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<th>NAME</th>
<th>Andrade-Sanchez, Pedro</th>
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<td>Authors</td>
<td>Pedro Andrade-Sanchez</td>
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<tr>
<td>Title</td>
<td>Field electronics to measure above ground plant traits of crops under irrigated conditions</td>
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<tr>
<td>Abstract</td>
<td>This presentation will provide a review of field methods developed for plant characterization of crops grown under irrigation conditions in the low-elevation desert of the US. The materials will make emphasis on the use of ground platforms, sensors, and auxiliary electronics that are integrated to enable rapid field deployment and high resolution data acquisition.</td>
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<td>Affiliation</td>
<td>University of Arizona, Maricopa, USA</td>
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<th>NAME</th>
<th>Byrne, Patrick</th>
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<tr>
<td>Authors</td>
<td>Patrick Byrne, Gayle Volk, Candice Gardner, Mike Gore, Phil Simon, Stephen Smith</td>
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<td>Title</td>
<td>GERmplasm Morgue or Gold Mine? Enhancing the Value of Plant Genetic Resource Collections for Plant Breeding</td>
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<tr>
<td>Abstract</td>
<td>GERmplasm Morgue or Gold Mine? Enhancing the Value of Plant Genetic Resource Collections for Plant Breeding Patrick Byrne1, Gayle Volk2, Candice Gardner3, Mike Gore4, Phil Simon5, and Stephen Smith6 1Dept. of Soil and Crop Sciences, Colorado State University 2USDA-ARS National Laboratory for Genetic Resources Preservation, Fort Collins, CO 3USDA-ARS, Plant Introduction Research Unit, Iowa State University 4Plant Breeding and Genetics Section, School of Integrative Plant Science, Cornell University 5USDA-ARS, Vegetable Crops Research Unit, University of Wisconsin 6Dept. of Agronomy, Iowa State Univ. Genetic diversity is the raw material that plant breeders require to develop cultivars that are productive, nutritious, pest and stress tolerant, and water and nutrient use efficient. The USDA-ARS National Plant Germplasm System (NPGS) contains a wealth of genetic diversity, including improved varieties, breeding lines, landraces, and crop wild relatives (CWR). However, too often the promise of benefits from our plant genetic resources is not matched by their actual usage in breeding programs. The Genetic Diversity Work Group of the Plant Breeding Coordinating Committee has analyzed this situation and believes the NPGS will enhance its relevance to plant breeding with (1) continued attention to filling the gaps in NPGS collections, especially for CWR; (2) a concerted effort to phenotype and genotype accessions using standardized methods; (3) enriched information content of the GRIN-Global System and improved interoperability with other databases; (4) more attention to pre-breeding activities; (5) better training opportunities in practices for incorporating PGR in breeding programs; and (6) expanded outreach efforts to strengthen public support for the NPGS. These steps will be implemented most effectively through coordinated efforts among stakeholders, including USDA-ARS, universities, the private sector, and international partners.</td>
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<td>Affiliation</td>
<td>Colorado State University, Fort Collins, CO, USA, USDA-ARS National Laboratory for Genetic Resources Preservation, Fort Collins, USA, USDA-ARS, Plant Introduction Research Unit, Ames, IA, USA, Iowa State University, Ames, IA, USA, Cornell University, Ithaca, NY, USA, USDA-ARS Vegetable Crops Research Unit, Madison, WI, USA, University of Wisconsin, Madison, WI, USA</td>
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<th>NAME</th>
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<td>Authors</td>
<td>Brett Carver, Liuling Yan, Carol Powers</td>
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<td>Title</td>
<td>Wheat Breeding: Lessons I have Learned</td>
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| Abstract      | LESSONS LEARNED IN WHEAT BREEDING Brett Carver, Liuling Yan, and Carol Powers Oklahoma State University Department of Plant and Soil Sciences. A career devoted to wheat (T. aestivum) breeding and genetics, with more recent emphasis on the former, has provided the senior author no shortage of unforeseen moments. As much as plant breeders are motivated, if not trained, to accurately predict outcomes, breeding success may hinge nonetheless on the ability to respond favorably to those outcomes exempt from prediction. Case in point can be offered not once, but four times. First, lessons on breeding a wheat variety truly aligned with the demands of southern Plains wheat production did not come from wheat. A fundamental breeding system was borne out of scholarly work performed elsewhere with Festuca arundinacea. Second, a significant advance in bread wheat quality was discovered with a common glutenin subunit that bread wheat breeders are commonly warned against deploying, serving as a reminder that an imperfect correlation should not be mistaken as perfect. Third, in ‘Duster’, one of the most widely utilized hard
red winter wheat cultivars in the southern Plains, likely resides one of the most underutilized yield-promoting genes in winter wheat germplasm. Only by chance was it discovered. Only by tedious design will it be identified and reliably tagged. Fourth, consumer reaction to wheat gluten provides a worthy reminder that beyond our clear professional duty to establish competence at the farm may be an obscure social obligation to establish trust beyond the farm.

**Affiliation**
Oklahoma State University, Stillwater, USA

**NAME**
Micaela Colley

**Authors**
Micaela Colley, James Myers, Edith Lammerts van Bueren

**Title**
“Organic plant breeding”: the evolving landscape of seed and breeding strategies to advance organic agriculture

**Abstract**
“Organic plant breeding”: the evolving landscape of seed and breeding strategies to advance organic agriculture

Micaela Colley 1, Jared Zystro1, James Myers2, Edith Lammerts van Bueren3

1 Organic Seed Alliance, WA
2 Oregon State University, OR
3 Wageningen University, Netherlands

Organic plant breeding is an emerging field of science and industry with rapid expansion over the last fifteen years, but the field is still nascent and continually evolving. Organic certification regulations are incentivising development of the organic seed supply, but the framework of organic breeding is much broader than the market or regulatory forces, often driven by environmental and philosophical values. Organic plant breeding presents an opportunity to enhance the agronomic success of organic agriculture and deliver environmental benefits while also reflecting the social and economic values of the organic movement. A diversity of approaches are clearly needed to fulfill the broad gap in genetics suited to the spectrum of organic producers, but participatory plant breeding (PPB) is one approach gaining momentum in the US and Europe. PPB leverages a low economic barrier to entry, selection within the environment of intended use, and engagement of stakeholders in the breeding process. The range of current breeding strategies contributing to the development of the organic seed supply are presented along with promising examples of participatory approaches employed in the US and Europe. Four case-studies in organic corn, potato, and kale breeding demonstrate the range of farmer’s roles; public and private partnerships leveraging access to germplasm and resources; and complimentary field and lab-based methodologies.

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**NAME**
Keo Corak

**Authors**
Keo Corak, Shelby Ellison, Claire Luby, Doug Senalik, Massimo Iorizzo, David Spooner, Irwin Goldman, Phil Simon, Julie Dawson

**Title**
DEVELOPMENT OF GENOMIC-BASED STRATEGIES FOR SCREENING AND SELECTION OF ACCESSIONS FROM GERMPLASM COLLECTIONS

**Abstract**
To efficiently utilize the diversity present in large germplasm collections, breeders often identify a subset of accessions that represents the larger collection. Methods for creating these “core collections” rely on partitioning collections into sub-clusters based on geographic, morphologic or neutral genetic similarity. These methods do not consistently capture functional diversity and may be inappropriate for highly admixed species. We are interested in using a collection of domesticated carrot (Daucus carota) accessions to test genomic-based strategies that will allow breeders to create custom subsets of germplasm collections that maximize trait values of interest. Our preliminary work has established carrot as an appropriate species in which to study these strategies. We used a large dataset of cultivars and wild accessions to study the genetic structure of carrot germplasm resources available to breeders. We found a genetic distinction between Eastern and Western domesticated carrots, as well as between cultivated and wild accessions. Within Western cultivars, genetic diversity is present but there has been continuous gene flow and admixture. The results support the conclusion that domesticated carrot form one large breeding pool. We plan to develop two genomic-based selection schemes that a) balance genetic and phenotypic diversity and b) incorporate genomic prediction models to identify interesting accessions. While these strategies will likely not identify subsets that maximize the
diversity of the subset and are a departure from the traditional core collection concept, we expect that they will help us identify accessions and develop breeding populations that are more relevant for specific breeding goals.

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**NAME**
Dawson, Julie

**Authors**
Julie Dawson

**Title**
New methods for incorporating rapid sensory evaluation in selection for vegetable quality

**Abstract**
Selection for flavor is gaining more attention among plant breeders and seed companies, driven in large part by increasing expectations of consumers. Where this is most apparent is in breeding vegetables for organic and local foods markets. It is also of interest more broadly as vegetables must have good flavor in order for people to consume the recommended amounts for optimal health. Selection for flavor is often considered difficult or impractical due to the differing perceptions of flavor, different environmental and processing influences on flavor and different market demands. However, plant breeders have been able to improve many complex traits successfully. There have been recent developments in rapid sensory evaluation methods that may make flavor evaluation more practical in plant breeding programs. These methods decrease the time and expense of conducting flavor evaluations and make these evaluations more relevant to the context in which the final product will be used and often involve end-users directly in the evaluation process. We will present several different rapid sensory methods developed recently, the statistical techniques that have made these methods feasible, and examples of how they have been used.

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**NAME**
Dever, Jane

**Authors**
Jane Dever, Neha Kothari

**Title**
INDUSTRIAL AND NUTRITIONAL CONSIDERATIONS IN COTTON BREEDING

**Abstract**
Cotton fiber is primarily an industrial-use crop, though cotton seed is recently garnering more attention as an oilseed commodity. Cottonseed oil has relatively high mono- and polyunsaturated fat content, long shelf life, and vitamin E content; however, cottonseed pricing in the USA market has been consistently low, with farmgate prices lower than corn, peanuts, canola, sunflower, flaxseed and soybeans. Cotton yield and aspects of fiber quality have improved consistently over the last few decades from breeding and management technology while seed oil and protein content has stagnated. Initiatives specific for fiber improvement have yielded success in genetic gain. Quality aspects are complex, and breeding objectives must be appropriately aligned with both technical and market indicators. Breeding beyond yield for cotton improvement considers both industrial and nutritional components, to reap additional value to the acre for this seed-fiber crop.

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**NAME**
Famula, Randi

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Randi A. Famula, James H. Richards, Thomas R. Famula, David B. Neale

**Title**
ASSOCIATION GENETICS OF WATER-USE EFFICIENCY TRAITS IN WALNUT (JUGLANS REGIA L)

**Abstract**
English walnut (Juglans regia L.) is the major nut producing species of the family Juglandaceae. Domestically, California produces >99% of US walnuts, with a farm gate value of $1.8 Billion in 2014. The Walnut Improvement Program (WIP) at the University of California, Davis is the only walnut breeding program in California. The program utilizes a phenotype-based breeding approach, presenting many of the common limitations seen in perennial breeding programs (e.g. cost, time, space). However, recent developments in genomic resources, such as a high-density SNP array, have created new opportunities for marker assisted breeding in walnut. California’s most recent drought has raised concerns about the future of nut production and responsible water use in Californian agriculture. In addition to modified irrigation practices, studies in
other species have indicated breeding for efficient water use as a potential strategy for mitigating future water limitations. Current breeding objectives of WIP do not include measurements of water-use efficiency; therefore a pilot study was carried out to estimate the breeding potential of ecophysiological traits among significant breeding cultivars of WIP.

We used a genome wide association genetics approach in conjunction with new phenotyping methods in an effort to identify potential loci among significant cultivars within the germplasm of the WIP. High-throughput measurements of stable isotope discrimination and leaf area were used to assess phenotypic diversity. An association model incorporating a marker-based kinship matrix reduced bias in a two-step polygenic analysis, yielding possible associations to linkage groups and genomic breeding values for new cultivar trait rankings.

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NAME  
Isik, Fikret

Authors  
Fikret Isik, Juan Acosta, Richard Sniezko, Andrew Eckert, Jill Wegrzyn

Title  
Towards Genomic Selection in Forest Trees

Abstract  
Genomic selection has the potential to revolutionize forest tree breeding. Our efforts funded by the USDA-NIFA (Award Number 2016-67013-24469) aim to develop genomic resources for the pine genetics and breeding community. During the 18 months of the project implementation, we improved the genome assembly of loblolly pine by aligning deep transcriptomic sequence (PacBio Iso-Seq and Illumina short reads) for scaffolding purposes. This resulted in a total of 11,951 linked scaffolds to create 4,545 new super scaffolds. This improved assembly (v2.01) has been released to the PineRefSeq project website and TreeGenes database. It reports an N50 of 111 Kbp across a total of 1.76 million scaffolds (~1 million of 1Kbp and longer). This release served as the primary reference for an updated gene (29,213 models) and repeat (84%) annotation. The final gene selection totaled 29,213 full-length high-quality gene models with an additional 14,045 partial models. Genomic information generated from publicly funded research projects in the USA have been aligned against v2.01 genome assembly. We have identified 168,922 high quality SNPs for loblolly pine using multiple strict critera, with no polymorphisms on either side of their 50 bp flanking region. About 52,244 SNPs are in and around genic regions. Further quality control of the polymorphic sites is being implemented. This phase involves the calculation of genome-wide patterns of diversity, population differentiation and linkage analysis. Additionally, our team is leading the establishment of a Pine SNP chip consortium in coming months to start large scale genotyping of samples for genomic selection.

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NAME  
Jansky, Shelley

Authors  
Shelley Jansky

Title  
Increasing genetic gain by reducing ploidy in potato

Abstract  
INCREASING GENETIC GAIN BY REDUCING PLOIDY IN POTATO
Shelley Jansky
USDA-ARS Vegetable Crops Research Unit and UW-Madison Department of Horticulture

While potato cultivars in major world production regions are tetraploid, wild and cultivated potatoes in the crop’s center of origin range from diploid to hexaploid. Landrace potato varieties cannot be distinguished based on ploidy. Contrary to popular belief, tetraploidy does not appear to be necessary for superior performance. The advantages of breeding diploid cultivars are significant and worthy of exploration. We are using naturally occurring dominant self-incompatibility inhibitor genes to allow us to self-pollinate diploid germplasm. In addition, we have access to pollinators that produce diploid haploids (dihaploids) from tetraploid clones via parthenogenesis. These germplasm resources are providing the foundation for our plan to develop hybrid potato cultivars from diploid inbred lines. We have generated recombinant inbred lines and are developing an introgression line population. In addition, we have begun hybridizing partially inbred dihaploids with partially to fully inbred germplasm to evaluate combining ability and heterosis.

Affiliation  
USDA-ARS, Madison, USA

NAME  
Luby, Claire

Authors  
Claire Luby

Title  
Open Source Plant Breeding: Experiences from the Open Source Seed Initiative
OPEN SOURCE PLANT BREEDING: EXPERIENCES FROM THE OPEN SOURCE SEED INITIATIVE

Claire Luby1
1Open Source Seed Initiative, University of Wisconsin-Madison

The Open Source Seed Initiative (OSSI) was developed as an educational and outreach 501(c)3 non-profit organization to raise awareness of and provide an alternative to the current intellectual property rights regime. The tool OSSI uses to keep germplasm available is the OSSI Pledge, which is based on ideas from the free and open source software movement. Using the OSSI Pledge, OSSI is a conduit for germplasm to remain in a ‘protected commons’, where OSSI-Pledged germplasm can be freely used in plant breeding, seed saving, and production as long as the user does not restrict the rights of others to use OSSI-Pledged seeds or their derivatives for these same purposes. OSSI now works with 37 plant breeders, who have pledged some 375 varieties of 50 crops, and 48 partnering seed companies who sell OSSI-Pledged varieties. OSSI plant breeders are diverse and include freelance plant breeders, farmer-breeders and those based at land grant universities and seed companies. While there are challenges to using open source material in a plant breeding program, we also know that OSSI and the OSSI-Pledge do serve the needs and interests of plant breeders. OSSI is working to strengthen and grow a community of practice comprised of plant breeders, seed companies, farmers, gardeners and concerned citizens who are committed to the development and use of OSSI-Pledged, open source seeds. Come learn about how OSSI works, and how you might work with us.

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NAME
Pincot, Dominique

Authors

Title
FoR2U-1, A DOMINANT GENE CONFERRING RESISTANCE TO FUSARIUM WILT IN STRAWBERRY

Abstract
Fusarium wilt, a devastating disease caused by the soil-borne pathogen Fusarium oxysporum f. sp. fragariae, causes economic losses in strawberry (Fragaria x ananassa) nearly worldwide. This disease was first identified in California in 2006 following the 2005 phaseout of methyl bromide, an ozone-depleting soil fumigant. Fusarium wilt has since become a serious threat to production in California, which supplies 88% of strawberries produced in the US. Here, we describe phenotypic diversity for resistance to F. oxysporum f. sp.fragariaeamong 566 historically and commercially important F. x ananassa germplasm accessions. These were phenotyped for resistance in 2016 and 2017 by artificially inoculating field-grown plants with spores of a virulent isolate of F. oxysporum f. sp.fragariae found in California (AMP132) and were genotyped with 38,506 single-nucleotide polymorphisms (SNPs) using the iStraw35 Affymetrix Axiom array. The phenotypic distribution was bimodal with 192 resistant and 374 susceptible accessions and high repeatability (0.98). Genome-wide association mapping using a diploid Fragaria vesca reference genome identified a statistically significant (-log10(p) > 40) block of nine SNPs on chromosome 2 in linkage equilibrium with resistance phenotypes. The haploblock spanned one Mb. Genetic mapping is currently underway in two self-pollinated mapping populations to confirm the segregation of a single dominant resistance gene. The R-gene traces to early cultivars, predates the appearance of F. oxysporum f. sp. fragariaein California by decades, and appears to provide complete resistance to the F. oxysporum f. sp.fragariaeisolate AMP132.

Affiliation
University of California, Davis, Davis, USA

NAME
Poland, Jesse

Authors
Jesse Poland

Title
Application of UAVs to increase genetic gain

Abstract
To realize a new level of yield potential, breeding programs must increase the rate of genetic gain by evaluating larger populations, making more accurate selections, and decreasing the length of the breeding cycle. Genomic advancements during the past decade have enabled genomic prediction and selection of complex traits on larger number of breeding lines and at early stages in the breeding cycle. At the same time, however, phenotyping of breeding lines under field conditions has seen minimal advancement and is a critical bottleneck for evaluating large populations. We are applying novel developments in remote sensing with unmanned aerial vehicles (UAVs) combined with deep learning
to implement yield prediction and advanced selection methodology directly within breeding programs. Spectral reflectance from proximal sensing can give assessment of plant physiology and contribute to yield prediction models. To dig into more ‘complex traits’ we can apply deep learning to ‘breeder trained datasets’ consisting of millions of UAV collected images paired with ‘ground-truth’ values to score traits directly from images. These multiple layers of secondary traits can be integrated for more powerful yield predictions and combined with genomic information for in-season prediction of tens of thousands of early generation breeding lines. Using these new tools we can investigate optimized selection strategies using the full array of genomic and phenotypic information available.

Affiliation Kansas State University, Manhattan, KS, USA

NAME Poland, Jesse
Authors Jesse Poland, Robert Pless, Allan Fritz, Ravi Singh, Mitchell Neilsen, Matthew Reynolds
Title Wheat yield prediction and advanced selection methodologies through field-based high-throughput phenotyping with UAVs
Abstract Jesse Poland1, Robert Pless2, Allan Fritz1, Ravi Singh3, Mitchell Neilsen1, Matthew Reynolds3
1Kansas State University
2George Washington University
3CIMMYT

To realize a new level of yield potential, breeding programs must increase the rate of genetic gain by evaluating larger populations, making more accurate selections, and decreasing the length of the breeding cycle. Genomic advancements during the past decade have enabled genomic prediction and selection of complex traits on larger number of breeding lines and at early stages in the breeding cycle. At the same time, however, phenotyping of breeding lines under field conditions has seen minimal advancement and is a critical bottleneck for selection in large populations. We are applying novel developments in remote sensing with unmanned aerial vehicles (UAVs), machine vision and deep learning to implement yield prediction and advanced selection methodology directly within breeding programs in the US and internationally at the International Maize and Wheat Research Center (CIMMYT). We are developing “breeder trained datasets” consisting of millions of UAV collected images paired with “ground-truth” values of complex target traits that will be used for deep learning and directly scoring these traits using only the UAV images. We target to generate in-season yield predictions on tens of thousands of breeding lines by combining genomic information with multiple levels of proximal sensing and deep learning. We are also focused on optimized selection strategies using the full array of genomic and phenotypic information.

Affiliation Kansas State University, Manhattan, KS, USA, George Washington University, Washington D.C., USA, CIMMYT, Texcoco, Mexico

NAME Simon, Phillip
Authors Philipp Simon
Title CARROT BREEDING TO REDUCE INPUTS FOR GROWERS AND INCREASE OUTPUTS FOR CONSUMERS
Abstract Carrot is a relative newcomer to agriculture, with the first extensive evidence for its cultivation as a root crop 1100 years ago in Central Asia. The traits that differentiate domesticated carrots from its wild progenitor reflect selection for meeting both grower and consumer needs that continues today. The discovery of cytoplasmic male sterility in wild carrot in the 1950’s provided a foundation to launch the development of hybrid cultivars that expanded the role of carrot in modern agriculture, with hybrids dominating carrot production. Today’s carrot breeders place a major focus on improved pest and disease resistance, and more recently on weed competitiveness, to reduce both grower inputs and environmental impact of production. With the dominant and expanding role of carrot in U.S. organic agriculture, the need for effective disease resistance and weed competitiveness is heightened. The development of “baby” carrots in recent decades added value to the carrot crop and increased attention to carrot quality including flavor, color, and nutritional value—in familiar orange carrots as well as “new” colors including purple, red, yellow, and white. This broadened range of market products has stimulated carrot breeders to draw upon a greater breadth of genetic diversity and incorporate traits into cultivars that will expand consumer demand in the marketplace. Continued success in breeding will rely upon diverse germplasm as a source new alleles and traits. The recent sequencing of the
A carrot genome provides a foundation for expanding the application of genomic tools to further accelerate genetic improvement of the carrot crop.

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**NAME**  Tracy, William

**Authors**  Julie Dawson, Virginia Moore, William Tracy

**Title**  Establishing best practices for germplasm exchange, intellectual property rights, and revenue return to sustain public cultivar development

**Abstract**  Establishing best practices for germplasm exchange, intellectual property rights, and revenue return to sustain public cultivar development
JC Dawson1, VM Moore2, WF. Tracy2,  
1Department of Horticulture, 2Department of Agronomy, University of Wisconsin-Madison WI 53706;  
Intellectual Property Rights can play critical roles in protecting the genetic integrity of varieties and generating revenue to support continued breeding. Exchange of germplasm is critical for continued innovation and relevance of public plant breeding programs. To ensure continued germplasm exchange among public programs, we need a united professional voice to counter increasing restrictions on germplasm sharing and reduced funding for public cultivar development. Yet among public sector institutions there are numerous approaches to IPR and royalty distribution, resulting not only in confusion, but, in some cases, damage to the associated breeding programs. To address challenges and opportunities surrounding IPRs and funding for public cultivar development, a two-day conference was held before the National Association of Plant Breeders’ annual meeting in Raleigh, NC, in August 2016. The following recommendations are a result of the presentations and discussions at this conference.

1. Develop a professional standard similar to the wheat workers code of ethics for exchanging and releasing germplasm from public sector breeding programs.
2. Develop best practices for dispersing royalty revenue to plant breeding programs and for joint release of cultivars from collaborative plant breeding projects.
3. Increase Farm Bill authorization and appropriations to support cultivar development capacity at public institutions, including increased base funding for programs and better targeting and availability of competitive grants.

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**NAME**  Weathery, James

**Authors**  James Weatherly

**Title**  WHY DOES SEED INNOVATION MATTER?

**Abstract**  Innovations from the seed industry are helping to address many of the economic, environmental and health issues we face as a global society. Seed improvements allow us to produce more food from the same land, which is essential to feed our growing population. Seed improvements result in produce that is healthier and more nutritious. And seed improvements mean less food waste because new varieties create produce that stays fresh longer and have more consistent quality. This presentation will discuss the need to communicate the value of these innovations to the agriculture industry, the need for investments in seed research and the critical importance of protecting new discoveries—all so plant breeders can continue to focus on developing seed improvements that benefit us all.

The U.S. Seed Industry is estimated to have a total annual value between $16 and $17 billion.[i] [^edn1] Data shows that it can cost up to $1 million or more to bring a new variety to market and it can cost upwards of $100 to $150 million to bring a new seed technology to market.[ii] [^edn2] A recent survey concluded that individual intellectual property violations can cost the industry between $300,000 to $500,000—and sometimes more than $1 million—depending of the scale of the infraction and the specific seed technology. The cost of seed IP violations limit seed companies and universities ability to focus on bringing new products to market that can address larger societal challenges, including enhancing agricultural productivity to feed the growing global population.

[i] [^ednref1] sigma™ Seed, Kynetec (2016)
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[ii] [https://croplife.org/plant-biotechnology/regulatory-2/cost-of-bringing-a-biotech-crop-to-market/]
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<th><strong>NAME</strong></th>
<th>Akhunov, Eduard</th>
<th>Poster Number</th>
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<tr>
<td><strong>Authors</strong></td>
<td>Wei Wang, Quanli Pan, Fei He, Alina Akhunova, Sarah Davidson Evanega, Liuling Yan, Harold Trick, Eduard Akhunov</td>
<td>TU58</td>
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<tr>
<td><strong>Title</strong></td>
<td>GENOME EDITING FOR IMPROVING WHEAT YIELD AND YIELD-RELATED TRAITS</td>
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<td><strong>Abstract</strong></td>
<td>Our USDA NIFA-funded project explores the capabilities of the gene editing technology to unlock the yield potential of the complex wheat genome, and build a foundation for transformative approaches to wheat improvement. We have optimized the CAS9 gene editing platform for effective multiplex gene editing in wheat. Our pipeline includes: 1) wheat codon-optimized CAS9 enzyme; 2) high-throughput screen of the designed gRNAs for editing efficiency using the wheat protoplast assays; 3) procedures for the quick assessment of the frequency and types of editing events by the next-generation sequencing of multiplexed amplicons; 4) simplex and multiplex gene editing construct assembly based on the Golden Gate strategy. For gene editing, we selected genes that have a potential to affect yield component traits in wheat. For 13 genes, the CRISPR/CAS9 constructs were designed and successfully tested for editing efficiency using the protoplast assay and next-generation sequencing. Biolistic transformation was used to target eight homoeologous gene sets in cultivar Bobwhite and the phenotypic effects of induced mutations were assessed. Our results demonstrated that the CAS9 system’s selective editing capability is a powerful tool for creating the beneficial combinations of homeo-allelic variants in the allopolyploid crops. For example, the mutagenesis of all three homeologous copies of the TaGW2 gene controlling grain size in wheat had more substantial effect on phenotype than the mutagenesis of only one copy. For the newly developed variants of genes affecting yield components, we initiated the transfer into the adapted cultivars for deploying in the wheat breeding programs.</td>
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<tr>
<td><strong>Affiliation</strong></td>
<td>Department of Plant Pathology, Kansas State University, Manhattan, USA, Integrated Genomics Facility, Kansas State University, Manhattan, USA, Cornell Alliance for Science, Cornell University, Ithaca, USA</td>
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<th><strong>NAME</strong></th>
<th>Alsahlany, Maher</th>
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<tr>
<td><strong>Authors</strong></td>
<td>Maher Alsahlany, Daniel Zarka, Joseph Coombs, David Douches</td>
<td>TU02</td>
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<tr>
<td><strong>Title</strong></td>
<td>IMPROVING SELF-COMPATIBILITY AND MAINTAINING GENETIC DIVERSITY IN DIPLOID POTATO THROUGH RECURRENT SELECTION</td>
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<tr>
<td><strong>Abstract</strong></td>
<td>Exploiting inbreeding in diploid potato breeding was difficult before the discovery of Solanum chacoence clone (M6) with self-incompatibility inhibitor locus (Sli). In this study, we are using a recurrent selection (RS) strategy to introgress self-compatibility (SC) into a population of clones derived from six diploid potato species (S. berthaultii, S. chacoence, S. microdontum, S. tuberosum Grp. Phureja, S. tuberosum Grp. Tuberorum and S. tarijense). The RS project goals are to introduce SC into diverse potato species germplasm and adapt the population to a long-day photoperiod while selecting for cultivated tuber traits such as tuber yield and shape for the round white market class. Four cycles of RS have been completed (first cycle was cycle 0). The percentage of SC in the RS population increased in the fourth cycle compared with previous cycles. On the family basis, SC increased from 23% in cycle one to 100% in cycle three. Based on the total number of the individuals evaluated in the population, SC increased from 12% in cycle one to 54% in cycle three. Male sterility decreased from 18% to 2%, and progeny with no flowers decreased from 44% to 4% in cycles one and three. To characterize the germplasm diversity in four RS cycles, we used genome-wide SNPs (SolCAP Infinium 8303, 12K and 22K Potato SNP Arrays). Principle component analysis of over 5000 quality-filtered SNPs was used to determine that genetic diversity is maintained in first cycles of recurrent selection. SNP genotype analysis and trait evaluations demonstrate that RS population is a valuable source of diploid germplasm for developing inbred potato germplasm.</td>
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<td><strong>Affiliation</strong></td>
<td>Michigan State University, East Lansing, USA</td>
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<th><strong>NAME</strong></th>
<th>Ando, Kaori</th>
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<td><strong>Authors</strong></td>
<td>Kaori Ando, James D. McCreight</td>
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<td>Title</td>
<td>POTENTIAL FOR PRODUCTION OF TURKMEN MELONS IN CALIFORNIA</td>
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<tr>
<td>Abstract</td>
<td>Melons (Cucumis melo L.) are national treasures of Turkmenistan, well known for their large variation in color, shape, size, and flavor. They are produced to a limited extent in the U.S. Moreover, it is unknown how Turkmen melon will perform in California, the leader in U.S. melon production. Seventy-four Turkmen melons were collected during the 2008 Cucumis and Citrullus plant exploration in Turkmenistan and deposited in the U.S. National Plant Genetic Resources System. Fifty-seven of them were evaluated in un-replicated field trials at the University of California, Desert Research and Extension Center, Holtville (DREC) for growth and fruit quality from 2012–2016. Six of them were chosen for further characterization at DREC in a replicated trial in 2017. One was resistant and five were susceptible to natural cucurbit powdery mildew (CPM) infection incited by Podosphaera xanthii race 1, with an overall mean disease rating of 3.8 on a 1 (no disease) to 9 (&gt;75 % of the adaxial leaf surface covered with hyphae) scale. Mean fruit weight ranged from 1.6 to 4.2 kg per fruit. Mean soluble solids (SS) ranged from 10.9 to 13.3 %. Despite being susceptible to CPM, the Turkmen melons maintained high soluble solids, they were comparable to SS observed in Turkmenistan. Responses from non-melon specialist scientists and laypersons were highly positive for their organoleptic properties: aroma, color, succulence, flavor, and sweetness. Hence, these selected Turkmen melons have high potential to be well adapted to California melon production to grow commercially and marketed as a specialty melon.</td>
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<td>Affiliation</td>
<td>USDA-ARS, Crop Improvement and Protection Research Unit, Salinas, USA</td>
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<td>Authors</td>
<td>M. Rokebul Anower, Christy M. Motes, Maria J. Monteros</td>
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<td>Title</td>
<td>DIVERGENT SELECTION APPROACHES FOR IMPROVING DROUGHT TOLERANCE AND WATER USE EFFICIENCY (WUE) IN ALFALFA (Medicago sativa L.)</td>
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<td>Authors</td>
<td>M. Rokebul Anower, Christy M. Motes, Maria J. Monteros</td>
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<td>Affiliation</td>
<td>Noble Research Institute, LLC., Ardmore, USA</td>
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<td>NAME</td>
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<td>Amber Bassett, Karen Cichy</td>
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<td>Title</td>
<td>COOKING TIME AND SENSORY EVALUATION OF A YELLOW DRY BEAN RECOMBINANT INBRED LINE POPULATION</td>
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| Abstract | COOKING TIME AND SENSORY EVALUATION OF A YELLOW DRY BEAN RECOMBINANT INBRED LINE POPULATION  
Amber Bassett12 and Karen Cichy21  
1Michigan State University Department of Plant, Soil, and Microbial Science  
2USDA Sugarbeet and Bean Research Unit  
Dry beans are a nutrient-rich food that often require long cooking times, particularly without prior soaking. They also display a range of sensory characteristics. Cooking time and sensory quality are two important traits considered when consumers select dry beans, but have largely been overlooked by breeders in favor of other traits. In order to increase consumption of dry beans and access to the associated nutritional benefits, the barriers of long cooking time and perceived poor flavor must be addressed. In this study, a yellow dry bean (Phaseolus vulgaris L.) recombinant inbred line population of 227 genotypes were assessed for cooking time, flavor characteristics, and texture. Cooking times ranged from approximately 17 to 46 minutes. A trained sensory panel determined flavor and texture profiles of each genotype using 5-point hedonic scales. A texture analyzer with a 2mm cylindrical probe was used to determine work to bite for each genotype and to support the texture data obtained from the panel. QTL mapping of cooking time, flavor profiles, and texture will identify genomic regions influencing these traits. This information can enable breeders to target faster cooking times and specific flavor and texture profiles in their programs, as well as allow agronomic traits of dry bean varieties to be improved without sacrificing desirable cooking time and flavor. |

| Affiliation | Michigan State University, East Lansing, USA, USDA Sugarbeet and Bean Research Unit, East Lansing, USA |
| NAME | Bastos Martins, Lais |
| Authors | Lais Bastos Martins, Luis Lopez Zuniga, Randall Wisser, James Holland, Peter Balint-Kurti |
| Title | Validation of Multiple Disease resistance loci in Maze using families derived from segment substitution lines |
| Abstract | Southern leaf blight (SLB), northern leaf blight (NLB), and gray leaf spot (GLS) caused by Cochliobolus heterostrophus, Setosphaeria turcica, and Cercospora zeae-maydis and Cercospora zeina respectively, are among the most important corn diseases worldwide. In this project, we identified loci underlying disease resistance in multiple disease resistant (MDR) lines by the creation of chromosome segment substitution line (CSSL) populations in multiple disease susceptible (MDS) backgrounds. Four MDR lines (NC304, NC344, Ki3 and NC262) were used as donor parents and two MDS lines (Oh7B, H100) were used as recurrent parents to produce eight BC3F4:5CSSL populations comprising 1,749 inbred lines in total. Each population was assessed for each disease in replicated trials in two environments. Moderate to high heritabilities on an entry mean basis were observed. Several lines in each population were significantly more resistant than the susceptible recurrent parental lines for each disease. For most populations and most disease combinations, significant correlations were observed between scores and between marker effects for each disease. We were able to detect quantitative trait loci for disease resistance for each disease: 36 for SLB; 16 for NLB; and 20 for GLS. Among these, 30 QTLs were associated with variation in resistance to a single disease, 17 to two diseases, and four to all three diseases. During summer 2017, we will validate and fine map QTLs associated with MDR using F2:3 backcross families derived from 13 of the lines showing highest MDR. |

