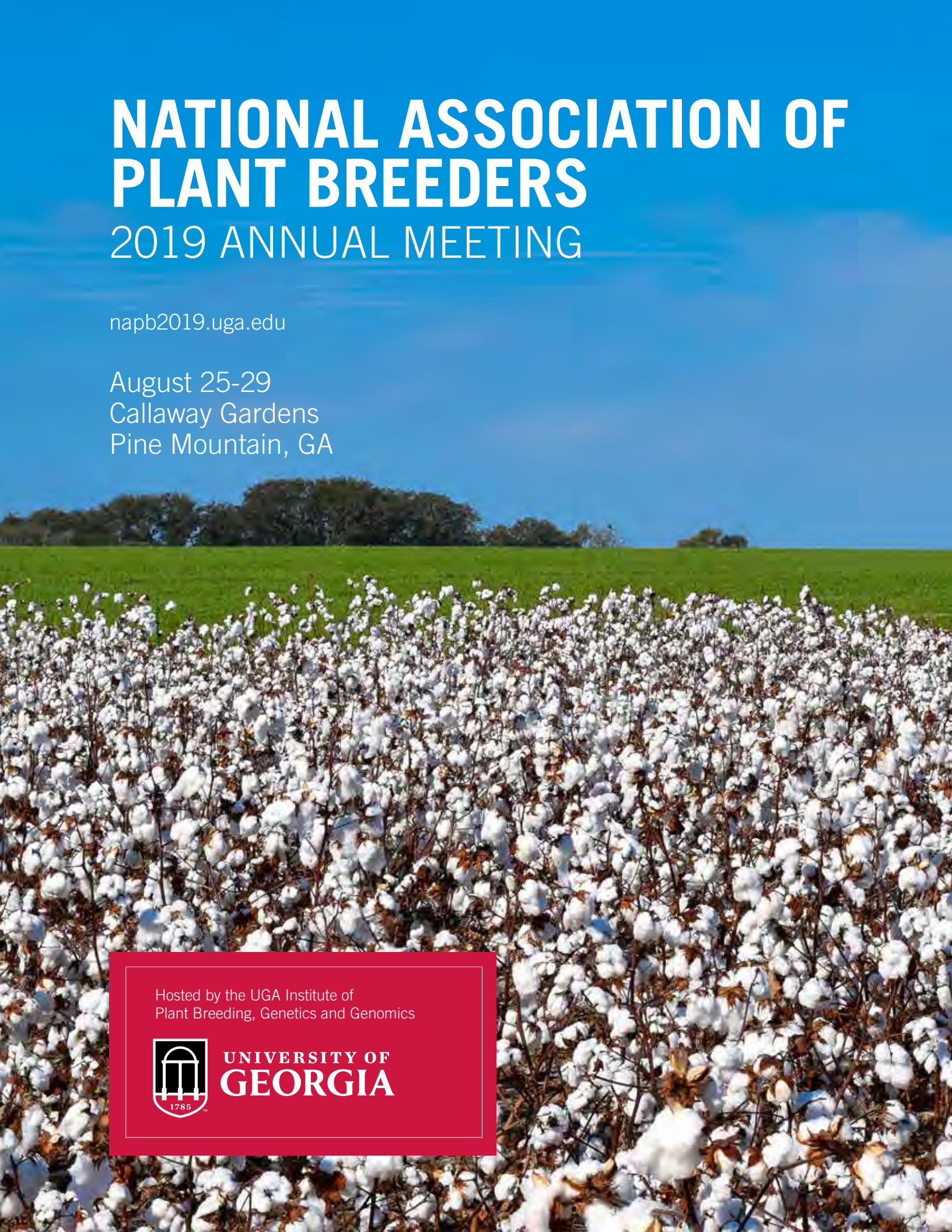
NATIONAL ASSOCIATION OF PLANT BREEDERS

2019 ANNUAL MEETING

napb2019.uga.edu

August 25-29
Callaway Gardens
Pine Mountain, GA



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Plant Breeding, Genetics and Genomics

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Evaluation of triploid hybrid watermelon cultivars for fruit quality and yield (Photo by Tim Coolong)

Planning Committee, UGA 2019

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THE INSTITUTE OF PLANT BREEDING, GENETICS & GENOMICS

The University of Georgia offers MS and PhD degrees through the Institute of Plant Breeding, Genetics, and Genomics. Established in 2008, the Institute enrolls about 40 graduate students at any given moment, offers a full slate of plant breeding-related courses, with 28 faculty, five adjunct faculty, and seven affiliated faculty.

