSUM* AND *V. ARBOREUM*
GENOMES BASED ON MOLECULAR MARKER ANALYSIS OF AN INTERSPECIFIC PSEUDO-
BACKCROSS POPULATION

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Highbush blueberries (*Vaccinium corymbosum*; Vc) are characterized as autotetraploids based on the tetrasomic inheritance patterns of single loci. In order to use in direct crosses with Vc, we used colchicine to double the chromosome number of the diploid related species, *V. arboreum* (Va). However the degree of genome similarity between the species is unknown, and the expectation of random chromosome segregation may not be correct in hybrids between Vc and Va. The objective of this research was to evaluate the segregation pattern of multi-allelic simple sequence repeat markers in a pseudo-backcross population between a Vc cultivar and a Vc x Va hybrid to determine whether the expectation of tetrasomic inheritance was correct when considering the interaction of the two divergent genomes. We utilized a pseudo-backcross population resulting from a cross of 'Southern Belle' x 'FL08-467'. 'FL08-467' is an interspecific hybrid from a cross between 'Primadonna' (Vc) and the selection 'FL06-753', a tetraploid Va selection created by colchicine chromosome doubling of a diploid individual. Ninety four individuals, the parents and two grandparents were genotyped using SSR markers. Individual marker analysis confirmed the expected tetrasomic inheritance Vc homologous chromosomes in 'Southern Belle' due to random chromosome pairing. 'FL08-467' showed predominantly disomic inheritance with preferential pairing between homologous chromosomes from the same genome, confirming the amphidiploid nature of this hybrid. However, up to 13% of the progeny showed allele segregation at marker loci indicating random pairing between Vc and Va genomes. A better understanding of the degree of genome similarity between these species will be important as we attempt to introgress specific traits from Va into the Vc genome.

POSTER 55

HETEROSIS IN SOYBEAN AS A PREDICTOR OF DROUGHT TOLERANCE

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Applied methods for drought tolerance breeding are needed to aid soybean breeders in developing drought-tolerant high-yielding soybeans lines. A possible method is an early generation test for heterosis (hybrid vigor) in F_1 or F_2 hybrids that could be used as an inbred line predictor for seed yield. Another possible predictor of inbred line performance is genetic distance between parental lines. To test if heterosis and genetic distance could be used as breeding tools to improve drought tolerance, we evaluated whether heterosis is expressed in hybrid soybeans when grown under water stress. Field trials of F_1 and F_2 bulk hybrids were conducted for three populations under limited and full irrigation in Nebraska. Significant ($P < 0.05$) and positive mid-parent heterosis (MPH) was detected in F_1 yield trials under limited irrigation for two families (+17% and +15%). Under full irrigation, we detected significant and positive MPH for one family (+12%) indicating that it is possible to use heterosis as a tool for drought tolerance breeding. Significant high-parent heterosis (HPH) was also detected under limited irrigation (+12%) for one family, but HPH was not detected under full irrigation. F_2 bulk yield trials showed significant MPH under limited irrigation for two families, indicating that F_2 field trial evaluations are also a viable early generation screening procedure. As genetic distance between two parental lines increased, heterosis increased under limited and full irrigation. The findings suggest that genetic distance between two parents could be used as a tool to predict hybrid performance and derived inbred performance. Heterosis could be a valuable tool for soybean breeders to detect the most advantageous populations to develop drought tolerant soybeans. The heterosis prediction method could increase speed to market and decrease resources required to develop drought tolerant cultivars.

POSTER 56

WHY WAIT FOR THE FRUIT? DNA-INFORMED BREEDING IN ROSACEAE: PREDICTION OF APPLE, PEACH, AND SWEET CHERRY SKIN COLOR AS A CASE STUDY.

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Much hype has been generated over the past 30 years regarding the potential positive impact of “molecular markers” on plant breeding. These “molecular markers”, more appropriately termed DNA tests, were expected to have substantial impact in tree fruit breeding, due to long juvenility periods, expensive phenotyping procedures, and space requirements. To date, there are few examples of successful application of DNA tests to enhance breeder decision confidence, termed DNA-informed breeding, for fruit quality traits in perennial crops. A limited number of reliable, predictive DNA tests for breeding-relevant traits is likely a major contributor to this failure to meet expectations. Due to recent dedicated efforts to develop such tools, specifically those of RosBREED and FruitBreedomics projects, the tree fruit breeding community is reaching a point at which this technology can begin to play a valuable role in the breeding process. DNA tests for the prediction of apple, peach, and sweet cherry fruit skin color are examples of some of the tools successfully developed and deployed for direct use in breeding programs. Based on genomic regions discovered by collaborators to be associated with anthocyanin-based fruit color traits, DNA tests were developed. In all three crops, the resulting simple sequence repeat tests differentiated alleles associated with various levels of red skin pigmentation. With the apple and peach tests, it is now possible to select parents with the genetic potential to produce high-blush seedlings and select seedlings predicted to have high-blush levels years before fruit evaluation if desired. In sweet cherry, blush and mahogany skin color are market-defining classes, each having different breeding targets and trait thresholds. Consequently, selecting parents that will produce seedlings of the desired class with the sweet cherry color DNA test can improve crossing outcomes. All three tests developed allow for the synergistic improvement of apple, peach, and sweet cherry fruit color, thanks in part to a conserved *MYB10* genetic mechanism in each crop. In addition to the skin color DNA tests, tests are available for the prediction of other valuable fruit quality traits including apple and peach texture and flavor and sweet cherry size and maturity date. So, why wait for the fruit to select germplasm with genetic potential to produce superior quality fruit? With skin color and other fruit quality DNA tests now developed, apple, peach, and sweet cherry breeders are well equipped to take the leap into DNA-informed breeding.