<p>| Affiliation | Dept. of Crop and Soil Science - North Carolina State University, Raleigh, USA, Dept. of Plant and Soil Science - University of Delaware, Newark, USA, USDA-ARS, Plant Science Research Unit, Raleigh, USA |
| NAME | Bhattacharya, Sourabh |
| Authors | Sourabh Bhattacharya, Baskar Ganapathysubramanian, Soumik Sarkar, Arti Singh, Asheesh Singh |</p>
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<th>Title</th>
<th>Saliency-driven Robotic Networks for Spatio-temporal Plant Phenotyping</th>
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| Abstract | **SALIENCY-DRIVEN ROBOTIC NETWORKS FOR SPATIO-TEMPORAL PLANT PHENOTYPING**  
Sourabh Bhattacharya1, Baskar Ganapathysubramanian1, Soumik Sarkar1, Arti Singh2,  
Asheesh Singh2  
1Iowa State University, Department of Mechanical Engineering  
2Iowa State University, Department of Agronomy  
The objective of this project is to build a network of ground robots that can collect multi-modal data in research farms for high throughput modular plant phenotyping. The robotic network will have the following capabilities (i) Navigate in a farm to collect data with minimal human intervention during operation (ii) Autonomous decision making i.e, it can take its own decisions for maximizing the value of information of the acquired data (iii) Scalable in terms of the size of the farmland (iv) Work in collaboration with humans to improve their situational awareness in multi-dimensional genome wide studies. Our approach will leverage opportunistic sensing, task partitioning and scout-task allocation and spatio-temporal importance map building, to enable resolution of the above science questions that cannot be addressed without the use of robotic systems. While our focus is driven by fundamental questions in plant sciences and genomics, the research possibilities that such a platform generates are much broader. |
| Affiliation | Iowa State University, Ames, USA |
| **NAME** | Gehendra Bhattarai, Jun Qin, Yuejin Weng, John Bradley Morris, Waltram Ravelombola, Wei Wang, Ainong Shi |
| **Title** | Association analysis of cowpea mosaic virus resistance in the USDA cowpea germplasm collection |
| **Abstract** | Cowpea [Vigna unguiculata (L.) Walp.] is an important legume crop, widely grown in Africa, South America, South Asia, Southeast Asia, and the southern United States. Cowpea is consumed as both fresh vegetable and dry grain, and also as an animal feed and fodder, and it is a major dietary protein source that complements cereal-based diet. Cowpea mosaic virus (CPMV) causes a severe yield loss of cowpea in many areas worldwide notably in the Africa. Identification and utilization of host genetic resistance are the most effective control method for the viral disease. The objective of this research is to conduct genome-wide association analysis (GWAS) and identify single nucleotide polymorphism (SNP) markers associated with CPMV resistance. A total of 333 cowpea germplasm accessions, originally collected from 39 different countries around the world were used in this study and 1033 SNPs identified from genotyping by sequencing (GBS) approach were used as genotyping. Single marker regression (SMR), general linear model (GLM), and mixed linear model (MLM) in Tassel 5, and compressed mixed linear model (cMLM) and enriched compressed mixed linear model (EcMLM) in the GAPIT R package were used for association analysis of CPMV resistance. Seven SNP markers (C35069548_1883, C35069548_1934, scaffold46144_3677, scaffold65342_6794, scaffold66293_6549, scaffold95805_2175, and scaffold17319_4417) were strongly associated with the CPMV resistance, and the markers were consistent with all tested models. SNP markers identified in this research will be a potential tool to use in cowpea molecular breeding to develop CPMV resistant cultivars through marker-assisted selection (MAS). |
| Affiliation | University of Arkansas, Fayetteville, USA, Plant Genetic Resources Conservation Unit (USDA), Griffin, USA |
| **NAME** | Anju Biswas |
| **Title** | GENOMIC AND BIOCHEMICAL CHARACTERIZATION OF STRAWBERRY (FRAGARIA x ANANASSA) GENOTYPES |
| **Abstract** | Strawberry is an important fruit crop for its nutritional value. Higher amounts of antioxidants and attractive taste are some of the positive components of strawberry. Antioxidants in strawberry act against cardiovascular diseases, cancer and other health issues. Strawberries |
are not only important for its health benefits but also have some commercial aspects in food and cosmetics industries. Nowadays, molecular markers are becoming popular for strawberry breeding. The majority of markers are used for cultivar identification, genetic diversity and taxonomic analysis, marker assisted breeding and cloning. SSR markers are single sequence repeats present in DNA in every organism. SSR markers are used as rapid, robust and inexpensive means of polymorphism identification. However, they differ from organism to organism and plant to plant. It is easier to identify some desirable traits in any variety within short time if known SSR markers are available. Cultivated strawberries have wide range of SSR markers available which permits to identify polymorphism among closely related genotypes. In our experiment, we are using five strawberry genotypes including Albion, Early glow, Honeoye, Jewel varieties and a wild type to identify polymorphism for 72 SSR markers. We have selected primers considering some desirable traits like antioxidants, flavor, disease resistance etc. After SSR analysis, we will perform association mapping with the above traits, which can be utilized by strawberry breeding programs during cultivar development and authentic genotype identification. Biochemical analysis will also be done to link the markers related with flavonoids or anthocyanin.

Affiliation Delaware State University, Dover, USA

NAME Brasier, Kyle

Authors Kyle Brasier, Joseph Oakes, Maria Balota, Wade Thomason, Carl Griffey

Title COMPARISON OF REMOTE SENSING DEVICES TO EVALUATE NITROGEN USE EFFICIENCY IN SOFT RED WINTER WHEAT

Abstract COMPARISON OF REMOTE SENSING DEVICES TO EVALUATE NITROGEN USE EFFICIENCY IN SOFT RED WINTER WHEAT

Braier K.G.1, Oakes J.2, Balota M.2, Thomason W.E.1 and Griffey C.G.1

1Department of Crop, Soils and Environmental Sciences, Virginia Tech, Blacksburg, Virginia, USA; 2Plant Pathology, Physiology, and Weed Science, Virginia Tech, Suffolk, Virginia, USA; Contact: Kyle Brasier, brasier1@vt.edu

Nitrogen (N) fertilization is a significant expense to winter wheat (Triticum aestivum L.) growers and can contribute to the degradation of aquatic and terrestrial ecosystems. Thus, prompting efforts to develop wheat varieties that can more reliably take up and utilize applied N under normal and reduced N growing conditions. This study explores the effectiveness of high-throughput phenotyping platforms and sensors in predicting winter wheat response to N fertilizer.

Thirteen soft red winter wheat varieties were grown under normal (134 kg N ha⁻¹) and reduced (67 kg N ha⁻¹) N treatments in eight Virginia environments. Two indices, normalized difference vegetative index (NDVI) and canopy temperature depression (CTD), were estimated using handheld and unmanned aerial vehicle (UAV) sensors to predict N-related traits.

Under reduced N conditions, handheld NDVI at anthesis exhibited a positive relationship with above-ground biomass (r² = 0.56) and N-uptake efficiency (r² = 0.53), while CTD was negatively correlated with above-ground biomass (r² = 0.52) and N-uptake efficiency (r² = 0.44). The handheld tools were unable to significantly discriminate wheat varieties under normal N conditions (r² values ranging from 0.01 to 0.30 for the same traits). Findings from both platforms will be presented in the poster.

Affiliation Virginia Tech, Blacksburg, USA

NAME Brewer, Brittney

Authors Brittney Brewer, Nancy Blake, Hwa-Young Heo, Jay Kalous, Talbert Luther

Title Contribution of introgressed durum wheat QTL alleles to yield components in bread wheat

Abstract Hexaploid bread-wheat and tetraploid durum-wheat have been cultivated in similar geographic areas for approximately 10,000 years. Based on the crossing barrier due to ploidy differences, it is probable that different favorable alleles for yield-related traits have
accumulated in the two crops. However, alleles from durum impacting quantitative traits in bread wheat have not previously been identified. We developed a recombinant inbred line population from a cross of Mountrail durum wheat and Choteau bread wheat in order to identify QTL for yield components in a hexaploid background. The purpose of this study is to determine the impact of durum wheat alleles impacting yield components using NIL in a hexaploid wheat background. The NIL were developed by crossing three hexaploid spring bread wheat varieties with five hexaploid lines derived from the original Choteau/Mountrail cross. Based on 2016 data, productive tiller number (PTN) and seeds per spike (SPS) QTL had a significant impact on several yield related traits. The durum allele at the QTL for PTN showed a significant postponement of heading and senescence; an increase in spikelets per spike, and kernel hardness; and a decrease in yield, kernel diameter, kernel weight and thousand-kernel-weight (TKW). Additionally, the durum allele at QTL for SPS, showed a postponement in heading data, increase in TKW, kernel weight and kernel diameter; and a decreased kernel hardness. Results suggest that alleles from durum wheat impacting grain yield may be useful for the improvement of cultivated hexaploid spring wheat varieties grown in the Great Plains of North America.

Affiliation | Montana State University, Bozeman, USA
---|---
NAME | Byrnes, David
Authors | David Byrnes, Fekadu Dinssa, Ondego Nyabinda, Stephen Weller, James Simon
Title | Genotype, environment, and genotype x environment interaction effect on elemental micronutrient content in vegetable amaranth grown in the United States, Kenya, and Tanzania
Abstract | Micronutrient content is fundamental to the consumer-side value of horticultural crops. Crops such as vegetable amaranth (Amaranthus sp.), which are aligned with cultural preference in regions of limited-resources are often promoted to improve the health status of micronutrient deficient people, making stability of micronutrient contents at high source levels neccessary to have this utility. Disputes in the literature exist on the elemental micronutrient content of vegetable amaranth as well as on the extent of genotype, environment, and genotype by environment interaction (GEI) effects on micronutrient content in both staple and horticultural crops. In this study, multi-environment trial data from USA, Kenya, and Tanzania was analyzed using the Additive Main effects and Multiplicative Interaction (AMMI) method to observe the effect by genotype, environment, and GEI on contents of Fe, Ca, Mg, and Zn, in 10 lines of vegetable amaranth. With respect to high source thresholds as defined by Codex Alimentarius, all entries in each environment fell well below high source threshold for Zn (4.5 mg/100 g Zn); all entries in each environment exceeded high source threshold for Mg (90 mg/100 g Mg); all entries in each environment exceeded Ca threshold (300 mg/100 g) with the exception of one trial in which all but two entries fell slightly below the threshold; and Fe content had the greatest variability of range across environments: all entries fell below the threshold (4.2 mg/100 g Fe) at least twice with the exception of RUAM24 which fell only slightly below the threshold in one trial.

Affiliation | Rutgers University, New Brunswick, USA, World Vegetable Center, Arusha, Tanzania, United Republic of, Moi University, Eldoret, Kenya
NAME | Cademartiri, Rebecca
Authors | Lin Ma, Yichao Shi, Asheesh Singh, Rebecca Cademartiri, Ludovico Cademartiri
Title | Transparent Soil Technologies for Root and Rhizosphere Phenotyping
Abstract | Transparent Soil Technologies for Root and Rhizosphere Phenotyping

Lin Ma1, Yichao Shi1, Asheesh Singh2, Rebecca Cademartiri1,3 and Ludovico Cademartiri1,3
1Iowa State University Department of Materials Science and Engineering
2Iowa State University Department of Agronomy
3Iowa State University Department of Chemical and Biological Engineering

Root phenotypes are a great indicator for the interaction between plants and their
environment, such as the uptake of water and nutrients and the effect of microorganisms. However physiological media (e.g., soil) is opaque, which complicates the phenotyping of roots in vivo. Hydroponic conditions are transparent but lead to high non-physiological root development.

To address this issue we are creating ‘transparent soil’, which combines the granularity and air pockets of soil with the transparency of hydroponics. The material is transparent in 0.5 MS or 1 MS media, which enables the phenotyping of root systems in vivo during the growth of the plant. The granularity of the soil can be changed to affect the effective porosity of the transparent soil, ranging between that of sand and that of loam. We will show the optical and mechanical characterization of the transparent soil, as well as evidence of its effect on root phenotypes on model plants such as Arabidopsis thaliana, Brassica rapa and Glycine max. Importantly we will show our current results on the comparisons of the root phenotypes of soybean plants with field grown plants.

Affiliation

Iowa State University, Ames, USA

NAME

Cai, Xiwen

Authors

Wei Zhang, Mingyi Zhang, Yaping Cao, Xianwen Zhu, Shuangfeng Ren, Yuming Long, Yadav Gyawali, Shiaoman Chao, Steven Xu, Xiwen Cai

Title

Enriching and understanding the wheat B genome by meiotic homoeologous recombination

Abstract

Wheat contains three homoeologous subgenomes (A, B, and D) originated from diploid ancestors. The ancestors of the subgenomes A and D were identified, but not for the subgenome B although the S genome of Aegilops speltoides (2n=2x=14, SS) has been considered most closely related to the B genome. The ancestral species and their relatives represent an invaluable gene pool for wheat improvement. Here, we report our research progress toward expanding genetic variability of the wheat B genome using Ae. speltoides and Thinopyrum elongatum (2n=2x=14, EE), and determining B-S genome homology. We have induced B-S and B-E homoeologous meiotic recombination using the ph1b mutant and recovered homoeologous recombinants using molecular markers and genomic in situ hybridization (GISH). To date, we have identified 858 recombinants involving 11 B-S and B-E homoeologous pairs. The Ae. speltoides- and Th. elongatum-derived resistance genes for multiple diseases and environmental stresses have been incorporated into the B genome. Some of the recombinants containing the genes of interest are readily utilized in wheat breeding for variety development. Molecular marker and GISH analyses of the recombinants have generated integrated genetic and physical maps of B-genome chromosomes. In addition, we discovered an Ae. speltoides-originated segment on wheat chromosome 1B, indicating the involvement of Ae. speltoides in the origin of the B genome. However, Ae. speltoides should not be considered an exclusive ancestor of the B genome. Furthermore, we have been deploying the ph1b mutant in the US wheats for direct gene introgression from wild grasses into US wheats.

Affiliation

North Dakota State University, Fargo, USA, USDA-ARS, Fargo, USA

NAME

Campbell, Todd

Authors

Kari Hugie, Tariq Shehzad, Min Liu, Andrew Paterson, Todd Campbell

Title

2017 Update-NIFA award 15-0584, Enriching the gene pool of upland cotton

Abstract

2017 Update-NIFA award 15-0584, Enriching the gene pool of upland cotton

Kari Hugie1, Tariq Shehzad2, Min Liu2, Andrew Paterson2, and B. Todd Campbell1

1 USDA-ARS Coastal Plains Soil, Water, and Plant Research Center, Florence, SC
2 University of Georgia Plant Genome Mapping Laboratory, Athens, GA

Cotton has a very narrow gene pool resulting from its evolutionary history, domestication, and modern crop improvement practices. The elite Upland cotton gene pool derives from only a small subset of progenitors from the Mexican-Guatemalan border that were brought into the USA and also dispersed into China, India, Australia and other countries. In contrast,
exotic G. hirsutum accessions are rich in diversity that was ‘left behind’ during crop domestication and improvement, but these accessions have been shunned by mainstream breeding programs because most are photoperiod-sensitive and flower too late in the season for temperate crop production. Recently, we discovered that naturally occurring day-neutral cotton genotypes are sufficiently abundant to capture a surprisingly large portion of the diversity available among exotic cotton races, in a breeder friendly form. In this project, we seek to quantify the phenotypic and genetic diversity of naturally occurring day-neutral exotic cottons in relation to one another, other exotic cottons, and elite cottons. Ultimately, we will conduct an integrative analysis to predict phenotype from genotype, providing a framework for development and application of tools and information to accelerate breeding of finished cultivars. Here, we provide an update on our progress towards meeting these goals.

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USDA-ARS Coastal Plains Soil, Water, and Plant Research Center, Florence, USA, University of Georgia Plant Genome Mapping Laboratory, Athens, USA

**NAME**  
Carpenter, Neal

**Authors**  
Neal Carpenter, Carl Griffey, Gina Brown-Guedira, Priyanka Tyagi, Paul Murphy, Marla Hall, Mark Christopher

**Title**  
Identification of quantitative trait loci for adult plant resistance to Puccinia triticina in soft red winter wheat cultivar 2013412

**Abstract**  
Leaf rust caused by Puccinia triticina is a destructive pathogen of wheat (Triticum aestivum). Host resistance is the most economical solution for providing full season control and reducing damage due to diseases as opposed to use of multiple fungicide applications. Pyramiding of multiple genes into single cultivars and use of quantitative trait loci (QTL) conferring adult plant resistance (APR) is the best strategy to achieve durable resistance. Soft red winter wheat cultivar 2013412 (SS8412) is a broadly adapted, high yielding, full-season, short height semi-dwarf producing grain that is well suited for dual end uses in both pastry and cracker products with exceptional adult plant resistance to Puccinia triticina. A doubled haploid population (2013412/ VA10W-21) was evaluated for leaf rust resistance in headrows at Blacksburg and Warsaw, VA. Genotyping was completed using double digest rad-seq or often referred to as GBS using the enzymes PstI and MseI. SNPs were aligned using the International Wheat Genome Sequencing Consortium’s whole genome assembly v0.4. Four traits from each location (Warsaw, Blacksburg) were analyzed using Interval Mapping and Composite Interval Mapping. The results were conclusive in that a few SNPs found on chromosome 1B conferred the majority of variance associate with each trait. Logarithm of Odd (LOD) scores were as high as 35 and accounted for 49% of the variation. These results were evaluated again and validated in four additional doubled haploid populations in VA, NC, IL, and TX in 2017.

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**NAME**  
Chang, Sam

**Authors**  
Sam Chang, Anne Gillen, Pengyin Chen, Bo Zhang

**Title**  
Enhancing Protein Composition in Soybeans For Improving Tofu Quality Using A3 Subunit As A Marker

**Abstract**  
Soybean has been traditionally used for making nutritious foods, including soymilk and tofu, in Asia for thousands of years. World food-grade soybean market is growing rapidly. The market growth presents an opportunity for the US growers due to a higher premium, and necessitates the selection and production of high-quality specialty soybean that possess high protein content and unique protein composition to compete in the international market. There is a strong need to search for soybean varieties with compositional improvement to enhance food, nutritional and health characteristics. The A3 peptide, a component present in the major storage protein in soybean, has been proven to be quantitatively related the firmness of tofu products in our laboratory. The
s study objective is to investigate the effect of production environment on the performance of the soybean lines containing various A3 peptide concentrations in multiple US locations to further sustain this structure-functional relationship.

**Affiliation**
Mississippi State University, MS State, USA, USDA-ARS CGRU, Stoneville, USA, University of Missouri, Portageville, USA

**NAME**
Chen, Andy (Yi)

**Authors**
Yi Chen, Harwinder Singh Sidhu, Mina Kaviani, Alireza Navabi

**Title**
High-Throughput Phenotyping Tool for Winter-Survival of Winter Wheat

**Abstract**
High-Throughput Phenotyping Tool for Winter-Survival of Winter Wheat

Yi Chen, Harwinder Singh Sidhu, Mina Kaviani, Alireza Navabi
University of Guelph Department of Plant Agriculture

The harsh and unpredictable winters in the high latitude regions of the northern hemisphere often leads to high risk of winterkill for winter wheat (Triticum aestivum L.). This emphasizes the need for more winter-hardy varieties that are adapted to specific winter-wheat growing regions in the world along with better management practices to reduce winterkill incidents. Current methods used in breeding programs to evaluate winter-hardiness are inefficient, have low differentiation power, and are often not quantitative. This research aimed to develop a high-throughput screening protocol to screen for genotypes with superior winter-hardiness, using quantitative data generated from images captured by unmanned aerial vehicle (UAV). A diversity panel of 450 winter wheat genotypes from Canada, with various levels of winter-hardiness, was planted in 1m² plots in October 2016. The aerial images were taken with a quadcopter at 30 m above the ground level in November 2016 at the 3 to 5 leaf stage and again in April 2017 right after plants started to recover from winter. The images were taken in the red, green, blue and near-infrared spectrum. This was used to calculate the normalized difference vegetation index (NDVI) for each plot, which can reflect the amount of green vegetation that survive through the winter. Ground-level images were taken to use as an in-field confirmation of UAV data. Initial results demonstrated a high correlation between the readings generated with UAV and the ground-level images (r=0.83).

**Affiliation**
University of Guelph, Guelph, Canada

**NAME**
Coggins, Jamie

**Authors**
Jamie Coggins, Kate Evans

**Title**
**UTILIZING VISIBLE/NEAR-INFRARED SPECTROSCOPY AS A NON-DESTRUCTIVE PHENOTYPING METHOD IN THE WSU APPLE BREEDING PROGRAM**