Prior to the establishment of the Institute, the University of Georgia already had conducted highly successful plant breeding programs for decades. Part of the legacy of UGA plant breeding is attributed to the highly productive and globally recognized program of Dr. Glenn Burton, conducted at the Coastal Plain Experiment Station and Tifton Campus, and jointly supported by USDA-ARS and UGA. Dr. Burton's achievements included the development and release of Coastal Bermudagrass in the 1940s, after which the College of Agricultural and Environmental Sciences (CAES) became internationally recognized for breeding successful forage and turfgrass cultivars. These cultivars presently have wide-spread usage on golf courses and athletic fields throughout the southern United States and in several countries, notably present on athletic fields hosting World Cup, Olympic, and Super Bowl events. Peanut cultivars bred on the Tifton Campus have dominated the peanut market in the Southeast where Georgia produces almost half of the US peanuts. Among woody ornamentals, UGA is well known for the breeding and selection program of Mike Dirr, which released 'Endless Summer' hydrangea. Numerous other cultivars licensed by the University of Georgia Research Foundation (UGARF) include soybean, alfalfa and other forages, wheat, cotton, blueberry, muscadine, citrus, pecan, and vegetable and ornamental species.

Sanford Stadium in Athens, GA is planted with Tifway bermudagrass, which was developed by Dr. Burton.

Dr. Glenn Burton developed Coastal Burmudagrass in the 1940s.

UGA plant breeding programs have developed over 400 commercialized plant cultivars since 1990. Of those, 40% are agronomic crop cultivars, 30% are cultivars of horticultural food crops, 27% are ornamental plant cultivars, and 4% are turfgrass cultivars. UGA plant cultivars contribute to over $1 billion in farm-gate value annually. The royalties returned to UGARFare approaching $100 million, much of which is returned through a variety of mechanisms that support plant breeding programs. With the formation of the Institute of Plant Breeding, Genetics and Genomics, most UGA breeding programs were able to enhance their breadth and efficiency with the incorporation of molecular genetic tools, facilitated by graduate student research, and fulfilling the Institute's mission to "train graduate students, conduct research, and develop improved crop cultivars through the integration of classical and modern genetic technologies."

As a College of Agricultural and Environmental Sciences where Plant Breeding is one of four designated focus areas, we are proud to host the 2019 annual meeting of the National Association of Plant Breeders, and the chance to share our research programs with you.

Ripe fruit of 'Lane' muscadine, a recent release of the UGA muscadine grape breeding program.

Code of Conduct

By participating, you voluntarily agree to abide by the NAPB meeting code of conduct below.

Video/Photography

Pre-registered members of the media and NAPB-designated individuals are authorized to photograph or record presentations. Photographs may be posted for promotion of Society activities. Presentations will be posted for public access only with separate written consent of the presenter.

Social Media

Registered members are free to discuss presentations and posters through social media unless the presenter opts-out. Presenters who wish to opt out should state so in their presentation slides/posters. All participants are expected to honor opt-out requests.

Harassment and Safety

NAPB is a community of plant breeders and associated professionals that finds strength through diversity and is committed to providing a safe and productive meeting environment. We seek to foster open dialogue and exchange of scientific ideas, to promote equal opportunities and treatment for all participants, in an environment that is free of harassment and discrimination. All meeting participants are expected to treat others with respect and consideration, and follow venue rules. Presenters are expected to uphold standards of scientific integrity, and professional ethics.

NAPB prohibits any form of harassment, including, but not limited to, offensive comments related to ethnicity, religion, disability, gender, or sexual orientation and inappropriate physical contact, intimidation, unwelcome attention, or unwarranted photography. Continued disruption of talks or other events is also prohibited. Retaliation for reporting harassment is also a violation of this policy, as is reporting an incident in bad faith.

NAPB reserves the right to expel any individual from its annual meetings if he/she does not comply with the above guidelines to ensure a safe and productive meeting, and to report the complaint leveraged against them to their employer.