POSTER 57

EVALUATION OF A HISTORICAL DATA SET OF SOUTHEASTERN US WINTER WHEAT FOR GENOMIC SELECTION

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Genomic Selection (GS) for complex or multi-genic traits requires the use of genotypic and phenotypic information from individuals in a training population (TP) to create a prediction model to produce genomic estimated breeding values (GEBV). Use of historical, unbalanced phenotypic data sets on lines in cooperative nurseries that are genotyped as training populations (TPs) is one strategy to develop selection models to predict the performance of breeding lines having only genotypic information. Advances in next generation sequencing (NGS) technologies allow generation of high-density genome wide molecular markers at a cost that makes the use of GS attractive to plant breeders. The genotyping by sequencing (GBS) approach takes advantage of restriction enzymes to capture a reduced representation of the target genome and DNA barcodes adapters to sequence multiple samples in parallel in a single run of NGS platform. Our objective was to evaluate the use of seven years of historical nursery phenotypic data and GBS genotypes for selected nursery entries to develop prediction models for southeastern soft red winter wheat. In this study, the training population consisted of 334 wheat lines from different Southeastern U.S.A. breeding programs evaluated in the Gulf-Atlantic Wheat Nursery that were genotyped using GBS. The phenotypic data was unbalanced, with few varieties repeated across years and included yield, test weight, plant height, and heading date from 2008 to 2014, where the most complete trait across years and locations was yield. Statistical analysis of phenotypic information was made using mixed model analysis in ASReml 3.0. The linear model utilized was $Y = \mu + E + B(E) + G + GE + \epsilon$, where Y = observed value for each observation, μ = overall mean, E = effect of environment, $B(E)$ = effect of block nested within environment, G = effect of genotype, GE = effect of interaction between genotype and environment, ϵ = experimental error. The BLUE (best linear unbiased estimate) for each variety was used in the genomic selection model. Missing data were imputed for 24,597 SNP obtained from TASSEL GBS after filtering (<50% missing data, $MAF > 0.05$, and $r^2 < 0.80$). The GS model utilized in this study was G-BLUP through the R-package Synbreed. GEBV were obtained for each individual for each trait, then the accuracy of the model was tested with a 2-fold random cross validation procedure for 100 randomized cycles for each trait. The Pearson correlation coefficients between observed phenotypes and GEBVs for yield, test weight, plant height and heading data were 0.59, 0.48, 0.52, and 0.53 respectively. When the models were used to predict yield of 65 breeding lines evaluated in the 2014 SunWheat Nursery, an accuracy of 0.63 was observed. This included the identification of 10 of the 15 highest yielding lines in the nursery. The prediction accuracies for each trait of our GS model were similar to accuracies reported in the literature and indicate the potential of GS in these populations. Our data suggest that this historical data set could be used in Southeastern breeding programs as an aid to select for yield of preliminary lines having only genotypic information.

POSTER 58

NOVIC II: A PARTICIPATORY PROJECT TO TRIAL AND BREED VEGETABLE VARIETIES FOR ORGANIC SYSTEMS

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The overall goal of the Northern Organic Vegetable Improvement Collaborative II (NOVIC II) is to increase the proportion of US agriculture that is managed organically by increasing the number of vegetable varieties tailored to organic systems, and available as certified organic seed. Currently, nearly all contemporary vegetable varieties have been bred in conventional systems, and are not necessarily adapted to organic production. The USDA NOP requires that growers use certified organic seed, but allows untreated, conventionally produced seed if certified organic seed of an equivalent variety is unavailable. Seed companies have been slow to produce organic seed and growers have been reluctant to buy it. Hence, farmers continue to use conventional untreated seed because their preferred varieties are not available organically. NOVIC II seeks to break this impasse by increasing the number of organically produced, well-adapted varieties available to growers through creation of new, improved varieties and identification of existing commercial varieties found to perform well in organic systems.

The project involves researchers and farmers collaborating to evaluate breeding lines for creation of new varieties, and to identify the best performing existing commercially available varieties (both organic and conventional seed sources) for organic systems. NOVIC II has four hubs (OR, NY, WA, WI) across the northern tier of vegetable producing states and employs a mother-daughter trial design that integrates varied farming environments into the trialing process. The breeding efforts on five vegetable crops (tomato, cabbage, sweet pepper, winter squash and sweet corn) are conducted with active involvement of collaborating farmers, seed growers and independent plant breeders. This project is a continuation of NOVIC I (2009-2013), with an original genesis in the USDA-OREI funded Organic Seed Partnership (OSP), and employed the farmer-researcher networks developed under OSP to design a management approach for the NOVIC projects to emphasize farmer involvement in project planning and implementation. The project collaborative design has also borrowed from the international research community. During NOVIC I, farmers and researchers acquired crucial data on variety performance; farmers implemented changes during farm planning based on project results; and breeders obtained data on the performance of their breeding lines across multiple farming environments. Communication within the network of researchers and growers developed by NOVIC I has allowed plant breeders to understand, identify and focus their work on traits that are most critical to organic growers. Improved varieties developed in NOVIC I have been or will be released for broccoli, sweet corn, snap peas, snow peas, and butternut squash. New breeding lines are also available for the same crops.

POSTER 59

IDENTIFYING GENETICALLY DIVERSE REPRESENTATIVE CORE SET FROM *AEGILOPS TAUSCHII* COLLECTION USING GENOTYPING-BY-SEQUENCING

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D-genome of hexaploid wheat is least diverse of all three sub-genomes. *Aegilops tauschii*, D-genome donor of hexaploid wheat, remains a great resource for bringing novel genetic diversity for resistance against several abiotic and biotic stresses in wheat. Despite its unmatched potential, *Ae. tauschii* has not been much used in wheat improvement for the yield and quality related traits. In conventional breeding, its use has been limited by the identification of best accessions based on phenotypic performance only. Here we present a procedure to identify and select a genetically diverse core set of *Ae. tauschii* accessions guided by their phenotypic performance and geographical distribution. Whole *Ae. tauschii* collection (~600 accessions) at Wheat Genetics Resource Center (WGRC) was genotyped using genotyping-by-sequencing (GBS) that is a robust, faster and cheaper method for genotyping. More than 145k SNPs were discovered and filtered for less than 50% missing data. Filtered SNPs were used for cluster analysis and the calculation of population statistics F_{ST} and nucleotide diversity (π). Based on cluster analysis, phenotypic performance and their geographical distribution, we developed a core set of 40 accessions that captures more than 90% genetic diversity present in whole collection, and represent great extent of geographical distribution. In addition to core set development, these accessions will be used to introgress novel genes for resistance against leaf rust, stem rust, Hessian fly and abiotic stresses such as heat and drought tolerance to wheat.

