Poster Abstract Submissions

Note: All abstracts appear exactly as they were submitted. No changes have been made to the original files.

NAME	Akhunov, Eduard	Poster Number
Authors	Wei Wang, Quanli Pan, Fei He, Alina Akhunova, Sarah Davidson Evanega, Liuling Yan, Harold Trick, Eduard Akhunov	TU58
Title	GENOME EDITING FOR IMPROVING WHEAT YIELD AND YIELD-RELATED TRAITS	
Abstract	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.	
Affiliation	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	

NAME	Alsahlany, Maher	Poster Number
Authors	Maher Alsahlany, Daniel Zarka, Joseph Coombs, David Douches	TU02
Title	IMPROVING SELF-COMPATIBILITY AND MAINTAINING GENETIC DIVERSITYIN DIPLOID POTATO THROUGH RECURRENT SELECTION	
Abstract	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. Tuberosum 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.	
Affiliation	Michigan State University, East Lansing, USA	

NAME	Ando, Kaori	Poster Number
Authors	Kaori Ando, James D. McCreight	TU59

Title	POTENTIAL FOR PRODUCTION OF TURKMEN MELONS IN CALIFORNIA	
Abstract	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 trails 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 (>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.	
Affiliation	USDA-ARS, Crop Improvement and Protection Research Unit, Salinas, USA	
<mark>NAME</mark>	Anower, Rokebul	Poster Number
Authors	M. Rokebul Anower, Christy M. Motes, Maria J. Monteros	TU04
Title	DIVERGENT SELECTION APPROACHES FOR IMPROVING DROUGHT TOLERANCE AND WATER USE EFFICIENCY (WUE) IN ALFALFA (Medicago sativa L.) M. Rokebul Anower1, Christy M. Motes1, and Maria J. Monteros1* 1Noble Research Institute, LLC, Ardmore, OK 73401. USA. *Email: mjmonteros@noble.org [mjmonteros@noble.org]	
Abstract	Alfalfa (Medicago sativa L.) is an important forage legume species worldwide due to its biomass yield, persistence and symbiotic nitrogen fixation capabilities. However, alfalfa biomass yields are limited by drought stress. The objectives of this study are to identify genetic variation for drought tolerance in alfalfa and generate new breeding populations. Genotypes contrasting for biomass productivity under drought conditions were identified from over 233 diverse alfalfa accessions and evaluated under rain-fed field conditions. Specific traits evaluated include biomass yield, field performance, relative water content, forage quality, and persistence and these were used to select the top-performing accessions. Genotypes from the top 20 accessions were further evaluated for drought responses and drought physiology parameters in the greenhouse. Selected genotypes were also used to generate half-sib families harvested separately for each plant. Half–sib progenies were evaluated in the greenhouse under drought stress and used to implement a divergent selection scheme. The top 35 drought-tolerant and bottom 35 drought-susceptible plants from within each half-sib family will be used to generate new populations. The drought-tolerant plants had over 200% higher biomass yields compared to the drought-sensitive plants. The parental genotypes were also evaluated using transcriptomic and metabolomics approaches to identify underlying drought tolerance strategies in alfalfa. Overall, the divergent selection approaches could enable the detection of shifts in allele frequencies for drought tolerance loci and ultimately lead to the development of alfalfa cultivars that continue to be productive under drought stress conditions.	
Affiliation	Noble Research Institute, LLC., Ardmore, USA	
<mark>NAME</mark>	Bassett, Amber	Poster Number
Authors	Amber Bassett, Karen Cichy	TU05

Title	COOKING TIME AND SENSORY EVALUATION OF A YELLOW DRY BEAN RECOMBINANT INBRED LINE POPULATION	
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	Poster Number
Authors	Lais Bastos Martins, Luis Lopez Zuniga, Randall Wisser, James Holland, Peter Balint-Kurti	TU06
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 byCochliobolus heterostrophus, Setosphaeria turcica, andCercospora zeae-maydisandCercospora zeinarespectively, 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.	
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	Poster Number
Authors	Sourabh Bhattacharya, Baskar Ganapathysubramanian, Soumik Sarkar, Arti Singh, Asheesh Singh	TU60

Title	Saliency-driven Robotic Networks for Spatio-temporal Plant Phenotyping
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	Bhattarai, Gehendra	Poster Number
Authors	Gehendra Bhattarai, Jun Qin, Yuejin Weng, John Bradley Morris, Waltram Ravelombola, Wei Wang, Ainong Shi	TU07
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	Biswas, Anju	Poster Number
Authors	Anju Biswas, Benjamain Bougouneau, Sathya Elavarthi, Kalpalatha Melmaiee	TU08
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	
<mark>NAME</mark>	Brasier, Kyle	Poster Number
Authors	Kyle Brasier, Joseph Oakes, Maria Balota, Wade Thomason, Carl Griffey	TU09
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 Brasier 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	
<mark>NAME</mark>	Brewer, Brittney	Poster Number
Authors	Brittney Brewer, Nancy Blake, Hwa-Young Heo, Jay Kalous, Talbert Luther	TU10
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	Poster Number
Authors	David Byrnes, Fekadu Dinssa, Ondego Nyabinda, Stephen Weller, James Simon	TU12
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 neccesary 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	Poster Number
Authors	Lin Ma, Yichao Shi, Asheesh Singh, Rebecca Cademartiri, Ludovico Cademartiri	TU61
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 area 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	
<mark>NAME</mark>	Cai, Xiwen	Poster Number
Authors	Wei Zhang, Mingyi Zhang, Yaping Cao, Xianwen Zhu, Shuangfeng Ren, Yuming Long, Yadav Gyawali, Shiaoman Chao, Steven Xu, Xiwen Cai	TU62
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	
<mark>NAME</mark>	Campbell, Todd	Poster Number
Authors	Kari Hugie, Tariq Shehzad, Min Liu, Andrew Paterson, Todd Campbell	TU63
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.	
Affiliation	USDA-ARS Coastal Plains Soil, Water, and Plant Research Center, Florence, USA, University of Georgia Plant Genome Mapping Laboratory, Athens, USA	
NAME	Carpenter, Neal	Poster Number
Authors	Neal Carpenter, Carl Griffey, Gina Brown-Guedira, Priyanka Tyagi, Paul Murphy, Marla Hall, Mark Christopher	TU13
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 duel 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.	
Affiliation	Dept. of Crop and Soil Environmental Sciences, Virginia Tech, Blacksburg, VA 24060, USA, Eastern Regional Small Grains Genotyping Laboratory USDA-ARS, Raleigh, 10 27695, NC, USA, Department of Crop Science, North Carolina State University, Raleigh, 10 27695, NC, USA	
NAME	Chang, Sam	Poster Number
Authors	Sam Chang, Anne Gillen, Pengyin Chen, Bo Zhang	TU64
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. Thi	

	s study s objective is to investigate the effect of production environment on the performance of the s oybean lines containing various A3 peptide concentrations in multiple US locations to further sustain this structure-functional re	
Affiliation	Mississippi State University, MS State, USA, USDA-ARS CGRU, Stoneville, USA, University of Missouri, Portageville, USA	
NAME	Chen, Andy(Yi)	Poster Number
Authors	Yi Chen, Harwinder Singh Sidhu, Mina Kaviani, Alireza Navabi	TU14
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	Poster Number
Authors	Jamie Coggins, Kate Evans	TU15
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 4oC. 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.	