**Abstract**
Washington state is the number one domestic apple (Malus ?domestica Borkh.) producer in the U.S. and grows at least 28 varieties commercially. Of those varieties, none have been bred for the Washington state growing region. The Washington State University Apple Breeding Program (WABP) aims to develop new and improved varieties with higher eating qualities that are better suited for the WA apple growing region. WABP uses a variety of destructive analytical tests, such as firmness, soluble solids and titratable acidity (instrumental), as well as appearance and eating quality (sensory) traits, to evaluate selections throughout the season, both at harvest and after several months of refrigerated storage. Seedling trees typically have low fruit numbers; incorporating non-destructive evaluations could increase the number of traits evaluated per selection, including dry matter content (DM). In 2015 and 2016, fruit from the WABP advanced selections were harvested and stored for two months at 4°C. Fruit was evaluated after storage using the above-mentioned analytical and sensory tests as well as destructive DM measurements. Data was compared to both visible (VIS) and near-infrared (NIR) spectral outputs to determine non-destructive measurement models. Correlations between DM and sensory fruit quality traits were calculated. A model was successfully developed for DM, confirming previously published studies showing the potential of using the NIR spectroscopy region between 729-925nm to measure DM. Models for firmness, soluble solids content and titratable acidity were developed with varying degrees of predictive accuracy. The potential for utilizing these results in the WABP are presented.
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<th>NAME</th>
<th>Craig, Valerie</th>
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<tr>
<td>Authors</td>
<td>Valerie Craig, Elizabeth Lee, Hugh Earl, Steve Bowley, Aaron Berg</td>
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<tr>
<td>Title</td>
<td>Identification of a Unique Spectral Signature of Black Layer Formation in Maize (Zea mays L.)</td>
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<tr>
<td>Abstract</td>
<td>Physiological maturity in maize is reached at the developmental stage black layer, where photosynthates are no longer able to move into the developing kernels. Currently, there is no high-throughput field-based phenotyping method available for detecting black layer, although remotely sensed spectral data may offer a solution to this problem. The aim of this project is to identify a unique reflectance signature associated with physiological maturity in maize. Being repeatable across genotypes, different environmental conditions, different senescence patterns, etc., is essential. Several types of remotely sensed data have been used including hyperspectral data generated with a dual-channel reflectance spectrometer and an unmanned aerial vehicle (UAV) mounted multispectral camera. Accompanying the remotely sensed data are ground-truthed data consisting of visual determination of black layer and chlorophyll measurements. Initial experiments consisted of two planting dates at one location and involved four short-season hybrids that exhibited two different senescence patterns at maturity, a rapid “die and dry” phenotype and an extended “stay green” phenotype. The hybrids differed in the accumulation of anthocyanins in the leaf tissues. We have tentatively identified a region of the spectrum that exhibits a change as black layer approaches. This region is consistent across the four genotypes and the two planting dates. To confirm our initial findings, we are now examining additional genotypes and adding a second growing season to the data set.</td>
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<th>De La Torre, Amanda</th>
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<tr>
<td>Authors</td>
<td>Amanda De La Torre, Daniela Puiu, Steven Salzberg, Marc Crepeau, Charles Langley, John Gleason, Richard Sniezko, Douglas Savin, David Neale</td>
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<tr>
<td>Title</td>
<td>TOWARDS GENOMIC-BASED BREEDING OF SUGAR PINE</td>
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<td>Abstract</td>
<td>White pine blister rust (WPBR) caused by the exotic Cronartium ribicola is a devastating fungal disease causing great damage in Strobus pines in North America. This project aims to find the genes underlying resistance to WPBR in order to develop genomic-based breeding for resistance in sugar pine (Pinus lambertiana). This will be a highly valuable tool for a faster, simpler and less expensive identification of resistant individuals that will ultimately translate in a reduction of the breeding cycle in more than 15 years. This project leverages resources newly generated by our group such as the draft genome of sugar pine, re-sequencing of the whole-genomes of ten individuals, whole transcriptome of sugar pine, and the cloning of the major resistance gene Cr1. The re-sequenced data is being used to generate a dense genotypic array comprising 100k SNP markers. The combination of a large number of SNP markers and a large phenotypic data set will allow the development of genome-wide association studies to identify the genes involved in WPBR quantitative and dominant resistance. In addition, this project will build high-resolution genetic maps to locate the genes in the genome, and identify co-expression networks and pathways.</td>
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<td>NAME</td>
<td>de Leon, Natalia</td>
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<td>Authors</td>
<td>Bridget McFarland, Shawn Kaeppler, Natalia de Leon, G2F Consortium</td>
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<td>Title</td>
<td>The effect of artificial selection on the genetic control and modulation of genotype-by-environment interaction in maize</td>
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<td>Abstract</td>
<td>Plant genotypes have the ability to produce different phenotypes in response to environmental influences, also known as genotype by environment (GXE) interaction. Despite the relevance of this phenomenon in terms of plant performance, little is known about how artificial selection for high productivity has affected that adaptation capacity in crop species. This project aims to determine what types of genetic variants explain most of the GXE variation observed and what types of genetic factors affect its modulation. During the summer of 2016, we evaluated hybrids generated from the cross of 100 fully genotyped inbred lines that span the range from highly selected (recently expired plant variety protection) to founder lines from the Iowa Stiff Stalk maize population, to tester 3IIH6. The resulting set of hybrids was evaluated in replicated trials across 15 North American locations as part of the Genomes2Fields Maize GXE project. Grain yield, agronomic and phenological characteristics were measured for the collection of hybrids. Significant genotypic variation was observed for all traits. Overall, founder lines consistently had the most variation in response across locations with the largest range and smallest R2 value. A second year of testing is currently underway. Collectively, results from this work are expected to generate information and resources that will enhance our understanding of the biological phenomenon affecting GXE and therefore enhance breeding outcomes. This material is based upon work that is supported by the National Institute of Food and Agriculture, U.S. Department of Agriculture, under award number 2015-05837</td>
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<th>NAME</th>
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<tr>
<td>Authors</td>
<td>Bandana Dhungana, Melanie Caffe-Treml, Shaukat Ali, Padmanaban Krishnan, Emmanuel Byamukama</td>
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<tr>
<td>Title</td>
<td>Methodology for Screening Oat Genotypes for Ochratoxin A Accumulation in Grain Inoculated with Penicillium verrucosum. B. Dhungan1, S. Ali1, E. Byamukama1, P. Krishnan2, and M. Caffe-Treml1</td>
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<td></td>
<td>1Department of Agronomy, Horticulture and Plant Science. 2Dairy and Food Science Department, South Dakota State University, Brookings, SD 57006</td>
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<tr>
<td>Abstract</td>
<td>Oat (Avena sativa), like any other cereal grain, can be contaminated with Ochratoxin A (OTA) when the grain is infested with Penicillium verrucosum and storage conditions are favorable for fungal growth and toxin production. Currently, the main preventative method used to limit OTA contamination in grains is to maintain unconducive storage conditions for toxin production. The level of OTA contamination in infested oat grain depends on several factors including water activity, temperature, and the ability of P. verrucosum isolates to produce OTA. It is not known if the oat genotype also influences OTA accumulation in grains. The use of oat genotypes that exhibit resistance to OTA accumulation can be an effective way to further reduce risks of OTA contamination in oat-based products. To our knowledge, a precise and simple protocol for evaluation oat genotypes for OTA production is not available. In this study, our primary objective was to develop methodology to screen oat genotypes for OTA accumulation. To achieve our objective, oat grain from three cultivars were inoculated with three different isolates of P. verrucosum and incubated at two water activity levels (0.85 and 0.90) and at two temperatures (22.5°C and 27.5°C) for 10 weeks. Significant differences among the isolates of P. verrucosum for OTA production were observed when inoculated grains samples were incubated with a water activity of 0.90 at 22.5°C for all the cultivars studied. This precise and simple protocol will help pathologists and breeders in evaluating oat germplasm for OTA production</td>
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<td>Affiliation</td>
<td>South Dakota State University, Brookings, USA</td>
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<td>NAME</td>
<td>Dzakovich, Michael</td>
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<tr>
<td>Authors</td>
<td>Michael Dzakovich, Jessica Cooperstone, Ken Riedl, Steven Schwartz, David Francis</td>
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<tr>
<td>Title</td>
<td>PURÉE TO PEAKS IN 15 MINUTES: A RAPID CAROTENOID EXTRACTION AND UHPLC-PDA ANALYSIS WORKFLOW FOR TOMATO BREEDING</td>
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<td>Abstract</td>
<td>Tomatoes (Solanum lycopersicum) are an economically and nutritionally important crop that owe their color to carotenoid pigments such as lycopene and ?-carotene. Public and private breeding programs have focused on manipulating fruit carotenoid content to improve consumer acceptability and enhance potential health benefits associated with consuming tomatoes. However, accurate phenotyping of carotenoids requires lengthy extraction protocols and chromatographic separation methods creating analytical bottlenecks that can reduce genetic gain per year. We developed both a rapid tomato carotenoid extraction protocol and an ultra-high performance liquid chromatography photodiode array detector (UHPLC-PDA) analysis method. To validate our extraction and quantitation methods, backcross populations of processing and cherry tomatoes were created with varying fruit concentrations of lycopene and ?-carotene by exploiting natural variation in the fruit-specific lycopene beta cyclase (Cyc-B). These populations were phenotyped using established extraction and high performance liquid chromatography photo diode array detector (HPLC-PDA) methods in addition to our new rapid tomato carotenoid workflow. We estimated variance components for genetic and environmental variables for both methods and determined that our new extraction and UHPLC-PDA analysis method performed comparably to established protocols while taking substantially less time. Notably, our methods were approximately 2x (~5 minutes/sample) and 5x (4.2 minutes/sample) faster than current extraction and HPLC-PDA methods, respectively. Our UHPLC-PDA method was able to resolve most cis-carotenoid isomers from all-trans carotenoids. Our rapid carotenoid extraction and analysis workflow could greatly enhance tomato breeding programs by drastically increasing throughput without sacrificing analytical performance or heritability.</td>
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<td>Affiliation</td>
<td>The Ohio State University Department of Horticulture and Crop Science, Columbus, USA, The Ohio State University Department of Food Science and Technology, Columbus, USA, The Ohio State University Department of Horticulture and Crop Science, Wooster, USA</td>
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<th>NAME</th>
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<td>Authors</td>
<td>Samira El Hanafi, Wuletaw Tadesse, Najib Bendaoui</td>
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<td>Title</td>
<td>Genetic variability and association mapping of floral traits for hybrid wheat production</td>
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<td>Abstract</td>
<td>Genetic variability and association mapping of floral traits for hybrid wheat production Samira El Hanafi1,2, Najib Bendaou2 and Wuletaw Tadesse1 1International Center for Agricultural Research in the Dry Areas, Rabat, Morocco 2Mohammed V University Agdal, Faculty of sciences, Rabat, Morocco Hybrid wheat is a promising technology to increase yields worldwide. High seed production costs due to low outcrossing rates and low heterosis are the main hybrid wheat constraints. Maximizing heterosis and appropriate morphological, floral and flowering traits to optimize outcrossing are mandatory for hybrid seed production. In bread wheat, our understanding of the genetic factors that govern floral traits and their role as determinants of grain yield is still limited. Exploitation of existing diversity is anticipated to be strongly used for better standardization of this technology and efficiently improve the cross-pollination ability. Utilization of marker/trait association for outcrossing traits will greatly help to simply identify heterotic group which express high heterosis and consequently high hybrid performance. This study aimed to dissect the genetic architecture of floral traits and identification of QTLs underlying floral traits. To this end, 200 ICARDA elite spring bread wheat genotypes were characterized for floral and phenogical traits and genotyped using 15K-SNP markers. Wide genotypic variances for important traits like pollen mass and anther extrusion and a wide range in trait values were observed. Besides, positive association between degree of openness of florets and duration of foral opening were observed. Furthermore, an association mapping will be carried out and new QTL for outcrossing traits will be identified.</td>
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<td>NAME</td>
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<td>Authors</td>
<td>Ammar A. Elakhdar, Toshihiro Kumamaru, Khairy Amer, Calvin O. Qualset, Kevin P. Smith, Robert S. Brueggeman</td>
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<td>Title</td>
<td>ASSOCIATION ANALYSIS OF YIELD RELATED-TRAITS IN BARLEY (HORDEUM VULGARE L.) UNDER SALT AND DROUGHT STRESSES</td>
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<td>Abstract</td>
<td>Increased food costs goods are the initial indication of strong edible yield-loss; therefore, crop productivity is irreversibly inhibited by environmental stresses. One of the most important abiotic stresses affecting agricultural crops is high soil salinity and act as a major obstacle to increasing them production in growing areas worldwide, particularly in the dry region. This situation has compelled plant scientists to develop climate change-resilient crops, which can withstand broad-spectrum of stresses. With the increasing demand for barley, an emphasis on developing elite barley cultivars conferring greater tolerant to relevant stress is needed in order to meet the current and future demands of this grain crop. Elite inbred and advanced breeding lines are highly adapted and have been subjected to numerous recombinations. The main purpose of this study was to implement association analysis for eighteen-trait using 111-elite barley lines. The genotypes have been developed by the ear-to-row selection method at, Agricultural Research Center (ARC), Egypt. Effects of stress were induced at the seedling stage for drought stress using polyethylene glycol (PEG) and salinity stress using sodium chloride (NaCl). A total of 261 SSRs and SNPs polymorphic specific alleles were used to characterize the panel for linkage disequilibrium (LD), population structure and kinship. Preliminary results show that broad-sense heritability (H2) of the agronomic traits was high (&gt; 0.65), highly significant marker-trait associations were identified for most traits. Our results show the potential of an elite inbred panel in association studies in targeting agronomic traits for drought and salinity stress.</td>
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<td>Affiliation</td>
<td>Kyushu University, Institute of Genetic Resources, Fukuoka, Japan, Agricultural Research Center, Field Crop Research Institute, Giza, Egypt, University of California-Davis Department Plant sciences, California, USA</td>
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<td>NAME</td>
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<td>Authors</td>
<td>Mitchell Feldmann, Steven Knapp, William Bridges</td>
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<td>Title</td>
<td>Heritability of an Individual Quantitative Trait Locus</td>
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<td>Abstract</td>
<td>Heritability is a fundamental concept in studying genotypic and phenotypic variation in natural and experimental populations in biology, agriculture, and medicine. The advent of technologies for routinely genotyping DNA variation opened the way to the application of linkage disequilibrium and association mapping and other approaches for identifying genes or quantitative trait loci (QTL) underlying biologically or economically important phenotypes, quantifying genetic versus non-genetic causes of phenotypic variation, and applying estimated parameters in marker-assisted selection. Here, we investigate a statistical problem associated with estimating the genetic variance linked to a QTL and show that this metric is often over-estimated due to the non-additivity of expected mean squares. The magnitude of the over-estimation depends on the effect of the locus, the number of loci affecting the trait under study, and the assortment of main and interaction effects included in the statistical model. When data are balanced, algebraic solutions exist for estimating and correcting the over-estimation with predicted coefficients that follow Pascal’s triangle.</td>
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<td>Affiliation</td>
<td>University of California, Davis, Davis, USA, Department of Plant Sciences, University of California, Davis, Davis, USA</td>
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<tr>
<td>NAME</td>
<td>Focht, Eric</td>
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<tr>
<td>Authors</td>
<td>Eric Focht, Rodrigo Iturrieta, Mary Lu Arpaia</td>
<td>TU24</td>
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<td>Title</td>
<td>QUANTIFYING FRUIT SHAPE IN AVOCADO: A BETTER WAY FORWARD</td>
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<td>Abstract</td>
<td>QUANTIFYING FRUIT SHAPE IN AVOCADO: A BETTER WAY FORWARD  Eric Focht 1, Rodrigo Iturrieta 1 and Mary Lu Arpaia 1 1University of California-Riverside Department of Botany and Plant Sciences</td>
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For decades now, the rating of avocado fruit shape has been tied to an arbitrary system containing discrete values that do not coexist on a linear scale. The goal of this presentation is to present a new methodology using pre-existing, commonly available software and equipment to capture and analyse images of fruit. Through use of Adobe Photoshop, pictures taken w/a DSLR or other digital camera can be reduced in scope to the length and width of the fruit. These resulting images can then be mined for the volume of negative and positive space, the length and width of these spaces, and the overall ratio of length to width of the entire image. This mined data allows for comparison of regularity through the entire shape of the fruit and ratio of volume between hemispheres, among other possible analyses. Analysis thus generated can be used to identify desirable phenotypic traits and to correlate them to environmental, genetic, and physiological measurements.

| Affiliation    | University of California, Riverside, USA                  |

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<th>NAME</th>
<th>Fong, Stephanie</th>
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<td>Authors</td>
<td>Stephanie Fong, Yifei Wang, Jennifer Johnson-Cicalese, Nicholi Vorsa</td>
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<td>Title</td>
<td>LOCI IMPACTING MALIC AND CITRIC ACID CONTENT IN CRANBERRY FRUIT</td>
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<td>Abstract</td>
<td>Malic and citric acids are the primary contributors to acidity in American cranberry (Vaccinium macrocarpon) fruit. Citric acid contributes a sour taste while malic acid contributes tartness. This sour taste is quantified in terms of titratable acidity (TA), measured in citric acid equivalents. Commercially grown cranberries have an average TA of 2.3-3.0%, while Granny Smith apple has a TA of about 0.8%. Malic acid concentrations typically range from 6 to 8 mg/g FW, while citric acid concentrations range from 8 to 11 mg/g FW in cranberry. Two unique wild germplasm accessions were identified with reduced TA, resulting from low citric acid (&lt;1 mg/g) and low malic acid (&lt;3 mg/g) levels. Observed segregation indicate both the low citric and low malic acid traits are independent, recessive, and consistent with single locus Mendelian inheritance. A SSR for the low citric acid allele indicated the SSR region to be within 1 cM of the locus. However, multiple SSR marker alleles indicate the locus has multiallelic ‘normal’ alleles with partial dominance. Identification of a molecular marker for the low malic acid locus is underway. Populations segregating for both loci indicate the low malic acid locus has a greater effect on reducing TA than the low citric acid locus. Homozygous genotypes for the respective low acid alleles gave TA ranging from 0.5% (malic) to 1.0% (citric). These markers will facilitate marker assisted selection in breeding for lower citric and malic acid phenotypes, allowing the development of cranberry varieties with reduced acidity.</td>
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<td>Authors</td>
<td>David Francis, Eduardo Bernal, Debora Liabeuf, Darlene De Jong, Taylor Anderson, Stella Zitter, Martha Mutschler-Chu</td>
<td>TU67</td>
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<tr>
<td>Title</td>
<td>Prebreeding to combine resistances to pathogens from three kingdoms in processing and fresh-market tomato</td>
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<td>Abstract</td>
<td>The goals of this project are to merge fungal, oomycete and bacterial resistances developed by our separate breeding programs, and create complementary sets of fresh market and processing tomato lines possessing genetic control of resistance to five diseases not combined in current tomato cultivars. We target the most persistent causes of foliar blight and tomato fruit loss in humid growing regions such as the North East, Atlantic Coast and</td>
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Midwestern US. Diseases include bacterial spot (Xanthomonas vesicatoria, X. perforans, X. euvesicatatoria, and X. gardneri), bacterial speck (Pseudomonas syringae), Early blight (fungal: Alternaria solani), Septoria leaf spot (fungal: S. lycopersici), and late blight (oomycete: Phytophthora infestans). The genetic control for these diseases involves at 9-12 genes or QTL in 5 linkage groups. As many of these resistance loci are clustered, we propose to select for recombination that will bring several genes into “coupling phase”. Developing these cassettes of linked resistance loci will allow plant breeders to breed for as few as 3-5 loci in order to control multiple diseases. The specific objectives are: 1) use marker assisted selection (MAS) to bring loci into coupling phase; 2) use MAS with background genome selection to generate a set of near isogenic lines containing different subsets of genes/QTL on Chromosome 11 that provide resistance to multiple species of Xanthomonas; 3) improve breeding strategies, including background genome selection and genome wide selection methods for combining resistance to multiple diseases into elite germplasm for distinct market uses; 4) release the resulting lines and information for use by private and public breeding and research programs.
Three gamma radiation dosages were studied (2,3,4 Gy), and a non-irradiated control was used for comparison. Surviving explants were rooted and established in a greenhouse. DNA was extracted from the plants after greenhouse establishment to obtain Genotyping By Sequencing (GBS) data. Traits measured include LD50 taken in tissue culture and after greenhouse establishment, height (as an estimate of vigor), powdery mildew resistance, and mutation rate estimate from GBS data. Results from this study will help determine the gamma radiation dosage necessary to induce subtle but meaningful mutations to Cascade and Centennial hop for improvement purposes and may also lead to gene discovery for important traits.

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NAME | Gibson, Kimberly
Authors | Kimberly Gibson, Stephanie Smolenski Zullo, Antonia Palkovic, Paul Gepts
Title | The Pursuit of Lygus Resistance/Tolerance in Phaseolus lunatus: Can Volatile Organic Compounds Provide a Solution?
Abstract | THE PURSUIT OF LYGUS RESISTANCE/TOLERANCE IN PHASEOLUS LUNATUS: CAN VOLATILE ORGANIC COMPOUNDS PROVIDE A SOLUTION? Kimberly Gibson1, Stephanie Smolenski-Zullo1, Antonia Palkovic1, Paul Gepts1 1University of California-Davis Department of Plant Sciences

Lygus hesperus is the most damaging pest for Phaseolus lunatus (Lima bean) in California, with the potential to create losses of up to 70% of yield by chewing on flowers and young pods. This prevents cultivation of P. lunatus without insecticides and thus, under organic cropping systems. In order to identify mechanisms of resistance to or tolerance of Lygus, and to improve breeding projects, we have started a multipart study of a recombinant inbred population developed from the cross between a viny baby lima bean variety (with some tolerance to Lygus) and a bush large lima bean variety (susceptible to Lygus). Three consecutive years of field testing have confirmed the tolerance of one of the parent lines as well as two progeny lines. This population was sequenced by RADseq and then BLASTed onto the common bean reference sequence. The sequence conservation between these two Phaseolus species was confirmed and we identified some 50,000 potential SNPs. The RI population was sequenced by GbS and is currently being analyzed for QTLs. Going forward we plan to analyze VOC emissions from this population to test the hypothesis that this may play a role in Lygus tolerance, alone or in combination with other putative resistance mechanisms like growth habit, polygalacturonase inhibiting protein, and cyanogenesis.

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NAME | Gimode, Winnie
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Title | FINE MAPPING OF A MAJOR FLOWERING TIME QUANTITATIVE TRAIT LOCUS IN WATERMELON
Abstract | Flowering time is important in determining time of fruit set in watermelon (Citrullus lanatus) and is therefore a major determinant of earliness. It is also crucial in production of seedless watermelon, which relies on synchronized flowering between pollenizers and triploid cultivars. Incorporation of single nucleotide polymorphisms (SNPs) for marker assisted selection (MAS) of flowering time in watermelon would potentially aid in selection for the early flowering trait, which would shorten the production time of watermelon cultivars. Moreover, seedless watermelon breeding would be enhanced by selecting for the most suitable pollenizers for the triploid cultivars. A major QTL associated with flowering time (Qdff3-1) was previously identified on chromosome 3 of watermelon and candidate genes underlying this QTL include FT and TEMPRANILLO. The objective of this study was to identify SNPs that are significantly associated with flowering time in order to fine-map the Qdff3-1 locus. QTL-seq was employed and SNPs with the highest absolute ?SNP-index were selected. The potential markers were validated in a recombinant inbred line mapping population as well as a cultivar panel. SNPs around the 10.5-11.5Mb region show significant association with the flowering trait, and may be applicable in MAS of flowering time in
watermelon. This study has identified another potential candidate gene (Cla002795, Phosphatidylinositol-4-phosphate 5-kinase) within the region that may also be involved in the regulation of flowering time in watermelon. A SNP within this gene, UGA3_11046548, shows a significant association with the flowering trait and its effect on flowering time may have functional significance.

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<th>Affiliation</th>
<th>University of Georgia, Athens, Georgia</th>
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<td><strong>NAME</strong></td>
<td>Giri, Anju</td>
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<td><strong>Authors</strong></td>
<td>Anju Giri, Robert Aiken, Floyd Dowell, Allan Fritz, Allan Fritz, Jesse Poland</td>
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<td><strong>Title</strong></td>
<td>Analysis of water soluble carbohydrates accumulation in wheat stem using NIR spectroscopy</td>
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<td><strong>Abstract</strong></td>
<td>The capacity for storage and utilization of water soluble carbohydrates (WSC) in the stem is an important trait to support grain filling, particularly under limited water availability. WSC have been found to be an important contributor to yield, biomass, and harvest index under drought. The main objectives of this study were to develop a near-infrared spectroscopy model to dissect genotypic differences in water soluble carbohydrates in diverse wheat genotypes. A set of 400 diverse breeding lines, 30 varieties and 3 check varieties, were planted in western Kansas, to evaluate their performance under two treatments: irrigated and limited irrigation. The breeding lines were planted in a type II modified augmented design and the 30 varieties were replicated 6 times and arranged in a randomized complete block design (RCBD) with three blocks in each treatment. The NIR reflectance was measured in finely ground wheat stems fifteen days after mid-flowering. The NIR data were calibrated and cross-validated to WSC using multivariate calibration technique Partial Least Square Regression with 105 diverse set of samples at R2of 0.83 and SECV (Standard Error of Cross Validation) of 40.8 mg/g. There were significant differences between the varieties with a mean value ranging from 132 mg/g to 340mg/g. Accumulation was significantly higher below top node compared to the stem part above top node. NIR spectroscopic techniques have been shown to be effective in monitoring plant physiological process rapidly and nondestructively. These results suggest that breeding for high WSC will be possible in wheat.</td>
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<th>Affiliation</th>
<th>Department of Agronomy, Kansas State University, Manhattan, USA, Northwest Research-Extension Center, Kansas State University, Colby, USA, USDA-ARS-CGAHR-SPIERU, Manhattan, USA</th>
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<tr>
<td><strong>NAME</strong></td>
<td>Giroux, Michael</td>
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<td><strong>Authors</strong></td>
<td>Emma Jobson, Andy Hogg, Rachel Johnston, John Martin, Michael Giroux</td>
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<tr>
<td><strong>Title</strong></td>
<td>Wheat Yield and Quality Improvement via Testing of New Semi-Dwarf Alleles</td>
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| **Abstract**      | WHEAT YIELD AND QUALITY IMPROVEMENT VIA TESTING OF NEW SEMI-DWARF ALLELES  
Emma Jobson, Andy Hogg, Rachel Johnston, John Martin, and Mike Giroux.  
Department of Plant Sciences, Montana State University  
Plant height is an important characteristic in wheat varieties since modern semi-dwarf varieties have more productive tillers and higher yields compared to standard height wheat varieties. Semi-dwarf wheat is the result of mutations in the Reduced Height (Rht) gene that limits the plant’s ability to respond to GA. Only two Rht dwarfing alleles, Rht-B1b and Rht-D1b, are used in commonly grown semi-dwarf wheat varieties. We have created a set of new Rht alleles varying in function that should prove useful in creating improved wheat yield and quality traits. Alleles were selected for further testing based on based on SIFT scores, reduced GA responsiveness, and intermediary coleoptile length compared to current Rht dwarfing alleles and the wildtype. Further studies will examine the relationship between the level of Rht function and plant growth, seed quality, and yield. Our objectives are:  
Characterization of new Rht-A1, B1, and D1 alleles in in vitro assays and in plants. This will include evaluation of the degree to which individual alleles interact in yeast two hybrid assays and measurements of plant growth, yield, and seed development under standard agronomic conditions. Create populations of wheat segregating for different combinations of Rht alleles. These populations could then be used in further experiments to determine the allelic combinations best suited to optimize wheat yield and product quality. |

<p>| Affiliation       | Montana State University, Bozeman, USA |</p>
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<th>Name</th>
<th>Greenhut, Rachel</th>
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<tr>
<td>Authors</td>
<td>Rachel Greenhut, Juliana Osorio Marin, E. Charles Brummer, Allen Van Deynze</td>
<td>TU32</td>
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<td>Title</td>
<td>DEVELOPING BABY LEAF SPINACH WITH LOWER CADMIUM UPTAKE</td>
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<td>Rachel Greenhut, Juliana Osorio Marin, E. Charles Brummer, and Allen Van Deynze</td>
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<td>Department of Plant Sciences, University of California, Davis, CA</td>
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Spinach (Spinacia oleracea) is an agronomically important crop in the Salinas Valley of California and a known hyper-accumulator of cadmium (Cd). The Valley has areas with anomalously high Cd in bedrock and agricultural soils. Because Cd accumulation can cause health risks, understanding the genetic mechanisms by which spinach accumulates Cd so that new varieties with reduced Cd content can be developed is an important goal for spinach production. Our long-range objective is to develop superior cultivars with reduced Cd uptake. In the first year, we evaluated 625 spinach accessions from germplasm collections for Cd uptake in a soil-based greenhouse assay, with duplicate testing of 95 selections. We found a 3-fold difference in Cd accumulation across tested accessions. In addition, we identified fifty candidate genes associated with Cd accumulation in other crops to test for association with the trait. We are currently looking at DNA sequence diversity in these genes to evaluate their relationship Cd accumulation in leaves. We will then begin cultivar development between low Cd lines and breeding populations as a first step to incorporate the trait into cultivars and to enable genetic mapping of genes associated with Cd uptake.

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<td>Authors</td>
<td>Lucia Gutierrez, Jean-Luc Jannink, Kevin Smith, Melanie Caffe, Mark Sorrells</td>
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<td>Title</td>
<td>TRANSCRIPTOMICS AND METABOLICOMICS TO IDENTIFY DRIVERS OF SEED COMPOSITION IN OAT</td>
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<td>Abstract</td>
<td>Oat is uniquely valued among grain crops for the health-promoting composition of its seeds. Enhancing the ability of breeders to select for higher concentrations or new combinations of compounds will increase the value of the crop and ensure its continued role in sustainable cropping systems. This project will generate detailed information on seed composition and its genetic control in global diversity and elite North American oat panels, and develop and evaluate methods enabling breeders to leverage that information for selection decision support and to discover new mutations affecting composition. The specific objectives of the project are: i) to identify metabolites and gene transcripts that are hubs in networks of these features in a global oat diversity panel, ii) to evaluate methods to incorporate this information in genomic evaluation and determine its value in selecting improved progeny in an elite Upper-Midwest panel, and iii) to sequence an oat TILLING population at sites suggested by this analysis and characterize new mutations for their impact on seed composition. The project will elucidate genetic drivers of oat seed composition to show how to increase accuracy of composition prediction. It will also deliver new alleles affecting composition. The project fits well with program priorities as data and methodological outputs will be published in the user-friendly environment of the online breeding research database T3/Oat. Specifically all datasets will be available and coupled to network analysis tools to analyze them or other similar data, thereby implementing systems-level predictive modeling for seed composition in oat.</td>
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<tr>
<td>Authors</td>
<td>Wesley Hancock, Roberto Cantor-Barreiro, Susan Copeland, Joyce Hollowell, Thomas Isleib, Thomas Stalker, Shyam Tallury</td>
<td>TU33</td>
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<tr>
<td>Title</td>
<td>Utilizing Wild Arachis Species as a Source of Genetic Variation for the Improvement of Disease Resistance in Peanut</td>
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### Abstract

Spotted wilt of peanut (Arachis hypogaea L. (2n=4x=40)) is caused by the tomato spotted wilt tospovirus (TSWV) and is one of the major causes of yield and quality loss for peanut growers in the U.S. Planting resistant cultivars is the preferred disease management strategy for growers but complete resistance is not available in cultivated germplasm. The wild diploid species A. diogoi (2n=2x=20) has been shown to have high levels of resistance to multiple diseases including TSWV. An interspecific hybrid-derived population was produced via the triploid-hexaploid method and evaluated for resistance to TSWV using greenhouse and field evaluations. A sterile triploid hybrid (2n=3x=30) resulting from the cross between a large-seeded virginia-type peanut cultivar ‘Gregory’ and A. diogoi GKP10602 (PI 276235) was chromosome doubled to restore fertility at the hexaploid level (2n=6x=60). The hexaploid plant and resulting progeny were allowed to self-pollinate for 12 generations during which spontaneous chromosome loss occurred resulting in approximately 90 fertile tetraploid introgression lines. Morphologically the introgression lines varied for traits such as growth habit, pod and seed size, with the majority being intermediate to the two parents. Nine lines were highly resistant to TSWV. These results are being confirmed in additional replicated field evaluations as well as in greenhouse inoculations to better understand the underlying genetic mechanisms for TSWV resistance. The presence of TSWV resistant introgression lines will aid in the long term goal of developing multiple disease resistant high yielding peanut cultivars.

### Affiliation

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<th>NAME</th>
<th>Hardigan, Michael</th>
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### Title

Domestication History of Strawberry: Population Bottlenecks and Restructuring of Genetic Diversity Through Time

### Abstract

Domestication History of Strawberry: Population Bottlenecks and Restructuring of Genetic Diversity Through Time

Michael Hardigan1, Thomas J. Poorten1, Charlotte Acharya1, Glenn S. Cole1, Kimberley Hummer2, Nahla Bassil2, Patrick Edger3, and Steven J. Knapp1

1University of California-Davis Department of Plant Sciences
2USDA-ARS, National Clonal Germplasm Repository
3Michigan State University Department of Horticulture

Garden strawberry (Fragaria x ananassa, 2n=8x=56) arose from hybrids of F. virginiana from North America and F. chiloensis from South America. Subsequent breeding occurred within this hybrid complex. Beginning in the 1920s, important germplasm development and cultivar releases took place in the University of California strawberry program. The UC strawberry germplasm collection and diverse USDA holdings were fingerprinted on the Axiom iStraw35 array. A panel of 1,305 genotypes, including 1,043 UC varieties, 157 non-U.C. varieties and 105 wild accessions was used to assess genetic bottlenecks in the history of California strawberry breeding and restructuring of germplasm diversity. Analysis of population structure revealed UC germplasm, particularly varieties developed since the 1960s, are genetically distinct from other American and European genotypes. Increased theoretical population numbers maintained this pattern while splitting UC germplasm into sub-clusters with differing rates of day-length neutrality and release years, showing structuring of diversit y along photoperiod sensitivity phenotypes. Reflecting strawberry s recent hybrid domestica

### Affiliation

UC Davis, Davis, USA

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<th>NAME</th>
<th>Harshman, Julia</th>
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### Authors

Julia Harshman, Mitchell F, Dominique Pincot, Tom Poorten, Glenn Cole, Alexander Putman, Thomas Gordon, Steve Knapp

### Title

RESISTANCE TO CHARCOAL ROT IN STRAWBERRY

### Poster Number

TU34
### RESISTANCE TO CHARCOAL ROT IN STRAWBERRY

Harshman J.M.1, Feldmann, M.J.1, Pincot D.D.A.1, Poorten T.J.1, Cole G.S.1, Putman, A.I.2, Gordon T.3, Knapp S.J.1

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2 Department of Plant Pathology and Microbiology, University of California, Riverside, California, 92521
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Charcoal rot, caused by the soil-borne pathogen Marophomina phaseolina, causes devastating economic losses in strawberry (Fragaria x ananassa) in many major production regions worldwide. This disease was first reported in California in 2005 and has since become a serious threat to all production regions in California, which supplies 88% of the strawberries produced in the US. However, resistance is low to non-existent among currently available cultivars. To identify novel sources of resistance for this emerging disease, resistance to M. phaseolina among 566 historically and commercially important F. x ananassa germplasm accessions was characterized in 2016 and again in 2017. These were phenotyped for resistance by dipping roots of field-grown plants in a slurry containing propagules of a virulent M. phaseolina isolate found in California (GL1310) and were genotyped with 38,506 single-nucleotide polymorphisms (SNPs) using an Affymetrix Axiom array. Results from a genome wide association study on these 566 individuals revealed a complex genomic landscape composed of many loci each of small effect. The complexity of the underlying genetics, low trait heritability, and low prediction accuracy from the genome wide markers suggest that breeding for this necrotrophic pathogen will be a continuous effort.