All concerns or complaints should be communicated promptly to any member of the NAPB Executive Committee or conference staff listed below, either in person or by calling 706-623-3010. All complaints will be treated seriously and action taken.

· Wayne Smith, *Past-president*
· Peggy Ozias-Akins, *Vice President*
· Dave Bubeck, *Secretary*
· Deborah Franco, *Meeting Staff*
· Alex Lipka, Web Editor

Internet access

There is complimentary Wi-Fi at the Lodge and Spa and it does not require a password.
To logon, go to "The Lodge Wi-Fi" and a picture of the Lodge and Spa will appear, then login.

PROGRAM

Abstracts for all talks and posters are in the online program book at napb2019.uga.edu.

SUNDAY, AUGUST 25

9 a.m.-3 p.m. Soft skills workshop hosted by Bayer and Corteva ..... Longleaf E

12-6 p.m. Registration ..... Hall leading to Longleaf

1-5 p.m. PBCC committee meeting ..... Sourwood 4/5

2:30 p.m. Poster set up ..... Loblolly
NIFA Poster set up ..... Cypress

3-5 p.m. **NIFA poster session** (open to all) ..... Cypress
Session Chair: Pushpa Kathir, Program Specialist NIFA
Includes NIFA grantsmanship table with handouts
3 p.m. Even numbered posters
4 p.m. Odd numbered posters

5:30-6:30 p.m. **Opening session** ..... Longleaf
5:30 p.m. **Peggy Ozias-Akins, University of Georgia,** *NAPB 2019 Welcome*
5:35 p.m. **Sam Pardue, University of Georgia, CAES Dean**
5:45 p.m. **Gary Black, Georgia Commissioner of Agriculture**
6 p.m. **Todd Campbell,** *NAPB Welcome and PBCC connection*
6:15 p.m. **Ksenija Gasic,** *PBCC Report*

6:30-7:30 p.m. **Opening keynote** ..... Longleaf
Jeff Bennetzen, University of Georgia
Sources of genetic variation in breeding materials, and how it might be enhanced (O-01)

7:30-9:30 p.m. **Opening reception** ..... Longleaf
Micah Levinson improvisation on the piano

MONDAY, AUGUST 26

7-8:30 a.m. Borlaug Scholar breakfast (awardees and mentors) ..... Sourwood 2/3
Sponsored by Inari, Cotton Inc., and Nutramaize

7-8:30 a.m. Diversity Travel Awardee breakfast (awardees and mentors) ..... Bayberry 3/4

7 a.m.-12 p.m. Registration ..... Hall leading to Longleaf

8:30-10 a.m. **NIFA Plant Breeding Project Director presentations** (Open to all) ..... Longleaf
Welcome by Session Chair: Ed Kaleikau, NIFA National Program Leader
8:35 a.m. **Scott Angle, Director NIFA,** Opening Remarks
8:50 a.m. **Soraya Bertioli, University of Georgia**
Unlocking novel wild alleles in cultivated peanut to increase disease resistance and productivity (O-02)
9:10 a.m. **Zachary Lippman, Cold Spring Harbor Laboratory**
Merging breeding and gene editing: Lessons from tomato (O-03)
9:30 a.m. **George Kantor, Carnegie Mellon University**
Robotic field measurements for plant breeding and crop management (O-04)
9:50 a.m. **Allen Van Deynze, University of California Davis**
Breeding for food safety (O-05)

10-10:20 a.m. Coffee Break ..... Longleaf prefunction area

MONDAY, AUGUST 26 continued

10:20 a.m.-12 p.m. **NIFA Plant Breeding Project Director Presentations** *continued* ..... Longleaf
Session Chair: Liang-Shiou Lin, NIFA National Program Leader

- 10:20 a.m. **Seth Murray, Texas A&M University**
  Transdisciplinary plant phenomics and unmanned aerial system phenotyping for maize crop improvement (O-06)
- 10:40 a.m. **Julie Dawson, University of Wisconsin**
  Facilitating the increased use of genetic resources: Custom core collections and genomic prediction with carrot as a model crop (O-07)
- 11 a.m. **Xiwen Cai, North Dakota State University**
  Genomics-enabled chromosome engineering for alien introgression and genome characterization in wheat (O-08)
- 11:20 a.m. **Karen Cichy, USDA-ARS**
  Optimizing the convenience, nutrition, and taste of yellow dry beans (*Phaseolus vulgaris* L.) to promote pulse consumption in the U.S. (O-10)
- 11:40 a.m. **Dusti Gallagher, Heartland Plant Innovations**
  Establishment of a winter wheat organic breeding pipeline in the Great Plains (O-09)
- 11:50 a.m. Closing remarks