Affiliation	Washington State University - Tree Fruit Research and Extension Center, Wenatchee, WA, USA, Roy Farms, Inc., Moxee, WA, USA	
NAME	Craig, Valerie	Poster Number
Authors	Valerie Craig, Elizabeth Lee, Hugh Earl, Steve Bowley, Aaron Berg	TU16
Title	Identification of a Unique Spectral Signature of Black Layer Formation in Maize (Zea mays L.)	
Abstract	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.	
Affiliation	University of Guelph, Guelph, Canada	
NAME	De La Torre, Amanda	Poster Number
Authors	Amanda De La Torre, Daniela Puiu, Steven Salzberg, Marc Crepeau, Charles Langley, John Gleason, Richard Sniezko, Douglas Savin, David Neale	TU65
Title	TOWARDS GENOMIC-BASED BREEDING OF SUGAR PINE	
Abstract	TOWARDS GENOMIC-BASED BREEDING OF SUGAR PINE Amanda R De La Torre 1, Daniela Puiu2, Steven Salzberg2, Marc Crepeau1, Charles H Langley1, John Gleason3, Richard Sniezko4, Douglas Savin4, David B Neale1 1 University of California-Davis. 2 John Hopkins University, Baltimore, MD. 3 US Forest Service Region 6 4 US Forest Service Region 5 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.	
Affiliation	UCDavis, Davis, USA, John Hopkins University, Batimore, USA, John Hopkins University, Baltimore, USA	

NAME	de Leon, Natalia	Poster Number
Authors	Bridget McFarland, Shawn Kaeppler, Natalia de Leon, G2F Consortium	TU66
Title	The effect of artificial selection on the genetic control and modulation of genotype-by-environment interaction in maize	
Abstract	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 | |
Affiliation	Department of Agronomy, Plant Breeding and Plant Genetics, University of Wisconsin, Madison, USA	
NAME	Dhungana, Bandana	Poster Number
Authors	Bandana Dhungana, Melanie Caffe-Treml, Shaukat Ali, Padmanaban Krishnan, Emmanuel Byamukama	TU17
Title	Methodology for Screening Oat Genotypes for Ochratoxin A Accumulation in Grain Inoculated with Penicillium verrucosum. B. Dhungana1, S. Ali1, E. Byamukama1, P. Krishnan2, and M. Caffe-Treml1 1Department of Agronomy, Horticulture and Plant Science. 2Dairy and Food Science Department, South Dakota State University, Brookings, SD 57006	
Abstract	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	
Affiliation	South Dakota State University, Brookings, USA	

NAME	Dzakovich, Michael	Poster Number
Authors	Michael Dzakovich, Jessica Cooperstone, Ken Riedl, Steven Schwartz, David Francis	TU18
Title	PURÉE TO PEAKS IN 15 MINUTES: A RAPID CAROTENOID EXTRACTION AND UHPLC-PDA ANALYSIS WORKFLOW FOR TOMATO BREEDING	
Abstract	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.	
Affiliation	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	
NAME	El Hanafi, Samira	Poster Number
Authors	Samira El Hanafi, Wuletaw Tadesse, Najib Bendaoui	TU19
Title	Genetic variability and association mapping of floral traits for hybrid wheat production	
Abstract	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/traits 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.	

Affiliation	International Center for Agricultural Research in the Dry Areas, Rabat, Morocco, Mohammed V University Agdal, Faculty of sciences, Rabat, Morocco	
NAME	Elakhdar, Ammar	Poster Number
Authors	Ammar A. Elakhdar, Toshihiro Kumamaru, Khairy Amer, Calvin O. Qualset, Kevin P. Smith, Robert s. Brueggeman	TU20
Title	ASSOCIATION ANALYSIS OF YIELD RELATED-TRAITS IN BARLEY (HORDEUM VULGARE L.) UNDER SALT AND DROUGHT STRESSES	
Abstract	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-traits 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 (> 0.65), highly significant marker-traits 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.	
Affiliation	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	
NAME	Feldmann, Mitchell	Poster Number
Authors	Mitchell Feldmann, Steven Knapp, William Bridges	TU22
Title	Heritability of an Individual Quantitative Trait Locus	
Abstract	Heritability of an Individual Quantitative Trait Locus Mitchell J. Feldmann1, William C. Bridges2 and Steven J. Knapp1 1Department of Plant Sciences, University of California, Davis 2Department of Mathematical Sciences, Clemson University 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.	
Affiliation	University of California, Davis, Davis, USA, Department of Plant Sciences, University of California, Davis, Davis, USA	

NAME	Focht, Eric	Poster Number
Authors	Eric Focht, Rodrigo Iturrieta, Mary Lu Arpaia	TU24
Title	QUANTIFYING FRUIT SHAPE IN AVOCADO: A BETTER WAY FORWARD	
Abstract	QUANTIFYING FRUIT SHAPE IN AVOCADO: A BETTER WAY FORWARD Eric Focht 1, Rodrigo Iturrieta 1and Mary Lu Arpaia1 1University of California-Riverside Department of Botany and Plant Sciences 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	
NAME	Fong, Stephanie	Poster Number
Authors	Stephanie Fong, Yifei Wang, Jennifer Johnson-Cicalese, Nicholi Vorsa	TU25
Title	LOCI IMPACTING MALIC AND CITRIC ACID CONTENT IN CRANBERRY FRUIT	
Abstract	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 (? 1 mg/g) and low malic acid (? 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.	
Affiliation	Rutgers University- Department of Plant Biology, NEW BRUNSWICK, USA, NJAES – Marucci Blueberry & Cranberry Research & Extension Center, Chatsworth, USA	
NAME	Francis, David	Poster Number
Authors	David Francis, Eduardo Bernal, Debora Liabeuf, Darlene De Jong, Taylor Anderson, Stella Zitter, Martha Mutschler-Chu	TU67
Title	Prebreeding to combine resistances to pathogens from three kingdoms in processing and fresh-market tomato	
Abstract	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	

	Midwestern US. Diseases include bacterial spot (Xanthomonas vesicatoria, X. perforans, X. euvesitcatoria, 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.	
Affiliation	The Ohio State University, Wooster, USA, Cornell, University, USA	
<mark>NAME</mark>	Ge, Yufeng	Poster Number
Authors	Atefi Abbas, Yufeng Ge, Santosh Pitla, James Schnable	TU26
Title	High-throughput plant phenotyping robot	
Abstract	Image-based high throughput phenotyping has gained momentum recently and demonstrated their usefulness in plant genetics and breeding research. Image-based plant traits extracted from images, however, do not measure plant physiological or chemical traits per se. In many cases, validation of imaged data with true measurements taken by human are required – which are in nature expensive and low throughput. In this project we focus on developing plant phenotyping robot that can take in vivo leaf-level measurements like a human. We develop a computer vision system to identify plants and localize the potential grasping points on plant leaves. We also develop a specialized gripper that integrates a fiber optics bundle to measure leaf reflectance. The prototyped system is tested in UNL's high throughput plant phenotyping greenhouse with maize and sorghum plants. At the same time, human measurements were also taken concurrently on the same set of leaves for these plants. Metrics including robotized measurement speed, successful rate, and consistency with human measurements are summarized. Our final goal, with the automated robotic system, is to collect leaf-level plant traits which can be used to validate image data, or used directly in quantitative genetic analyses (QTL mapping, GWAS, training GS models).	
Affiliation	University of Nebraska-Lincoln, Lincoln, USA	
<mark>NAME</mark>	Getty, Brooke	Poster Number
Authors	Brooke Getty, Shaun Townsend, John Henning	TU27
Title	EFFECTIVE GAMMA RADIATION DOSAGE FOR MUTATION BREEDING IN CASCADE AND CENTENNIAL HOP	
Abstract	EFFECTIVE GAMMA RADIATION DOSAGE FOR MUTATION BREEDING IN CASCADE AND CENTENNIAL HOP Brooke Getty1, Shaun Townsend1, John Henning2 1Oregon State University- Department of Crop Science, Corvallis, OR 2USDA- ARS, Corvallis, OR Hop (Humulus lupulus L.) is a long-lived, herbaceous, climbing perennial in the Cannabaceae family. The female plant produces flowers that mature into cone-like structures which are used as the principal bittering and flavoring agent in beer. Mutation breeding may be a useful technique for developing replacement aroma hop cultivars by inducing minor but significant DNA alterations with a mutagen to improve agronomic quality without significantly changing the brewing profile. The objective of this experiment is to evaluate various gamma radiation doses to establish an LD50 in Cascade and Centennial hop and acquire preliminary data to characterize changes in agronomic performance. Nodal explant segments of micropropagated hops were placed on Petri plates of NCGR Humulus medium.	