### Epicuticular Waxes and Thrips Resistance in Onion

#### Abstract

Thrips (Thrips tabaci) is the most serious insect pest of onion and is the vector for Iris yellow spot virus (IYSV), a devastating disease of onion across the US. Onion selections showing less thrips damage and lower IYSV incidence in the field were evaluated for amounts and types of epicuticular waxes and thrips damage in field plots in Wisconsin. The ketone hentriocontanone-16 (H16) is the most prevalent wax on the leaves of wild-type “waxy” (WX) onions, and is significantly less abundant on foliage of the thrips-resistant [“semi-glossy” (SG)] selections. Importantly, some SG selections had more total epicuticular waxes than WX onions, due primarily to increased amounts of fatty alcohols and alkanes. SG phenotypes suffered significantly less feeding damage by thrips as compared to waxier onionod. This study supports the development of onion cultivars with unique profiles of epicuticular waxes in order to avoid losses due to thrips and IYSV and reduce pesticide applications.

### Micropropagation of Immature Inflorescences of Little Bluestem (Schizachyrium scoparium)

#### Abstract

**MICROPROPAGATION OF IMMATURE INFLORESCENCES OF LITTLE BLUESTEM (SCHIZACHYRIUM SCOPARIUM)**

Susan Hawkins and Carol Robacker

University of Georgia Department of Horticulture

Little bluestem (Schizachyrium scoparium) is a long-lived perennial bunchgrass native to the United States. Little bluestem is increasingly popular as an ornamental landscape plant.
Cultivars are usually reproduced by division, which greatly limits the number of new plants that can be produced. Micropropagation was investigated as a way to rapidly propagate little bluestem in greater numbers. Immature inflorescences of eight genotypes were cultured using four combinations of 2,4-D and kinetin and three levels of light. Cultures were scored after 30 days, subcultured onto rooting media either containing NAA or not containing NAA, and placed under light. Cultures that initiated shoots and roots were transplanted onto rooting media and placed under mist in a greenhouse to acclimate. Two initiation media, 0.5 mg/L 2,4-D with 1 mg/L kinetin and 1 mg/L 2,4-D with 1 mg/L kinetin, had higher scores than the other two combinations \((p=0.0002)\). Light treatment \((p=0.1360)\) made no difference in the scores of the cultures. Rooting media made no difference in the number of cultures rooted and transplanted to the greenhouse \((p=0.1081)\). Cultures originally held under semi-light produced more rooted plants than those held under dark \((p=0.0206)\) while initiation media made no difference \((p=0.1886)\). An interaction was found between the combination of 2,4-D and kinetin and light treatment \((p=0.0005)\). Our study showed that micropropagation of immature inflorescences is a viable way to increase little bluestem cultivars.

**Affiliation**
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**NAME**
Hinds, Zach

**Authors**
Zach Hinds, Eric Hequet

**Title**
Impact of Breeding Methods on Fiber Length Distribution Improvement

**Abstract**
Cotton fiber length distributions generated from the Advanced Fiber Information System (AFIS) have been shown to better capture information related to yarn properties than High Volume Instrument (HVI) measurements. Previous results demonstrated that breeding cotton for improved fiber length distributions would result in better spinning performance and ultimately greater market access. However, traditionally utilized pedigree selection may not be an ideal method for enhancing the length distributions of cotton germplasm. While effective for improving qualitative traits where superior phenotypes can be effectively observed and selected, pedigree selection becomes limited, because of individual plant selection, when trying to improve quantitative traits controlled by a large number of genes and influenced by environmental factors. Additionally, making selections within heterogeneous germplasm can lead to inefficient breeding progress by advancing segregating materials and therefore delaying the development of homogeneous lines, while potentially inadvisably eliminating germplasm that could contribute to the quantitative trait of interest.

In this study, 8 F2 populations were generated using obsolete cotton varieties developed prior to widespread cotton characterization with the HVI. Concurrent but separate from pedigree selection, these populations are under development using a modified single seed descent strategy (single boll descent) where selection for fiber length distribution will be delayed to later generations when a greater degree of homogeneity within the population has been established. Both the genetic improvement and the economic cost of the two breeding schemes will be compared to identify the most appropriate breeding method for improving cotton fiber length distributions.

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**NAME**
Hinojosa, Leonardo

**Authors**
Leonardo Hinojosa, Kevin Murphy

**Title**
EVALUATION OF QUINOA POLLEN IN HEAT CONDITIONS

**Abstract**
Quinoa (Chenopodium quinoa Willd.) is a pseudocereal with high nutritional value and health benefits. Quinoa cultivation and consumption has expanded around of the world over the last decade, however, high temperatures during critical growth stages has led to moderate to extreme reductions in yield. Male gametophyte development is the most critical stage for many crops in high temperatures conditions. The objective of this study was to evaluate the pollen morphology in quinoa after exposure to high temperature. Pollen morphology was
analyzed with transmission electron microscopy and scanning electron microscopy in the
quinoa genotypes QQ74 and 17GR, subjected to 22°C/16°C (day/night) as control conditions
and 40°C/24°C as high-heat conditions in anthesis in growth chamber experiments. Pollen
germination and viability was recorded. Our results show that heat stress reduced the pollen
viability and pollen germination. Although no morphological differences were observed in
the pollen surface, both the pollen wall (intine and extine) thickness and the germ pore
increased due to heat stress. In conclusion, pollen viability could be a good parameter to
identify heat tolerant quinoa genotypes. Continued evaluation of quinoa pollen in field
conditions is necessary to determine the effect high temperature on pollen germination,
viability and morphology.

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NAME
Hoogland, Traci

Poster Number
TU40

Authors
Traci Hoogland, Jack Martin, Jamie Sherman

Title
GENETIC DISSECTION OF FORAGE QUALITY IN A WORLD CORE POPULATION
OF SPRING 2-ROW BARLEY

Abstract
Forages quality is where plant breeding meets animal nutrition. Even a 1% increase in forage
digestibility has been shown to substantially increase the average daily weight gain of
livestock and results in reduced inputs for the farmer and rancher alike. Despite its
importance, much remains unclear about the genetics controlling forage nutritional quality in
barley or the quality of publically available germplasm resources. A germplasm resource of
particular interest is the Barley World Core (BWC) held by the National Small Grains
Collection (NSGC). As part of the Triticeae CAP, the BWC population was created to
capture the full genetic diversity of the NSGC and was genotyped with a genome-wide, 9k
SNP-chip panel. A set of the most genetically diverse, spring 2-row lines were selected from
the BWC for a genome-wide association study to map forage quality and to assess the
BWC’s potential to contribute novel positive alleles. The selected lines were phenotyped in
Bozeman, MT, USA to determine their economically important forage quality traits under
both irrigated and dryland conditions. Based on the forage quality field results, an association
analysis was performed and lines with positive characteristics selected for introgression into
the barley forage breeding program. The long-term goal of this study is the genetic dissection
of forage quality traits and the utilization of QTLs in forage quality improvement.

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NAME
Hoyos Villegas, Valerio

Poster Number
TU41

Authors
Valerio Hoyos-Villegas, Jessica O’Connor, Angus Heslop, Anthony Hilditch, Zulfi Jahufer,
John Ford, Brent Barrett

Title
New Zealand's little giant: Genetic gain in white clover breeding across 90 years of
population improvement

Abstract
White clover is the predominant legume companion for grasses in pasture based, animal
production systems in New Zealand and other temperate countries due to numerous
environmental and productivity benefits. White clover was first introduced into New Zealand
in 1834 but breeding and cultivar release has only been known since the mid 1900s with
‘Grasslands Huia’ as the first recorded cultivar. White clover improvement has mainly
occurred via the use of recurrent phenotypic selection methods. The last report of genetic
gain in white clover was published in 1994 and included trials of cultivars across 60-years of
breeding. Genetic improvement in white clover was previously reported on an annual basis to
be 1.44 g m-2 for forage yield and 0.14% for clover percentage in a sward. In addition to
delivering a renewed report of genetic gain after over 20 years, the enabling of genomic
selection (GS) in white clover in New Zealand will require that an updated benchmark for
genetic gain be established to allow for initial cycles of GS to be compared with the historical
rate of gain and determine the effectiveness of genomic selection. In the current report, we
surveyed germplasm from across 90 years of white clover breeding. The 80 cultivars are
planted in trials in three locations across New Zealand managed under sheep and dairy
grazing and measurements are being taken every season for three years from 2016-2018.
Variables collected include clover content in sward, forage yield and leaf size.
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<td><strong>Title</strong></td>
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<td></td>
<td>Modification of plant determinacy to increase yield in fresh market tomato</td>
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<td><strong>Abstract</strong></td>
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<td>Plant architecture is one of the most important determinants of crop productivity. In several crops, modifications to plant architecture facilitated hand and mechanical harvesting and permitted higher planting densities. In tomato, the primary driver of yield during domestication was fruit size. Recent studies in tomato (Solanum lycopersicum), have revealed that the Self pruning (SP), and Single flower truss (SFT) genes play a key role in plant determinacy, with Sp acting to repress flower development while SFT promotes this. The suppressor of sp (SSP) likewise acts to restore indeterminate growth in sp backgrounds. In processing tomato, sft and ssp mutations were found to quantitatively manipulate determinacy to improve yield. We hypothesize that through modification of flowering signal-related genes, we can improve yield in fresh-market tomato. To test this, we backcrossed two mutant alleles of sft (viz., sft-tmf and sft-1906) and two mutant alleles of ssp (viz., ssp-2129 and ssp-610) into two large-fruited and one small-fruited background. We have produced BC3F2 or BC4F2 seed for each trait*background combination. Crosses will be made in fall 2017 to generate single and double-heterozygotes for each gene combination in Fla. 8059, Fla. 8153, and NC3grape. Field trials will be conducted under commercial production settings in 2018 and 2019 to determine effects of these genes on yield and marketability. We have also used CRISPR/Cas9 gene editing to engineer loss of function mutations in a related family member of SP that provides early flowering and yield. These mutant lines will be used for architectural evaluations in parallel with the introgressions.</td>
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<td>Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA, University of Florida, GCREC, Wimauma, FL, USA</td>
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<td><strong>NAME</strong></td>
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<td>HIGH-THROUGHPUT PHENOTYPING FOR EFFECTIVE WATER USE WITH DISPERSBLE SENSORS</td>
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<td>HIGH-THROUGHPUT PHENOTYPING FOR EFFECTIVE WATER USE WITH DISPERSBLE SENSORS</td>
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<td>Piyush Jain1, Duke Pauli3, Nicholas Kaczmar3, Michael Gore3, Abraham D Stroock2</td>
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<td>1Sibley School of Mechanical and Aerospace Engineering,</td>
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<td>3School of Integrative Plant Science, Cornell University, Ithaca, New York 14853 USA</td>
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<td>Leaf water potential ((?leaf)) represents the best single indicator of plant water status because it integrates environmental conditions (e.g.: water availability and evaporative demand) and genotype specific plant responses (e.g.: stomatal regulation and anatomy). The lack of high-throughput phenotyping methods to measure (?leaf)on an individual plant basis poses a significant challenge to decoupling the environment and genotype contributions in the assessment of effective water use (EWU) in plants. This poster will present initial steps toward the development of a dispersible sensor of water potential that will allow for remote measurement of (?leaf)at the level of individual plants. The presentation will cover: 1) the characterization of delivery of sensors to the leaf tissue in maize, 2) optical characterization of embedded sensors, and 3) design considerations for materials that respond optically to changes in water potential. We will also discuss opportunities to define new traits that capture EWU and their use within a phenotyping and statistical genetics framework to access the associated quantitative trait loci.</td>
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<td>Jillian A. Jastrzembski, Madeleine Y. Bee, Gavin L. Sacks</td>
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<td>Title</td>
<td>Faster, cheaper, smellier – accelerating throughput and achieving spatial resolution of plant volatiles with extractive meshes coupled to ambient ionization mass spectrometry</td>
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<tr>
<td>Abstract</td>
<td>Trace-level plant volatiles (ng/L – mg/L) are of interest to plant breeding and other disciplines due to their role in plant protection and communication, as well as their impact on the sensory qualities of foodstuffs and fragrances. However, standard methods for targeted quantification of trace volatiles (e.g. gas chromatography – mass spectrometry, GC-MS) are low-throughput as compared to analysis of other important traits (e.g., major metabolites, color). We demonstrate that sorbent-coated meshes (SPMESH) or laser-etched polymeric thin-films (eSPMESH) can be used to extract and pre-concentrate volatiles from sample headspaces. The extracted volatiles can then be rapidly analyzed (&lt;30 s) under ambient conditions using chromatography-free Direct Analysis in Real Time (DART)-MS. Using a high resolution SPMESH-DART-MS, detection limits in the range of 2-3 ng/L can be achieved for certain odorants (3-isobutyl-2-methoxypyrazine (IBMP), 7-damascenone) with precisions of &lt; 10 %RSD. Good correlation could be achieved between SPMESH-DART-MS and GC-MS analyses for volatiles in grape samples from commercial vineyards. The eSPMESH format is amenable to parallel extraction of volatiles from multiple samples on multi-well plates, which makes it well suited for high-throughput phenotyping of volatiles of large numbers of samples (e.g. mapping populations). Preliminary work shows that samples can be analyzed by eSPMESH-DART-MS using an automated positioning stage in less than 1 min, as compared to 30 min or more for a conventional GC-MS analysis. Furthermore, because eSPMESH retains the original spatial distribution of volatiles, it could potentially be used to create volatile images of plant samples, although further improvements must be made to limit leakage of volatiles between adjacent wells.</td>
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<td>Jiang, Tao</td>
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<td>Authors</td>
<td>Charles Chen, Tao Jiang, Phat Dang, Mingli Wang</td>
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<tr>
<td>Title</td>
<td>Association mapping of SSR markers to sweet, bitter and roasted peanut sensory attributes in cultivated peanut</td>
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<tr>
<td>Abstract</td>
<td>Certain roasted peanut quality sensory attributes are very important breeding objectives for peanut manufactory and consumers. Currently the only means of measuring these traits is the use of a trained sensory panel. This is a costly and time-consuming process. It is desirable, from a cost, time and sample size perspective, to find DNA marker and the trait association for the implementation of marker-assisted selection (MAS) in a breeding program. One hundred and four accessions of the U.S. mini core collection are used for sweet, bitter and roasted peanut sensory attributes analysis including tocopherols, fatty acids and sugars. One hundred and thirty-three SSR (Simple Sequence Repeats) markers were applied for genotyping the panel of 104 peanut genotypes. Association mapping analysis indicated that the four markers (pPGPseq5D5, GM2745, pPGSseq18G1, GM2723) are associated with sensory attributes, while five makers (GM1609, Ah32, pPGPseq2C11, XIP297, Ah3) associated with tocopherols, three makers (GM2690, GM2774, GM2791) associated with fatty acids and two markers (GM2690, GM1609) associated with sugars, respectively. These SSR markers are consistently associated with corresponding traits by four models: Q model, PCA model, Q+K model, and PCA+K model and resulting in a high R2. It is noteworthy that GM1609 and GM2690 are common markers for two traits. These highly associated markers would be used for the development of flavor-desirable and nutrient-rich cultivars in peanut breeding programs after further validation of the markers.</td>
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<td>Affiliation</td>
<td>Auburn University, Auburn, USA, Auburn University, Auburn, China, USDA, Dawson, USA</td>
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<td>NAME</td>
<td>Jimenez, Randi</td>
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<td>Authors</td>
<td>Randi Jimenez, Saarah Kuzay, Mengyuan Xiao, Kimberly Gibson, Jake Uretsky, Stephanie Smolenski Zullo, Travis Parker, Zachary Dashner, Jorge Berny, Nisha Marwaha, Allen Van Deynze, Dina St. Clair, Paul Gepts, Antonia Palkovic, Carol Hillhouse, Raoul Adamchak, Mark Van Horn, Jared Zystro, E. Charles Brummer</td>
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<td>Title</td>
<td>An experiential learning-based public plant breeding pipeline for organic cultivar development: Student Collaborative Organic Plant Breeding Education (SCOPE) at UC Davis</td>
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<tr>
<td>Abstract</td>
<td>AN EXPERIMENTAL LEARNING-BASED PUBLIC PLANT BREEDING PIPELINE FOR ORGANIC CULTIVAR DEVELOPMENT: SCOPE PROJECT at UC Davis. Randi Jiménez1, Saarah Kuzay1, Mengyuan Xiao1, Kimberly Gibson1, Jake Uretsky1, Stephanie Smolenski Zullo1, Travis Parker1, Zachary Dashner1, Jorge Berny1, Nisha Marwaha1,2, Allen Van Deynze1, Dina St.Clair1, Paul Gepts1, Antonia Palkovic1,2, Carol Hillhouse2, Raoul Adamchak2, Mark Van Horn2, Jared Zystro3, and E. Charles Brummer1 1Plant Breeding Center, University of California, Davis 2Agricultural Sustainability Institute, University of California, Davis 3Organic Seed Alliance. Student Collaborative Organic Plant Breeding Education (SCOPE) is a student-led collaborative of student and faculty plant breeders working with local organic growers on improving crop varieties for organic farming systems in Northern California with the possibility of future expansion to other regions. The organic plant-breeding project was developed in direct response to California organic growers, who have reported a scarcity of seeds for cultivars that meet the needs of organic farming systems. Using traditional, field-based plant breeding methods, new varieties of heirloom-like tomatoes, jalapeno peppers, bell peppers, pest resistant common bean and lima bean are being developed on certified organic land at The Student Farm at UC Davis. The breeding objectives of these projects were selected based on input from local organic farmers as well as input from one of the collaborators, the Organic Seed Alliance. In addition to the breeding projects, the students participate in seminars focused around how to conduct outreach activities, organic farming methods, project management as well as participate in Field Days to showcase their work to a broader audience.</td>
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<td>Affiliation</td>
<td>University of California, Davis, Davis, CA, USA, Organic Seed Alliance, Port Townsend, WA, USA</td>
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<td>NAME</td>
<td>Jimenez, Randi</td>
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<td>Poster Number</td>
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<td>Authors</td>
<td>Randi Jimenez, Theresa Hill, Allen Van Deynze</td>
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<td>Title</td>
<td>Utilizing Wild Capsicum annuum Germplasm for Breeding Resistance to Curtovirus (Family: Geminiviridae) in Cultivated Pepper (Capsicum annuum L.)</td>
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<td>Abstract</td>
<td>Utilizing Wild Capsicum annuum Germplasm for Breeding Resistance to Curtovirus (Family: Geminiviridae) in Cultivated Pepper (Capsicum annuum L.) Randi Jiménez1, Theresa Hill1, and Allen Van Deynze1 1University of California-Davis Department of Plant Sciences. Geminiviruses are the largest family of viruses threatening global vegetable production. Additionally, Beet curly top virus (BCTV) is one of the most damaging geminivirus of chili pepper (Capsicum annuum) in the United States that can cause yield losses of 20-80%. BCTV is transmitted by leafhoppers (Circulifer tenellus) and infect a wide range of plants, such as pepper, bean, sugar beet, tomato, cucurbits and spinach. Both the virus and the insect vector continue to be difficult to control. Our goal is to investigate novel germplasm, as well as lines from the literature for resistance to BCTV. To identify sources of resistance, we utilize a rapid Agrobacterium-mediated inoculation assay. Resistance has been confirmed using a leafhopper assay for some of the wild accessions. Several accessions identified as resistant have been crossed into a cultivated, susceptible jalapeño variety to generate and test populations segregating for BCTV resistance and desirable traits. These populations are being used to determine the genetics of BCTV resistance in pepper using a bulk segregant analysis. They have already been used to determine the most likely number of major genes controlling the trait. Our long-term goals are to develop and release pepper breeding lines that combine resistance from wild pepper germplasm to BCTV, as well as to determine the genetic basis of this resistance.</td>
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<td>Affiliation</td>
<td>University of California, Davis</td>
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**Title**: SUSCEPTIBILITY OF DENT-STERILE POPCorns TO THE GA1-M GAMETOPHYTE FACTOR: RISK ASSESSMENT AND OPPORTUNITIES

Zachary Jones, and Major Goodman  
Department of Crop and Soil Sciences, North Carolina State University  
The Ga1-s allele is the foundation of dent-sterile popcorns where it is used as a genetic barrier to prevent pollen contamination, but it’s known genetic susceptibility to another allele at the same locus is problematic for the sustainability of Ga1-s popcorns. The Ga1-m allele overcomes Ga1-s, opening any system using it to potential contamination. The Ga1-m allele, although previously thought rare, has been shown to be abundant in tropical maize. The requirement for specific evaluation to detect the allele creates a considerable risk of the unintentional release of Ga1-m-carrying materials. Through field evaluation, we tested commercial popcorns for resistance to Ga1-m, all of which were uniformly susceptible. There is, therefore, a need to identify and integrate Ga1-m resistance into commercial popcorn breeding materials. To assess the risk of Ga1-m entering US commercial maize through use of tropical germplasm, we screened a set of Germplasm Enhancement of Maize (GEM) lines for the Ga1-m allele. Choice of a replacement gametophytic system should be predicated on the rarity or absence of a corresponding “m-type” allele in commonly used commercial maize backgrounds. Based on this idea, we assessed the gametophytic allele content of the maize NAM founder lines to explore the prevalence of “m-type” alleles of the three most prevalent gametophytic systems to potentially identify any unknown presence of gametophytic alleles.

**Affiliation**: North Carolina State University, Raleigh, USA

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**Title**: QTL MAPPING OF SEED AND SPIKE TRAITS IN TRITICUM CARTHLICUM, A TETRAPLOID WHEAT WITH HEXAPLOID WHEAT SEED MORPHOLOGY

Triticum carthlicum, (Black Persian wheat) has been used as a source of disease resistance for durum and common bread wheat breeding. Triticum carthlicum is a tetraploid that resembles Triticum durum in many ways. It, however, differs in seed shape, having rounded seeds resembling that of bread wheat, and possessing a ‘keel’. The understanding of the genetic control of these traits could facilitate the introgression of large, round seeds into the durum gene pool, as well as correct the archaeobotanical record, as seed shape is often used to discriminate between wheat species grown at a given archeological site. Triticum carthlicum spike morphology also differs from that of durum wheat. Triticum carthlicum possesses a unique awn morphology, having four long awns originating from the outer glumes, whereas durum typically has three awns originating from the inner glumes. The glumes are black. Mapping of these traits could be important, as awns are an important source of photosynthates for the developing seed. To study genetics of these traits, a recombinant inbred line (RIL) population was developed between T. carthlicum and T. durum cv. Langdon, and 224 of them were genotyped with the wheat 90k iSelect Infinium platform. They were field-grown at UC Davis and Intermountain Research and Extension Center in Tulelake, California.

**Affiliation**: UC Davis, Davis, USA

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**Title**: Effect of missing data rates on imputation accuracy using LD-knni method

The aim of association mapping studies is to identify genetic polymorphisms that are responsible for phenotypic variation. Methods that use reduced representation libraries and
multiplex barcoding, such as GBS, while produces large amounts of data aligned with drastically reduced costs, and thus, becoming the choice of many GWAS studies for many different crops, also generates high levels of missing data, which ultimately reflects in a large loss of information. Therefore, imputation methods have become increasingly important with the rising of GBS method. One of such methods, LD-knni use the SNP's that in most LD with the SNP that will be imputed, to measure the genetic distance between genotypes, and with so, greatly increasing imputation accuracy. To investigate the effect that missing data have over imputation accuracy, a GBS dataset consisting of 183 maize inbred lines with 835,525 SNP's was used. Different sub-sets of the original dataset were generated using the minimum count filter, and inside each sub-set, different proportions of masked data (5% to 95%, with increments of 5%) were created following by imputation using LD-knni method with a 1,000,000 Ld window size and 10 as k-nearest neighbours. A graphic analysis of the imputation accuracy implied that ranging from 5% to approximately 30% proportion of missing rate didn't present significant differences. Therefore, for the present dataset, instead of 8,971 SNP's with a 93.05% accuracy, it could be used a dataset with 177,827 SNP's with the same imputation accuracy, greatly increasing the amount of information used for this study.

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<th>Affiliation</th>
<th>North Carolina State University, Raleigh, USA, Universidade Estadual de Maringá, Maringá, Brazil</th>
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<tr>
<td>NAME</td>
<td>Kantar, Michael</td>
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<tr>
<td>Authors</td>
<td>Plant Breeding Coordinating committee (PBCC), Michael Kantar</td>
<td>TU49</td>
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<td>Title</td>
<td>Sustaining the Future of U.S. Plant Breeding</td>
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<tr>
<td>Abstract</td>
<td>Plant breeding is essential to the long-term sustainability of agricultural production to supply the world with food, feed, fiber, fuel, green space, and shelter. The PBCC was established in the federal-state partnership in 2006, to support plant breeding “to solve problems that concern more than one state” (SAES Directors et al., 2006). PBCC’s core membership are representatives of State Agricultural Experiment Stations (SAES) that have plant breeding programs. PBCC seeks to bolster long-term SAES plant breeding programs to (1) educate plant breeders of the future; (2) contribute to breeding methods and germplasm enhancement; and (3) develop cultivars, especially for specialty and commodity crops. PBCC fills unique roles as a working committee and in communicating with USDA and other federal agencies on issues of national importance concerning plant breeding as a voice of the states.</td>
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<th>Affiliation</th>
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<td>NAME</td>
<td>Kantor, George</td>
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<td>Authors</td>
<td>George Kantor, Wenhao Luo, Changjoo Nam, Katia Sycara</td>
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<td>Title</td>
<td>ADAPTIVE ROBOTIC SAMPLING FOR HIGH THROUGHPUT PHENOTYPING</td>
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<td>Carnegie Mellon University Robotics Institute</td>
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<td>Autonomous robots equipped with a variety of sensing technologies have the potential to alleviate the phenotyping bottleneck. Such platforms provide the capability to gather measurements of plants as they grow in the field at higher resolution and larger scale than is currently possible. This poster reviews our prior work in robotic phenotyping, and it describes preliminary efforts and plans for a newly funded NSF/NIFA Cyber-Physical Systems project that is investigating methods of predicting the importance of potential measurements and using those predictions to plan for optimal deployment of robotic phenotyping.</td>
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<th>Affiliation</th>
<th>Carnegie Mellon University Robotics Institute, Pittsburgh, PA, USA</th>
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<td>NAME</td>
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<td>Authors</td>
<td>Stephanie Karhoff, Sungwoo Lee, Rouf Mian, Anne Dorrance, Leah McHale,</td>
<td>TU51</td>
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<tr>
<td>Title</td>
<td>TRANSCRIPTOMIC ANALYSIS OF NEAR-ISOGENIC LINES TO IDENTIFY CANDIDATE GENES FOR MAJOR PHYTOPHTHORA ROOT AND STEM ROT RESISTANCE QTL</td>
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<td><strong>Abstract</strong></td>
<td>Phytophthora root and stem rot is a major yield-limiting disease in soybean [Glycine max (L). Merr.] caused by the soil-borne oomycete Phytophthora sojae. The widespread use of isolate specific Rps genes has led to a shift in pathogen virulence. Thus, there is an increased need for higher partial resistance, which is polygenic and non-isolate specific. Quantitative trait loci (QTLs) are a valuable resource for broad spectrum resistance. However, major QTLs are relatively rare in this pathosystem and the majority of QTLs explain less than 20% of the phenotypic variance. Recently, we identified a major QTL on Chromosome 18 which explains up to 45% of the phenotypic variance. We hypothesize that resistant and susceptible near isogenic lines (NIL) segregating for the QTL will significantly differ in gene expression under inoculated and non-inoculated conditions. We used RNA-Seq to analyze differential gene expression of five resistant and five susceptible NILs 3, 24, and 48 hours after inoculation (hai) to identify candidate genes associated with the major resistance QTL. Differential expression analysis revealed 20 and 59 genes upregulated and downregulated, respectively, in resistant relative to susceptible NILs under inoculated treatment. In total, among all comparisons 71 differentially expressed genes (DEG) are located within the QTL interval, with four unique to the resistant QTL allele. This work will provide candidate genes for further functional analyses and contribute to our growing knowledge of the trait’s genetic architecture. Ultimately, the identification of the gene(s) controlling this QTL will facilitate the use of the resistance source in breeding programs.</td>
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<td><strong>Affiliation</strong></td>
<td>The Ohio State University Translational Plant Sciences Graduate Program, Columbus, USA, Ohio State Center for Soybean Research, Columbus, USA, North Carolina State University Department of Crop Science, Raleigh, USA</td>
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<td><strong>NAME</strong></td>
<td>Kinczyk, Jonathan</td>
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<td><strong>Authors</strong></td>
<td>Jonathan Kinczyk, Kenneth Pecota, Bode Olokulu, Ragy Ibrahim, G. Craig Yencho</td>
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<td><strong>Title</strong></td>
<td>IDENTIFYING KEY PROCESSING TRAITS IN SWEETPOTATO THROUGH GENOTYPING BY SEQUENCING</td>
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<td><strong>Abstract</strong></td>
<td>Sweetpotato (Ipomoea batatas) is one of the fastest growing commodities in the agricultural marketplace. With acreage and interest increasing as consumers become more aware of the nutritional benefits of sweetpotatoes, this trend is sure to continue. While a staple food in many regions of sub-Saharan Africa, the majority of production takes place in China. Likely due to its relative status as a minor crop in European and American markets, there has been little interest in developing genomic resources for crop improvement in sweetpotato. Advances in genomics, however, have opened up new research avenues for this important food crop. The purpose of this research is to identify single nucleotide polymorphisms (SNPs) associated with quantitative trait loci (QTL) for key processing quality traits segregating in progeny of a cross between ‘DM04-001’ and ‘Covington.’ Our mapping population consists of 413 genotypes, and we propose to identify SNPs via genotyping by sequencing (GBS) and conduct high-throughput storage root chemistry phenotyping using near-infrared spectroscopy (NIRS). During Summer 2017, we are planting trials in two separate environments using randomized complete block design with three repetitions. These experiments will be repeated in 2018. Traits targeted for analysis include storage root glucose, fructose, sucrose, beta-carotene, asparagine, dry matter, and starch content. The parents differ significantly for these processing traits and we believe this will allow us to identify SNP markers associated with these traits in the progeny. Future work will likely include marker validation studies and implementation of a marker-assisted breeding program for these important processing quality traits in different materials.</td>
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<td><strong>Affiliation</strong></td>
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<td><strong>NAME</strong></td>
<td>King, Kevin</td>
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<td><strong>Authors</strong></td>
<td>Kevin King, Huang Li, Chaofu Ly</td>
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<td><strong>Title</strong></td>
<td>Mapping Quantitative Trait Loci to Understand Seed Size Variation in Camelina sativa</td>
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<td><strong>Abstract</strong></td>
<td>Kevin King, Huang Li, and Chaofu Lu Department of Plant Science and Plant Pathology, Montana State University</td>
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Camelina sativa (L.) Crantz is an emerging Brassica oilseed crop. Camelina oil is high in polyunsaturated C18-fatty acids, and uses for the oil range from bio-fuels and bio-lubricants to an animal feed additive and cooking oils. A major breeding objective for camelina is to develop varieties with increased seed size. Understanding seed size variation would help breeders develop varieties that are easier to plant and harvest, better for oil processing, and could increase oil yield. For this study, a quantitative traits loci (QTL) map will be identified using a bi-parental recombinant inbred population created between the variety “Suneson”, which has an average seed size of 1.51mm2, and the variety “Pryzeth” with an average seed size of 2.21 mm2. Field trials are being conducted over the next two years in both dryland and irrigated environments in Montana. The aim is to locate areas in the camelina genome that are linked to important agronomic traits including flowering time, seed size, seed weight, and oil content. The results of this study could lead to the marker-assisted breeding of varieties better adapted to fit the needs of Montana farmers.
highly specific environmental conditions necessary for disease development. This complicates selection for tolerant wheat lines, as does the quantitative nature of snow mold tolerance, which involves several major and minor genes. Therefore, marker-assisted selection has the potential to greatly facilitate breeding for snow mold tolerant wheat varieties, by enabling the selection of lines with the most, or most impactful, quantitative trait loci (QTL). The aim of this study is to determine the effectiveness of marker-assisted selection for such quantitative traits as snow mold tolerance in winter wheat. Selected and unselected populations of recombinant inbred lines (RILs), derived from a cross between susceptible and tolerant parents, were compared to determine the effect of marker-assisted selection on population parameters such as tolerance score mean and distribution. Impacts of QTL singly and in combination were analyzed by dividing the RIL population into groups based on which QTL were present. Here we detail the analysis of these comparisons. This knowledge can be used to improve breeding for snow mold tolerance and to better leverage marker-assisted selection of highly-quantitative traits.