POSTER 60

AGRONOMIC AND CULINARY EVALUATION OF ELITE FRESH MARKET POTATO GERMPLASM

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In the fresh market potato industry, the most widely grown cultivars were developed anywhere from 20 to more than 100 years ago. Compared with other field crops, the rate of new variety development is limited by the autotetraploid genetic structure of potato and the large number of traits required for commercial acceptance. The goal of this study was to measure the agronomic and culinary properties of elite fresh market breeding lines. The agronomic properties, which included total yield, tubers per plant, tuber size distribution, tuber disease incidence, and the incidence of internal defects, were measured with a replicated complete block design at two commercial locations and one research station in Wisconsin. The multi-environment trial structure enabled a comparison of the broad-sense heritability for each location as well as the genetic correlation between sites, estimated using a multivariate mixed model. The culinary traits, which included two different analytical measurements of texture and the results of a human sensory panel, were only evaluated for tubers from one location due to their labor-intensive nature. Results from the first year showed that, except for disease incidence, the heritability of the agronomic traits was consistently high (> 0.7). The genetic correlation between sites was high for some traits, such as tubers per plant (> 0.8), but was more variable and lower for yield. A second year of the study is underway to assess the repeatability of the genotype \times environment interactions observed in the first year. This research has helped identify several breeding lines with superior agronomic and culinary properties as candidates for variety release. These new varieties should provide a higher economic return for growers and packing sheds, as well as better quality for consumers.

POSTER 61

HERITABILITY AND REPEATABILITY PREDICTIONS FOR TREE HEIGHT FROM DIALLEL PROGENY TEST DATA OF COAST REDWOOD (*SEQUOIA SEMPERVIRENS*)

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A repeatability model was fit to predict repeatability and heritability for tree height from a sample of full-sib families from a coast redwood (*Sequoia sempervirens*) breeding population for timber production. Linear mixed models (LMMs) using Bayesian Markov chain Monte Carlo (MCMC) methods were used for prediction. Height repeatability was predicted to be 0.23 and height heritability to be 0.09 for height measurements in growth years 2, 4, and 9 after planting across three locations. Repeatability and heritability predictions and accuracy were compared for each location individually. Tree height means and variances vary by location resulting in changes in variance component estimates and genetic parameter predictions due to heterogeneity of the environment and different numbers of entries tested. The field trial location with the most entries and multiple trees per block had the highest accuracy. This study can be used to guide coast redwood breeding program management decisions and is insightful for breeding in other similar forest systems.

UTAH TREFOIL (*LOTUS UTAHENSIS*): A UNIQUE NATIVE FORAGE LEGUME FOR WESTERN RANGELAND HABITAT RESTORATION AND REHABILITATION

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With an increased emphasis being placed on native forbs and grasses used in federal land management projects. There is an increased need for native plant materials development. We investigate the breeding potential of several Utah trefoil germplasm collections because this species provides essential ecological functions such as soil stability, pollinator habitat, and valuable high quality forage for both wildlife and livestock grazing. Additionally, Utah trefoil produces condensed tannins which make this species a bloat free forage legume; condensed tannins may also improve the absorption of nutrients during digestion, and reduce parasite infection rates in ruminant animals. In 2012 seed collections were made from 19 sites in Arizona, Nevada, and Utah. Plants were grown in the greenhouse and in 2013 were planted into three common gardens in northern Utah. Collections were evaluated for dry matter yield (DMY), seed production, and forage quality factors including condensed tannins (CT), crude protein (CP), and neutral detergent fiber (NDF) content. The domesticated birdsfoot trefoil (*Lotus corniculatus*) was included as a check species for forage quality comparisons. Our 2014 evaluations found that collection e5 had the highest DMY with a mean of 23.49g per plant, but was not significantly higher than collections e20, e13, e16, and e15 with means of 22.3g, 17.98g, 15.16g, and 13.71g DMY per plant respectively. Collection e5 had the highest seed production of a mean of 5.42g per plant, and was significantly higher than all collections except e20, and e15 with means of 5.11g, and 4.83g per plant respectively. The CT content was extremely variable. The birdsfoot trefoil check was significantly lower than all native collections at 0.92% CT content and a p-value of <0.0001. The next separation was between all of the germplasm collections originating from Arizona e22, e10, e14, e12, and e13 with CT concentrations of 7.44%, 8.11%, 8.41%, 8.44%, and 8.9% respectively. These were significantly less than all germplasm collections from Utah and Nevada with a p-value of <0.0001. The CT concentrations of the other germplasm collections CT content ranged from 11.57% in e20 to 17.93% in e8. Birdsfoot trefoil had a significantly higher NDF content of 35.11% than all native germplasm collections except e10, e14, e13, e22, e12, e5, and e15 with NDF content of 38.38%, 37.09%, 36.07%, 35.8%, 34.45%, 33.22%, and 30.2% respectively. The NDF content of e20 (28.79%) was not significantly less than collections e5 and e15. The only germplasm collection that had significantly higher CP than birdsfoot trefoil (0.29%) was e15 (0.32%) with a p-value of 0.0177. Birdsfoot trefoil was only significantly higher than e2 (0.27%) with a p-value of 0.0435. We will be collecting the final year of data during the summer of 2015. Judging from our preliminary data, the optimal native Utah trefoil collections to be used in a plant breeding and domestication program will be e5, e15, and e20. These native germplasm collections have forage quality factors similar to the domesticated birdsfoot trefoil, with the exception of significantly higher CT, and have some of the greatest biomass and seed productions of all native germplasm collections evaluated in our trials. We foresee in the coming years that this species will be used in arid rangeland restoration projects throughout the intermountain west.