	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.	
Affiliation	Oregon State University, Corvallis, USA, USDA- ARS, Corvallis, USA	
NAME	Gibson, Kimberly	Poster Number
Authors	Kimberly Gibson, Stephanie Smolenski Zullo, Antonia Palkovic, Paul Gepts	TU28
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. | |
Affiliation	University of California, Davis, Davis, USA	
NAME	Gimode, Winnie	Poster Number
Authors	Winnie Gimode, Josh Clevenger, Cecilia McGregor	TU29
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.	
Affiliation	University of Georgia, Athens, Georgia	
NAME	Giri, Anju	Poster Number
Authors	Anju Giri, Robert Aiken, Floyd Dowell, Allan Fritz, Allan Fritz, Jesse Poland	TU30
Title	Analysis of water soluble carbohydrates accumulation in wheat stem using NIR spectroscopy	
Abstract	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 R^2 of 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.	
Affiliation	Department of Agronomy, Kansas State University, Manhattan, USA, Northwest Research-Extension Center, Kansas State University, Colby, USA, USDA-ARS-CGAHR-SPIERU, Manhattan, USA	
NAME	Giroux, Michael	Poster Number
Authors	Emma Jobson, Andy Hogg, Rachel Johnston, John Martin, Michael Giroux	TU68
Title	Wheat Yield and Quality Improvement via Testing of New Semi-Dwarf Alleles	
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.	
Affiliation	Montana State University, Bozeman, USA	

NAME	Greenhut, Rachel	Poster Number
Authors	Rachel Greenhut, Juliana Osorio Marin, E. Charles Brummer, Allen Van Deynze	TU32
Title	DEVELOPING BABY LEAF SPINACH WITH LOWER CADMIUM UPTAKE	
Abstract	DEVELOPING BABY LEAF SPINACH WITH LOWER CADMIUM UPTAKE Rachel Greenhut, Juliana Osorio Marin, E. Charles Brummer, and Allen Van Deynze Department of Plant Sciences, University of California, Davis, CA 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.	
Affiliation	UC Davis, Davis, USA	
NAME	Gutierrez, Lucia	Poster Number
Authors	Lucia Gutierrez, Jean-Luc Jannink, Kevin Smith, Melanie Caffe, Mark Sorrells	TU69
Title	TRANSCRIPTOMICS AND METABOLOMICS TO IDENTIFY DRIVERS OF SEED COMPOSITION IN OAT	
Abstract	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.	
Affiliation	University of Wisconsin at Madison, Madison, USA, Cornell University, Ithaca, USA, USDA-ARS, Ithaca, USA	
NAME	Hancock, Wesley	Poster Number
Authors	Wesley Hancock, Roberto Cantor-Barreiro, Susan Copeland, Joyce Hollowell, Thomas Isleib, Thomas Stalker, Shyam Tallury	TU33
Title	Utilizing Wild Arachis Species as a Source of Genetic Variation for the Improvement of Disease Resistance in Peanut	

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 GKP 10602 (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	N.C. State Univ., Raleigh, USA, Plant Germplasm Resources Conservation Unit, USDA-ARS, Griffin, USA	
NAME	Hardigan, Michael	Poster Number
Authors	Michael Hardigan	TU34
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 ofF. 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 diversity along photoperiod sensitivity phenotypes. Reflecting strawberry s recent hybrid domesticat	
Affiliation	UC Davis, Davis, USA	
NAME	Harshman, Julia	Poster Number
Authors	Julia Harshman, Mitchell F, Dominique Pincot, Tom Poorten, Glenn Cole, Alexander Putman, Thomas Gordon, Steve Knapp	TU35
Title	RESISTANCE TO CHARCOAL ROT IN STRAWBERRY	

Abstract	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 1Department of Plant Science, University of California, Davis, California, 95616 2 Department of Plant Pathology and Microbiology, University of California, Riverside, California, 92521 3Department of Plant Pathology, University of California, Davis, California, 95616 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.	
Affiliation	University of California, Davis, Davis, USA, University of California, Riverside, Riverside, USA	
NAME	Havey, Michael	Poster Number
Authors	Eduardo Munaiz, Michael Havey	TU36
Title	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 oniond. 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.	
Affiliation	University of Wisconsin, Madison, WI, USA, USDA-ARS and University of Wisconsin, Madison, WI, USA,	
NAME	Hawkins, Susan	Poster Number
Authors	Susan Hawkins, Carol Robacker	TU37
Title	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 or**NAME**ntal 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	University of Georgia, Griffin, GA, USA	
NAME	Hinds, Zach	Poster Number
Authors	Zach Hinds, Eric Hequet	TU38
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.	
Affiliation	Texas Tech University, Lubbock, USA	
NAME	Hinojosa, Leonardo	Poster Number
Authors	Leonardo Hinojosa, Kevin Murphy	TU39
Title	EVALUTION OF QUINOA POLLEN IN HEAT CONDITIONS	
Abstract	EVALUTION OF QUINOA POLLEN IN HEAT CONDITIONS Leonardo Hinojosa1 and Kevin Murphy1 1 Sustainable Seed Systems Lab, Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164 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 determinate the effect high temperature on pollen germination, viability and morphology.	
Affiliation	Washington State University, Pullman, USA	
NAME	Hoogland, Traci	Poster Number
Authors	Traci Hoogland, Jack Martin, Jamie Sherman	TU40
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.	
Affiliation	Montana State University, Bozeman, MT, USA	
NAME	Hoyos Villegas, Valerio	Poster Number
Authors	Valerio Hoyos-Villegas, Jessica O'Connor, Angus Heslop, Anthony Hilditch, Zulfi Jahufer, John Ford, Brent Barrett	TU41
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.	

Affiliation	AgResearch, Lincoln, New Zealand, PGGW Seeds, Lincoln, New Zealand	
<mark>NAME</mark>	Hutton, Samuel	Poster Number
Authors	Zachary Lippman, Samuel Hutton, Andrew Krainer, Sebastian Soyk	TU70
Title	Modification of plant determinacy to increase yield in fresh market tomato	
Abstract	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.	
Affiliation	Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA, University of Florida, GCREC, Wimauma, FL, USA	
<mark>NAME</mark>	Jain, Piyush	Poster Number
Authors	Piyush Jain, Duke Pauli, Nicholas Kaczmar, Michael Gore, Abraham D Stroock	TU71
Title	HIGH-THROUGHPUT PHENOTYPING FOR EFFECTIVE WATER USE WITH DISPERSIBLE SENSORS	
Abstract	HIGH-THROUGHPUT PHENOTYPING FOR EFFECTIVE WATER USE WITH DISPERSIBLE SENSORS Piyush Jain1, Duke Pauli3, Nicholas Kaczmar3, Michael Gore3, Abraham D Stroock2 1Sibley School of Mechanical and Aerospace Engineering, 2Robert Frederick Smith School of Chemical and Biomolecular Engineering, 3School of Integrative Plant Science, Cornell University, Ithaca, New York 14853 USA 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 ?leafon 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 ?leafat 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.	
Affiliation	Cornell University, Ithaca, USA	
<mark>NAME</mark>	Jastrzembski, Jillian	Poster Number
Authors	Jillian A. Jastrzembski, Madeleine Y. Bee, Gavin L. Sacks	TU42

Title	Faster, cheaper, smellier – accelerating throughput and achieving spatial resolution of plant volatiles with extractive meshes coupled to ambient ionization mass spectrometry
Abstract	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 (<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), ?-damascenone) with precisions of < 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.
Affiliation	Cornell University, Ithaca, USA

NAME	Jiang, Tao	Poster Number
Authors	Charles Chen, Tao Jiang, Phat Dang, Mingli Wang	TU43
Title	Association mapping of SSR markers to sweet, bitter and roasted peanut sensory attributes in cultivated peanut	
Abstract	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.	
Affiliation	Auburn University, Auburn, USA, Auburn University, Auburn, China, USDA, Dawson, USA	

NAME	Jimenez, Randi	Poster Number
Authors	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	TU44

Title	An experiential learning-based public plant breeding pipeline for organic cultivar development: Student Collaborative Organic Plant Breeding Education (SCOPE) at UC Davis
Abstract	AN EXPERIMENTAL LEARNING-BASED PUBLIC PLANT BREEDING PIPELINE FOR ORGANIC CULTIVAR DEVELOPMENT: SCOPE PROJECT at UC Davis Randi Jiménez[1], Saarah Kuzay[1], Mengyuan Xiao[1], Kimberly Gibson[1], Jake Uretsky[1], Stephanie Smolenski Zullo[1], Travis Parker[1], Zachary Dashner[1], Jorge Berny[1], Nisha Marwaha[1,2], Allen Van Deynze[1], Dina St.Clair[1], Paul Gepts[1], Antonia Palkovic[1,2], Carol Hillhouse[2], Raoul Adamchak[2], Mark Van Horn[2], Jared Zystro[3], and E. Charles Brummer[1] 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 poppers, 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.
Affiliation	University of California, Davis, Davis, CA, USA, Organic Seed Alliance, Port Townsend, WA, USA