12-8:30 p.m. GRIFFIN CAMPUS TOUR*

Grab a boxed lunch (in front of The Lodge) and board buses to the Griffin Campus. Buses will be numbered 1-5. Your bus number will be your group throughout the tour. The buses will park at the Student Learning Center (301 Higgins Rd, Griffin, Georgia). We will spend about 45 minutes here for a break and welcome from the campus director, Dr. Lew Hunnicutt. We will also take a photo of the group. Tours of the breeding programs will follow. This will include short walks between buildings and a tram to the ornamental and turf plots. Carts will be available for those who cannot walk. Tours end at 5:10 p.m. Buses depart campus at 5:15 p.m. and stop for dinner at Barnstormer's Grill (349 Jonathans Roost Rd, Williamson, GA). After dinner, buses will return to Callaway Gardens.

TIME	ACTIVITY				
12:30-1:30 p.m.	Load buses with boxed lunch, drive to Griffin Campus, lunch on the bus				
1:30-2:15 p.m.	Break at Student Learning Center, welcome by director and group photo				
2:15-5:10 p.m. *Each group rotates through all programs*	Ornamental Breeding *Carol Robacker*	Turf Breeding *Paul Raymer*	USDA National Plant Germplasm System *Melanie Harrison*	Sensory Science Laboratory *Dario Chavez* *Rachel Itle* *Koushik Adhikari*	Food Product Innovation and Commercialization Center *Kirk Kealey* *Dick Phillips* *Kevin Mis Solval* *Lauren Hatcher*
5:10-5:30 p.m.	Travel to Barnstormers Grill				
5:30-8 p.m.	Dinner and return to Callaway Gardens				

**Closed-toe shoes or boots are recommended. Bring hats and sunscreen. Water will be provided throughout the tour.*

Continued on next page

PROGRAM

Abstracts for all talks and posters are in the online program book at napb2019.uga.edu.

TUESDAY, AUGUST 27

7-8 a.m. GSWG networking breakfast ..... Bayberry 3/4

7-8 a.m. ECWG networking breakfast ..... Sourwood 2/3

7 a.m.-5 p.m. Registration ..... Hall leading to Longleaf

8-10 a.m. **Plenary session and lightning talks** ..... Longleaf

Moderator: Jason Wallace, University of Georgia

8 a.m. **Marlin Edwards, retired plant breeder and consultant**
Plant breeding: A lifetime passion (O-11)

8:45 a.m. **Scott Jackson, University of Georgia**
The application of machine learning to trait prediction and the underlying genetic architecture of complex traits (O-12)

9:30 a.m. Graduate student lightning talks

9:50 a.m. **Beatrice Ifie, WACCI**
Introduction to newly formed African Plant Breeders Association (APBA)

9:55 a.m. **Rob Duncan, Education Committee Chair**
Introduction to ASTA/NAPB plant breeding video competition

10-10:30 a.m. Break ..... Longleaf prefunction area
Sponsored by TAMU Plant Breeding

10:30 a.m.-12 p.m. Posters (odd numbered presenting) ..... Loblolly/Loblolly prefunction area/Cypress

11:30 a.m.-1 p.m. Lunch and viewing of plant breeding video competition winners ..... Longleaf prefunction area/Longleaf

12-1 p.m. Industry Committee Lunch ..... Sourwood 4/5

1-3 p.m. **General session, Plant Breeding Innovations** ..... Longleaf

Moderator: Wayne Parrott, University of Georgia

1 p.m. **Fredy Altpeter, University of Florida**
Editing the complex sugarcane genome (O-13)

1:20 p.m. **Fenggao Dong, Bayer**
Doubled haploid technology and utilization in plant breeding (O-14)

1:40 p.m. **Marissa Simon, Corteva**
Achieving apomixis in sorghum (O-15)