POSTER 63

EFFICACY OF JUVENILE, FIRST YEAR, AND SECOND YEAR SELECTION ON IMPROVING BIOMASS YIELD AND ETHANOL YIELD IN SWITCHGRASS

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Switchgrass (*Panicum virgatum* L.) is a perennial, warm season grass that can be used as a biofuel. Switchgrass does not reach full biomass yield potential until the third year of production. This can delay selection, increasing time and expense of a switchgrass breeding program. The objective of this research was to determine the efficacy of early selection of juvenile, first year, and second year switchgrass on improving biomass and ethanol yield. Eight parents, representing the varieties 'Kanlow', 'Alamo', and 'Miami' were crossed in a diallel design to create fifty-six full sib families. Greenhouse started seedlings were planted at Knoxville, TN and Crossville, TN in single plant plots in a RCB design with four blocks and twenty replications per family. Plants were evaluated for biomass yield at 8 weeks post-emergence. After transfer to the field, plants were evaluated for biomass and ethanol yield in the fall of the first, second, and third year. Biomass yield was measured by weighing individual plants. Ethanol yield was predicted by grinding a representative sample from each plant using a Wiley Mill with a 2 mm mesh and analyzing using near infrared spectroscopy. An ANOVA was performed to test the year effect and year by family interaction effect. Additionally, a rank correlation was calculated between year three (Y3) yields and juvenile (YJ), year one (Y1), and year two (Y2) yields respectively. Biomass yield differed significantly by year (YJ = 0.33 g plant⁻¹, Y1 = 95 g plant⁻¹, Y2 = 1081 g plant⁻¹, Y3 = 1434 g plant⁻¹). Ethanol yield did not differ significantly by year ($\mu = 64 \text{ mg g}^{-1}$). A significant ($p < 0.05$) family by year interaction was observed for both biomass and ethanol yield. For biomass yield, rank correlations were significant ($p < 0.05$) but were weak between Y3 and YJ ($R^2 = 0.07$) with much stronger correlations between Y3 and Y1 ($R^2 = 0.74$) and Y3 and Y2 ($R^2 = 0.88$). For ethanol yield, rank correlations were also significant, but were weak between Y1 and Y2 ($R^2 = 0.36$). Ethanol yield for Y3 is currently being processed and will be presented at the meeting. Results indicate early selection based on first or second year biomass might be effective in selecting for full biomass yield potential. Early selection for ethanol yield may be less effective due to greater differences in ranking between years.

POSTER 64

IN VITRO PHENOTYPING OF TALL FESCUE FOR SUMMER DORMANCY

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Mediterranean tall fescue exhibits partial summer dormancy during extreme summer conditions. Genetic improvement of tall fescue by exploiting summer dormancy can be a key strategy to improve persistence of tall fescue in the south-central USA. Identifying traits associated with summer dormancy along with phenotyping method is very critical and yet to develop in tall fescue. In vitro experiments were conducted in growth chambers using four Mediterranean (summer dormant) and four Continental (summer active) tall fescue cultivars following completely randomized design with five replications. One growth chamber was maintained at 24/16°C day and night temperature and 10 h photoperiod as optimum growing condition, while another chamber was maintained at 34/26°C day and night temperature and 16 h photoperiod as summer environmental condition. Among the measured traits, electrolytic conductivity was significantly higher in Mediterranean cultivars under both optimum and summer dormant condition by 20-60%, porosity was higher only under summer dormant condition by almost 150%, while leaf growth rate and plant height was lower under summer dormant condition by almost 150%. Overall, all the Mediterranean genotypes showed higher electrolytic conductivity and leaf porosity than any continental genotypes. The two morphotypes did not show any significant differences for osmotic potential, leaf chlorophyll content, pH of the conductivity solution, number of stomata, length of stomata, width of stomata, length of stoma and width of stoma under any of the two conditions. This study with some additional verification will lead to identify traits and phenotyping procedures for summer dormancy under green house and growth chamber conditions, which will help breeders selecting Mediterranean genotypes under controlled environmental condition.

POSTER 65

PREDICTING GENETIC VARIANCE IN BREEDING POPULATIONS: USING HISTORICAL BREEDING RECORDS TO EMPIRICALLY EVALUATE SIX PREDICTION METHODS

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Robust methods to predict genetic variance (σ_G^2) of bi-parental breeding populations would facilitate greater gains per breeding cycle. To illustrate its utility, consider a crossing block of 100 elite parents – making all 4,950 pairwise crosses is impractical and evaluating all such crosses at a scale appropriate to quantify σ_G^2 is impossible. Previously, metrics such as the phenotypic, genetic (measured as the proportion of non-matching markers), and kinship-based (estimated from genome wide markers) distances between parents have been tested for their ability to predict σ_G^2 . In general there is little to no correlation between these metrics and σ_G^2 . One explanation for this is the inability of such methods to explicitly model the segregation of associated genetic loci (i.e. QTL). Now, the commonplace use of genome wide markers and genomic selection (GS) in breeding programs, along with recent theoretical work in the area, has enabled the development of three additional methods that, at varying levels, explicitly model the segregation of QTL. The accuracies of six σ_G^2 prediction models were evaluated using field-based estimates of σ_G^2 from 40 bi-parental barley breeding populations. The accuracies of phenotypic distance, genetic distance, and kinship-based distances between the two parents were all low and non-significant. In contrast, the accuracies of the three methods that explicitly integrate the effects of associated genetic loci were all significant. The method that directly measures variation using the GEBVs of simulated bi-parental populations was the most accurate. The results indicate that σ_G^2 predictions based on genome-wide markers may enable plant breeders to target specific parent combinations, or at the least winnow out low- σ_G^2 predicted crosses.