<mark>NAME</mark>	Jimenez, Randi	Poster Number
Authors	Randi Jimenez, Theresa Hill, Allen Van Deynze	TU45
Title	Utilizing Wild Capsicum annuum Germplasm for Breeding Resistance to Curtovirus (Family: Geminiviridae) in Cultivated Pepper (Capsicum annuum L.)	
Abstract	Utilizing Wild Capsicum annuum Germplasm for Breeding Resistance to Curtovirus (Family: Geminiviridae) in Cultivated Pepper (Capsicum annuum L.) Randi Jiménez[1], Theresa Hill[1], and Allen Van Deynze[1] 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.	
Affiliation	University of California, Davis	

NAME	Jones, Zachary	Poster Number
Authors	Zachary Jones, Major Goodman	TU46
Title	SUSCEPTIBILITY OF DENT-STERILE POPCORNS TO THE GA1-M GAMETOPHYTE FACTOR: RISK ASSESSMENT AND OPPORTUNITIES	
Abstract	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 its 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	
NAME	Jorgensen, Chad	Poster Number
Authors	Chad Jorgensen, Jan Dvorak	TU47
Title	QTL MAPPING OF SEED AND SPIKE TRAITS IN TRITICUM CARTHLICUM, A TETRAPLOID WHEAT WITH HEXAPLOID WHEAT SEED MORPHOPLOGY	
Abstract	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	
NAME	Jose Camargo Senhorinho, Henrique	Poster Number
Authors	Henrique Jose Camargo Senhorinho, Marlon Dacal Mathias Coan, Thiago Pablo Marino, Ronald Jose Barth Pinto, Carlos Alberto Scapim, James Brendam Holland	TU48
Title	Effect of missing data rates on imputation accuracy using LD-knni method	
Abstract	The aim of association mapping studies is to identify genetic polymorphisms that are responsable 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 did'nt present significant differences. Therefore, for the present dataset, insted 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.	
Affiliation	North Carolina State University, Raleigh, USA, Universidade Estadual de Maringá, Maringá, Brazil	
<mark>NAME</mark>	Kantar, Michael	Poster Number
Authors	Plant Breeding Coordinating committee (PBCC), Michael Kantar	TU49
Title	Sustaining the Future of U.S. Plant Breeding	
Abstract	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.	
Affiliation	USDA, DC, USA, University of Hawaii, Honolulu, USA	
<mark>NAME</mark>	Kantor, George	Poster Number
Authors	George Kantor, Wenhao Luo, Changjoo Nam, Katia Sycara	TU50
Title	ADAPTIVE ROBOTIC SAMPLING FOR HIGH THROUGHPUT PHENOTYPING	
Abstract	ADAPTIVE ROBOTIC SAMPLING FOR HIGH THROUGHPUT PHENOTYPING George Kantor, Wenhao Luo, Changjoo Nam, and Katia Sycara Carnegie Mellon University Robotics Institute

Autonomous robots equipped with a variety of sensing technologies have the potential to alle viate the phenotyping bottleneck. Such platforms provide the capability to gather measureme nts of plants as they grow in the field at higher resolution and larger scale than is currently po ssible. This poster reviews our prior work in robotic phenotyping, and it describes preliminar y efforts and plans for a newly funded NSF/NIFA Cyber-Physical Systems project that is inv estigating methods of predicting the importance of potential measurements and using those pr edictions to plan for optimal deployment of robotic phenotyping | |
Affiliation	Carnegie Mellon University Robotics Institute, Pittsburgh, PA, USA	
<mark>NAME</mark>	Karhoff, Stephanie	Poster Number
Authors	Stephanie Karhoff, Sungwoo Lee, Rouf Mian, Anne Dorrance, Leah McHale,	TU51
Title	TRANSCRIPTOMIC ANALYSIS OF NEAR-ISOGENIC LINES TO IDENTIFY CANDIDATE GENES FOR MAJOR PHYTOPHTHORA ROOT AND STEM ROT RESISTANCE QTL	

Abstract	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.	
Affiliation	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	
NAME	Kinczyk, Jonathan	Poster Number
Authors	Jonathan Kinczyk, Kenneth Pecota, Bode Olokulu, Ragy Ibrahem, G. Craig Yencho,	TU52
Title	IDENTIFYING KEY PROCESSING TRAITS IN SWEETPOTATO THROUGH GENOTYPING BY SEQUENCING	
Abstract	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.	
Affiliation	NC State University, Raleigh, USA	
NAME	King, Kevin	Poster Number
Authors	Kevin King, Huang Li, Chaofu Ly	TU53
Title	Mapping Quantitative Trait Loci to Understand Seed Size Variation in Camelina sativa	
Abstract	Mapping Quantitative Trait Loci to Understand Seed Size Variation in Camelina sativa Kevin King, Huang Li, and Chaofu Lu Department of Plant Science and Plant Pathology, Montana State University	

	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.	
Affiliation	Montana State University, Bozeman, USA	
NAME	Korani, Walid	Poster Number
Authors	Walid Korani, Ye Chu, Corley Holbrook, Peggy Ozias-Akins	TU54
Title	ALPHA-LINOLENIC ACID METABOLISM DIFFERENTIALLY REGULATES POST-HARVEST AFLATOXIN ACCUMULATION IN PEANUTS	
Abstract	ALPHA-LINOLENIC ACID METABOLISM DIFFERENTIALLY REGULATES POST-HARVEST AFLATOXIN ACCUMULATION IN PEANUTS Walid Ahmed Korani1, Ye Chu1, C. Corley Holbrook2, and Peggy Ozias-Akins1 1Institute of Plant Breeding, Genetics and Genomics, University of Georgia, Tifton, Georgia 31793. 2USDA-ARS, Crop Genetics and Breeding Res. Unit, Tifton, Georgia, 31793 Aspergillus spp. infection, and the subsequent aflatoxin accumulation, is an intricate issue facing peanut production as the process includes many genetic factors and is sensitive to environmental effects such as water deficit and heat stress. In our previous study, we showed that peanut genotypes do not differ in their ability to support fungal growth. However, they differ in rate of aflatoxin formation, **NAME**ly retardation in the peanut genotype ICG 1471. Therefore, we used this genotype alongside Florida-07, a cultivar known to be susceptible for post-harvest aflatoxin contamination to differentiate the responsive genes between the two genotypes upon the fungal growth. 4272 genes were differentially expressed. In addition, 3845 genes were found affected by the environmental effects. An R package was designed to apply KEGG enrichment analysis for polyploids utilizing the progenitors' sub-genomes by combining them into a single genome, designated 'keggseq'. The implementation of 'keggseq' identified five significant pathways, i.e., protein processing in endoplasm reticulum, spliceosome, carbon fixation and metabolism, and alpha-linolenic acid metabolism. A further study showed the particular importance of the latter pathway in regulation of aflatoxin accumulation in the resistant peanut genotype.The results pointed out the important factors controlling the resistance of peanut aflatoxin formation that may open new avenues to breed resistant lines.	
Affiliation	the University of Georgia, Tifton, USA, USDA-ARS, Tifton, USA	
NAME	Kruse, Erika	Poster Number
Authors	Erika B. Kruse, Timothy D. Murray, Arron H. Carter	TU55
Title	Evaluating Marker-Assisted Selection in Breeding for Tolerance to Snow Mold in Winter Wheat	
Abstract	Evaluating Marker-Assisted Selection in Breeding for Tolerance to Snow Mold in Winter Wheat Erika B. Kruse1, Timothy D. Murray2, and Arron H. Carter1 1 Washington State University, Dept of Crop & Soil Science 2 Washington State University, Dept of Plant Pathology The disease pressure of snow molds on winter wheat is highly unpredictable due to the	

	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.	
Affiliation	Washington State University, Pullman, USA	
NAME	Lemes, Cristiano	Poster Number
Authors	Cristiano Lemes da Silva, Allan Fritz, Robert Bowden, Jesse Poland, John Fellers, Yue Jin, Matt Rouse	TU56
Title	Genome-Wide Association Study of Seedling Stem Rust Resistance in a Historical Data of Elite Winter Wheat Lines	
Abstract	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.	
Affiliation	Kansas State University - Departament of Agronomy, Manhattan, USA, Kansas State University - USDA, Manhattan, USA, Kansas State University - Dept. of Plant Pathology, Manhattan, USA	
NAME	Levina, Anna	Poster Number
Authors	Anna Levina, Owen Hoekenga, Corey Broeckling, Walter De Jong	TU57
Title	Network analysis of potato tuber metabolome to enhance potato tuber quality and accelerate potato breeding efforts	
Abstract	NETWORK ANALYSIS OF POTATO TUBER METABOLOME TO ENHANCE POTATO TUBER QUALITY AND ACCELERATE POTATO BREEDING EFFORTS Anna Levina1, Owen Hoekenga2, Corey Broeckling3, Walter De Jong1, 1Cornell University School of Integrative Plant Science, Section of Plant Breeding and Genetics 2Cayuga Genetics, Ithaca NY 3Colorado State University	