2 p.m. **Charlie Li, University of Georgia**
Robot-assisted and machine learning-enabled in-field high throughput plant phenotyping (O-16)

2:20 p.m. **Katrien Devos, University of Georgia**
Trait mapping in non-model crops: Challenges and successes (O-17)

2:40 p.m. **Khushi Goda, North Carolina State University**
Optimal mating in Pinus taeda (O-18)

2:55 p.m. Announcements ..... Longleaf

3-3:30 p.m. Break ..... Longleaf prefunction area

TUESDAY, AUGUST 27 continued

3:30-5 p.m. **General session, Plant Breeding Perspectives** ..... Longleaf
Moderator: Melanie Harrison, USDA-ARS

- 3:30 p.m. **Susan Mayne, FDA**
  FDA's role in supporting plant biotechnology including genome editing (O-19)
- 4 p.m. **Roger Boerma, Georgia Seed Development**
  GICRS: Bringing UGA-developed varieties into the marketplace (O-20)
- 4:20 p.m. **Wayne Hanna, University of Georgia**
  Don't forget to follow and complete the scientific process (O-21)
- 4:40 p.m. **Qi Mu, Iowa State University**
  Exploring plant height plasticity observed in natural field environments (O-22)
- 4:55 p.m. **Donn Cummings, Borlaug Scholar Committee Chair**
  Introduction to Borlaug Scholars Program

5:30 p.m. Student networking – pool and beach options with swimming, volleyball, putt putt and table tennis

7 p.m. All-student cookout ..... Ironwood and Courtyard
Dinner on your own for non-students

7:30 p.m. Social for all participants, with entertainment by Cotton Bird ..... Ironwood

WEDNESDAY, AUGUST 28

7 a.m.-5 p.m. Registration ..... Hall leading to Longleaf

8-10 a.m. **General session, Awardee Presentations and lightning talks** ..... Longleaf
Moderator: Josh Clevenger, Mars-Wrigley Confectionery

- 8 a.m. **Shawn Kaeppler, Lifetime Achievement Awardee 2018, University of Wisconsin**
  Breeding for future food systems (O-23)
- 8:30 a.m. **Donald Bockelman, Plant Breeding Impact Awardee 2018**
  Reflections on 38 years of corn breeding and diversity (O-24)
- 9 a.m. **Jeffrey Endelman, Early Career Awardee 2018, University of Wisconsin**
  Genomics-assisted breeding in potato (O-25)
- 9:30 a.m. **Nathan Taitano, University of Georgia**
  Exploring a shared organ shape regulatory network in three solanaceous crops (O-26)
- 9:45 a.m. Graduate student lightning talks

10:05-10:30 a.m. Break ..... Longleaf prefunction area
Sponsored by UGA Plant Breeding

10:30 a.m.-12 p.m. Posters (even numbered presenting) ..... Loblolly/Loblolly prefunction area/Cypress

11:30 a.m.-1 p.m. Lunch ..... Longleaf prefunction area/Longleaf

Continued on next page

PROGRAM

Abstracts for all talks and posters are in the online program book at napb2019.uga.edu.

WEDNESDAY, AUGUST 28 continued

1-3 p.m. **General session, Breeding Specialty Crops** ..... Longleaf
Moderator: Cecilia McGregor, University of Georgia

1 p.m. **Shelley Jansky, USDA-ARS**
My mother is also my father: Tales of inbreeding and redemption through the eyes of a potato (O-27)

1:20 p.m. **Michael Mazourek, Cornell University and Row 7 Seed Co.**
Breeding for flavor: Field and kitchen co-selection (O-28)

1:40 p.m. **John Ruter, University of Georgia**
Herbaceous ornamental plant breeding at the University of Georgia (O-29)

2 p.m. **Patrick Conner, University of Georgia**
Pecan tree breeding at the University of Georgia (O-30)

2:20 p.m. **Ksenija Gasic, Clemson University**
Starting from scratch: 10 years of peach breeding program at Clemson University (O-31)

2:40 p.m. **Sarah Kostick, Washington State University**
Identifying fire blight resistance/susceptibility loci in apple for breeding use (O-32)