POSTER 66

QTL ANALYSIS AND HERITABILITY ESTIMATION FOR TSWV RESISTANCE IN THE PEANUT CULTIVAR, FLORIDA-EPTM'113'

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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 heritability of spotted wilt resistance is also important in helping breeders to predict breeding values of future generations. The two objectives of this study are 1) to identify molecular markers linked to spotted wilt resistance in peanut through genetic mapping using a bi-parental population, and 2) to estimate the heritability of TSWV disease resistance among different years and locations with two different disease measurement methods.

A total of 163 F₂ progenies were derived from a cross between Florida-EPTM'113', a TSWV resistant cultivar and Georgia Valencia, a susceptible cultivar. The F_{2:3}, F_{2:4}, and F_{2:5} populations were phenotyped by visual rating and/or immunostrip test in two different locations, Marianna and Citra, FL. More than 2500 markers were screened through the whole peanut genome against two parental lines. Around 100 markers flanking known QTLs were tested and the polymorphic markers were used to genotype the whole F₂ population. The QTL analysis showed that 14 markers on linkage group A01 were linked with a TSWV resistant QTL region, which was the same QTL region identified previously. This QTL is validated by different populations and fine mapping will be conducted by utilizing F_{5:6} population. More markers located within the region will be developed in order to obtain markers closely linked to spotted wilt resistance.

The heritability of TSWV resistance was estimated using ASReml 3.0 with a linear mixed model. The dataset included three years (2012, 2013, 2014), two locations (Citra and Marianna, FL) and two disease measurement methods (visual rating and immunostrip). Pedigree information was incorporated and spatial analysis was applied to better control environmental errors and increase the heritability and genetic gains. Multi-environment trial (MET) and bivariate analysis were conducted. The results indicated that heritability of TSWV resistance using immunostrip measurement was higher than the overall plot visual rating on single site analysis. The MET analysis also supported the results: both the type B genetic correlation and heritability of immunostrip results (correlation: 0.84; heritability: 0.69) were higher than visual rating (correlation: 0.75; heritability: 0.39), which suggested that the selection based on the immunostrip can be more efficient regardless of the seasonal impacts (years, locations, high/low disease pressure).

POSTER 67

DIALLEL ANALYSIS OF TOP SIZE IN CARROT (*DAUCUS CAROTA*, L.)

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Crop establishment in carrot (*Daucus carota*, L.) is limited by erratic germination, poor seedling growth, and delayed canopy closure. This growth habit translates to ineffective competition with weeds and thus weed control is often a substantial cost of production. Varieties with rapid top growth are one option to improve weed management, but little is known about the inheritance and genetic basis of top size in carrot. This project aims to analyze the genetic components contributing to top size and facilitate future breeding efforts. Useful parental stocks and superior hybrid combinations will be identified using a diallel mating design. Six diverse carrot inbred lines representing a range of top sizes were crossed, including reciprocals, in Madison, WI in 2014. F1 progenies and parents were grown out in a randomized complete block design (RCBD) with two blocks in El Centro, CA in 2014 and are currently planted in Hancock, WI. Midseason and harvest measurements were taken for canopy height, canopy width, shoot biomass, and root biomass. Data will be analyzed using Griffing's Method I, Model I to estimate general combining ability (GCA), specific combining ability (SCA), and reciprocal effects. Additionally, graphical representation of the data using the GGE biplot method will further elucidate relationships among genotypes, traits, and environments. Results of this analysis will provide valuable insight into desirable hybrid combinations, determine the relative importance of additive and non-additive gene action, and inform selection strategies for top size.

POSTER 68

ASSOCIATION ANALYSIS OF STEM SOLIDNESS AND WHEAT STEM SAWFLY RESISTANCE IN A PANEL OF NORTH AMERICAN SPRING WHEAT GERMPLASM

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The wheat stem sawfly (WSS) is historically a pest of major economic importance in wheat in the Northern Great Plains of North America. Damaging WSS populations have recently expanded southward, increasing concerns about wheat susceptibility to this pest over a large vulnerable area. Limitations constraining traditional control measures have driven pest management efforts towards resistance breeding, but selection for resistance has mainly target stem solidness due to its effectiveness and easy of phenotyping. Resistance based on stem solidness is not always reliable, partially because the degree of solidness is influenced by photoperiod and light intensity during stem elongation. A better characterization of resistance genes will provide additional tools for breeders. An association mapping analysis for stem solidness and wheat stem sawfly resistance was conducted using a set of 244 elite spring wheat lines from 10 North American breeding programs. All lines were genotyped using the wheat 90K iSelect SNP assay and 25,728 polymorphic markers were detected. Field data were collected in three environments during four years of trials. Early and late stem solidness were shown to be associated with the solid stem quantitative trait locus (QTL) on chromosome 3B, but variation for early solidness was also affected by chromosomal regions on 1B and 5D. Lines that become solid later in the growing season are likely to be less effective against WSS than those that develop pith early. Therefore, breeding programs that rely on stem solidness to breed for WSS resistance should consider its temporal and structural components for best results. Despite the original expectation of having a single haplotype conferring solidness on the 3B locus, two lines from CIMMYT had haplotypes that differed from that of Rescue, the first solid-stemmed line developed in North America. This may indicate a different origin of the solid stem alleles in these lines. Previously identified QTLs for resistance were confirmed, including QTLs for heading date and stem cutting on chromosomes 1B and 4A, respectively. Association analysis revealed that the favorable allele of the 4A QTL is present in a high frequency among germplasm from WSS infested and uninfested areas. This suggests that this chromosomal region is either under selection throughout North America for reasons other than WSS resistance, or at least does not confer a cost in terms of other agronomic traits. Potential sources of a novel resistance mechanism causing larval mortality were identified among the panel lines. Larval mortality was associated with QTLs on chromosomes 2A, 3A, and 5B. The use of this panel allowed us to determine the genetic basis of WSS resistance available within North American breeding programs. The genetic diversity for traits associated with WSS resistance uncovered in this study can be exploited by breeders through marker assisted selection and will potentially benefit both historically impacted areas and regions vulnerable to future outbreaks.