	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.	
Affiliation	Cornell University, Ithaca, USA, Cayuga Genetics, Ithaca, USA, Colorado State University, Fort Collins, USA	
NAME	Li, Wanlong	Poster Number
Authors	Wanlong Li, Marie Langham, Qin Ma, Steven Xu	TU73
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.	
Affiliation	South Dakota State University Department of Biology & Microbiology, Brookings, SD, USA, South Dakota State University Department of Agronomy, Horticulture & Plant Science, Brookings, SD, USA, USDA-ARS Red River Valley Agricultural Research Center Cereal Crops Research Unit, Fargo, ND, USA	
NAME	Li Wang, Ming	Poster Number
Authors	Ming Li Wang, Brandon Tonnis, David Pinnow, Shyam Tallury	WED01
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.	
Affiliation	USDA-ARS, PGRCU, Griffin, USA	
NAME	Lin, Yu-Ming	Poster Number
Authors	Yu-Ming Lin, Luis De Santiago, Sukumar Saha, Robert Vaughn, Johnie N. Jenkins, Jack McCarty, Russell W. Hayes, Benjamin Todd Campbell, Amanda Hulse-Kemp, David Stelly	WED02
Title	High-density SNP-based Mapping and Multi-trait QTL Analysis of Isogenic Chromosome-specific CS-B17 RILs in Upland Cotton (Gossypium hirsutum L.)	
Abstract	High-density SNP-based Mapping and Multi-trait QTL Analysis of Isogenic Chromosome-specific CS-B17 RILs in Upland Cotton (Gossypium hirsutumL.) Yu-Ming Lin[1], Luis De Santiago[1,2], Sukumar Saha[3], Robert Vaughn[1], Johnie N. Jenkins[3], Jack C. McCarty[3], R. W. Hayes[3], B.T. Campbell[4], Amanda M. Hulse-Kemp[5,6], and David M. Stelly[1] [1]Soil and Crop Sciences Department, and [2]Program in Genetics, TAMU, [3,4]USDA-ARS, [3]Crop Science Research Laboratory, Mississippi State, MS, [4]Coastal Plains Soil, Water, and Plant Research Center, Florence, SC, [5]USDA-ARS, Genomics and Bioinformatics Research Unit, Raleigh, NC, [6]Crop and Soil Sciences Department, NCSU, Raleigh, NC Abstract Quantitative genetic effects are often complicated by interactions among loci and/or environments, especially when interspecific hybridization is involved. We report here on QTL analysis of agronomic and fiber traits using a set of interspecific isogenic chromosome-specific CS-B17 RILs, where each line is theoretically homozygous for a unique array of sub-chromosome-17 segments from two homozygous lines -- 'TM-1' G. hirsutum and '3–79' G. barbadense. Fifty CS-B17 RILs were phenotyped for 10 traits across 2 years at a total of 4 locations, and were genotyped via the Illumina CottonSNP63K Array. We applied 500 chromosome-17 SNPs for linkage mapping and QTL analysis using programs JoinMap, R/OneMap and R/qtl package. One or two QTLs were detected for each trait. Positions of the QTLs for lint percentage, fiber length, and micronaire were environmentally consistent, but for other traits varied. Epistatic interactions were evident, in that the low-quality recurrent parent contributed the desirable alleles for some of the traits but not others.	
Affiliation	Plant Breeding Program, Department of Soil and Crop Science, Texas A&M University, College Station, USA, Genetics Program, Department of Soil and Crop Science, Texas A&M University, College Station, USA, USDA-ARS, Genetics and Sustainable Agriculture Research, Mississippi, USA	
NAME	MacDonell, Edward	Poster Number
Authors	Edward MacDonell, Chris Grainger, Gordon Hoover, Barry J. Shelp, Istvan Rajcan,	WED04
Title	IDENTIFICATION OF QUANTITATIVE TRAIT LOCI ASSOCIATED WITH SOYBEAN SEED SOYASAPONIN I CONCENTRATION	
Abstract	IDENTIFICATION OF QUANTITATIVE TRAIT LOCI ASSOCIATED WITH SOYBEAN SEED SOYASAPONIN I CONCENTRATION Edward MacDonell, Chris Grainger, Gordon Hoover, Barry J. Shelp and Istvan Rajcan. University of Guelph Department of Plant Agriculture Soyasaponin B forms are a group of secondary plant metabolites naturally found in soybean (Glycine max (L.) Merr.) seeds, which have putative health benefits and are of interest for their functional food properties. The predominant form of soyasaponin B derived from	

	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.	
Affiliation	University of Guelph, Guelph, Canada	
NAME	Mancero, Daniel	Poster Number
Authors	Daniel Mancero-Castillo, Jose Chaparro, Philip Harmon, Thomas Beckman	WED05
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 familyBotryosphaeriaceae,and this disease has become an important problem for the peach industry in the Southeastern United States since the 1970s. Furthermore,Botryosphaeriaceaespecies 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 toBotryosphaeriaspecies 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.?	
Affiliation	University of Florida, Gainesville, USA, USDA-ARS, Byron, USA,	
NAME	Marino, Thiago	Poster Number
Authors	Thiago Marino, Heather Manching, Randall Wisser, James Holland	WED06
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, Department of Plant and Soil Sciences – University of Delaware, Newark, USA, USDA-ARS - Plant Science Research Unit, Raleigh, USA	
NAME	Mazourek, Michael	Poster Number
Authors	Michael Mazourek	WED07
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	Poster Number
Authors	Michael Mazourek, Rachel Hultengren, Michael Glos	TU74
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	Poster Number
Authors	Christopher Hernandez, Michae Ma	TU75
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 be used to profile gene expression in four squash cultivars from C. mosachata 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	Poster Number
Authors	Shawn Mehlenbacher, Rebecca McCluskey	TU76
Title	DEVELOPING EASTERN FILBERT BLIGHT RESISTANT HAZELNUT CULTIVARS USNG MODERN TOOLS AND TRADITIONAL BREEDING METHODS	
Abstract	DEVELOPING EASTERN FILBERT BLIGHT RESISTANT HAZELNUT CULTIVARS USNG MODERN TOOLS AND TRADITIONAL BREEDING METHODS Shawn Mehlenbacher[1] and Rebecca McCluskey[1] [1]Department of Horticulture, Oregon State University The United States ranks fourth in world hazelnut production, yet it produces only 4.5% of the world s 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 into the breeding program. RAPD and microsatellite markers have been developed for the Gasaway re	
Affiliation	Department of Horticulture, Oregon State University, Corvallis, OR 97331, USA	

NAME	McCluskey, Rebecca	Poster Number
Authors	Thomas J. Molnar, Josh Honig, Shawn A. Mehlenbacher, Rebecca McCluskey	TU77
Title	SECURING AND EXPANDING THE U.S. HAZELNUT INDUSTRY THROUGH BREEDING FOR RESISTANCE TO EASTERN FILBERT BLIGHT USDA-NIFA Agriculture and Food Research Initiative Competitive Grant 2014-67013-22421	
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 fromC. 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.	
Affiliation	Plant Biology and Pathology Dept. Rutgers University, New Brunswick, NJ, USA, Dept. of Horticulture, Oregon State University, Corvallis, OR, USA,	
NAME	McMahon, Paul	Poster Number
Authors	Paul McMahon, Gregoire Hummel, Vincent Vadez	WED10
Title	FieldScan – a novel semi-field platform to phenotype traits controlling plant water budget	
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	Poster Number
Authors	Kylie Mendonca, Lauren Garner	WED 60
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	California Polytechnic State University	
NAME	Michelmore, Richard	Poster Number
Authors	Richard Michelmore, Lien Bertier, Lorena Parra, Maria-Jose Truco, Dean Lavelle, Brett Pike, Daniel Ellison	WED61
Title	GENE STACKING TO GENERATE MULTI-DISEASE RESISTANT LETTTUCE	
Abstract	GENE STACKING TO GENERATE MULTI-DISEASE RESISTANT LETTTUCE Richard Michelmore, Lien Bertier, Lorena Parra, Maria-Jose Truco, Dean Lavelle, Brett Pike, Daniel Ellison. The Genome Center, University of California, Davis, CA 95616. http://michelmorelab.ucdavis.edu [http://michelmorelab.ucdavis.edu/] 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	