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<th>Affiliation</th>
<th>Washington State University, Pullman, USA</th>
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<td>NAME</td>
<td>Lemes, Cristiano</td>
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<td>Authors</td>
<td>Cristiano Lemes da Silva, Allan Fritz, Robert Bowden, Jesse Poland, John Fellers, Yue Jin, Matt Rouse</td>
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<td>Title</td>
<td>Genome-Wide Association Study of Seedling Stem Rust Resistance in a Historical Data of Elite Winter Wheat Lines</td>
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<td>Abstract</td>
<td>Stem rust is a devastating wheat disease with multiple race variations. TTKSK (Ug99) is the most virulent race which defeated several genes deployed in Africa and Asia, representing a threat to wheat production and food security. Hence, wheat breeders and pathologists are constantly evaluating germplasm and elite lines to find genes for durable resistance against stem rust races. This study used 533 unique elite lines from the Southern Regional Performance Nursery that were inoculated in the greenhouse for 34 races of stem rust from 2000 to 2015. The race TTKSK was added to the set of races in 2008. Infection types (IT) were scored in the greenhouse 2 weeks after inoculation using the Stakman scale. ITs were converted into a linear scale (1-9) using a pipeline in Perl and averaged across races, except for TTKSK, which was analyzed separately. All advanced lines were genotyped with GBS and the sequence data were analyzed using a pipeline in Tassel 5 to call and filter SNPs. Markers with ≥50% of missing data and minor allele frequency ≥5% were discarded. The association mapping analysis was conducted with GAPIT using an enhanced compression of the mixed linear model. Due to the high stringency of the significance test used by GAPIT, only two genomic regions located on the short arms of 2A and 2D were significantly associated with stem rust resistance to multiple races at the seedling stage. No significant markers were found associated with TTKSK. Further analysis will be performed to confirm if these candidate genes are novel or already reported in other studies.</td>
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The potato Solanum tuberosum is an important staple crop worldwide. This project aims to facilitate the selection of potatoes with improved composition by developing genetic markers linked to individual, as well as groups of, important metabolites. Methanol extracts of cooked tubers from 206 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, and of these, half were strongly associated with at least one SNP marker by GWAS analysis. Weighted Gene Correlation Network Analysis (WGCNA) was used to cluster individual features, resulting in 27 groups (modules). As several closely related compounds clustered into different modules, it appears that linkage disequilibrium, and not just membership in biochemical or developmental pathways, influences module composition. Regression with module eigenvalues revealed that fourteen modules were significantly correlated with potato chip color and that one of the modules, containing eighty-one features, explained a comparable level of variation to that explained by levels of the reducing sugar glucose.

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**Title**
Dissecting the sea wheatgrass genome to transfer biotic stress resistance and abiotic stress tolerance into wheat

**Abstract**
Wheat production is facing numerous challenges from biotic and abiotic stresses. Alien gene transfer has been an effective approach for wheat germplasm enhancement. Sea wheatgrass (SWG) (Thinopyrum junceiforme, 2n = 4x =28, genomes J1J1J2J2), is a distant relative of wheat and a relatively untapped source for wheat improvement. We have identified high tolerance to waterlogging, manganese toxicity, heat and low nitrogen and resistance to wheat streak mosaic virus (WSMV), Fusarium head blight and wheat stem sawflies (due to solid stem) in SWG. To facilitate simultaneous discovery and transfer of quantitative trait loci (QTL) for the biotic stress resistance and abiotic stress tolerance more efficiently, we are dissecting the SWG genome with two objectives: (1) to develop a draft SWG genome assembly for genome-specific markers; and (2) to construct a SWG chromosome library in wheat consisting of 14 wheat-SWG addition lines. Our long-term goal is to broaden the wheat genetic basis and develop novel germplasm that will contribute to a more sustainable wheat industry. We crossed and backcrossed wheat-SWG amphiploid with wheat and developed large backcross populations, which showed great segregation in plant height, architecture, spike morphology, fertility, and resistance to waterlogging and WSMV. We also isolated DNA from these populations. We have sequenced 40-fold coverage of the SWG genome, and effort is underway to assemble the SWG draft genome, from which SWG-specific markers will be developed and used to genotype backcrossed populations.

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Li Wang, Ming

**Authors**
Ming Li Wang, Brandon Tonnis, David Pinnow, Shyam Tallury

**Title**
Identification of Natural High-Oleate Mutants from the USDA Peanut Germplasm Collection

**Abstract**
Natural genetic variation may exist in plant germplasm collections. Identifying genetic variation may provide useful materials for breeders to develop new cultivars. After screening 8,846 cultivated peanut germplasm accessions by gas chromatography analysis, we identified three natural mutant lines with 80% oleic acid. Two accessions, PIs 342664 and 342666, were originally collected from West Pakistan. The third, PI 162805, was originally collected from Liberia. FAD2A and FAD2B are the two major genes in peanuts coding for a fatty acid desaturase which converts oleic to linoleic acid. Functional mutations in one or both genes can alter the oleate level. By sequencing the coding region of these two genes, we identified a
substitution of G448A in FAD2A and a substitution of C301G in FAD2B for the first two mutant lines. The mutation on FAD2A and FAD2B for PI 162805 were identical to the high-oleate line F435 containing a substitution of G448A on genome A and an “A” insertion on genome B. All of these mutants belong to subspecies hypogaea based on their morphology with no flowers on the main stem; but F435, a previously identified natural high oleate mutant, is classified as subspecies fastigiata since it does have flowers on the main stem. Therefore, we have identified a class of natural mutants from the subspecies hypogaea and provided new genetic resources for breeders to use.
soybean seeds is soyasaponin I. Understanding the genetic control of soyasaponin I accumulation in soybean seeds is an important step toward development of soybean lines with improved soyasaponin profiles. The objective of this study was to identify Quantitative Trait Loci (QTL) associated with the accumulation of soyasaponin I using a population consisting of 186 F4:7 recombinant inbred lines (RILs) derived from the cross of OAC Glencoe and OAC Wallace. The population was grown in two Southern Ontario locations in 2015 and 2016 and the concentration of soyasaponin I in seeds was determined using high-performance liquid chromatography (HPLC). Putative QTL associated with accumulation of soyasaponin I were identified through simple interval mapping (SIM) and composite interval mapping (CIM) on chromosome 10 and chromosome 16 explaining 7 to 11% of the phenotypic variation. Additional QTL were identified on additional seven chromosomes using single-marker ANOVA. The use of marker-assisted selection in the development of soybean lines with improved soyasaponin I profiles may benefit from the QTL regions identified in the present study.

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**NAME**
Mancero, Daniel

**Authors**
Daniel Mancero-Castillo, Jose Chaparro, Philip Harmon, Thomas Beckman

**Title**
A MAJOR LOCUS FOR TOLERANCE TO BOTRYOSPHAERIA DOTHIDEA IN PRUNUS

**Abstract**
A MAJOR LOCUS FOR TOLERANCE TO BOTRYOSPHAERIA DOTHIDEA IN PRUNUS
Daniel Mancero-Castillo, Thomas G. Beckman2, Philip F. Harmon3, José X. Chaparro1
1 Horticultural Sciences Department, University of Florida, FL.
2 USDA-ARS Southeastern Fruit and Tree Nut Research, GA.
3 Department of Plant Pathology, University of Florida, FL
Peach fungal gummosis (PFG) is a vascular disease caused by fungi in the family Botryosphaeriaceae, and this disease has become an important problem for the peach industry in the Southeastern United States since the 1970s. Furthermore, Botryosphaeriaceae species have been associated with outbreaks of new diseases and the emergence of known diseases in more than 1000 plants. The climatic conditions in the Southeastern United States, southern China, South Africa and Western Australia have aggravated the development of the disease. In severe cases, peach tree trunks and limbs are damaged by PFG with an estimated yield reduction of up to 40%. However, there are no effective and suitable cultural or chemical control options. Identification of Botryosphaeriaceae species from diseased Prunus trees found three species in the SE United States. Screening of Prunus germplasm for resistance to Botryosphaeriaspecies was performed in the field and complemented with laboratory assays for four years. A source for genetic resistance was discovered in interspecific crosses and segregating backcross populations using Kansu peach (P. kansuensisRehder), almond [P. dulcis(Mill.) D.A. Webb], and peach [P. persica(L.) Batsch]. The mode of inheritance and closely linked molecular markers to PFG resistance were identified using three F2 segregating populations.

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**NAME**
Marino, Thiago

**Authors**
Thiago Marino, Heather Manching, Randall Wisser, James Holland

**Title**
Genomic selection for Fusarium ear rot and fumonisin resistance in maize

**Abstract**
Fusarium ear rot (FER) is a disease of maize caused by Fusarium verticillioides, which produces fumonisin (FUM), a mycotoxin linked to human and animal health risks. Sources of resistance to FER have been identified, but the resistance is polygenic and difficult to incorporate into elite hybrids. Extensive field trials, laborious inoculation, and expensive antibody assays are required to reliably assess resistances to FER and FUM contamination in breeding populations. Genomic selection (GS) could improve the efficiency of breeding for these complex disease resistance traits by training selection models on a subset of a breeding population and applying them to a larger sample of genotyped but untested lines from the population. This can increase the number of lines screened beyond the limits of field
screening capacity, effectively increasing selection intensity. To evaluate the potential utility of GS in an ongoing maize breeding program, we called 6131 SNPs on 508 S0:1 families from an advanced generation of a recurrent selection program using low coverage sequence. A training set of 263 S0:1 lines was evaluated for FER and FUM at three locations during two years. The remaining 245 S0:1 lines were evaluated as an independent validation set in a subsequent year. Preliminary results have shown that we can obtain high correlations between predicted and true genetic values for FER (>0.5) and FUM (>0.6). This provides evidence that GS is a very promising breeding strategy for Fusarium resistance and can be applied in a recurrent selection breeding program to increase the genetic gain.

**Affiliation**
Department of Crop and Soil Sciences – North Carolina State University, Raleigh, USA,
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**NAME**
Mazourek, Michael

**Authors**
Michael Mazourek

**Title**
Northern Organic Vegetable Improvement Collaborative

**Abstract**
Michael Mazourek1, Rachel Hultengren1, Erin Silva2, Bill Tracy2, Anne Pfeiffer2, Tessa Peters2, Ginny Moore2, Micaela Colley3, Laurie McKenzie3, Jared Zystro3, Joanne Labate4, Lane Selman5, Kara Young5, Ryan King5, Jim Myers5
1Cornell University, Ithaca, NY; 2University of Wisconsin, Madison, WI; 3Organic Seed Alliance, Port Townsend, WA; 4USDA-ARS PGRU, Geneva, NY; 5Oregon State University, Corvallis, OR; and over 30 organic farms in OR, WA, WI and NY

The goal of the Northern Organic Vegetable Improvement Collaborative (NOVIC) is to improve the profitability of organic farmers and the quality of organic produce for consumers through increasing choice in vegetable varieties and availability of certified organic seed. For optimal performance, varieties need to be adapted to organic production systems. The project uses a combination of farmer participatory breeding and trialing at four main locations in NY, WI, WA, and OR with satellite trials in regional farmers’ fields. The crops and traits include sweet corn (cold tolerance, quality), tomatoes (late blight resistance, flavor), sweet peppers (earliness, high yield, flavor), winter squash (short season, disease resistant delicata types) and cabbage (high yielding, good field holding capacity, flavor). NOVIC is in its second 4-year round of funding from OREI. The project has released several varieties that are now sold into over 40 states in the U.S., has trained 8 graduate students in organic/participatory plant breeding, and has held over 80 workshops and meetings with outreach to 19 states. Results have been published in trial reports that are closely followed by organically oriented seed companies and by growers.

**Affiliation**
Cornell University, Ithaca, USA

**NAME**
Mazourek, Michael

**Authors**
Michael Mazourek, Rachel Hultengren, Michael Glos

**Title**
Breeding Research and Education Needs Assessment for Organic Vegetable Growers in the Northeast

**Abstract**
BREEDING RESEARCH AND EDUCATION NEEDS ASSESSMENT FOR ORGANIC VEGETABLE GROWERS IN THE NORTHEAST
Rachel L. Hultengren, Michael Glos, and Michael Mazourek
Cornell University-SIPS-Plant Breeding and Genetics

This work seeks develop a vision for future breeding, research and outreach necessary to support the continued growth of organic vegetable production in the Northeast. In 2015, an electronic survey was sent to organic vegetable growers in the northeastern United States asking them to identify the varieties upon which they depend, the pests that constrain their production, and suggested improvements for future cultivar development work. A working group meeting was held to discuss themes arising from survey results and to identify opportunities for the seed community. The meeting's outcomes were twofold: prioritization of specific traits needed by organic vegetable growers in 18 vegetable crops (see report for full list) and identification of infrastructural challenges and opportunities around the effective delivery of those traits to growers: develop and produce more regionally and organically
adapted cultivars; maintain and improve open-pollinated varieties; expand and strengthen system for simplified and fairly compensated on-farm variety trials; increase education and training opportunities for farmers wanting to produce vegetable seed. A report, along with the survey and anonymized responses were published online through Cornell University’s eCommons and are available at: https://ecommons.cornell.edu/handle/1813/44636. This work was supported by a competitive grant of the Agriculture and Food Research Initiative, National Institute of Food and Agriculture, U.S. Department of Agriculture, under award number 2014-67013-22409.

Affiliation Cornell University, Ithaca, USA

NAME Mazourek, Michael

Authors Christopher Hernandez, Michae Ma

Title GENOMIC ENABLED QUALITY IMPROVEMENT IN BUTTERNUT SQUASH

Abstract GENOMIC ENABLED QUALITY IMPROVEMENT IN BUTTERNUT SQUASH
Christopher Hernandez and Michael Mazourek
Cornell University-SIPS-Plant Breeding

Three main cultivated species of squash Cucurbita pepo, Cucurbita moschata, and Cucurbita maxima are grown worldwide and provide an important nutritious vegetable in our diets. Due to scant genomic resources, progress in squash breeding has been made primarily through phenotypic selection. Our current project seeks to accelerate the production of superior winter squash cultivars through the application of genomic recurrent selection. Mirroring the effective phenotypic selection program, an index for the improvement of multiple fruit quality traits has been implemented in a biparental family derived from two elite butternut squash lines. Results from this analysis suggest that phenotypically correlated fruit quality traits are also strongly genetically correlated. This summer, selected populations will be grown in a multi-environment trial for an evaluation of gain from genomic selection. Concurrently, 3’ RNA-seq has been used to profile gene expression in four squash cultivars from C. moschata and C. maxima that cover the spectrum of fruit quality. Through comparison of gene expression across two key fruit developmental time points within and between cultivars, we have identified gene expression differences that may underlie variation in important fruit quality traits such as Brix, dry matter, starch, sugar, and carotenoid content. Cultivars developed by phenotypic selection are entering the marketplace and tools for vegetable phenotyping have been expanded. This material is based upon work that is supported by the National Institute of Food and Agriculture, U.S. Department of Agriculture, under award number 2013-67013-21232.

Affiliation Cornell University, Ithaca, USA

NAME McCluskey, Rebecca

Authors Shawn Mehlhenbacher, Rebecca McCluskey

Title DEVELOPING EASTERN FILBERT BLIGHT RESISTANT HAZELNUT CULTIVARS USING MODERN TOOLS AND TRADITIONAL BREEDING METHODS

Abstract DEVELOPING EASTERN FILBERT BLIGHT RESISTANT HAZELNUT CULTIVARS USING MODERN TOOLS AND TRADITIONAL BREEDING METHODS
Shawn Mehlhenbacher1 and Rebecca McCluskey1
1Department of Horticulture, Oregon State University

The United States ranks fourth in world hazelnut production, yet it produces only 4.5% of the world crop. Oregon produces 99% of the nuts produced in the United States. Eastern filbert blight (EFB), a fungal disease found only in North America, is devastating to the European hazelnut and threatens commercial production in Oregon. The hazelnut breeding program at Oregon State University has been active since 1969 and currently leads the world in new hazelnut cultivar development. Germplasm has been collected from eastern and western Europe, Asia, Chile, and the United States, and more than 100 new sources of resistance have been identified and incorporated during the breeding program. RAPD and microsatellite markers have been developed for the Gasaway re
NAME | McCluskey, Rebecca
---|---
Authors | Thomas J. Molnar, Josh Honig, Shawn A. Mehlenbacher, Rebecca McCluskey
Title | SECURING AND EXPANDING THE U.S. HAZELNUT INDUSTRY THROUGH BREEDING FOR RESISTANCE TO EASTERN FILBERT BLIGHT
---|---
Abstract | Hazelnuts are a low-input, high-value crop whose demand exceeds current supply. The United States is a significant leader in hazelnut breeding and research, yet US production amounts to <5% of the world's crop. Eastern filbert blight (EFB), a fungal disease found only in North America, is devastating to the European hazelnut, threatening commercial production in Oregon and restricting expansion of plantings in parts of the eastern US. Our research addresses the AFRI Program Area Plant Health and Production and Plant Products in the Priority Area Plant Breeding for Agricultural Production. It includes public breeding efforts to improve crop characteristics and adaptation, develops tools to predict phenotype from genotype to accelerate breeding, and trains graduate students in plant breeding. In this research, we 1) study the inheritance of EFB resistance from several new sources and mapped four of them, 2) characterize the genetic diversity of hazelnut germplasm, and 3) develop enhanced EFB-resistant germplasm to be systematically evaluated in OR and NJ. Joint efforts have identified > 100 sources of EFB resistance. We used simple sequence repeat (SSR) markers to map new EFB resistance genes. Resistance from the Serbian cultivar ‘Uebov’ maps to LG6. Resistance from C. americana ‘Rush’ and ‘Yoder #5’ (an American-European hybrid) maps to LG7, and from a Holmskij (Russia) selection to LG2. Evaluation of a new seed-based germplasm collection from the Republic of Georgia was completed and 79 of 1,394 plants were resistant.
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Affiliation | Plant Biology and Pathology Dept. Rutgers University, New Brunswick, NJ, USA, Dept. of Horticulture, Oregon State University, Corvallis, OR, USA,

NAME | McMahon, Paul
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Authors | Paul McMahon, Gregoire Hummel, Vincent Vadez
Title | FieldScan – a novel semi-field platform to phenotype traits controlling plant water budget
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Abstract | FieldScan – a novel semi-field platform to phenotype traits controlling plant water budget Gregoire Hummel1, Vincent Vadez2. Email: g.hummel@phenospex.com
1Phenospex, Heerlen, Netherlands.2ICRISAT, Patancheru, Telangana, India

We describe the concept and realisation of a high-throughput phenotyping platform (FieldScan) combined with lysimetric capacity, to assess canopy traits affecting water use. The platform is based on a novel 3D scanning technique to capture canopy development, a scanner-to-plant concept to increase throughput (2500 plants/h), and analytical scales to combine gravimetric transpiration measurements. We present how the technology functions, how data are visualised via a web-based interface, and how data extraction and analysis is interfaced through ‘R’ libraries. Close agreement between scanned and observed leaf area data of individual plants in different crops was found (R2 between 0.86 and 0.94). Similar agreement was found when comparing scanned and observed area of plants cultivated at densities reflecting the field conditions. Example of the monitoring, the plant transpiration by the analytical scales is presented. Moreover we present some on-going applications of the platform to target key phenotypes: (i) the comparison of the leaf area development pattern of fine mapping recombinants of pearl millet; (ii) the leaf area development pattern of pearl millet breeding material targeted to different agro-ecological zones; (iii) the assessment of the transpiration response to high VPD in sorghum and pearl millet.

Affiliation | Phenospex, Heerlen, Netherlands, ICRISAT, Patancheru, India,

NAME | Mendonca, Kylie
---|---
Authors | Kylie Mendonca, Lauren Garner
Title | Fruit and Flowering Habit of Mature ‘Wonderful’ Pomegranate (Punica granatum L.)
---|---
**Abstract**

‘Wonderful’ pomegranate’s flowering and fruiting habits are not well understood. Characterizing any relationship(s) between flowering habit and fruit size and quality could lead to effective cultural practices for producing high-value fruit. Five mature ‘Wonderful’ pomegranate trees were monitored every 5-14 days throughout the 2015 growing season. Newly emerged flowers were tagged and characterized with respect to sex (determined by ovary shape and style length at anthesis), clustering habit, age of wood on which floral buds were borne, and direction of wood growth. More than 1,100 hermaphroditic flowers were identified and ovary/fruit diameter was recorded throughout the season. In addition to tagging 1,800 staminate flowers at anthesis, approximately 14,000 abscised staminate flowers were collected and used to estimate total flower number and the ratio of hermaphroditic to staminate flowers. Trees were strip picked at harvest. Fruit weight, maximum hemispheric diameter and exocarp color were recorded. Arils (seeds with a fleshy seed coat) were removed and weighed; aril number was estimated from the weight of 100 arils, and aril titratable acidity and total soluble solids were measured. The age of wood on which flowers were borne was a significant predictor of gender. One-year-old wood produced the highest number of flowers (70% of total) with the smallest proportion of hermaphroditic flowers (5%) for any age of wood. Two-year-old wood produced fewer flowers (19% of total) with 10% hermaphroditic flowers. Wood that was greater than two years old produced 10% of total flowers and 20% were hermaphroditic. Overall, 93% of the flowers were staminate. Despite the low proportion of hermaphroditic flowers produced on one-year-old wood, 57% of marketable sized fruit were produced on one-year-old wood. There were three distinct bloom periods, the first lasting approximately 6 weeks. Bloom time was highly predictive of fruit quality. Late-blooming flowers produced low-quality fruit that were smaller in diameter with fewer arils and poor exocarp color. Such fruit accounted for approximately 13% of total fruit weight. Location within the canopy influenced fruit diameter significantly. Flowering rarely occurred in the typically “closed” interior of the canopy and flowers in the northwest tree quadrant were less likely to be early blooming or hermaphroditic than flowers in other quadrants. The results suggest that development of cultural methods that limit excessive production of staminate flowers, reduce late-season flowering and/or fruit production and/or increase light exposure to fruiting wood could increase the production of high-value fruit for ‘Wonderful’ pomegranate.

**Affiliation**

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**NAME**

Michelmore, Richard

**Authors**

Richard Michelmore, Lien Bertier, Lorena Parra, Maria-Jose Truco, Dean Lavelle, Brett Pike, Daniel Ellison

**Title**

GENE STACKING TO GENERATE MULTI-DISEASE RESISTANT LETTUCE

**Abstract**

Lettuce is an important crop plant that ranks as one of the top ten most valuable crops in the US with an annual value of over $2.3 billion. We have currently mapped 52 phenotypic loci that confer resistance in lettuce to ten diseases. We will clone major genes for resistance to downy mildew and Verticillium dahliae, refine gene editing technology for lettuce, generate gene stacks to combine resistance genes, and in the long term release advanced breeding lines that are resistant to multiple diseases. To isolate the causal resistance genes, we are using contemporary map-based cloning approaches that exploit high throughput sequencing and the availability of the lettuce genome sequence. This involves high-resolution mapping of resistance phenotypes and validation of candidate genes by genome editing. Germplasm will be analyzed to identify allelic variation and to provide a library of accessions with new alleles for resistance. These will be stacked using CRISPR/Cas9-mediated genome editing. This will be part of a pipeline of resistance genes that can be introduced into cultivated
let us from wild germplasm as part of resistance gene deployment strategies to provide durable disease resistance.

**Affiliation**  
University of California, Davis, Davis, USA

**NAME**  
Miller, Tamara

**Authors**  
Tamara Miller, Yayis Rezene, Luseko Chilagane, Susan Nchimbi Msolla, Paul Gepts, Ph.D.

**Title**  
Increasing Angular Leaf Spot resistance of common beans in East Africa by mapping genetic interactions in the Phaseolus vulgaris/Pseudocercospora griseola pathosystem

**Abstract**  
INCREASING ANGULAR LEAF SPOT RESISTANCE OF COMMON BEANS IN EAST AFRICA: MAPPING GENETIC INTERACTIONS IN THE PHASEOLUS VULGARIS/PSEUDOCERCOSPORA GRISEOLA PATHOSYSTEM  
Tamara Miller1, Yayis Rezene2, Luseko Chilagane3, Susan Nchimbi Msolla, Ph.D.4, Paul Gepts, Ph.D.5  
1 University of California – Davis, Department of Plant Sciences  
2 Southern Agricultural Research Institute – Ethiopia  
3 Sokoine University of Agriculture – Tanzania  
4 Sokoine University of Agriculture – Tanzania  
5 University of California – Davis, Department of Plant Sciences  

Common bean (Phaseolus vulgaris L.) production throughout Africa is limited by multiple diseases, foremost of which is Angular Leaf Spot (ALS), caused by the fungus, Pseudocercospora griseola. Identification and pyramiding of multiple host resistance genes into a single genetic background is the most effective means of controlling pathogen proliferation. The Mexican landrace, Mexico 54, is resistant to 94% of ALS races in East Africa and is used as a source of resistance in multiple breeding programs. Construction of reference genomes of three P. griseola races from Latin American and African populations will be performed, followed by population resequencing using Genotyping By Sequencing. Quantitative Trait Locus mapping of a recombinant inbred population derived from crossing Kablanketi and Mexico 54 will be used to identify resistance loci against diverse P. griseola from Ethiopia, Tanzania, Uganda, and Kenya. Gene expression analysis will be used to identify causal loci against specific pathogen races. Finally, markers identified through genetic mapping of the interaction between ALS and its common bean host will be deployed in breeding programs of the African Bean Consortium disease resistance breeding programs.

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**NAME**  
Mills, Cory

**Authors**  
Anthony Leddin, Cory Mills

**Title**  
Plant Breeders Without Borders

**Abstract**  
Plant Breeders Without Borders is the idea that plant breeders could go into developing countries to help farmers harness the new skills of plant breeding. Farmers were the original plant breeders so maybe it is time to go back to the beginning and allow the plant breeders of today to learn some lessons from the past. Farmers could also understand the importance of research and development by looking at the gains that could be achieved by doing just a limited amount of crossing and selection. By strengthening the link between farmers and plant breeders it could lead to a better uptake of newly bred varieties due to the farmers having first hand involvement. The main purpose of this project is to assist in improving quality of life through higher yield and nutrition.

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**NAME**  
Morris, Craig

**Authors**  
Craig F. Morris, Jessica C. Murray, Alecia M. Kiszonas, Jeffrey D. Boehm, Jr., Maria Itria Ibba, Karsta Heinze, Valerie Lullien-Pellerin

**Title**  
End-use quality of soft kernel durum wheat
### Abstract

Kernel texture is a major determinant of end-use quality of wheat. Durum wheat has very hard kernels. We developed soft kernel durum wheat via Ph1b-mediated homoeologous recombination. The Hardness locus was transferred from Chinese Spring to Svevo durum wheat via back-crossing. ‘Soft Svevo’ had SKCS kernel hardness, break flour yield, flour starch damage, and flour particle size similar to soft hexaploid wheat. Soft Svevo had greatly reduced Solvent Retention Capacity (SRC) -water, -carbonate, and -sucrose; whereas SRC-lactic acid was similar to Svevo. Similarly, Mixograph, Farinograph and Alveograph results indicated much reduced water absorption, but similar gluten strength. Cookie diameter of Soft Svevo was markedly larger and similar to soft wheat. The energy required to produce flour was dramatically reduced, one-quarter that of Svevo. When Soft Svevo was crossed to 10 CIMMYT durum parents, half-sib families and full-sib lines within families showed significant differences in SKCS hardness, break flour and total flour yields, starch damage, SRC-water, -carbonate, -sucrose, and -lactic acid, and flour SDS sedimentation volume. Cookie diameters ranged from 8.68 to 9.57 cm. Mean bread loaf volumes for families ranged from 680 to 838 cm³. Results illustrate the significant effect of the Puroindoline genes and the Hardness locus on kernel texture and end-use quality, and demonstrate that soft kernel durum wheat has properties similar to soft hexaploid wheat. Further, the hard durum parent has a significant effect on end-use quality traits by contributing superior alleles for soft wheat milling, flour properties, dough and bread quality.