POSTER 69

MAIZE GERMPLASM EXHIBITING AFLATOXIN RESISTANCE WITH GOOD YIELD POTENTIAL AS IDENTIFIED BY SOUTHEAST REGIONAL AFLATOXIN TRIALS (SERAT)

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Since 2003, a multi-environmental trial of public breeding maize (*Zea mays* L.) hybrids across multiple programs in the southeastern United States has evaluated stable resistance to the accumulation of aflatoxin following inoculation with *Aspergillus flavus*. Aflatoxins pose a potential serious health hazard to humans and livestock, requiring serious economic cost in identifying and disposing of contaminated grain. The Southeast Regional Aflatoxin Trial (SERAT) was formed to identify public breeding material with the most stable resistance to aflatoxin accumulation, and to evaluate their essential agronomic traits in different environments. Each year thirty to forty hybrids were tested in four locations in a randomized complete block design with three replications. Ears were machine harvested except for the randomly chosen ten that were selected in each plot to be inoculated with a suspension of *A. flavus*, and tested for aflatoxin concentration at maturity. Yield and other agronomic traits were measured as well. As expected there was significant genotype by environment (GxE) interaction for aflatoxin concentration, as inheritance of resistance to production of aflatoxin is known to be highly quantitative in nature. The entries tested as a group from 2006-2014 displayed relatively high resistance, as 71% had average levels that were lower than the average commercial check level at 182 ng g⁻¹, and ca. 25% had levels lower than the best check BLUP at 106 ng g⁻¹. Yield was negatively correlated with levels of aflatoxin in the two Texas locations, College Station and Lubbock, and only slightly positively correlated with aflatoxin in Starkville, MS and Tifton, GA. Twenty percent of the program hybrids had yields of 9.5 t ha⁻¹ or higher, which although lower than the average check yield at 10.5 t ha⁻¹ in this study, is excellent for material arising from tropical and subtropical germplasm. Most importantly, specific hybrids and lines (such as CY-1, Mp313E, NC300, S2B73, Tx777, and TZAR106) that were in multiple hybrids stood out for both resistance to aflatoxin accumulation and yield in a number of environments. Repeatability for yield over all locations based on best linear unbiased predictors was 0.73 and for log-transformed aflatoxin levels was 0.63. The SERAT program has been a valuable collaboration across southeastern US breeding programs by confirming the aflatoxin resistance in lines with desirable agronomic traits.

POSTER 70

GENOTYPE BY ENVIRONMENT INTERACTIONS OF FLAVOR TRAITS IN GREEN BEANS

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Several studies dating back to 1900s and 1900s have attempted to analyze the genetics of flavor traits in green beans, yet no concerted effort has been made to assess the impact of environment on green bean flavor. In this study, six cultivars of green bean were chosen representing three market classes of green beans. Two cultivars, 'Tendergreen' and 'Eagle', were chosen based on their close phylogenetic relationship to 'Tendercrop' and a close phylogenetic connection to the Andean gene pool. Two green bean cultivars, 'OR5630' and 'DMC04-88' were chosen based on their close phylogenetic relationship to 'Pole Blue Lake' and a close phylogenetic connection to the Mesoamerican gene pool. Finally, two cultivars, 'Ebro' and 'Bogota', were chosen as representatives of the romano market class of green beans. These six cultivars were grown at three locations with three randomized blocks at each location. Two locations were in Oregon and one in Wisconsin. Moreover, trials were planted in May and July at all locations. Samples were chosen based on their weight, seed development, and overall maturity. Fresh samples were ground into a fine powder in liquid nitrogen and analyzed using head space gas chromatography Mass spectrometry (GC-MS). GC-MS peaks for linalool and 1-octen-3-ol volatile compounds were quantified. Bartlett's tests, residual plots, and normality plots indicated that the data was not normally distributed and variances were not equal. Log transformation of the data resulted in the assumptions of ANOVA being met. ANOVA analysis was conducted in R on the main effects of bean cultivar, location, and month of planting and the interactions of the main effects. The main effect of bean cultivar was significant for linalool, but only date of planting was significant for 1-octen-3-ol. There were no significant interactions of the main effects. Tukey's multiple pairwise comparisons of bean cultivar for linalool showed that 'Eagle' was significantly different from all other varieties, except 'OR5630', and that it had the lowest mean level of linalool. The cultivar 'DMC04-88' had unexpectedly high levels of linalool for a green bean phylogenetically related to 'Pole Blue Lake'.

POSTER 71

CHARACTERIZATION OF PROGENY DERIVED FROM DISOMIC ALIEN ADDITION LINES FROM
INTERSUBGENERIC CROSS BETWEEN *GLYCINE MAX* AND *GLYCINE TOMENTELLA*