	lettuce 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	Poster Number
Authors	Tamara Miller, Yayis Rezene, Luseko Chilagane, Susan Nchimbi Msolla, Paul Gepts,	WED11
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.	
Affiliation	University of California - Davis, Davis, USA, Southern Agricultural Research Institute, Hawassa, Ethiopia, Addis Ababa University, Addis Ababa, Ethiopia	
NAME	Mills, Cory	Poster Number
Authors	Anthony Leddin, Cory Mills	WED12
Title	Plant Breeders Without Borders	
Abstract	Plant Breeders Without Borders 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.	
Affiliation	Valley Seeds Australian Seed Breeders, Victoria, Australia, Bayer Crop Science, Lubbock, USA	
NAME	Morris, Craig	Poster Number
Authors	Craig F. Morris, Jessica C. Murray, Alecia M. Kiszonas, Jeffrey D. Boehm, Jr., Maria Itria Ibba, Karsta Heinze, Valerie Lullien-Pellerin	WED13
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	
NAME	Motes, Brian	Poster Number
Authors	Brian Motes, Joe Bouton, Michael Trammell	WED14
Title	A New, Late Maturing Crabgrass Cultivar for the Southern USA	
Abstract	'Red River' crabgrass (Digitaria ciliaris (Retz.) Koeler) is the main commercial crabgrass cultivar for southern USA livestock operations. Based on farmer feedback, one limitation is the cultivar's short vegetative growth period that reduces its overall nutritive quality. Therefore, the forage breeding program at the Noble Research Institute began a breeding program to develop a crabgrass cultivar that was later maturing than Red River, with higher nutritive value, but competitive yield, adaptation, and reseeding ability. NFCG07-1 was essentially derived from Red River by recurrent phenotypic selection for late flowering and good individual plant growth. In trials established at Ardmore, OK, in 2014 and 2015, NFCG07-1 headed significantly (p < 0.05) later than Red River and the early maturing cultivar 'Quick-n-Big'; an average of 8 and 10 days later, respectively. The positive effect of NFCG07-1 later maturity was demonstrated by significantly higher (p < 0.05) in-vitro true dry matter digestibility (IVDMD) than Red River and Quick-n-Big (69.7% vs. 68.5% and 66.5%, respectively, across 11 harvests) and lower neutral detergent fiber (NDF; 63.5% vs. 65.4%) than Quick-n-Big. Crude protein (CP) content was not different among the three cultivars, but averaged 13.7% for NFCG07-1. In yield performance trials, there were no consistent differences in total dry matter yields when NFCG07-1 was compared to Red River. NFCG07-1 is currently under evaluation by a Barenburg Seed Company for licensing.	
Affiliation	Noble Research Institute, LLC, Ardmore, USA	
NAME	Mugabe, Deus	Poster Number
Authors	Deus Mugabe, Rebecca McGee, Clarice Coyne	WED15
Title	Identification of quantitative trait loci associated with cold tolerance in an interspecific chickpea recombinant inbred line population	
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	

	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	Poster Number
Authors	Seth C. Murray, Sorin Popescu, Dale Cope, Lonesome Malambo, Nathália Cruzato, Steven Anderson, Colby Ratcliff	WED64
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	Poster Number
Authors	Martha A. Mutschler, John R. Smeda, Andre Kessler, Anthony Schilmiller, Diane Ullman, Hugh Smith, George Kennedy	WED65
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	Cornell University, Ithaca, NY, USA, Michigan State University, East Lansing, MI, USA, University of California, Davis, Davis, CA, USA	
<mark>NAME</mark>	Neupane Adhikari, Sudha	Poster Number
Authors	Sudha Adhikari, Melanie Caffe-Treml, Jixiang Wu	WED16
Title	ACCURACY OF GENOMIC PREDICTION MODELS FOR MAJOR OAT MILLING AND NUTRITIONAL QUALITY TRAITS Sudha Neupane Adhikari, Jixiang Wu, and Melanie Caffe-Treml Department of Agronomy, Horticulture and Plant Science, South Dakota State University Brookings, SD 57007	
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.	
Affiliation	South Dakota State University, Brookings, USA	
<mark>NAME</mark>	Nguyen, Andy	Poster Number
Authors	Andy Nguyen, Cecilia Agüero, M. Andrew Walker	WED17
Title	Inheritance of GFLV Resistance in a 101-14 x Trayshed Population	
Abstract	INHERITANCE OF GFLV RESISTANCE IN A 101-14 X TRAYSHED POPULATION Andy V. Nguyen1, Cecilia B. Agüero1, M. Andrew Walker1 1University of California, Davis, Department of Viticulture and Enology 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 Trayshed 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.	
Affiliation	Univeristy of California, Davis, Davis, USA	
NAME	Park, Jaebum	Poster Number
Authors	Jaebum Park, Walter DeJong	WED18
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 re duce 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 effe ctive against pathotype Ro1, it is not effective against Ro2. To map Ro2 resistance gene(s), 1 95 F1 clones and their parents (NY121 Ro2 resistant and NY115 Ro2 susceptible) wer e genotyped with the SolCAP 8303 SNP chip and the resistance of each clone was assessed i n	
Affiliation	Cornell University, Ithaca, USA	
NAME	Parker, Travis	Poster Number
Authors	Travis Parker, Paul Gepts	WED19
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	Poster Number
Authors	Takshay Patel, Todd Wehner	WED20
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.	
Affiliation	North Carolina State University, Raleigh, USA	
NAME	Paudel, Dev	Poster Number
Authors	Dev Paudel, Baskaran Kannan, Fredy Altpeter, Jianping Wang	WED21
Title	GENOME SURVEY AND FIRST HIGH-DENSITY GENETIC LINKAGE MAP OF NAPIERGRASS (Pennisetum purpureum)	
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.	
Affiliation	University of Florida, Gainesville, USA	
NAME	Pfeiffer, Brian	Poster Number
Authors	Brian Pfeiffer, William Rooney	WED22
Title	What's changing from 55 years of sorghum breeding?	
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	Poster Number
Authors	Doug Phillips, Patricio Munoz	WED23
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	Poster Number
Authors	Julia Piaskowski, Craig Hardner, Lichun Cai, Yunyang Zhao, Amy Iezzoni, Cameron Peace	WED24
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	Poster Number
Authors	Thomas Poorten, Glenn Cole, Steven Knapp	WED25
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 identify-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	Poster Number
Authors	Xiaoqiong Qin, Meilian Tan, Diana Burkart-Waco, Yosuke Moritama, Tim Wills, Xiuwen Huo, Sergio Silva, Angel Fernandez, Roger Chetelat	WED66
Title	DEVELOPMENT OF SOLANUM SITIENS INTROGRESSION LINES TO ACCELERATE THE USE OF CROP WILD RELATIVES FOR TOMATO IMPROVEMENT	
Abstract	The genepool 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 introgession 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	Poster Number
Authors	Mohammad Rahman, Naresh Barma, Jesse Poland	WED26
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 Resesarch Institute, Jamalpur, Bangladesh, Bangladesh Agricultural Resesarch Institute, Joydebpur, Bangladesh	
NAME	Rahman, Mukhlesur	Poster Number
Authors	Mukhlesur Rahman, Danielle Fiebelkorn	WED27
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	Poster Number
Authors	Katy Rainey, Keith Cherkauer	WED28

Title	Development of Analytical Tools for Drone-based Canopy Phenotyping in Crop Breeding Katy Martin Rainey1, and Keith Cherkauer2 1Purdue University Department of Agronomy 2Purdue University Department of Agricultural and Biological Engineering	
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	Poster Number
Authors	Karin Cruzado, Mahnaz Rashidi, Nora Olsen, Erik Wenninger, Richard Novy, Arash Rashed	WED29
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	Poster Number
Authors	Casey Reagan, Anna, M. Locke, Thomas, E. Carter	WED67
Title	SCREENING ELITE SOUTHERN SOYBEAN GERMPLASM FOR GENETIC FLOOD TOLERANCE IN NORTH CAROLINA	