### Affiliation

USDA-ARS Western Wheat Quality Laboratory, Pullman, USA, Washington State University, Pullman, USA, UMR IATE, CIRAD INRA, Montpellier, France

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### NAME

Motes, Brian

**Title**

A New, Late Maturing Crabgrass Cultivar for the Southern USA

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### Affiliation

Noble Research Institute, LLC, Ardmore, USA

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### NAME

Mugabe, Deus

**Title**

Identification of quantitative trait loci associated with cold tolerance in an interspecific chickpea recombinant inbred line population

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### Abstract

Chickpea, Cicer arietinum L., is one of the oldest grain legumes in modern agriculture and is grown in more than 50 countries. The seeds are rich in carbohydrates, minerals, and protein. Increases in production are slowed by several abiotic and biotic stresses. In regions with Mediterranean climates that have mild winters, yields can almost double when chickpea is planted in the fall rather than the spring. However, there are no cultivars that can successfully overwinter in regions with harsher Continental climates. This project focuses on understanding the genetic basis of cold tolerance in chickpea. The objectives are to identify QTL and genomic regions associated with cold tolerance. An interspecific recombinant

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### Affiliation

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### NAME

Motes, Brian

**Title**

A New, Late Maturing Crabgrass Cultivar for the Southern USA

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Noble Research Institute, LLC, Ardmore, USA

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Mugabe, Deus

**Title**

Identification of quantitative trait loci associated with cold tolerance in an interspecific chickpea recombinant inbred line population

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### Abstract

Chickpea, Cicer arietinum L., is one of the oldest grain legumes in modern agriculture and is grown in more than 50 countries. The seeds are rich in carbohydrates, minerals, and protein. Increases in production are slowed by several abiotic and biotic stresses. In regions with Mediterranean climates that have mild winters, yields can almost double when chickpea is planted in the fall rather than the spring. However, there are no cultivars that can successfully overwinter in regions with harsher Continental climates. This project focuses on understanding the genetic basis of cold tolerance in chickpea. The objectives are to identify QTL and genomic regions associated with cold tolerance. An interspecific recombinant

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### Affiliation

ARS Western Wheat Quality Laboratory, Pullman, USA, Washington State University, Pullman, USA, UMR IATE, CIRAD INRA, Montpellier, France

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### NAME

Motes, Brian

**Title**

A New, Late Maturing Crabgrass Cultivar for the Southern USA

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### Affiliation

Noble Research Institute, LLC, Ardmore, USA

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### NAME

Mugabe, Deus

**Title**

Identification of quantitative trait loci associated with cold tolerance in an interspecific chickpea recombinant inbred line population

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### Abstract

Chickpea, Cicer arietinum L., is one of the oldest grain legumes in modern agriculture and is grown in more than 50 countries. The seeds are rich in carbohydrates, minerals, and protein. Increases in production are slowed by several abiotic and biotic stresses. In regions with Mediterranean climates that have mild winters, yields can almost double when chickpea is planted in the fall rather than the spring. However, there are no cultivars that can successfully overwinter in regions with harsher Continental climates. This project focuses on understanding the genetic basis of cold tolerance in chickpea. The objectives are to identify QTL and genomic regions associated with cold tolerance. An interspecific recombinant
An inbred line (RIL) population was evaluated for cold tolerance in field and controlled conditions and was genotyped using genotyping-by-sequencing (GBS). The RIL population, developed from the cross ICC 4958 / PI 489777, is F6-derived and consists of 129 lines. ICC 4958 is a cold sensitive desi type (C. arietinum); PI 489777 is a cold tolerant wild relative (C. reticulatum). The field evaluations were conducted at two locations with different winter conditions; Central Ferry, WA (46.63 N; 117.49 W; 195 m asl) and the Washington State University Spillman Research Farm, Pullman, WA (46.73 N; 117.17 W; 720 m asl).

Assessment of cold tolerance was based on stand counts and leaf damage, both assessed in late autumn and again in early-spring. A freezing experiment in controlled conditions will provide additional cold tolerance data for specific growth stages. Preliminary data indicate that post-winter plant leaf damage is highly correlated to mean spring stand count.

Affiliation | Washington State University, Pullman, USA
---|---
**NAME** | Murray, Seth
**Authors** | Seth C. Murray, Sorin Popescu, Dale Cope, Lonesome Malambo, Nathália Cruzato, Steven Anderson, Colby Ratcliff
**Title** | AERIAL AND GROUND PHENOTYPING ANALYTICAL TOOL DEVELOPMENT FOR PLANT BREEDERS USING THE MAIZE G2F PROJECT
**Abstract** | High throughput field phenotyping (HTFP) using unmanned aerial vehicle (UAV) or ground vehicle (GV) systems, equipped with sensors, are promising tools for breeders and geneticists to characterize germplasm and improve genotype-to-phenotype relationships. We have collected and analyzed temporal fixed-wing and copter UAV and GV data, in maize breeding plots, throughout the past two years. This identified gaps in scale, knowledge and tools for plant breeders to use sensing data in actionable decisions (e.g. automating plot boundary extraction, outlier detection). Here we will develop and test novel analytical and visualization tools for HTFP data, and deploy these tools for field breeding and genetics programs. Using the US-wide Genomes to Fields GxE experiment (G2F-GxE), grown under three abiotic stress levels (temperature and moisture), temporal plant height growth curves will be developed with HTFP to identify germplasm (and alleles) with differential tolerance of stressors; in addition to investigating other HTFP measurements. Strong positive correlations between terminal plant height and yield, previously identified in commercial and breeding hybrids in Texas, are likely due to vigor and stress tolerance, not maturity or shading. Temporal HTFP will identify different types of stress tolerance across genotypes to pyramid for development of more stress tolerant maize. The primary outputs of this project will be analysis and visualization methodology for HTFP, developed and deployed within the statistical computing environment ‘R’, and improved characterization of the maize G2F experiment.

Affiliation | Texas A&M University - Department of Soil and Crop Sciences, College Station, USA, Texas A&M University - Department of Ecosystem Science and Management, College Station, USA, Texas A&M University - Department of Mechanical Engineering, College Station, USA
**NAME** | Mutschler-Chu, Martha
**Authors** | Martha A. Mutschler, John R. Smeda, Andre Kessler, Anthony Schilmiller, Diane Ullman, Hugh Smith, George Kennedy
**Title** | Prebreeding Tomato For Optimized Acylsugar-Mediated Resistance To Insects
**Abstract** | Acylsugars produced by the wild tomato Solanum pennellii control major pests of tomato. Prior breeding created the first tomato lines producing acylsugar levels impacting major pests. Testing tomato lines producing different levels of the same acylsugars showed the importance of acylsugar level. Work with diverse acylsugars extracted from different S. pennellii accessions demonstrated that different acylsugar chemotypes also vary in efficacy. So alteration of acylsugar level and or of acylsugar chemotypes are both possible breeding approaches for optimizing insect control.

Using the benchmark line CU071026, tomato lines were bred that possess additional S. pennellii introgressions containing QTL that impact fatty acid components of acylsugars; these lines vary for the fatty acid profiles and complexity of their acylsugars. Three QTL
impacting acylsugar sugar moiety (glucose vs sucrose) were transferred creating an acylglucose producing tomato line. Lines with additional QTL impacting acylsugar level were also created by addition of acylsugar level QTL. Cooperative multi-state experiments demonstrated the efficacy of specific acylsugar breeding lines with increased acylsugar level or modified acylsugar chemotype against insects. Continued work to support the use of acylsugar mediated insect resistance in cultivated tomato includes: a) determining the types/levels of acylsugar that provide optimal control of targeted major pests to refine breeding goals. b) improving horticultural type of acylsugar lines by breaking thee linkage drag affecting fruit set/size.

Affiliation
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NAME
Neupane Adhikari, Sudha

Authors
Sudha Adhikari, Melanie Caffe-Treml, Jixiang Wu

Title
ACCURACY OF GENOMIC PREDICTION MODELS FOR MAJOR OAT MILLING AND NUTRITIONAL QUALITY TRAITS

Abstract
Oats can lower cholesterol, reduce risks of type-2 diabetes, and help prevent heart diseases when consumed daily. Therefore, it is important to evaluate and select breeding lines with desirable milling and nutritional quality traits. Genomic selection, which consists in using genotyping data to predict the breeding value of an individual, is a promising method to increase genetic gain by selecting for quality traits earlier in the line development process. In this study, we collected phenotypic data for test weight, thousand kernels weight, groat percent, percent plumps, percent thins, and beta glucan, protein, and fat content on grain samples from 227 oat genotypes grown at four locations in South Dakota in 2015. All 227 lines were genotyped with genotyping by sequencing. Genomic selection models were developed using five methods (RRBLUP, GAUSS, PLSR, Elastic Net, and Random Forest). Among the different milling and nutritional quality traits evaluated, prediction accuracy was highest for percent thin (0.56-0.78), percent plump (0.63-0.70), and fat content (0.50-0.69), while lowest for beta glucan (0.22-0.49), and test weight (0.23-0.56). Among these five methods, Random Forest resulted in higher prediction accuracy for most traits. For example, the average prediction accuracy for fat and beta glucan content obtained by Random Forest was 0.76 and 0.51, respectively, whereas those by the other four methods ranged from 0.56-0.75 and 0.41-0.48. Our results suggested that genomic selection offers a valuable strategy to improve genetic gain for major milling and nutritional quality traits in oats.

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NAME
Nguyen, Andy

Authors
Andy Nguyen, Cecilia Agüero, M. Andrew Walker

Title
Inheritance of GFLV Resistance in a 101-14 x Trayshed Population

Abstract
Grapevine fanleaf virus (GFLV) causes fanleaf degeneration, one of the most economically severe diseases affecting grapevines worldwide. The disease can result in crop losses of up to 80% by greatly reducing fruit set and causing formation of ‘shot berries,’ or very small seedless berries. Muscadinia rotundifolia, a North American grape species, has previously been shown as a valuable source of GFLV resistance. However, very little is known about the inheritance of this resistance. The objective of this work is to quantify GFLV resistance in a select number of individuals resulting from a cross between 101-14 Mgt. x Muscadinia rotundifolia cv. Trayshed to study the inheritance of this trait. For GFLV inoculation, 2-node cuttings of GFLV-infected Vitis vinifera cv. Cabernet Sauvignon obtained from a vineyard in
Rutherford, CA were grafted onto hardwood cuttings from 50 individuals of the 101-14 x Trayshad population. Approximately four months after grafting, the roots of the surviving plants were assayed for GFLV using RT-qPCR. We will present results of GFLV concentrations in the different genotypes and our preliminary findings on the inheritance of GFLV resistance from M. rotundifolia.

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NAME
Park, Jaebum

Authors
Jaebum Park, Walter DeJong

Title
MAPPING RESISTANCE IN TETRAPLOID POTATO FOR RESISTANCE TO Globodera rostochiensis PATHOTYPE Ro2

Abstract
MAPPING RESISTANCE IN TETRAPLOID POTATO FOR RESISTANCE TO Globodera rostochiensis PATHOTYPE Ro2
Jaebum Park1 and Walter S. DeJong1
1 Cornell University School of Integrative Plant Science Plant Breeding and Genetics Section
The golden cyst nematode (Globodera rostochiensis) is a serious pest that can dramatically reduce potato crop yield. Pathotype Ro2 of G. rostochiensis was first discovered in Long Island & South Lima, NY in 1994. Although the widely deployed H1 resistance gene is highly effective against pathotype Ro1, it is not effective against Ro2. To map Ro2 resistance gene(s), 195 F1 clones and their parents (NY121 Ro2 resistant and NY115 Ro2 susceptible) were genotyped with the SolCAP 8303 SNP chip and the resistance of each clone was assessed.

Affiliation
Cornell University, Ithaca, USA

NAME
Parker, Travis

Authors
Travis Parker, Paul Gepts

Title
IDENTIFICATION OF LOCI ASSOCIATED WITH RAPID EARLY SEASON GROWTH RATE IN COMMON BEAN

Abstract
IDENTIFICATION OF LOCI ASSOCIATED WITH RAPID EARLY SEASON GROWTH RATE IN COMMON BEAN
Travis Parker1 and Paul Gepts1
1University of California-Davis Department of Plant Sciences
Vigorous early season growth rate improves weed competitiveness and reduces the amount of labor required for manual weeding in many species. This has made it a major area of focus for plant breeders. Despite this, genetic improvement has been been hindered by the complex genetic basis for the trait and the difficulties associated with its precise evaluation. Using a novel sUAS based high-throughput phenotyping approach, we generated growth curves for each of the 280 member Middle American Diversity Panel of common bean developed by BeanCAP. Association mapping identified several loci in linkage disequilibrium with early season growth rate in the population. These markers could be used for rapid and efficient marker assisted selection to improve the weed competitiveness of common bean.

Affiliation
UC Davis Department of Plant Sciences, Davis, USA

NAME
Patel, Takshay

Authors
Takshay Patel, Todd Wehner

Title
Identification of new resistance sources and SNPs markers in watermelon for anthracnose (Colletotrichum orbiculare)

Abstract
IDENTIFICATION OF NEW RESISTANCE SOURCES AND SNPS MARKERS IN WATERMELON FOR ANTHRACNOSE
Takshay Patel, Todd Wehner
North Carolina State University Department of Horticultural Science

Anthracnose (Colletotrichum orbiculare) is reappearing as a major problem on watermelon (Citrullus lanatus). The latest resistance gene, Ar-2-1, to watermelon anthracnose was identified in 1959 is still durable today. The goals of this study are to find new and higher resistance sources to C. orbiculare races 1 and 2, and develop single nucleotide
polymorphism (SNP) markers. The available watermelon germplasm collection of 1408 PI accessions was screened for resistance to anthracnose races using seedling (greenhouse) and flowering stage plants (field). All accessions were also sequenced using genotyping-by-sequencing (GBS) protocol. We are finishing the greenhouse study and have found potential new resistance sources for each anthracnose race. A GWAS analysis will be performed using the GBS data and disease resistance data to identify SNPs and candidate loci for anthracnose R-genes. A bulk segregation analysis will be used to annotate the R-genes using an F2 population from a cross of resistant (PI 189225) and susceptible (New Hampshire Midget) parents. SNP data from the watermelon accession panel will help in the development of resistant cultivars using the new sources of resistance.

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<th>Affiliation</th>
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<td>NAME</td>
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<td>GENOME SURVEY AND FIRST HIGH-DENSITY GENETIC LINKAGE MAP OF NAPIERGRASS (Pennisetum purpureum)</td>
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| Abstract                  | GENOME SURVEY AND FIRST HIGH-DENSITY GENETIC LINKAGE MAP OF NAPIERGRASS (Pennisetum purpureum)
Dev Paudel, Baskaran Kannan, Fredy Altpeter and Jianping Wang
University of Florida, Agronomy Department

Napiergrass (Pennisetum purpureum Schumach) is one of the highest yielding tropical forage grass and a promising lignocellulosic biofuel feedstock owing to its high biomass, nutritive value, and yield. However, its utilization for breeding has been lagging other crops due to limited genomic studies and unavailability of reference genome and linkage maps. In this study, next-generation sequencing approach was used to carry out the genome survey and to construct a high-density linkage map of napiergrass for the first time. Genome sequence of napiergrass showed high synteny to the genome of pearl millet which could be used as a reference genome for mapping in napiergrass. For the linkage map, 1,917 markers were grouped into 14 linkage groups spanning a length of 1473.94 cM and a density of 1 marker per 0.76 cM. Using multiple programs (TASSEL, GBS-SNP-CROP, STACKS, Freebayes, Samtools, and GATK) for de-novo and reference based SNP identification, we present the first genetic map of napiergrass which can be used for genome assembly, genetic improvement of napiergrass, and comparative genomics research. QTL analysis for various yield related traits are underway.

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<th>Affiliation</th>
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<td>NAME</td>
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<td>Authors</td>
<td>Brian Pfeiffer, William Rooney</td>
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<td>Title</td>
<td>WHAT'S CHANGING FROM 55 YEARS OF SORGHUM BREEDING?</td>
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| Abstract                  | WHAT'S CHANGING FROM 55 YEARS OF SORGHUM BREEDING?
Brian K. Pfeiffer1, William L. Rooney1
1Texas A&M University Department of Soil & Crop Sciences
Estimating genetic gains in sorghum [Sorghum bicolor (L.) Moench] is necessary to review past and present research and to determine whether the current rates of improvement will meet future production demands. Defining the rate of yield gains has a profound impact on growers, land owners, input suppliers, scientists, investors, policy makers and others. This study was conducted to determine the rate of genetic gain in yield and associated traits in grain sorghum over the past 50--60 years. A panel of sixty hybrids representing 50+ years of hybrid breeding and their respective parental lines from the Texas A&M AgriLife Research Sorghum Breeding Program and fourteen historical DuPont Pioneer hybrids were grown and evaluated across Texas in 2016.
Based on data from these trials, grain sorghum yields have increased .008 t ha--1 annually in the both the Texas A&M and DuPont Pioneer sorghum breeding programs. Traits associated with yield including yield potential per plant, heterosis, test weight, panicle size, and grain number per panicle have also increased from long—term selection. Other traits such as leaf
angle, days to maturity, plant height and yield stability had little to no change. The portion of yield gains in sorghum production attributed to plant breeding was 61%.

Compared to other field crops, the rate of genetic gain in sorghum has been slower. Reasons to explain the slower gains include changes in production environments, shifts in trait priorities, reductions in research and development, and less than optimized heterotic groups. Despite a plurality of reasons for why the rate of genetic yield gains is slower in sorghum, emerging technologies in sorghum breeding (i.e., doubled haploids, genomic selection) could lead to future increases.

Affiliation | Texas A&M University, College Station, USA
---|---
NAME | Phillips, Doug
Authors | Doug Phillips, Patricio Munoz
Title | Heritability and Trait Segregation for Anthracnose Susceptibility in Southern Highbush Blueberry
Abstract | The success of Florida blueberry growers is due in large part to the development of southern highbush blueberry (SHB) cultivars that need significantly less chilling hours for fruit production than typical temperate cultivars. However, the humid summer conditions that also occur with the subtropical climate often result in a high degree of disease incidence and severity. Anthracnose, caused by the Colletotrichum fungal pathogen, is a disease typically associated with postharvest fruit rots, but can also produce stem lesions and dieback in susceptible cultivars. This disease has recently been reported on two cultivars (‘Flicker’ and ‘Scintilla’) grown primarily in central Florida; the degree of susceptibility of other cultivars is currently unknown. The objectives of this research are to screen several blueberry cultivars commercially grown in Florida for susceptibility to anthracnose, develop a laboratory assay that can be used to rapidly screen breeding selections, and inoculate seedling populations with a known susceptible parent to test for heritability of the susceptibility trait. Future work will identify molecular markers associated with susceptibility to allow for identification and selection of non-susceptible parents. The screening for anthracnose susceptibility will be performed using a spray inoculation of a virulent Colletotrichum isolate onto both whole plants and detached stems, followed by measurement of incidence and severity of disease over time. Non-inoculated control plants will be utilized to account for any latent infection present in the plant material. Heritability estimation for anthracnose susceptibility will be accomplished by inoculating multiple bi-parental populations using susceptible and assumed-resistant parents.

Affiliation | University of Florida, Balm, USA, University of Florida, Gainesville, USA
---|---
NAME | Piaskowski, Julia
Authors | Julia Piaskowski, Craig Hardner, Lichun Cai, Yunyang Zhao, Amy Iezzoni, Cameron Peace
Title | Cross Assist: on online tool for predicting progeny distribution in a new cross for multiple correlated traits in sweet cherry
Abstract | Plant breeding is a numbers game in which thousands of genetically distinct individuals are generated, largely through crosses, and most of those are discarded. This step is particularly costly for tree fruits because they are expensive to grow and have a long juvenility period. Selection of superior individuals requires a desirable population mean and sufficient genetic variation of the target traits to maximize the probability of obtaining a superior segregant. There are currently no easy-to-use tools for predicting the performance of new biparental crosses in outcrossing crops. Furthermore, these methodologies predict the progeny distribution for a single trait only. We have developed on online tool for predicting the distribution of F1 of a biparental cross of sweet cherry across multiple correlated traits. We used genome enabled approaches to estimate the breeding values and genetic variance of the RosBREED sweet cherry Crop Reference Set representing the foundational germplasm of sweet cherry in North America. Using breeding values of the parents, the population-wide genetic variance and genetic covariance across traits, an F1 population is simulated using the multivariate normal distribution. Several approaches will be tested for predicting the genetic variance of a new cross: the gametic model and modeling the segregation of alleles. The accuracy of this tool will be tested on cherry and apple full sib families. A prototype of this
tool is currently available online. This software allows users to predict the mean and genetic variance of a new cross across several traits, apply selection thresholds and calculate the probability of obtaining an individual meeting thresholds for all traits. This tool will help breeders of heterozygous outcrossing crops find cross combinations which maximize the probability of producing a superior individual.

Affiliation  Washington State University, Pullman, USA

NAME  Poorten, Thomas

Authors  Thomas Poorten, Glenn Cole, Steven Knapp

Title  Genealogical Reconstruction and Pedigree Authentication in Strawberry Using Genome-Wide DNA Profiling and Inferred Identity-by-Descent

Abstract  Challenges arise in genealogical reconstruction, germplasm conservation, breeding, sexual and asexual propagation, and intellectual property protection in plants where individuals, parents, and more distant relatives need to be identified, pedigrees need to be authenticated, and unknown pedigrees need to be ascertained. Highly accurate and robust statistical methods have been developed for inferring identity-by-descent (IBD) from DNA profiles. The present study was undertaken to assess the accuracy of these methods when applied to the problems of estimating genetic relationships, authenticating pedigrees, and inferring unknown pedigrees in octoploid (2n = 8x = 56) garden strawberry (Fragaria x ananassa). DNA profiles were produced by genotyping 1,539 individuals in the University of California and United States Department of Agriculture germplasm collections with 38,000 single nucleotide polymorphisms utilizing an Affymetrix Axiom Array. Genealogical records were available for 1,249 of the genotyped individuals, of which we collected genotype data for the focal individual and both parents in 522 cases. By estimating IBD statistics, 92.7% of the parents of individuals with pedigree records were verified. The fraction with unverified parentage (7.3%) was attributed to inaccurate pedigree records and uncertain provenance of samples over repeated cycles of asexual propagation in clonal germplasm preservation. For individuals lacking pedigree records, 70.3% of the probable parents were identified, thus vastly improving the completeness of the genealogies of individuals preserved in the germplasm collections surveyed. These analyses demonstrated the utility and accuracy of pedigree authentication and genealogical reconstruction in octoploid strawberry by inferring IBD from high-density genome-wide DNA profiles.

Affiliation  University of California, Davis, Davis, CA, USA

NAME  Qin, Xiaoqiong

Authors  Xiaoqiong Qin, Meilian Tan, Diana Burkart-Waco, Yosuke Moritama, Tim Wills, Xiuwen Huo, Sergio Silva, Angel Fernandez, Roger Chetelat

Title  DEVELOPMENT OF SOLANUM SITIENS INTROGRESSION LINES TO ACCELERATE THE USE OF CROP WILD RELATIVES FOR TOMATO IMPROVEMENT

Abstract  The gene pool of cultivated tomato (Solanum lycopersicum) has been improved by the introgression of genes from related wild species. Yet modern cultivars lack certain key traits such as tolerance to drought and high temperatures, and resistances to emerging diseases. The wild tomato relative Solanum sitiens, a species endemic to the Atacama Desert of Chile, grows under conditions of extremely limited rainfall, low temperatures, and high soil salinity. Until recently, strong breeding barriers prevented its hybridization and introgression with cultivated tomato. We bypassed these barriers using a ‘pseudo-double cross hybrid’ breeding strategy. The main objective of our research is to develop an introgression line (IL) population that captures the genome of S. sitiens in the genetic background of cultivated tomato. Approximately 75 ILs have been developed, each containing a single S. sitiens chromosome segment. The IL set together captures all 12 S. sitiens chromosomes except for the short arm of chromosome 6. While many lines are homozygous, others must be propagated through heterozygotes due to hybrid sterility and interspecific incompatibility loci. As a whole, the ILs exhibit extreme phenotypic variation for most traits, reflecting the wide phylogenetic distance between the parents, as well as a number of novel traits not seen in either parent. The crossover breakpoints of each segment will be precisely mapped by
GBS (Genotyping By Sequencing). This IL population should be a useful resource to study abiotic stress tolerances and other unique traits present in this wild nightshade, and to incorporate these traits into improved cultivars.

Affiliation: UC Davis, Davis, USA

NAME: Rahman, Mohammad

Authors: Mohammad Rahman, Naresh Barma, Jesse Poland

Title: SCOPE OF WHEAT PRODUCTION AND IMPROVEMENT IN BANGLADESH

Abstract: Wheat is the second most important cereal crop after rice in Bangladesh and its consumption increasing by more than 10% in recent years. The crop is subjected to various abiotic and biotic stresses with terminal heat stress as the greatest constraint. Recently the discovery of wheat blast, caused by Magnaporthe oryzae, poses significant additional challenges for wheat breeding and production. The Wheat Research Center (WRC) under Bangladesh Agricultural Research Institute (BARI) is the organization in Bangladesh tasked with wheat improvement. Using traditional breeding methods it usually takes 12 to 15 years to develop and release a new wheat variety. Classical breeding assisted with molecular breeding will accelerate the improvement. With the conjunction of low cost new high-throughput genotyping technologies and more routine statistical methods the genomic selection can greatly accelerate the breeding cycle and thus genetic gain beyond what is possible with phenotypic selection. Our objectives are - to harness genetic resources for wheat improvement through systematic characterization and use of genetic diversity to accelerate breeding gains to address climate change issues, - develop high-throughput phenotyping system and genomic selection models to identify useful alleles/traits for stress tolerance and rapidly make predictions and selections of the most promising candidate wheat varieties. In this context, breeding heat and drought tolerant cultivars, and developing new technologies comparable with those in more advanced countries in collaboration with various national and international organizations (i.e. CIMMYT, ICARDA, ICRISAT, CIDA, AusAID, USAID) are most important.

Affiliation: Kansas State University, Department of Plant Pathology, Manhattan, USA, Bangladesh Agricultural Reseasrch Institute, Jamalpur, Bangladesh, Bangladesh Agricultural Resesarch Institute, Joydebpur, Bangladesh

NAME: Rahman, Mukhlesur

Authors: Mukhlesur Rahman, Danielle Fiebelkorn

Title: STUDIES OF FREEZING TOLERANCE OF RAPESEED/CANOLA (Brassica napus L.)

Abstract: STUDIES OF FREEZING TOLERANCE OF RAPESEED/CANOLA (Brassica napus L.)
Mukhlesur Rahman and Danielle Fiebelkorn
North Dakota State University Department of Plant Sciences, Fargo, ND

Freezing temperature/frosts can cause significant damage of plants by rupturing plant cells. Rapeseed/canola (Brassica napus) is susceptible to freezing temperature at early seedling stage. Different freezing tolerance studies on rapeseed/canola germplasm accessions have been conducted in the laboratory, controlled plant growth chamber, and field. The phenotyping data were aligned with genotyping data obtained from genotyping-by-sequencing. Genome-wide association study (GWAS) was conducted on each of the three experiments separately to identify potential markers/genes those were related to frost tolerance traits. The laboratory study identified 12 QTL located on 11 chromosomes A01, A02, A03, A04, A05, A07, A10, C01, C01_rand, Cnn_rand, and Unn_rand of Brassica napus. The controlled plant growth chamber study identified one QTL on chromosome A02, while the field study also identified one QTL on chromosome C04. All the GWAS studies identified several orthologs of the functional candidate genes involved in freezing/cold tolerance, abiotic stress tolerance, and transcription factors.

Affiliation: North Dakota State University, Fargo, USA

NAME: Rainey, Katy

Authors: Katy Rainey, Keith Cherkauer
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<th>Title</th>
<th>Development of Analytical Tools for Drone-based Canopy Phenotyping in Crop Breeding</th>
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<td>Katy Martin Rainey1, and Keith Cherkauer2</td>
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<td>1Purdue University Department of Agronomy</td>
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<td>2Purdue University Department of Agricultural and Biological Engineering</td>
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| Abstract | Characterization and selection of phenotypes acquired from image analysis represents a low-hanging fruit for genetic improvement of yield potential in crops. In contrast to point or plant based spectral reflectance, image analysis allows direct measurement of spatial or field based traits that are known to be valuable, such as canopy coverage and vegetation indices, collected from the field with high-throughput platforms such as unmanned aircraft systems (UAS) (Cabrera?Bosquet et al. 2012, Liebisch et al. 2015). When applied to breeding pipelines, such phenomic tools are most effective when they overcome bottlenecks created by the limited quality, quantity, and reliability of phenotypic information, such as for early-season and early-generation selection. In addition, metrics derived from UAS imagery can increase the accuracy of yield estimation in advanced yield trials, and provide precision metrics for marketing. Since 2014, our team has been using UAS-based phenotypes in a soybean breeding pipeline and for association mappings and in 2017 we initiated a project to develop more analytical tools for multi-environment data. Preliminary rests are promising for use of canopy parameters for selection of soybeans in early generations. We also present some of our existing analytical tools, and progress for those under development. |

| Affiliation | Purdue University Agronomy Department, West Lafayette, USA, Purdue University, West Lafayette, USA |

| NAME | Rashed, Arash |

| Authors | Karin Cruzado, Mahnaz Rashidi, Nora Olsen, Erik Wenninger, Richard Novy, Arash Rashed |

| Title | Identification of resistance to zebra chip diseases in species-derived germplasm and international potato cultivars for use in the development of zebra chip resistant and tolerant potato cultivars for the U.S. |

| Abstract | Zebra Chip (ZC) disease has a negative impact on commercial potato production in the Americas and New Zealand. ZC has been associated with the bacteria “Candidatus Liberibacter solanacearum” (Lso) that is transmitted by the potato psyllid (Bactericera cockerelli). The disease reduces potato yield and quality of tubers. Development of ZC-resistant potato cultivars would be a significant step that could lead to establishing an integrated, and a relatively more sustainable, management strategy. The aim of the present study was to identify sources of resistance to Lso and/or its potato psyllid vector, by screening several potato genotypes. Greenhouse (12 potato genotypes) and field (8 potato genotypes, with 5 overlapping with greenhouse) experiments were set up to initiate the screening process. Lso transmission success, Lso titer (qPCR), and ZC symptom severity in fresh cut tubers were quantified. Significant variation in transmission success was observed among the 12 genotypes studied in the greenhouse, with A07781-3LB having the lowest rate of successful Lso transmission. Overall, A07781 siblings expressed relatively lower susceptibility to Lso (lower titer), and/or higher tolerance to ZC (lower symptom expression), than other genotypes, a pattern consistent between field and greenhouse trials. The commercial varieties, Western Russet and Russet Burbank were classified as relatively less susceptible, but intolerant to ZC. Comparisons of relative tolerance and resistance during storage are currently ongoing and will be presented. Based on findings to date, the Solanum chacoense-derived A07781 clones appeared to be promising candidates for use as parental material by breeding programs for the development of ZC-resistant varieties. |

| Affiliation | University of Idaho, Dept. Entomology, Plant Pathology and Nematology, Aberdeen, USA, Plant Science, Kimberly, USA, University of Idaho, Dept. Entomology, Plant Pathology and Nematology, Kimberly, USA |

| NAME | Reagan, Casey |

| Authors | Casey Reagan, Anna, M. Locke, Thomas, E. Carter |

| Title | SCREENING ELITE SOUTHERN SOYBEAN GERMLASM FOR GENETIC FLOOD TOLERANCE IN NORTH CAROLINA |
Soybean (Glycine max (L.) Merrill) growers in eastern North Carolina often face flooding as a result of massive rainfall, such as Hurricane Matthew in 2016. The effects of prolonged waterlogging can include weak root development, spindly plants and ultimately, a decrease in yield. However, yield response of regionally-adapted soybean genotypes to flooding has not been quantified well in NC. We conducted a 7 acre field trial at Tidewater Research Station in Plymouth, NC in 2016. A flooding treatment was imposed on the experimental plots at the R2 growth stage for approximately 7 days. 56 breeding lines and varieties from both the mid-south and North Carolina were evaluated for yield response (bu/ac), visual appearance (0-9 ratings where 0 indicates no damage) and agronomics (maturity date, lodging, and plant height). Results suggest that genetic variation exists for flood tolerance in soybean when grown in the Tidewater area of N.C. Flooding conditions significantly reduced overall seed yield as compared to controls. However, 2 varieties maintained ~25% greater yield after flooding, and several more varieties maintained yields equivalent to the control. Results from this 2016 experiment and follow-up experiments currently underway are the essential first steps in identifying parental stock for a breeding program to improve flood tolerance for the eastern USA. Further steps for this project will include identifying the mechanism(s) and genes that underlie this crucial stress tolerance and incorporating them into successful, high-yielding cultivars.