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Disomic alien addition lines (DAALs, $2n=42$) were obtained from an intersubgeneric cross between *Glycine max* [L.] Merr. cv. Dwight ($2n=40$, G1G1) and *Glycine tomentella* Hayata (PI 441001, $2n=78$, D3D3CC). They are morphologically uniform but distinct from either of the parents. These DAALs were all derived from the same monosomic alien addition line ($2n=41$), and theoretically they should breed true because they had a pair of homologous chromosomes from *G. tomentella* and 40 soybean chromosomes. However, in some selfed progenies of DAALs the extra *G. tomentella* chromosomes were eliminated resulting in plants with 40 soybean chromosomes. These progeny lines ($2n=40$) have a wide variation in phenotypes. The objectives of this research were to document the phenotypic variation among the progeny of these DAALs, and to understand the genetics behind this phenomenon. In the replicated field study, variation was observed among the $2n=40$ progenies for the qualitative traits such as flower, seed coat, hilum, pod, and pubescence color, and stem termination; as well as the quantitative traits protein and oil concentrations, plant height, lodging, and time of maturity. Three $2n=40$ lines had protein concentrations significantly higher than either the DAAL or Dwight. Studying the plant transcriptome via RNA-sequencing documented that many genes that are critical to fundamental plant growth processes and related to stress and defense responses were differentially expressed between the DAAL (LG13-7552) and one of the $2n=40$ progeny (LG12-7063). RNA-sequencing data indicated that the gray pubescence of LG12-7063 was not due to sequence change from *T-* to *t t* genotype, but the result of altered gene expression. The expression of *G. tomentella* sequences and higher expression of transposable elements (TEs) in the DAAL were also documented.

POSTER 72

YIELD DRAG ASSOCIATED WITH THE APHID RESISTANCE GENE RAG2 FROM PI 200538

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The soybean aphid (*Aphis glycines* Matsumura) is an exotic pest of soybean (*Glycine max* (L.) Merr.) first identified in North America during 2000. There are currently four known biotypes of soybean aphid and several genes that confer resistance to the pest. Two such genes are *Rag1*, which was mapped from Dowling, and *Rag2*, which was mapped from PI 200538. Both genes have been introgressed into Midwestern adapted soybean lines and in previous studies, the effect of both genes on yield and other agronomic traits was evaluated in aphid free environments. These tests showed that *Rag1* was not associated with a yield drag, but *Rag2* was associated in one of two backgrounds it was tested. In our current study, we compared the effect of both *Rag1* and *Rag2* on yield and other agronomic traits in a population of near isogenic lines that segregate for both genes. The populations were tested in three Illinois environments in 2013 and 2014 with no aphid infestation. Results from the tests showed that while *Rag1* was not associated with yield, *Rag2* was associated with reduced yield. Lines homozygous for *Rag2* yielded approximately 130 kg ha⁻¹ less than lines with *Rag1* or neither resistance gene. The reduced yield is likely the result of genes linked to *Rag2* instead of the *Rag2* gene itself and experiments are now being conducted to determine whether the association between *Rag2* and reduced yield can be broken.

POSTER 73

PUSHING AND PULLING ADDITIONAL METHIONINE INTO RICE SEED

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Rice is a staple food for approximately 3 billion people and can account for a significant proportion of their dietary protein, especially in the developing nations of Asia. However, rice protein is deficient in several amino acids essential in diets of non-ruminant animals, including lysine, tryptophan, and methionine. Unless the diet is supplemented with other protein sources, these amino acid deficiencies can result in significant health consequences for humans and significantly stunted growth in animals. Conventional rice breeding programs have developed high yielding varieties with higher seed protein levels, but these varieties are still deficient in several essential amino acids, including methionine. A more targeted approach to improve the amino acid balance is seed-specific expression of exogenous storage proteins to 'pull' essential amino acids into the seed. Linda Tabe's group at the CSIRO in Canberra, Australia pursued this strategy in rice with one of the most sulfur-rich storage proteins known, sunflower seed albumin (SSA). In addition to its very high methionine and cysteine contents (16% and 8% respectively), SSA is rumen stable, meaning that additional methionine "pulled" into the seed by SSA expression would likely be bioavailable, even to ruminant animals like sheep, goats, and cattle. However, despite achieving high SSA expression in transgenic rice seed, total seed methionine content remained nearly unchanged. This suggests that free amino acid pools of methionine limit seed protein expression and that limiting methionine is directed into SSA expression at the expense of endogenous seed proteins. An alternative approach pursued by our group to improve the nutritive quality of rice seed has been to increase the biosynthesis of free cysteine and methionine in source tissues. Extensive work in model organisms such as *Arabidopsis* and tobacco and crops such as potato suggests that increased expression of serine acetyltransferase (SAT) and feedback-insensitive cystathionine-gamma-synthase (CgS) may have the potential to increase the synthesis of cysteine and methionine to the point where these amino acids are no longer limiting for storage protein expression. These "push" approaches proved to be somewhat successful in increasing seed protein-incorporated methionine, but the gains fell short of producing greatly improved nutritive quality. Since neither manipulation of sink nor source strength proved to be sufficient on its own, we combined these two approaches by crossing the SSA transgenic "pull" line with SAT and CgS transgenic "push" lines. Quite strikingly, the "push plus pull" combination resulted in up to 50% increase in total seed methionine, the vast majority of which is protein-incorporated. We look forward to performing feeding trials with the high-methionine seed from these double transgenics. In addition to the demonstrated utility of the "push plus pull" transgenic approach to increase protein-incorporated methionine in rice, we anticipate that it may have wider utility in development of crops with greatly improved nutritive quality for human and animal consumption.