Abstract	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.	
Affiliation	North Carolina State University, Raleigh, NC, USA, USDA-ARS, Raleigh, NC, USA	
NAME	Rivera, Luis	Poster Number
Authors	Luis Rivera Bugos, Todd Wehner	WED30
Title	Evaluation of gummy stem blight resistance in a recombinant inbred line watermelon population	
Abstract	Evaluation of gummy stem blight resistance in a recombinant inbred line watermelon population Luis A. Rivera-Burgos and Todd C. Wehner North Carolina State University Gummy stem blight (GSB), caused by three related species of Stagonosporopsis [S. cucurbitacearum (syn. Didymella bryoniae), S. citrulli, and S. caricae], is a major disease of watermelon [Citrullus lanatus (Thunb.) Matsum. & Nakai] in most production areas of the United States. Plant breeders seek sources of resistance that can be incorporated into advanced lines and cultivars to help control the disease. We evaluated a watermelon population of 300 inbred lines under field and greenhouse conditions for resistance to gummy stem blight in North Carolina. The experiment was a randomized complete block design with 10 replications per plot. Artificial inoculation was used to induce a uniform and strong epidemics in the field and greenhouse. We evaluated the lines using a scale of 0=no damage to 9=plant dead). Data were used to estimate BLUPs for the trait. We found large variation among resistance lines suggesting a quantitative resistance possibly controlled by multiple loci of small effect.	
Affiliation	NC State University, Raleigh, USA	
NAME	Roose, Mikeal	Poster Number
Authors	Mikeal Roose, Yoko Hiraoka, Sergio Ferrante, Tulsi Dey, Marc Moragues,	WED68
Title	SNP arrays for citrus breeding and germplasm analysis	
Abstract	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	Poster Number
Authors	Juan José Quirós, Rebecca McGee, Sindhuja Sankaran	WED69
Title	REMOTE SENSING FOR PHENOTYPING YIELD POTENTIAL IN DRY PEA Juan José Quirós1,2, Rebecca McGee3, Sindhuja Sankaran1 1Department of Biological Systems Engineering, Washington State University, Pullman, WA, USA. 2Departamento de Engenharia de Biossistemas, Universidade de São Paulo, Piracicaba, SP, Brazil. 3USDA-ARS, Grain Legume Genetics and Physiology Research Unit, Pullman, WA, USA.	
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, USA	
NAME	Sapkota, Surya	Poster Number
Authors	Surya Sapkota, Jonathan Fresnedo-Ramirez, Li-Ling Chen, Lance Cadle-Davidson, Chin-Feng Hwang,	WED31
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 simple 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	Poster Number
Authors	Ismael Schegoscheski Gerhardt, Antonio Teixeira do Amaral Junior, Ismael Schwantes, Adriano dos Santos	WED32
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 enviroments, 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 enviroments, 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	Poster Number
Authors	Cari Schmitz Carley, Jeffrey Endelman	WED33
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.	
Affiliation	University of Wisconsin - Madison, Madison, USA	
NAME	Scruggs, Wesley	Poster Number
Authors	Wesley Scruggs, Dusty Pittman, Brian Motes, Michael Trammell	WED34
Title	Characterization of Red Clover Accessions from the National Plant Genetic Resource Center	
Abstract	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.	
Affiliation	Noble Research Institute, LLC, Ardmore, USA	
NAME	Septiningsih, Endang	Poster Number
Authors	Yuya Liang, Michael Baring, Shichen Wang, Endang Septiningsih	WED35
Title	Mapping QTLs for disease resistance and key agronomic traits in peanut using SNP-based next-generation sequencing markers	
Abstract	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.	
Affiliation	Department of Soil and Crop Sciences, Texas A&M University, College Station, Texas 77843, USA, Genomics and Bioinformatics Service, Texas A&M AgriLife Research, College Station, Texas 77845, USA,	
NAME	Shuler, Stacie	Poster Number
Authors	Stacie Shuler, Tracie Hennen-Bierwagon, Alan Myers, William Tracy	WED70
Title	Plant Breeding for Sweet Corn Improvement by Rational Design	

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.	
Affiliation	University of Wisconsin-Madison, Madison, USA, Iowa State University, Ames, USA,	
NAME	Sierra Orozco, Edgar	Poster Number
Authors	Edgar Sierra-Orozco, Reza Shekaste band, Eudald Illa Berenguer, Esther van der Knaap, Samuel Hutton,	WED36
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	University of Florida, Gainesville, USA, University of Georgia, Athens, USA	
NAME	Silva, Erin	Poster Number
Authors	Philipp Simon, Charlene Grahn, Ryan King, James Myers, Erin Silva	WED37
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.	
Affiliation	USDA-ARS, Madison, WI, USA, University of Wisconsin-Madison, Madison, WI, USA	
NAME	Simko, Ivan	Poster Number
Authors	German Sandoya, Maria-Jose Truco, Krishna Subbarao, Frank Martin, Richard Michelmore, Ryan Hayes, Ivan Simko	WED71
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	Poster Number
Authors	Daljit Singh, Xu Wang, Uttam Kumar, Jesse Poland	WED39
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	Poster Number
Authors	Kanwardeep Singh, Amita Mohan, Ramanjot Bhullar, Muhammad Khan, Kulvinder Gill	WED40
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 homoeologous recombination. Thus, suggestingPh1 gene evolved via neiofunctionalization to control pairing and recombination in polyploid wheat.	
Affiliation	Washington State University, Pullman, USA	
NAME	Singh, Narinder	Poster Number
Authors	Narinder Singh, Shuangye Wu, John Raupp, Sunish Sehgal, Sanu Arora, Vijay Tiwari, Prashant Vikram, Sukhwinder Singh, Parveen Chunneja, Bikram Gill, Jesse Poland	WED41
Title	EFFICIENT CURATION OF GENEBANKS 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.	
Affiliation	Kansas State University, Manhattan, USA, South Dakota State University, Brookings, USA, Punjab Agricultural University, Ludhiana, USA	
NAME	Sjoberg, Stephanie	Poster Number
Authors	Stephanie Sjoberg, Camille Steber, Kimberly Garland-Campbell, Arron Carter	WED42
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.	
Affiliation	Washington State University, Pullman, USA, USDA-ARS, Pullman, USA	
NAME	Smith, Matthew	Poster Number
Authors	Matthew Smith, James Holland, Sherry Flint-Garcia	WED44
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.	
Affiliation	North Carolina State University, Raleigh, USA, USDA-ARS, Raleigh, USA, University of Missouri, Columbia, USA	
NAME	St. Clair, Dina	Poster Number
Authors	David Slaughter, Dina St.Clair, Paul Bosland, Thuy Nguyen, Vivian Vuong, Bryce Kubond, Amanjot Kaur	WED72
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.	
Affiliation	University of California, Davis, Department of Biological and Ag. Engineering, Davis, CA, USA, University of California, Davis, Department of Plant Sciences, Davis, CA, USA, New Mexico State University, Las Cruces, Department of Plant and Environmental Sciences, Las Cruces, NM, USA	
NAME	Stapleton, Ann	Poster Number
Authors	Ann Stapleton, Weijia Xu, Silvia Liverani, Austin Gratton	WED73
Title	GENETICALLY-INFORMED ENVIROTYPING TOOLS 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 envirotype 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.	
Affiliation	University of North Carolina Wilmington, Wilmington, USA, Texas Advanced Computing Center, Austin, USA, Queen Mary University of London, London, United Kingdom	
<mark>NAME</mark>	Straley, Elizabeth	Poster Number
Authors	Elizabeth Straley, Jen Colcol Marzu, Michael Havey	WED45
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.	
Affiliation	University of Wisconsin-Madison, Madison, USA, USDA-ARS, Madison, USA,	
<mark>NAME</mark>	Subudhi, Prasanta	Poster Number
Authors	Prasanta Subudhi, Teresa De Leon, John Ontoy, Raman Rao V. Puram, Uttam Bhattarai, Ronald Tapia, Steven Linscombe	WED74
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.	