Evaluation of gummy stem blight resistance in a recombinant inbred line watermelon population

From genome sequences of 41 citrus accessions, including 30 new sequences, we developed two Affymetrix Axiom SNP arrays designed for analysis of citrus and closely related genera, one with about 1.4 million unvalidated SNPs (Citrus15AX) and a second with about 58,000 validated SNPs (Citrus56AX). The arrays target SNPs in genes and adjacent regions. Replicate samples have repeatability of 99.8% or better. These arrays are being used to analyze ancestry of about 900 accessions in the UCR Citrus Variety Collection and to construct linkage maps of several populations. Among 32 accessions compared between the Citrus56AX and Citrus15AX arrays, concordance ranged from 97 to 99.9% with only one accession having less than 99% concordance. Sequences of 19 Citrus accessions were compared with array genotype calls and concordance averaged 98.2%. PCA separates the major ancestral species groups (citron, mandarin and pummelo) and suggests that many other...
accessions are hybrids or introgressed, a result confirmed by admixture analysis. The larger array is useful for detection of heterozygous deletions in clonally-derived accessions by loss-of-heterozygosity and copy number analysis. The smaller array is being used to infer whole chromosome haplotypes of many accessions and breeding parents based on genotyping whole-genome amplifications a few single pollen grains or each accession. High density (14,000 to 16,000 marker) linkage maps developed with the 56K array will be illustrated. Breeding applications that require relative few markers can be efficiently pursued with SNP markers such as the KASP system since parental genotypes are known from the SNP arrays.

Affiliation  University of California - Riverside, Riverside, USA, National Research Council of Italy, Palermo, Italy, Kalyani Mahavidyalaya, Kalyani, India

NAME  Sankaran, Sindhuja

Authors  Juan José Quirós, Rebecca McGee, Sindhuja Sankaran

Title  REMOTE SENSING FOR PHENOTYPING YIELD POTENTIAL IN DRY PEA

Abstract  Dry pea (Pisum sativum) is an important grain legume and Palouse region of the Pacific Northwest U.S. is one of the major producing area. Grain legumes are typically grown in rotation with cereal grains such as wheat, as they disrupt the lifecycle of pathogens, help in fixing atmospheric nitrogen into soil, and complement the nutritional qualities of small cereal grains. The USDA-ARS dry pea breeding program focuses on developing varieties of both spring and autumn-sown peas that are high yielding and have high levels of resistance to biotic and abiotic stresses. Yield potential is one of the critical traits influencing the selection of high performing varieties. In this study, low-altitude aerial multispectral imaging was performed to phenotype yield potential differences early in the season. Two different dry pea panels with 25 and 16 varieties at two locations, and one additional panel with 10 varieties at one location were utilized for this purpose. Images were acquired at about 70 and 90 days after planting. Normalized difference vegetation index (NDVI) and green normalized vegetation index (GNDVI) image based features (SUM, MIN, MAX, MEAN) were extracted using image processing with ArcGIS. In most cases, the MEAN NDVI and GNDVI were found to be consistently correlated with yield potential (p<0.05).

Affiliation  Washington State University, Pullman, USA, Universidade de São Paulo, Piracicaba, Brazil, USDA-ARS, Pullman, WA, USA

NAME  Sapkota, Surya

Authors  Surya Sapkota, Jonathan Fresnedo-Ramirez, Li-Ling Chen, Lance Cadle-Davidson, Chin-Feng Hwang

Title  Construction of High-density Linkage Map and QTL Mapping for Botrytis Bunch Rot Resistance in Vitis aestivalis-derived ‘Norton’-based Population

Abstract  Botrytis bunch rot of grapevine, caused by Botrytis cinerea, is one of the most destructive diseases particularly in viticultural areas where post-bloom cooler temperatures coincide with higher humidity. The disease is controlled by a combination of routine fungicide applications and management practices, which are time consuming, costly and not environmentally friendly. Though several North American grapevines including Vitis aestivalis-derived ‘Norton’ show various levels of resistance to Botrytis bunch rot, the genetic mechanisms leading to the resistance are still unknown. To identify genetic resistance determinants in Norton grapes, a mapping population was developed in 2005 from a cross between ‘Norton’ and V. vinifera ‘Cabernet Sauvignon’ at the Missouri State Fruit Experiment Station, resulting in 95 hybrid progenies. This population was further expanded to 182 F1 individuals by repeating the same crosses in 2011, from which a consensus map was constructed via 411 single sequence repeat (SSR) markers. Using genotyping-by-sequencing (GBS), 3,825 single nucleotide polymorphism (SNP) markers were generated. Of these, 1,659 SNP and
406 SSR markers were clustered into 19 linkage groups for a total of 2,065 markers spanning a genetic distance of 2,203.5cM. Segregation of Botrytis bunch rot was studied 10 days’ post-inoculation for two consecutive years under controlled conditions. A quantitative trait loci (QTL) analysis indicated a resistance locus on chromosome 2 that explained 18% of the total phenotypic variation. Flanking markers closely linked with the trait can be used for marker-assisted selection in the development of new cultivars with resistance to Botrytis bunch rot.

Affiliation University of Missouri and Missouri State University Collaborative, Mountain Grove, USA, Ohio State University, Wooster, USA, Missouri State University, Springfield, USA

NAME Schegoscheski Gerhardt, Ismael

Authors Ismael Schegoscheski Gerhardt, Antonio Teixeira do Amaral Junior, Ismael Schwantes, Adriano dos Santos

Title Diallel analysis of popcorn lines for phosphorus responsiveness and use efficiency

Abstract DIALLEL ANALYSIS OF POPCORN LINES FOR PHOSPHORUS RESPONSIVENESS AND USE EFFICIENCY
Ismael Fernando Schegoscheski Gerhardt1, Antonio Teixeira do Amaral Junior1, Ismael Albino Schwantes1, Adriano dos Santos1
1State University of Northern Rio de Janeiro

The expansion of agriculture, coupled with the need for sustainable cropping, is one of the greatest challenges of the scientific community working on the generation of new cultivars adapted to abiotic stress conditions. The aim of this study was to evaluate additive and non-additive genetic effects of popcorn lines previously selected to responsiveness and efficiency in phosphorus use in a complete diallel design and for the implementation of an adequate breeding program for the production of superior genotypes. Eight contrasting popcorn lines for responsiveness and efficiency in phosphorus use were used in complete diallel crosses, resulting in 28 hybrids. The hybrids with its parentals were evaluated in two locations with different phosphorus levels, using a triple lattice design. The following traits were measured: grain yield, popping expansion and popping volume. For popping expansion, the quadratic components for GCA were higher than those for SCA in low and high phosphorus environments, demonstrating predominance of additive genetic effects to responsiveness and efficiency in phosphorus use. And for grain yield and popping volume, the quadratic components for SCA were superior in low and high phosphorus environments, demonstrating predominance of non-additive genetic effects to responsiveness and efficiency in phosphorus use, making feasible to explore the use of popcorn hybrids, using parents that provide an accumulation of additive genes for popping expansion.

Affiliation State University of Northern Rio de Janeiro, Campos dos Goytacazes, Brazil

NAME Schmitz Carley, Cari

Authors Cari Schmitz Carley, Jeffrey Endelman

Title GENOMIC SELECTION IN TETRAPLOID POTATO

Abstract GENOMIC SELECTION IN TETRAPLOID POTATO
Cari Schmitz Carley1, Jeffrey B Endelman1
1Dept. Horticulture, University of Wisconsin-Madison

Potato breeding cycles typically last 6-7 years because of the modest seed multiplication rate and large number of complex traits requiring multi-environment trials. Genomic selection has the potential to increase genetic gain per unit time, either through increased accuracy or a shortened breeding cycle. Both possibilities were explored using a training population (TP) of advanced chip (N = 365) and russet (N = 179) processing genotypes, evaluated for total yield and specific gravity across multiple years at one location. Potato clones were genotyped with an array of 8303 SNP markers, of which 5278 with accurate tetraploid dosage were used to construct additive and dominance relationship matrices for mixed model analysis. After one year of phenotyping, the expected reliability of genome-estimated breeding values (GEBV) was 0.4–0.5 for yield and 0.5–0.6 for specific gravity. By comparison, the narrow-
sense heritability, which equals the reliability of phenotypic selection, was 0.1–0.2 lower. To explore the feasibility of a rapid, two-year breeding cycle, which would require predictions for unphenotyped clones, four unselected F1 populations were evaluated for two years at the same location as the TP and used for validation. GEBV reliabilities were much lower than for the elite, phenotyped panel: 0.15–0.19 for yield and 0.01–0.16 for specific gravity. Random sampling of markers and clones established an increasing trend with little sign of saturation, so the prospects for genomic selection are expected to improve as higher density arrays and larger TPs become available.

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<th>Affiliation</th>
<th>University of Wisconsin - Madison, Madison, USA</th>
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<td><strong>NAME</strong></td>
<td>Scruggs, Wesley</td>
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<tr>
<td><strong>Authors</strong></td>
<td>Wesley Scruggs, Dusty Pittman, Brian Motes, Michael Trammell</td>
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<tr>
<td><strong>Title</strong></td>
<td>Characterization of Red Clover Accessions from the National Plant Genetic Resource Center</td>
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<tr>
<td><strong>Abstract</strong></td>
<td>Red clover (Trifolium pratense L.) is an important legume species for pastures in the southern USA. In addition to being used as a hay crop, red clover is often inter-seeded into grass pastures to improve forage yield and quality. One obstacle faced by producers in the southern USA is that persistence in pastures is greatly reduced due to disease and insect pressure. During the fall of 2016, the forage breeding group at the Noble Research Institute established a trial near Gene Autrey, OK in order to evaluate synthetic red clover populations and PI accessions from the National Plant Genetic Resource Center. The purpose of this trial is to characterize populations for various traits and evaluate their persistence under intensive grazing. The trial includes a total of 30 PI accessions representing 13 originating countries, 20 populations from the Noble Research Institute’s forage breeding program and 6 commercial check cultivars. Red clover plants were transplanted into an established pasture of Texoma MaxQ II tall fescue [Festuca arundinaceum (Schreb.) S.J. Darbyshire]. Trial design is a randomized complete block design with 4 replications. Information collected from this trial will be used to identify material of a high breeding value for our service area. Material selected will be integrated into our red clover breeding program for the development of a persistent cultivar for the southern USA.</td>
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<th>Affiliation</th>
<th>Noble Research Institute, LLC, Ardmore, USA</th>
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<td><strong>NAME</strong></td>
<td>Septiningsih, Endang</td>
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<td><strong>Authors</strong></td>
<td>Yuya Liang, Michael Baring, Shichen Wang, Endang Septiningsih</td>
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<tr>
<td><strong>Title</strong></td>
<td>Mapping QTLs for disease resistance and key agronomic traits in peanut using SNP-based next-generation sequencing markers</td>
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<tr>
<td><strong>Abstract</strong></td>
<td>High yielding peanut cultivars (Arachis hypogaea L.) with high grade ratings are preferable by the farmers. However, often this effort is hampered by major diseases in peanut. Leafspot is one of the important diseases of peanut that can cause more than 50% yield loss. The objective of this study is to identify and map quantitative trait loci (QTLs) for resistance to leafspot disease, yield, kernel weight, total sound mature kernels (TSMK) and other kernels (OK). A recombinant inbred line (RIL) population, derived from a released cultivar Tamrun OL07 and a highly tolerant breeding line Tx964117, was used as a mapping population. A total of 90 RILs were planted for phenotyping in Yoakum, Stephenville, and Brownfield, Texas. A genetic map spanning the 20 linkage groups was developed using 1,211 SNP markers based on double digest Restriction-site Associated DNA sequencing (ddRAD-seq). Some major and minor QTLs were detected for all traits. Several QTL clusters were also identified. Major QTLs identified in this study may be used as potential targets for peanut improvement through molecular breeding.</td>
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<th>Affiliation</th>
<th>Department of Soil and Crop Sciences, Texas A&amp;M University, College Station, Texas 77843, USA, Genomics and Bioinformatics Service, Texas A&amp;M AgriLife Research, College Station, Texas 77845, USA,</th>
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<td><strong>NAME</strong></td>
<td>Shuler, Stacie</td>
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<td><strong>Authors</strong></td>
<td>Stacie Shuler, Tracie Hennen-Bierwagon, Alan Myers, William Tracy</td>
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<tr>
<td><strong>Title</strong></td>
<td>Plant Breeding for Sweet Corn Improvement by Rational Design</td>
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</table>
**Abstract**  
This project integrates mechanism-based genetic design into a highly productive selection program for phytoglycogen-type sweet corn. Phytoglycogen, a water soluble polysaccharide (WSP), imparts desirable characteristics for culinary applications. Most phytoglycogen-type sweet corn uses su1-Ref as the causative agent of the phenotype. su1-Ref has potential drawbacks, however, including restricted genetic diversity in commercial germplasm and limited phenotypic characteristics for taste preferences and/or culinary quality. This project seeks to overcome these problems by breeding phytoglycogen-type sweet corn with novel genetic bases, and modifying su1-Ref sweet corn for novel qualities. Novel mutant combinations that condition phytoglycogen accumulation will be described, together with progress towards breeding these into lines suitable for commercial application. Detailed information is presented about a specific modification, specifically addition of a null mutation in the isa2 locus to the su1-Ref background. Five inbred su1-Ref isa2 double mutant lines were generated by marker-assisted selection that all varied from su1-Ref single mutants in bite test results. Populations segregating for isa2- in su1-Ref/su1-Ref backgrounds were generated in 15 different hybrid combinations. Sibling kernels varying for the isa2 genotype were characterized for starch and WSP content, and linear chain length distribution (CLD) amylopectin and phytoglycogen. Double mutants invariably were significantly increased in phytoglycogen content compared to su1-Ref single mutants. These results are best explained by concluding the su1-Ref product enzyme is partially functional. The data provide proof of concept that breeding based on mechanistic information regarding starch biosynthesis viable for modifying sweet corn quality and utility, as well as improving genetic diversity.

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**NAME**  
Sierra Orozco, Edgar

**Authors**  
Edgar Sierra-Orozco, Reza Shekaste band, Eudald Illa Berenguer, Esther van der Knaap, Samuel Hutton.

**Title**  
FINE-MAPPING OF A NOVEL FRUIT SHAPE LOCUS ON CHROMOSOME 12 IN TOMATO (Solanum lycopersicum L.)

**Abstract**  
Fruit size is essential for fresh market tomato (Solanum lycopersicum L.) because growers typically receive higher prices for larger fruit. Within large-fruited germplasm, fruit size is influenced by flat and round fruit shapes. Flat fruits are smaller but retain better marketability as larger round fruits are more prone to undesirable fruit imperfections such as cracking. Hybrids are developed from crosses between flat and round shaped breeding lines in most commercial fresh market tomatoes because flat shape is dominant but fruit size is intermediate in the hybrid. Knowledge of the location of the gene(s) controlling this trait may improve cultivar development efforts for fresh-market tomato. The objective of this study was to map a novel locus that underlies segregation of fruit shape in the progeny of a cross between flat and round fruited parents in the University of Florida fresh market tomato germplasm. Twenty-four single plant selections, 12 with flat and 12 with round fruits, from a F6 population derived from a cross between Fla. 8000 (flat) and Fla. 8111b (round), were genotyped using an array of 7,720 SNPs and a locus on chromosome 12 was detected controlling flat versus round fruit shape. Map-based cloning applied to recombinants in an F2 population from the same parents established the presence of the locus to an interval of approximately 400 kb on the upper arm. Measurements of fruit shape attributes evidenced that this locus significantly effects fruit mass, fruit depth, fruit shape index and fruit shoulder height.

**Affiliation**  
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**NAME**  
Silva, Erin

**Authors**  
Philipp Simon, Charlene Grahn, Ryan King, James Myers, Erin Silva

**Title**  
Assessing Genotype By Environment (G X E) Interaction And Heritability Of Vegetable Crops In Organic Versus Conventional Production Systems

**Abstract**  
Crop morphology and nutrient use efficiency influences crop weed competitiveness in organic systems; however, these traits are seldom the focus of breeding projects and research. This study seeks to elucidate the heritability of key traits of carrot and snap bean while
answering the question: “Is selection for carrots and beans organic production systems effective in a conventional environment, or must selection be made in an organic environment if it is to be relevant to organic growers?” To accomplish this goal, four diverse F2 and F3 segregating carrot populations were evaluated in 2015 and 2016, respectively, in adjacent certified organic and conventionally managed fields at the University of Wisconsin-Madison. Trait heritability and response to selection were compared between the two environments by selecting individual F2 plants with extremes in top size in 2015 and evaluating the top size of their F3 progeny in 2016. Additionally, F2 and F3 generations for two of the snap bean crosses made in the winter of 2015 and 2016, and then were grown in parallel in organic and conventional plots over the summer of 2016 and 2017 at Lewis Brown Farm in Corvallis, OR. Root measurements and dry weights were recorded for 10 of the parent plants in each system. The results of this research will inform breeders about the heritability of carrots and beans in organic and conventional environments and the need to manage breeding trials organically when developing new cultivars for organic growers.

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NAME

Simko, Ivan

Authors

German Sandoya, Maria-Jose Truco, Krishna Subbarao, Frank Martin, Richard Michelmore, Ryan Hayes, Ivan Simko

Title

BREEDING AND GENETICS OF LETTUCE FOR RESISTANCE AGAINST RACE 2 VERTICILLIUM WILT

Abstract

Verticillium wilt, caused by Verticillium dahliae Kleb., is an economically important disease of lettuce in coastal California. Most isolates of the pathogen detected in the Salinas Valley belong to race 1 for which complete resistance exists. However, adequate levels of resistance is not available against race 2 that is present in low frequency but may potentially spread throughout the main production areas. We have screened over 1,200 Lactuca sativa and L. serriola accessions from the U.S. National Germplasm System for their reaction to race 2 of V. dahliae. Partial resistance that could reduce yield loss has been identified in L. sativa accessions PI 171674, PI 204707, and L. serriola 11G99. Analyses of three bi-parental mapping populations that were developed by mating accessions with partial resistance revealed quantitative trait loci (QTL) for resistance. Though these QTLs were located on several linkage groups (LG), a common QTL was detected on LG6. Spectral analysis of accessions with resistance to race 1 (cv. La Brillante) and the susceptible check cv. Salinas were performed to quantitatively measure wilting following infection with race 2. No significant differences were observed between the inoculated plants and controls, with only a minor difference at wavelengths related to chlorophyll absorption. Similarly, in preliminary investigations limited differences between infected and healthy plants were detected using the chlorophyll fluorescence approach. Accessions with the highest partial resistance to race 2 were incorporated into our breeding program for introgression of resistance into breeding lines.

Affiliation

University of Florida, Belle Glade, USA, University of California - Davis, Davis, USA, University of California - Davis, Salinas, USA

NAME

Singh, Daljit

Authors

Daljit Singh, Xu Wang, Uttam Kumar, Jesse Poland

Title

GENETIC ANALYSIS OF CROP LODGING AND MULTI-SPECTRAL TRAITS IN CIMMYT WHEAT

Abstract

GENETIC ANALYSIS OF CROP LODGING AND MULTI-SPECTRAL TRAITS IN CIMMYT WHEAT
*Daljit Singh1,2, Xu Wang2, Uttam Kumar3, and Jesse Poland2,4
1Kansas State University Interdepartmental Genetics
2Kansas State University Department of Plant Pathology
3Borlaug Institute for South Asia, Ladhowal, Punjab, India
4Kansas State University Department of Agronomy

The current rate of genetic gains in wheat (Triticum Aestivum) (1%) must be increased to
meet the growing demand for this staple cereal crop. Next generation genotyping and phenotyping technologies can help achieve the desired rate of genetic gains (~2%) through the efficient selection of improved wheat germplasm. The rapidly evolving field phenomics tools can provide higher data throughput and spectral and temporal resolution compared to the conventional phenotyping tools. These high-resolution spectral and temporal traits will aid in better operational efficiency and decision making in the crop improvement programs. To test the feasibility of these approaches, we assessed different phenotyping platforms, sensors and genetic analysis strategies in CIMMYT wheat nurseries. A Small Unmanned Aerial Vehicle or sUAV equipped with the latest multi-spectral sensor was used to collect high-resolution imagery of wheat yield nurseries at regular intervals at three field locations in India. In this paper, we will discuss the feasibility of implementation of crop lodging and a variety of multi-spectral traits into the genomic analysis framework. The prediction accuracies of different genomic selection models for physiological and agronomic traits will be presented. The proposed strategies will facilitate more informed selection decisions and rapid genetic gains in wheat breeding programs.

Affiliation Kansas State University, Manhattan, USA, Borlaug Institute for South Asia, Ladhowal, India

NAME Singh, Kanwardeep

Authors Kanwardeep Singh, Amita Mohan, Ramanjot Bhullar, Muhammad Khan, Kulvinder Gill

Title Evolution of Ph1 gene in polyploid wheat and application in wheat breeding

Abstract Wheat is an allohexaploid that originated after two independent events of polyploidization with three sub-genomes that can pair with one another. To maintain integrity of the nucleus and reduce abnormal meiotic behavior, a precise mechanism to regulate chromosome pairing is required that not only differentiates homologous from non-homologous but also differentiates homoeologous chromosomes for normal bivalent formation and accurate recombination. In our previous study, we reported the cloning and functional characterization of major chromosome pairing control gene, Ph1 that regulates diploid-like pairing behavior of wheat (Bhullar et al 2014). We have also shown that the novel function of the Ph1-5B copy evolved via neofunctionalization that happened due to i) 29bp deletion and ii) 60bp insertion leading to the acquisition of unique motifs; iii) Alternate splicing; and iv) early PI to MI specific expression. Further cloning and structural comparison of gene in diploid progenitors of wheat revealed that 29bp deletion in the 5B copy is polyploidization specific. Similarly, expression analysis in diploid progenitors revealed that gene has highest expression during pollen developmental stages in comparison to hexaploid wheat, where maximum transcript of Ph1-5B copy is present during early meiotic stages. Ph1-5B copy from Triticum dicoccoides with varying level of chromosome pairing control (Ozkan et al 2001) show differences in gene expression, where high pairing lines show low expression during early meiotic stages compared to low pairing lines. Transient silencing of Ph1 gene was used to induce homeologous recombination. Thus, suggesting Ph1 gene evolved via neofunctionalization to control pairing and recombination in polyploid wheat.

Affiliation Washington State University, Pullman, USA

NAME Singh, Narinder

Authors Narinder Singh, Shuangye Wu, John Raupp, Sunish Sehgal, Sanu Arora, Vijay Tiwari, Prashant Vikram, Sukhwinder Singh, Parveen Chunneja, Bikram Gill, Jesse Poland

Title EFFICIENT CURATION OF GENE BANKS USING NEXT-GENERATION SEQUENCING METHODS

Abstract Eroding genetic diversity poses a limitation in crop improvement, which can be mitigated using crop wild relatives stored in genebanks. Genebanks not only facilitate ex-situ conservation of the germplasm, but also provides a platform for the sharing of germplasm. Over 1700 genebanks around the world store more than seven million accessions. In the wake of feeding 9.5 billion by 2050, the need to access the stored germplasm nowadays is more than ever before. However, the poor curation, existence of duplication accessions, and missing metadata coupled with confounding phenotypic characterization hinder their usage. Hence, we propose using next-generation sequencing technologies, such as genotyping-by-sequencing (GBS), to identify and remove phenotypically cryptic individuals, identify
duplicate accessions, and efficiently curate genebanks. In this study, we used the Aegilops tauschii collections from three different genebanks and compared them to identify duplicate accessions within and among genebanks. Using GBS, we could identify and remove few individuals that were incorrectly identify as Ae. tauschii. Our results also indicate that about 50% of the accessions are duplicated across all genebanks. If this holds true for other genebanks, we are vastly overestimating the genetic diversity we have at our disposal. Using this protocol, a globally unique set of accessions can be identified for any given species, which will facilitate the better use of germplasm by geneticists and breeders, and ultimately help in crop improvement.

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<th>Affiliation</th>
<th>Kansas State University, Manhattan, USA, South Dakota State University, Brookings, USA, Punjab Agricultural University, Ludhiana, USA</th>
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**NAME** Sjoberg, Stephanie

**Authors** Stephanie Sjoberg, Camille Steber, Kimberly Garland-Campbell, Arron Carter

**Title** The low Falling Number problem of wheat: applying knowledge about seed biology to a real world issue

**Abstract** The Hagberg-Perten Falling Number (FN) test is used by the wheat industry to measure starch degradation caused by alpha-amylase enzyme activity in flour. Grain with high alpha-amylase activity must be sold at a severe discount because it results in poor-quality baked goods. Problems with an excess of alpha-amylase result from two independent genetic causes, insufficient seed dormancy to resist preharvest sprouting (PHS) and a developmental defect called late maturing alpha-amylase (LMA). PHS is the germination of physiologically matured grains on the mother plant when rainy, cool conditions break dormancy and induce germination. Alpha-amylase is naturally produced to mobilize stored reserves during sprouting. In susceptible varieties, LMA is the induction of alpha-amylase in response to an extreme temperature shock can during late seed maturation. Over 8,000 FN data points in 4 years have been collected on WSU Cereal Variety trials at locations across the state. FN data in years without challenging weather didn’t predict FN in environments with LMA or sprouting. Moreover, ANOVA analysis of the entire dataset suggested that genetics accounted for only 15% of the variability for FN. However, such analyses fail to address that there is more than one cause of the problem. When weather data was used to tease apart which low FN events were due to LMA and/or PHS a different picture of heritability emerged. Being able to see the data in terms of separate components will help to making better breeding decisions, and serve as a first step to understanding the genetics of this problem.

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<th>Affiliation</th>
<th>Washington State University, Pullman, USA, USDA-ARS, Pullman, USA</th>
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**NAME** Smith, Matthew

**Authors** Matthew Smith, James Holland, Sherry Flint-Garcia

**Title** Toward a Low-Protein Maize for Amino Acid Metabolism Deficiency Diets

**Abstract** Toward a low-protein maize for amino acid metabolism deficiency diets

Matthew W. Smith1, James B. Holland1,2, and Sherry A. Flint-Garcia2,3
1 Dept. of Crop & Soil Science, NC State University
2 USDA-ARS
3 Div. of Plant Sciences, University of Missouri

Maize is one of the most important crop plants globally and a major source of calories in diets worldwide. The significance of maize in the global food system places undesirable constraints on individuals with phenylketonuria (PKU) and other inborn errors of amino acid metabolism, who must strictly limit intake of protein and specific amino acids (phenylalanine, in the case of PKU).

Substantial effort has gone into developing high-quality high-protein maize, and meaningful variation exists in the protein profile of maize landraces and commercial lines. However, no effort has yet been made to produce maize appropriate for PKU and similar conditions. We seek to develop a commercializable low-protein maize to meet the needs of this population. In 2016 and 2017 we planted a wide variety of maize hybrids, inbreds, and landraces in
Missouri and North Carolina. Using near-infrared spectroscopy we have identified the lowest-protein 2016 lines; this will be repeated for 2017. A selection of low- and high-protein lines underwent a full amino acid assay, and levels of phenylalanine were compared to total kernel protein. Early results suggest that total protein and total Phe are closely correlated, and breeding toward low total protein will be the most productive direction. A final season of identifying low-protein lines will lead us into a breeding program for quality low-protein maize.

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NAME St. Clair, Dina
Poster Number WED72

Authors David Slaughter, Dina St.Clair, Paul Bosland, Thuy Nguyen, Vivian Vuong, Bryce Kubond, Amanjot Kaur

Title HIGH-THROUGHPUT IN-FIELD PHENOTYPING SYSTEM TO ACCELERATE BREEDING OF VEGETABLE CROPS

Abstract High-throughput genomics technologies useful for crop breeding have become widely available and cost-effective to use, but there is a lack of in-field high-throughput trait phenotyping methodologies. Phenotyping remains a major bottleneck in crop breeding. The focus of our project is the development of novel high-throughput plant phenotyping (HTPP) technology designed to replace, advance and expedite plant phenotyping currently performed laboriously by humans in on-farm breeding trials and optimized to serve vegetable crop breeders as they work to accelerate new cultivar development. Breeding climate-resilient crops efficiently and effectively requires the parallel use of high-throughput genomics and HTPP (phenomics) in the field. Our hypothesis is that the development of field-deployable HTPP systems with advanced sensors that have both high-speed and high-performance can enable breeders to gather large amounts of objective plant phenotype data efficiently and cost-effectively. This project will develop and deploy a novel 2nd generation prototype in-field HTPP system for fruit-bearing vegetable crops. A sensor suite of high-resolution, digital color stereovision cameras simultaneously observing the crop plants from multiple vantage points and thermal infrared radiometry will be deployed from a customized high-clearance mobile platform with on-board RTK-GPS for centimeter-level geolocation in the field. Our novel proximal multiview sensor configuration will enable detailed, automated machine observation and characterization of important trait phenotypes specific to vegetable crops. The first year of replicated field experiments with tomato and pepper breeding lines are currently in progress at UC Davis.