POSTER 74

MOLECULAR CHARACTERIZATION OF THE *VRN1* GENES IN WINTER WHEAT AGS 2000 AND PIONEER 26R61

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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. Regulation of the vegetative to reproductive growth transition ensures that flowering occurs in environments when temperatures are warm and water is abundant to support growth. For winter wheat, time from planting to ear emergence is influenced by vernalization duration requirement, photoperiod response and earliness per se. Vernalization requirement can be variable requiring minimal vernalization to more than eight weeks duration. The objective of this study was to investigate the molecular differences for vernalization duration between winter wheat cultivars AGS 2000 and Pioneer 26R61. Analysis of a RIL mapping populations from the cross between AGS 2000 with Pioneer 26R61 detected major flowering QTLs co-located with the *VRN-A1* and *VRN-B1* loci on chromosomes 5A and 5B, respectively. Cloning and sequencing of the 13 kb *vrn-B1* winter allele from both cultivars revealed sequence variation in the first intron, particularly a 36 bp deletion detected in AGS 2000 was within the critical region associated for vernalization insensitivity in spring wheat and associated with short vernalization duration requirement. TaqMan gene copy number assays estimated that both cultivars had a single *vrn-B1* copy but differed at the *vrn-A1* locus with AGS 2000 having three *vrn-A1* copies and Pioneer 26R61 had two copies. The RILs were grouped into four genotypic classes based on *vrn-A1* gene copy number and the *vrn-B1* deletion polymorphism. The four RIL groups responded variably to different partial vernalization treatments and significant genetic interaction between *vrn-A1* copy number and *vrn-B1* polymorphism ($p < 0.001$) were observed. Flowering was not delayed among the four genotype classes when plants were fully vernalized. When plants were partially vernalized for two and four weeks, flowering time among the four genotype classes range from 75 to 133 days. Genotypes with the *vrn-B1* 36 bp deletion flowered 12 to 28 days earlier than lines without this deletion. Genotypes with two *vrn-A1* copies flower 11 to 33 days earlier than lines having three *vrn-A1* copies in the two and four week treatments, respectively. Our results suggest that the 36 bp deletion in the critical region of *vrn-B1* intron 1 is associated with reduced vernalization requirement in lines having either two or three copies of *vrn-A1*. However, this small deletion within intron 1 does not have the large effect of the large deletions found in the dominant *Vrn-B1* genes that confer spring growth habit. A broader understanding of the available genetic diversity of known and novel vernalization genes and the biology of flowering in winter wheat will enable precision approaches for breeding climate resilient cultivars.

POSTER 75

QUANTITATIVE TRAIT LOCI ASSOCIATED WITH STEM STRENGTH AND LODGING IN DRY PEAS

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Field pea is an excellent rotation crop which leaves nitrogen in the soil for the following wheat crop, breaks disease cycles, and facilitates rotational weed control. Since the year 2000, US pea acreage has increased 5 fold to over a million acres, and Montana pea acreage has increased 27 fold to 570,000 acres. The dramatic increase in pea acreage has made research in this crop very important. In order to discover the QTL associated with lodging in peas, a RIL population was created from a relatively wide cross between the commercial variety Delta and a wild type pea variety. Data was collected for 15 quantitative morphological traits, and several categorical traits which might be linked to lodging resistance. Based on a single year of data, the major genes influencing lodging in pea are Mendel's dwarfing gene (*le*) and the semileafless mutation (*af*), which together account for approximately 30% of the variation in lodging in pea. Another important QTL affecting basal branch number is near Mendel's flower color locus (*a*). Number of basal branches is positively correlated with lodging resistance and explains approximately 13% of the variation in lodging. Literature has indicated that increasing compressed stem thickness would decrease lodging in pea, but compressed stem thickness appears to be only mildly associated with lodging resistance. Compressed tiller diameter has a weak positive correlation with lodging indicating that wider stems may increase lodging due to added weight. Multiple pleiotropic effects were seen for such traits such as tendril length, which is positively correlated with plant height, lodging, yield, and tiller diameter. These and other associations need to be investigated further in pea. Genotype by sequencing and other methods will be used to discover genetic markers for major traits influencing lodging resistance and other important characteristics in pea, allowing for faster selection of desirable characteristics.

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EFFECT OF GENOTYPE, ENVIRONMENT, AND GENOTYPE-ENVIRONMENT INTERACTION ON FE CONTENT IN AMARANTHUS SPP.

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Amaranthus spp. is one of several African Indigenous Vegetables valued as a means of delivering essential micronutrients to resource-limited communities. However, the effect of phenotypic plasticity, or genotype-environment interaction (GEI) on the ability of this plant to deliver key nutrients is under-studied. Fe was selected as it is often cited as the most prevalent nutritional deficiency globally. The purpose of this study was to make observations on the extent of GEI on the Fe content of *Amaranthus* spp., ultimately toward making selections for high Fe content performance among otherwise advanced genotypes. Five genotypes were analyzed for Fe content, grown in randomized complete block design in Pittstown, New Jersey (NJ), USA, and Arusha, Tanzania. Samples analyzed are exclusively from first harvest foliar material. Fe content was quantified by Inductively Coupled Plasma (ICP) analysis at the Penn State Agricultural Analytical Services Lab. Analysis of variance (ANOVA) results indicate that genotype effect was highly significant ($p < .001$), environment effect was significant ($p < .05$) and the effect of GEI was also highly significant ($p < .001$).

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GENETIC CHARACTERIZATION OF ¹⁵N ABUNDANCE IN ZEA MAYS AND IMPLICATIONS FOR DIAZOTROPHIC RECRUITMENT

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Zea mays spp. *mays* (hereafter maize) landrace populations cultivated within indigenous communities of Mexico have been reported to be farmed using traditional cultivation practices without fertilizers or pesticides, and several fields have exhibited low NO₃⁻ levels. Interestingly, certain landrace maize populations perform well under such conditions, and may reach heights greater than 5 m at maturity. Many such landrace populations are characterized by the presence of thick, abundant aerial roots that secrete significant quantities of root exudate (a.k.a. mucilage). This polysaccharide-rich exudate may play a vital role in recruitment of diazotrophic microbes to facilitate nitrogen fixation within said landrace populations. The studies summarized hereafter utilize natural ¹⁵N abundance within maize leaf tissues to infer nitrogen fixation activity [via symbiotic diazotrophic microbes] within various subpopulations of *Zea mays*. These studies indicate distinct variation and significant heritability governing ¹⁵N abundance in *Z. mays* leaf tissue, which may be an indication of diazotrophic recruitment. Conclusive evidence and genetic elucidation of diazotrophic recruitment in maize would have profound impacts on global maize production, with the potential to drastically reduce both production costs and harmful effects on the environment.



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