Affiliation	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,	
NAME	Talbert, Luther	Poster Number
Authors	Andrea Varella, David Weaver, Jamie Sherman, Luther Talbert	WED75
Title	New Genes for Resistance to the Wheat Stem Sawfly from Geographically Targeted Landrace Selections of Wheat	
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.	
Affiliation	Montana State University, Bozeman, USA	
NAME	Thammapichai, Paradee	Poster Number
Authors	Paradee Thammapichai, Yiqun Weng	WED46
Title	Genomics-aided Development and Characterization of Cucumis hystrix Introgression Lines in Cucumber	
Abstract	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 chromatins 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 pursed 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.	
Affiliation	University of Wisconsin, Madison, Madison, USA, USDA-ARS, Vegetable Crops Research Unit, Madison, USA	

NAME	Tillman, Barry	Poster Number
Authors	Diane Rowland, Barry Tillman, Paxton Payton, Rao Kottapalli	WED76
Title	IDENTIFICATION OF TRAITS FOR OPTIMIZED ROOT SYSTEM ARCHITECTURE IN PEANUT	
Abstract	IDENTIFICATION OF TRAITS FOR OPTIMIZED ROOT SYSTEM ARCHITECTURE IN PEANUT Diane Rowland1, Barry Tillman1, Paxton Payton2, and Rao Kottapalli3 1University of Florida, Agronomy Department 2USDA-ARS, Lubbock, Texas 3Texas Tech University, Lubbock, Texas The Southeastern United States accounts for approximately 75% of peanut (Arachis hypogaeaL.) 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.	
Affiliation	University of Florida, Gainesville, USA, University of Florida, Marianna, USA, USDA-ARS, Lubbock, USA	
NAME	Trammell, Michael	Poster Number
Authors	Michael Trammell, Twain Butler, Carolyn Young, Brian Motes	WED48
Title	Chisholm: A New, Endophyte Free, Summer Dormant Tall Fescue Cultivar for the Southern Great Plains	
Abstract	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	

	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.	
Affiliation	Noble Research Institute, LLC., Ardmore, OK, USA	
NAME	Trampe, Benjamin	Poster Number
Authors	Benjamin Trampe, Ursula Frei, Thomas Lübberstedt	WED49
Title	Mapping of spontaneous haploid genome doubling in temperate maize	
Abstract	Mapping of spontaneous haploid genome doubling in temperate maize Benjamin Trampe1, Ursula Frei1, and Thomas Lübberstedt1 1Iowa State University Maize (Zea mays L.) is a globally important crop for food, feed, and fuel. The use of doubled haploids has dramatically reduced the time needed to produce inbred lines. Doubling agents (i.e., colchicine, oryzalin) are used to double the haploid genome to produce doubled haploid lines that are 100% homozygous. Maize haploids are typically treated in the greenhouse during the 2-leaf stage and then transplanted by hand into the field. Both of these steps are extremely labor intensive. Spontaneous haploid genome doubling (SHGD) does occurring naturally, though at low levels, and circumvents the need for these steps. This study will be conducted to identify QTL that influence SHGD. Progeny from a biparental mapping population (210 F2:3 families) will be evaluated for spontaneous haploid genome doubling in a replicated, multi-location experiment in the summer of 2017. Reproductive capacity will be determined for each family based on pollen production, silk production, and seed set.	
Affiliation	Iowa State University, Ames, USA	
NAME	Vetch, Justin	Poster Number
Authors	Justin Vetch, Robert Stougaard, John Martin, Mike Giroux	WED50
Title	Identification, analysis and implementation of genetic factors influencing pre-harvest sprouting tolerance in Montana spring and winter wheat populations	
Abstract	Identification, analysis and implementation of genetic factors influencing pre-harvest sprouting tolerance in Montana spring and winter wheat populations. J.M. Vetch, R.N. Stougaard, J.M. Martin, and M.J. Giroux. Department of Plant Sciences, Montana State University, 119 Plant Bioscience Building, Bozeman, MT 59717-3150 USA. Pre-harvest sprouting (PHS) is the premature germination of grain before harvest which negatively impacts seed and end use quality. PHS is typically measured using the falling number (FN) test which quantifies the degree to which seed starch has been degraded by alpha amylase. Harvested grain with low FN negatively impacts the price producers receive for their grain and global losses of up to $1 billion per year have been reported. Because of this, identifying and breeding wheat varieties resistant to PHS is of great economic importance. The goals of the project are to first, screen Montana wheat varieties for FN and PHS tolerance and then investigate previously reported PHS QTL markers and determine which may be useful in screening for PHS resistance. A PHS screening method was used to screen 145 Montana grown spring and winter wheat varieties. The PHS tolerance test results indicate that both spring and winter wheat varieties were highly variable in terms of their level of PHS tolerance with varieties falling within a range from totally susceptible to totally resistant. In an effort to develop PHS resistant varieties, the spring and winter wheat lines are	

	currently being screened to identify PHS QTL markers that are associated with both PHS tolerance and high FN.	
Affiliation	Montana State University, Bozeman, USA	
<mark>NAME</mark>	Vorsa, Nicholi	Poster Number
Authors	Nicholi Vorsa, Giovanny Covarrubias-Pazaran, Brandon Schlautman, Luis Diaz-Garcia, Guillaume Daverdin, James Polashock, Juan Zalapa, Jennifer Johnson-Cicalese	WED51
Title	GENOMIC REGIONS ASSOCIATED WITH AGRONOMIC TRAITS, FRUIT QUALITY AND DISEASE RESISTANCE IN THE AMERICAN CRANBERRY	
Abstract	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.	
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<mark>NAME</mark>	Welch, Stephen	Poster Number
Authors	Daniel Gomez-Garcia, Carl Leuschen, Nathan Albin, Stephen Welch, David Steward, Allan Fritz	WED53
Title	Microwave Radar Studies Of Wheat Morphology In Breeding Trials	
Abstract	MICROWAVE RADAR STUDIES OF WHEAT MORPHOLOGY IN BREEDING TRIALS Daniel Gomez-Garcia1, Carl Leuschen1, Nathan Albin2, Stephen Welch3, David Steward4, Allan Fritz3 University of Kansas: 1Center for Remote Sensing of Ice Sheets, Kansas State University: Depts. of 2Mathematics, 3Agronomy, and 4Civil Engineering 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	

	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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<mark>NAME</mark>	Wente, Rebecca	Poster Number
Authors	Rebecca Wente, Jian Li, Jeffrey Jones, Gerald Minsavage, Robert Stall, Samuel Hutton	WED54
Title	Fine mapping the pepper bacterial spot resistance gene bs6	
Abstract	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 <2.0 Mb region.	
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<mark>NAME</mark>	Westbrook, Jared	Poster Number
Authors	Jared Westbrook, Jason Holliday	WED55
Title	Accelerating the restoration of American chestnut with genomics	
Abstract	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.	
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<mark>NAME</mark>	Yarnes, Shawn	Poster Number
Authors	Shawn Yarnes	WED56
Title	Breeding Management System	

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.	
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NAME	York, Larry	Poster Number
Authors	Larry York, Felix Fritschi, Robert Sharp	WED77
Title	HIGH-THROUGHPUT PHENOTYPING OF MULTIPLE ION UPTAKE KINETICS IN MAIZE ROOTS	
Abstract	HIGH-THROUGHPUT PHENOTYPING OF MULTIPLE ION UPTAKE KINETICS IN MAIZE ROOTS Larry M. York[1], Felix B. Fritschi[2], and Robert E. Sharp[2] [1]Noble Research Institute, Ardmore, OK [2]University 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.	

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NAME	Yu, Shu	Poster Number
Authors	Shu Yu, Xiaoqiong Qin, Jorge Dubcovsky, Li Tian	WED57
Title	Enhancing ?-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 ?-carotene accumulation is expected to provide long term prevention of VAD. Vitamin A (?-carotene) biofortification of tetraploid wheat grains can be achieved by blocking the competing reactions (catalyzed by lycopene ?-ring cyclase/LCYe) and the catabolism of ?-carotene (catalyzed by ?-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 ?-carotene accumulation in tetraploid grains. Information obtained from this study will not only be directly applied to improving ?-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
Authors	Jianming Yu, Xianran Li, Jinyu Wang, Kevin Price	WED78
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 multidisciplinary 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.	
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NAME	Zhang, Hongbin	Poster Number
Authors	Yun-Hua Liu, Yang Xu, Meiping Zhang, Sing-Hoi Sze, Steve Hague, C. Wayne Smith, Shizhong Xu, Yanru Cui, Hong-Bin Zhang	WED79
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.	
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NAME	Zhao, Yang	Poster Number
Authors	Yang Zhao, Laura Perilla Henao, Ali Said Yusuf, Emily Bergmann, Lisa Vance, Douglas Cook	WED58
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.	
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