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NAME Stapleton, Ann
Poster Number WED73

Authors Ann Stapleton, Weijia Xu, Silvia Liverani, Austin Gratton

Title GENETICALLY-INFORMED ENVIROTYPING TO BETTER MATCH TEST AND TARGET ENVIRONMENTS

Abstract Better matching of test environments to target production environments is key for efficient crop breeding. We are optimizing PreMiuM Bayesian clustering-based envirotyping analysis and developing publicly accessible known-truth genotype-environment simulations. We will combine PreMiuM profile regression-based covariate variable selection with standard linear model selection and fit methods to create a combined analysis workflow that will allow breeders to fit SNP and environment variates to their data. To illustrate these new analysis methods and inform our breeding program modeling, we will analyze real crop datasets with our improved PreMiuM and PreMiuM+ model selection workflow. To leverage better envirotyping within breeding programs, we need modeling tools that allow exploration of program design constraints. We have begun development of accessible breeding simulation models that incorporate realistic environment covariate features of test and target environments and flexible, extensible specifications of genetic gain within an
open-source, widely used web-accessible modeling system that supports both student training and advanced breeder modeling. Modeling tools and better envirotyping tools will support breeders in allocating effort. Breeders will be able to determine optimal germplasm exchange programs for maximum genetic gain by using PreMiuM results to inform setup of test and target environments.

This material is based upon work that is supported by the National Institute of Food and Agriculture, U.S. Department of Agriculture, under award number 2017-67013-26188.

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NAME
Straley, Elizabeth

Authors
Elizabeth Straley, Jen Colcol Marzu, Michael Havey

Title
Resistance to Fusarium Basal Rot in Onion

Abstract
RESISTANCE TO FUSARIUM BASAL ROT IN ONION
Elizabeth Straley1, Jen Colcol Marzu1, and Michael Havey2
1 Department of Horticulture, University of Wisconsin, Madison WI
2 USDA-ARS and Department of Horticulture, University of Wisconsin, Madison WI

Fusarium Basal Rot (FBR) is major soil-borne disease of onion (Allium cepa) that routinely results in significant yield losses. The disease is caused by the fungus Fusarium oxysporum f. sp. cepae (Foc) and leads to browning of the basal plate, damping off, stunted growth, and rotting of bulbs during storage. Control options include treatments with fungicides or soil fumigants, rotation, and host plant resistance, with resistance being the most desirable and cost effective. Resistance to Foc has been proposed to be complexly inherited with evidence of dominance. We evaluated diverse sources of onion germplasm for FBR resistance using a seedling screen, and inbred W446 was identified as a source of resistance for genetic analysis. This inbred was crossed with susceptible inbred B5351 and segregating families developed. Preliminary screening of F3 families revealed that they segregate for FBR resistance and will be used to map this source of FBR resistance in onion.

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NAME
Subudhi, Prasanta

Authors
Prasanta Subudhi, Teresa De Leon, John Ontoy, Raman Rao V. Puram, Uttam Bhattarai, Ronald Tapia, Steven Linscombe

Title
WIDENING THE GENETIC BASE OF US RICE GERMPLASM THROUGH INTROGRESSION OF NOVEL ABIOTIC STRESS TOLERANCE GENES FROM EXOTIC DONORS

Abstract
Drought and salinity are major climate-related risks for sustainable rice production. Abiotic stress tolerant cultivars are needed to enhance food security under future climatic uncertainties. The major bottleneck to accomplish this goal is the narrow genetic base of US rice germplasm, which needs to be enhanced through introgression of novel abiotic stress tolerance genes from exotic donors. The overall goal of this study is to develop rice varieties with enhanced stress adaptation and to provide a better understanding of the genetic network of complex abiotic stress tolerance mechanisms. Several mapping populations such as recombinant inbred lines (RILs) and introgression lines (ILs) developed from crosses involving elite rice cultivars and well-known stress tolerant donors were genotyped using genotyping by sequencing (GBS). Phenotyping for seedling stage salt tolerance was done in hydroponics whereas root and shoot traits were evaluated for drought tolerance at vegetative stage. Quantitative trait loci (QTL) for both morphological and physiological attributes conferring salt tolerance and drought tolerance were discovered and validated. Increased saturation of linkage map due to GBS based SNP markers helped us to identify candidate genes in the QTL regions which can be used for marker-assisted pyramiding to develop climate resilient rice varieties. Moreover, the genomic and germplasm resources will accelerate discovery of genes involved in abiotic stress tolerance mechanisms using both map-based and functional genomics strategies in future.
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<tr>
<th>Affiliation</th>
<th>School of Plant, Environmental, and Soil Sciences, Louisiana State University Agricultural Center, Baton Rouge, USA, Rice Research Station, Louisiana State University Agricultural Center, Baton Rouge, USA,</th>
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<tr>
<td>NAME</td>
<td>Talbert, Luther</td>
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<td>Authors</td>
<td>Andrea Varella, David Weaver, Jamie Sherman, Luther Talbert</td>
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<tr>
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<td>New Genes for Resistance to the Wheat Stem Sawfly from Geographically Targeted Landrace Selections of Wheat</td>
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| Abstract    | New Genes for Resistance to the Wheat Stem Sawfly from Geographically Targeted Landrace Selections of Wheat  

Andrea Varella, David Weaver, Jamie Sherman and Luther Talbert  
Montana State University Plant Sciences and Plant Pathology Department

The objective of this study is to use wheat landrace accessions to identify new genes for resistance to the wheat stem sawfly (WSS) (USDA-NIFA 2013-67013-21106). Genetic resistance due to stem solidness has been the most widely used control measure for the WSS. However, lack of reliability dictates the need for identification of additional resistance mechanisms. Plant landraces are potential pools for biotic and abiotic stress-related genes. Identification of WSS resistance genes in landrace accessions may improve our ability to breed for WSS resistance. Landrace accessions targeted areas of the world where WSS is endemic. Accessions were screened in fields naturally infested by WSS for antixenosis and antibiosis types of resistance between 2012 and 2015. Resistant accessions were crossed to a local susceptible cultivar to generate recombinant inbred lines (RIL). Two RIL populations were screened for antixenosis and antibiosis types of resistance in replicated field trial in 2016. RIL populations derived from landrace accessions from Turkey and Portugal were used for QTL analysis. Previously identified QTLs for reduced stem cutting and increased stem solidness were detected. Novel resistance QTLs were also identified. These initial results suggest that novel genes to complement current genes for WSS resistance will be identified for deployment in wheat varieties for WSS-impacted areas.

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<th>Affiliation</th>
<th>Montana State University, Bozeman, USA</th>
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<td>NAME</td>
<td>Thammapichai, Paradee</td>
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<td>Authors</td>
<td>Paradee Thammapichai, Yiqun Weng</td>
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<tr>
<td>Title</td>
<td>Genomics-aided Development and Characterization of Cucumis hystrix Introgression Lines in Cucumber</td>
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<tr>
<td>Abstract</td>
<td>Cucumis hystrix (2n = 2x = 24) is the only known species in the genus Cucumis that is cross-compatible with cucumber (C. sativus, 2n = 2x = 14) and has a great potential for cucumber improvement. To facilitate introgression of C. hystrix chromatin into cucumber genetic background, we sequenced two accessions, TH1 and CN1, of the C. hystrix genome and conducted de novo draft genome assembly. Sixty percent of 378 million reads were assembled for TH1 with an estimated genome size of 447.0 Mbp. The resulting assembly contained 16,865 scaffolds (~78x coverage) with the largest scaffold being 342 kb and N50 scaffold size of 23.3 kb. For the CN1 accession, 72.4 out of 117 million reads (61.9%) were assembled into 88,371 contigs (N50 size: 4.0kb) with 24x coverage and an estimated genome size of 478.8 Mbp. Scaffold assembly was not pursued for CN1 due to low genome coverage. Through genotyping-by-sequencing (GBS), a genetic map of 1,669 SNP loci in 12 linkage groups was developed for C. hystrix using 113 TH1 x CN1 F2 plants. A synthetic tetraploid was developed from interspecific cross between C. sativus and C. hystrix and induction of chromosome doubling, which was used as the bridge to develop an introgression library through marker-assisted backcrossing. These genetic and genomic resources allowed refinement of syntenic relationships among the chromosomes of cucumber, C. hystrix and melon, as well as quick and reliable detection and molecular tagging of over 300 introgression lines. These ILs were morphologically characterized in field trials.</td>
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| Affiliation | University of Wisconsin, Madison, Madison, USA, USDA-ARS, Vegetable Crops Research Unit, Madison, USA |


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<tr>
<th>NAME</th>
<th>Tillman, Barry</th>
<th>Poster Number</th>
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<tbody>
<tr>
<td>Authors</td>
<td>Diane Rowland, Barry Tillman, Paxton Payton, Rao Kottapalli</td>
<td>WED76</td>
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<tr>
<td>Title</td>
<td>IDENTIFICATION OF TRAITS FOR OPTIMIZED ROOT SYSTEM ARCHITECTURE IN PEANUT</td>
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<tr>
<td>Abstract</td>
<td>Diane Rowland1, Barry Tillman1, Paxton Payton2, and Rao Kottapalli3 1University of Florida, Agronomy Department 2USDA-ARS, Lubbock, Texas 3Texas Tech University, Lubbock, Texas</td>
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<td>The Southeastern United States accounts for approximately 75% of peanut (Arachis hypogaea L.) production in the United States (NASS, 2015). Soils where peanut is produced are sandy and characterized as well drained and highly high permeable. The objective of this research was to quantify genotypic responses to irrigation during phenological development that would allow identification of periods of crop development where water savings can occur without reducing production. Field studies were conducted over three years at the University of Florida and the USDA-ARS in Lubbock, TX. Rainout shelters were used to shed rainfall on plots until first bloom and irrigation treatments included: 1) 1.9 cm (100%) for the entire season; 2) 1.1 cm until mid-bloom and 1.9 cm following mid-bloom (60% of optimum treatment). Results were similar in 2015 and 2016, with the genotype COC 041 responding to the 60% irrigation treatment by producing a greater amount of root area deeper in the soil, while no differences in root area were observed between the two irrigation treatments with TUFRunnerTM‘511’. These results indicate that root growth plasticity exists among peanut genotypes in their response to varying amounts of soil water. A second major effort enhanced the web based irrigation and harvesting tool known as PeanutFARM. The model is based on adjusted growing degree day (aGDD) calculations for assessing crop coefficient values. Accumulated aGDD values can be used to predict crop developmental stage in-season and predict harvest and schedule irrigation. During the project, the web based tool was launched on a smart-phone platform that allowed weather data download based on GPS coordinates. These tools are freely accessible to growers across the southeast, with 218 growers and researchers registered as users during the 2015 growing season. Further validation occurred with adjustments being made through model calibrations and adjustment of the Kc values and seasonal duration of particular developmental stages. These adjustments were based on simulations of results determined in 2015 through soil tension based irrigation scheduling. Lastly, efforts have also been focused on whole genome sequencing of a drought-tolerant runner genotype (as determined in the experiments listed above and utilized for transcriptome analysis) using single molecule real time sequencing (PacBio) at the Interdisciplinary Center for Biotechnology Research at the University of Florida. The data (25X coverage) was analyzed and reads, after error correction, were assembled with an Illumina assembly generated by the Texas Tech University Center for Biotechnology and Genomics (Kottapalli Lab) to obtain scaffolds. These data are being processed for annotation.</td>
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<tr>
<td>Affiliation</td>
<td>University of Florida, Gainesville, USA, University of Florida, Marianna, USA, USDA-ARS, Lubbock, USA</td>
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<th>NAME</th>
<th>Trammell, Michael</th>
<th>Poster Number</th>
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<tr>
<td>Authors</td>
<td>Michael Trammell, Twain Butler, Carolyn Young, Brian Motes</td>
<td>WED48</td>
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<tr>
<td>Title</td>
<td>Chisholm: A New, Endophyte Free, Summer Dormant Tall Fescue Cultivar for the Southern Great Plains</td>
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<tr>
<td>Abstract</td>
<td>Chisholm is a phenotypic selection from the cultivar Flecha, a perennial, forage type tall fescue [Festuca arundinaceum (Schreb.) S.J. Darbyshire] from Tunisia. Chisholm belongs to the group of Mediterranean-type (summer-dormant) tall fescues which are characterized by increased growth in mild winters and dormancy in dry, hot summers. Selections were made</td>
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from Flecha in north Texas and southern Oklahoma emphasizing persistence under grazing and drought tolerance. Chisholm differs (p < 0.05) from Flecha by possessing a later heading date (4 days), a more semi-erect growth habit, and wider (≥ 0.7 mm wider) flag and tiller leaves. When tested in small plot grazing trials for persistence in southern Oklahoma and north Texas from 2011–2016, final stands of Chisholm were 21% greater (p < 0.05) than those of the Mediterranean cultivars Flecha and Prosper when averaged across all locations. Chisholm tall fescue was released for its improved persistence under grazing when compared to Flecha. It is intended for livestock producers needing a grazing persistent, endophyte free, cool-season perennial forage option for the hot, dry summer’s common to the southern Great Plains. Chisholm tall fescue is capable of producing high quality pasture from autumn through spring to provide a perennial forage option to complement or replace dual-purpose wheat.
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<th>Affiliation</th>
<th>Montana State University, Bozeman, USA</th>
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<td><strong>NAME</strong></td>
<td>Vorsa, Nicholi</td>
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<tr>
<td><strong>Authors</strong></td>
<td>Nicholi Vorsa, Giovanny Covarrubias-Pazaran, Brandon Schlautman, Luis Diaz-Garcia, Guillaume Daverdin, James Polashock, Juan Zalapa, Jennifer Johnson-Cicalese</td>
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<tr>
<td><strong>Title</strong></td>
<td>GENOMIC REGIONS ASSOCIATED WITH AGRONOMIC TRAITS, FRUIT QUALITY AND DISEASE RESISTANCE IN THE AMERICAN CRANBERRY</td>
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<tr>
<td><strong>Abstract</strong></td>
<td>The American cranberry, Vaccinium macrocarpon Ait., being a recently domesticated North American crop species, has undergone only a few breeding and selection cycles. Rate of genetic improvement/gain for horticultural traits, e.g., yield, fruit rot resistance (FRR), fruit quality, is impeded by a long generation interval, biennial bearing habit, large and long (6-8 yrs) field space commitment for phenotyping, impact of a variable fruit rot fungal complex and reliance on relatively small breeding populations. Grant objectives included: development of a cranberry, high-resolution genetic map with QTL for horticultural traits, association mapping of traits, identification of inter and intra-locus allelic effects, estimation of selection accuracy and prediction of the genetic gain under genome wide selection emphasizing FRR. Genotyping-by-sequencing (GBS) of biparental breeding populations has provided several well characterized high density linkage maps encompassing diverse genetic backgrounds. Parental linkage map lengths varied from 1165 to 2223 cM. Mapping identified a FRR variety as being heterozygous for a reciprocal translocation. GBS and SSR markers identified QTL for yield (3), biennial bearing, fruit size (3), fruit organic acids and FRR (19). Four QTL accounted for 33% of FRR variation. GWAS was more powerful and accurate in estimating proportion of variation accounted for by genetic components compared to single and composite QTL mapping. Multivariate genomic best linear unbiased predictor (GBLUP) provided higher predictive ability (PA) than multiple-linear-regression. PA from GBLUP did not statistically differ from the univariate GBLUP. Validation of QTL for horticultural traits, e.g., FRR, is underway in subsequent breeding populations. Supported by USDA-NIFA-AFRI Grant 2013-67013-21107.</td>
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<tr>
<th>Affiliation</th>
<th>Rutgers University, New Brunswick, USA, Marruci Center, Chatsworth, USA, University of Wisconsin, Madison, USA</th>
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<td><strong>NAME</strong></td>
<td>Welch, Stephen</td>
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<td><strong>Authors</strong></td>
<td>Daniel Gomez-Garcia, Carl Leuschen, Nathan Albin, Stephen Welch, David Steward, Allan Fritz</td>
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<td><strong>Title</strong></td>
<td>Microwave Radar Studies Of Wheat Morphology In Breeding Trials</td>
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<td><strong>Abstract</strong></td>
<td>Wheat is achieving barely 50% of the gain rate needed to meet food needs at 2050. However, technology limits collection of the massive phenotype data, especially canopy geometry, needed to accelerate progress. This proof-of-concept project is combining microwave radar sensing with a novel, inversion algorithm to ameliorate the situation. We believe (1) it is unnecessary to sense the 3D position, angle, and size of all plant parts in a plot - rather one desires the genetic markers and effect sizes associated with statistical distributions of these quantities; (2) suitable morphological models exist; (3) if field radar data from plant canopies can be obtained and calculations accelerated, then such models can be inverted to yield genetics; and (4) extending the Analytical Element Method from hydrology to electromagnetic wave propagation can provide such a speed up. A prototype system has been built and tested in a wheat breeding field trial. Echograms clearly show canopy tops, the ground surface and dry down effects. As yet undiagnosed within-canopy features reflect morphological differences. Preliminary mathematical derivations and numerical work are underway. Using the observed distribution of radar returns and radiation boundary...</td>
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**conditions, we seek to solve for plant phenotype probability density functions. Current work is 2D and we will move to 3D next year.**

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<tr>
<th>Affiliation</th>
<th>University of Kansas, Center for Remote Sensing of Ice Sheets, Lawrence, KS, USA, Kansas State University, Dept. Mathematics, Manhattan, KS, USA, Kansas State University, Dept. Agronomy, Manhattan, KS, USA</th>
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<td><strong>NAME</strong></td>
<td>Wente, Rebecca</td>
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<tr>
<td><strong>Authors</strong></td>
<td>Rebecca Wente, Jian Li, Jeffrey Jones, Gerald Minsavage, Robert Stall, Samuel Hutton</td>
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<td><strong>Title</strong></td>
<td>Fine mapping the pepper bacterial spot resistance gene bs6</td>
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<td><strong>Abstract</strong></td>
<td>Bacterial spot is a major disease of pepper (Capsicum annuum) and tomato (Solanum lycopersicum) in warm and humid production environments. The disease is caused by various Xanthomonas spp. and is characterized by leaf and fruit lesions that result in significant crop losses. Host resistance has been an objective in various tomato and pepper breeding programs. Although a number of dominant resistance genes have been identified, they have lacked durability due to shifting bacterial populations and instability of the avirulence genes in the pathogen. In contrast, the combination of the bs5 and bs6 recessive resistance genes in pepper have so far provided a high and durable level of resistance to bacterial spot. The location of bs5 was recently ascertained, but the position of bs6 remains unknown. An F2 population and F2:3 lines derived from the cross between ‘Early Calwonder’ (ECW) and an ECW near-isogenic line containing bs6 (60R) were developed to map and fine map bs6. Genotyping by sequencing (GBS) of the parents and 93 F2 plants identified a 27 Mb region on chromosome 6 which co-segregated with resistance. Using a map-based cloning approach, two rounds of screening for recombination were employed, and phenotyping of recombinant inbred lines delimited the bs6 locus to a &lt;2.0 Mb region.</td>
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<tr>
<th>Affiliation</th>
<th>Gulf Coast Research &amp; Education Center, University of Florida, Balm, FL, USA, Department of Plant Pathology, University of Florida, Gainesville, FL, USA</th>
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<td><strong>NAME</strong></td>
<td>Westbrook, Jared</td>
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<td><strong>Authors</strong></td>
<td>Jared Westbrook, Jason Holliday</td>
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<td><strong>Title</strong></td>
<td>Accelerating the restoration of American chestnut with genomics</td>
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<td><strong>Abstract</strong></td>
<td>The American chestnut is a unique example of a tree species, decimated by exotic pathogens, that is on the verge of restoration through breeding and biotechnology. The chestnut blight fungus Cryphonectria parasitica, introduced from Asia, girdled 3.5 billion stems throughout the eastern U.S. by the 1950s. The root pathogen Phytophthora cinnamomi eradicated American chestnut from low elevation forests in this region prior to the introduction of chestnut blight. For over thirty years, The American Chestnut Foundation (TACF) has used backcross breeding to introgress disease resistance alleles from Chinese chestnut into American chestnut. Third backcross hybrids (BC3s) were intercrossed to generate large populations of BC3-F2 trees segregating for resistance to C. parasitica and P. cinnamomi. At TACF’s Meadowview Research Farms, over 60,000 BC3-F2 trees have been inoculated with C. parasitica. After culling individuals with significant canker expansion, 5,000 trees remain from which to make the final selections of 500 of the most disease-resistant trees. To increase the speed and accuracy of selection in seed orchards, genomic prediction models for resistance to both pathogens are being developed with restriction-associated DNA sequencing of BC3-F2 mother trees whose progeny have been screened for resistance to chestnut blight and/or . Cross validation using 20 K SNPs demonstrates that the accuracy of genomic selection exceeds the accuracy of phenotypic selection and progeny testing. Work is ongoing to genotype remaining trees seed orchards to accelerate selection of the most disease-resistant trees.</td>
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<tr>
<th>Affiliation</th>
<th>The American Chestnut Foundation, Asheville, NC, USA, Virginia Polytechnic Institute, Blacksburg, VA, USA,</th>
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<td><strong>NAME</strong></td>
<td>Yarnes, Shawn</td>
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<tr>
<td><strong>Authors</strong></td>
<td>Shawn Yarnes</td>
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<tr>
<td><strong>Title</strong></td>
<td>Breeding Management System</td>
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Abstract

Created by the not-for-profit Integrated Breeding Platform (IBP), the Breeding Management System (BMS) software is designed to support plant breeders manage a diversity of data: genealogy, inventory, nurseries, trials, genetic markers, and data analysis. The BMS has recently been scaled up from a single user desktop application to a high-performance multi-user server application suitable for institutional breeding programs. The BMS has an open source breeding API (BrAPI), developed in collaboration with other publically funded software initiatives, like GOBii, which allows plug-and-play interoperability with external applications.

Improved data management and analysis increases breeding efficiency, thus reducing the time and resources required to improve crops under local target conditions. Standardized data terminology through curated crop ontologies facilitates data exchange and comparison across teams, enabling meta-analyses. Large projects, like the Tropical Legumes 3 (TLIII), are using the BMS to standardize their trial designs, data collection, and analysis among participating breeders and technicians.

In the developing world, BMS implementation and maintenance are subsidized by government and donor funds. Many national programs, CGIAR centers, universities, and private companies in Africa and SE Asia are using the BMS to efficiently manage breeding activities and data. In the developed world, application and support packages are commercially available for private sector, government agencies, and educational use. The IBP has extensive experience providing professional support to plant breeders, and offers a customizable BMS service package that can include support for system administrators and users.

Affiliation

Integrated Breeding Platform, Winters, CA, USA

NAME

York, Larry

Authors

Larry York, Felix Fritschi, Robert Sharp

Title

HIGH-THROUGHPUT PHENOTYPING OF MULTIPLE ION UPTAKE KINETICS IN MAIZE ROOTS

Abstract

Larry M. York1, Felix B. Fritschi2, and Robert E. Sharp2
1Noble Research Institute, Ardmore, OK
2University of Missouri, Columbia, MO

Roots that are more efficient at acquiring nutrients from soil could lead to greater crop yields and decreased pollution from applied fertilizers. However, little is known about the maximum uptake rate of roots at high concentrations of nutrients, nor the ability to uptake nutrients at lower concentrations (affinity), collectively known as Michaelis-Menten uptake kinetics. Optimizing these parameters without sacrificing other aspects of crop performance could dramatically improve the nutrient use efficiency of crops. This research will develop a high throughput phenotyping (HTP) platform that allows uptake kinetics for several nutrients to be measured simultaneously in hundreds of plants, in turn facilitating genetic analyses and breeding.

The proposed HTP platform will measure the uptake of the most important nutrients in NAM genotypes of maize grown across a range of nutrient concentrations. Each genotype will initially be grown in standard nutrient solution, then individual plants will be placed into small volumes of solutions containing a range of nutrient concentrations, and nutrient uptake will be measured as the difference between the nutrient concentration at the beginning and at the end of the uptake period as measured by ion chromatography. Using curve fitting, the maximum uptake rate and affinity are computed. The combination of the phenotyping platform and powerful maize genetic resources will facilitate genetic mapping to identify genomic regions and possibly specific genes underlying different parameters associated with the uptake of several important mineral nutrients. Combined with physiological work, these measurements could allow a new field of phenomics to contribute to global breeding.
This work is funded by the Agriculture and Food Research Initiative 2017-03911 of the USDA National Institute of Food and Agriculture.

Affiliation Noble Research Institute, Ardmore, OK, USA, University of Missouri, Columbia, MO, USA

NAME Yu, Shu
Poster Number WED57

Authors Shu Yu, Xiaoqiong Qin, Jorge Dubcovsky, Li Tian

Title Enhancing β-carotene Accumulation in Tetraploid Wheat Grains by TILLING

Abstract Vitamin A deficiency (VAD) is a leading cause of childhood blindness in developing countries. Generating staple foods with high β-carotene accumulation is expected to provide long term prevention of VAD. Vitamin A (β-carotene) biofortification of tetraploid wheat grains can be achieved by blocking the competing reactions (catalyzed by lycopene β-ring cyclase/LCYe) and the catabolism of β-carotene (catalyzed by β-carotene hydroxylases/HYDs and carotenoid cleavage dioxygenases/CCDs). Targeting Induced Local Lesions in Genomes (TILLING) mutants were screened and functional characterized to block the carotenoid metabolic pathway. Phenotypic analysis along with spatial gene expression results enabled the selection of single mutants to generate specific higher level mutant combinations which will lead to increased β-carotene accumulation in tetraploid grains. Information obtained from this study will not only be directly applied to improving β-carotene accumulation in tetraploid wheat grains through breeding, but also facilitate future provitamin A biofortification in hexaploid wheat.

Affiliation University of California, Davis, Davis, USA

NAME Yu, Jianming
Poster Number WED78

Authors Jianming Yu, Xianran Li, Jinyu Wang, Kevin Price

Title Canopy geometry analysis at different solar angles and phenological stages through sUAS

Abstract Lack of efficient and high throughput physiological screening and phenotyping processes hampers the realization of the full potential of genomic technologies. In this project, our interdisciplinary team aims to research into detailed spatial data acquisition and feature extraction using the small unmanned aircraft system (sUAS) to study plant canopy geometry. This project represents a collaboration between biologists, who want to know whatever phenomic tools can help us learn more about plants, and engineers, who want to figure out whatever can be done to make it happen. Our proposed research includes three areas: Specific Aim 1 is to conduct extensive acquisition of the ultra-high spatial resolution remotely sensed data using sUAS at different solar angles and across different phenological stages; Specific Aim 2 is to extend the phenotype characterization to night time and identify the difference in canopy geometry patterns; and Specific Aim 3 is to develop automatic, accurate, and high throughput field plot boundary delineation algorithms through machine learning. Two existing genetic mapping populations are leveraged for this project. Both populations were specifically developed to study the plant canopy architecture. The first one is a maize population with 400 doubled haploid lines derived from inbreds with contrasting leaf angle and leaf size. The second is a sorghum population of 250 recombinant inbred lines derived from parental inbreds with contrasting plant height, leaf angle, and photoperiod response.

This work is funded by the Agriculture and Food Research Initiative (2015-06894) of the USDA National Institute of Food and Agriculture.

Affiliation Iowa State University, Ames, USA, AgPixel, Des Moines, USA

NAME Zhang, Hongbin
Poster Number WED79

Authors Yun-Hua Liu, Yang Xu, Meiping Zhang, Sing-Hoi Sze, Steve Hague, C. Wayne Smith, Shizhong Xu, Yanru Cui, Hong-Bin Zhang

Title A GENE-BASED BREEDING (GBB) SYSTEM FOR ENHANCED AND ACCELERATED BREEDING IN COTTON

Abstract Continued crop improvement will largely depend on application of new technologies. We previously constructed a genetic map consisting of 145,395 SNP markers, mapped 209 QTLs (LOD ≥ 5.00) controlling cotton fiber length, strength, uniformity, elongation, lint percentage, lint yield and seed yield, and cloned 10,954 genes controlling these traits. This
study has demonstrated the utility of these genes and developed a gene-based breeding (GBB) system in cotton using the 474 cloned GFL (Gossypium Fiber Length) genes. GBB designs and breeds for superior cultivars based on (i) the number of favorable alleles, (ii) genotypes and (iii) expression profiles of the genes controlling the targeted trait(s). Importantly, it allows continuously pyramiding the favorable alleles or genotypes of the trait controlling genes into elite cultivars, thus realizing continued crop improvement. We found that when one of these three genic datasets was used for fiber length prediction, a prediction accuracy of $r = 0.82 - 0.85$ was obtained. When the prediction results of two or all of the three datasets were jointly used, the prediction of fiber length was completely ensured. Therefore, the cloned genes are capable of accurately predicting the targeted trait(s), thus improving the ability, accuracy and efficiency of plant breeding. Furthermore, we developed a GBB system for cotton, through which we have further confirmed the ability, utility and efficiency of GBB for enhanced and accelerated breeding in plants. This project is supported by Agriculture and Food Research Initiative competitive grant no. 2013-67013-21109 of the USDA National Institute of Food and Agriculture.

**Affiliation**
Texas A&M University, College Station, USA, University of California, Riverside, USA

**NAME**
Zhao, Yang

**Authors**
Yang Zhao, Laura Perilla Henao, Ali Said Yusuf, Emily Bergmann, Lisa Vance, Douglas Cook

**Title**
Comparing cultivated and wild chickpea for effectiveness of nitrogen fixation with different Mesorhizobium species

**Abstract**
Chickpea (Cicer arietinum) is the second most widely grown pulse legume after common bean, and an important staple food in developing countries. Like other legumes, chickpea is a pivotal agricultural species due to its nitrogen-fixation ability in symbiosis with a genus of Gram-negative soil bacteria, Mesorhizobium. The interaction between Mesorhizobium and chickpea species offers a model system to study the effectiveness of nitrogen fixation. Here, we conducted an agricultural experiment with various chickpea accessions and Mesorhizobium strains. The chickpea accessions included the sequenced domesticated (C. arietinum) cultivar ICCV_96029 and four wild chickpea species (C. reticulatum), Oyali084, Savur063, CudiA152 and Kalkan064. The bacterial strains included two predominant types from Turkey, Kar-203 (M. ciceri) and B2O3/Rse19 (M. mediterraneum), and two from Ethiopia, 43P5 and 43P2 (M. plurifarium). Five plant genotypes and four bacterial strains were inoculated in all combinations and grown to late vegetative stage when the biomass, nodule morphology, and plant architecture were assessed.

The data reveal that wild relatives performed with differing effectiveness when treated with different Mesorhizobia strains. In a second experiment, two representative plant accessions, ICCV_96029 and Oyali084, were inoculated with Kar-203 and B2O3/Rse19. The plant tissue and nodules were harvested over a developmental time course. Our results showed that Oyali084 developed more nodule fresh weight upon inoculation with B2O3/Rse19 than did ICCV_96029 and that the difference in nodule development became significant at flowering growth stage.

Our results reveal difference in nitrogen fixation among domesticated and wild chickpea species.

**Affiliation**
Shandong University, Jinan, China, University of California, Davis, Davis, USA