2:55 p.m. NAPB2020 and other announcements

3-3:15 p.m. Break ..... Longleaf prefunction area

3:15-4:15 p.m. **General session, Advances in Field Crop Breeding and Genetics** ..... Longleaf
Moderator: Mohamed Mergoum, University of Georgia

3:15 p.m. **Michael Casler, USDA-ARS**
Design optimization in field experiments (O-33)

3:35 p.m. **Jenny Koebernick, Auburn University**
Importance and impact of cotton breeding in the U.S. (O-34)

3:55 p.m. **David Bertioli, University of Georgia**
The peculiar genetics of peanut – breeding with a segmental allotetraploid (O-35)

4:15-4:30 p.m. Break ..... Longleaf prefunction area
Begin poster removal

4:30-6 p.m. NAPB Committee Breakout Sessions and General Meeting ..... Longleaf

6-7 p.m. Pre-dinner social featuring boiled peanuts
and entertainment by our own Albert Culbreath ..... Longleaf prefunction area
Complete poster removal

7-9 p.m. Banquet and award presentations ..... Longleaf

Evaluation of interspecific bermudagrass (Cynodon spp.) hybrids for turfgrass quality and persistence over years to drought, diseases, plant parasitic nematodes and other stresses in Tifton, GA.

THURSDAY, AUGUST 29

8 a.m.- 8 p.m.	DEPART CALLAWAY GARDENS FOR POST-MEETING TOURS*	
	Participants need to grab a boxed breakfast and board bus and vans in front of THE LODGE for transport to Plains. The first stop will be at UGA's Southwest Research and Education Center, 108 Experiment Station Rd., Plains, GA. The group will split in two groups as shown below.	
TIME	**ACTIVITIES**	
8 a.m.	Load bus/vans, drive to SWREC in Plains	
9:30-10 a.m.	Break in conference room; welcome by Assistant Dean for Research, Bob Stougaard and SWREC superintendent, Scott Rogers	
	Group 1	**Group 2**
10- 10:40 a.m.	Zenglu Li – soybean breeding Bill Branch – peanut breeding	Roger Boerma – Georgia Seed Development Terry Hollifield – Georgia Crop Improvement Association
10:40- 11:20 a.m	Roger Boerma – Georgia Seed Development Terry Hollifield – Georgia Crop Improvement Association	Zenglu Li – soybean breeding Bill Branch – peanut breeding
11:20 a.m.- 12:10 p.m.	Jimmy Carter boyhood farm/museum	
12:10-1 p.m.	Lunch in SWREC Conference room Board bus/vans and depart for Tifton	

**Closed-toe shoes or boots are recommended. Bring hats and sunscreen. Water will be provided throughout the tour.*

Zenglu Li, Professor/Soybean Breeder at University of Georgia visited an early planted soybean field in Vienna, GA.

PROGRAM

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THURSDAY, AUGUST 29 continued

8 a.m.- 8 p.m. POST-MEETING TOURS CONTINUED*

After the morning tours and lunch at the Plains Research and Education Center, the bus and vans will travel to the Tifton campus, National Environmentally Sound Production Agricultural Laboratory [(NESPAL) 2353 Rainwater Rd., Tifton, Georgia]. We will spend about 30 minutes here for a break and welcome from the Assistant Dean, Dr. Joe West. The group will split in two groups as shown below.

TIME	ACTIVITIES	
1-2:30 p.m.	Travel to Tifton Campus	
2:30-3 p.m.	Break at NESPAL, welcome by Assistant Dean	
	Group 1	**Group 2**
3-4 p.m.	Peng Chee – cotton breeding Corley Holbrook – peanut breeding Bill Anderson – forage breeding	Patrick Conner – muscadine breeding Brian Schwartz & Wayne Hanna - turf/ornamentals Peggy Ozias-Akins - centennial garden
4-5 p.m.	Patrick Conner – muscadine breeding Brian Schwartz & Wayne Hanna - turf/ornamentals Peggy Ozias-Akins - centennial garden	Peng Chee – cotton breeding Corley Holbrook – peanut breeding Bill Anderson – forage breeding
5:15 p.m.	Hotel check-in	
5:45 p.m.	Travel to Blackshank Farm	
6-7 p.m.	Pre-dinner social featuring boiled peanuts	
7 p.m.	Dinner	
8:15 p.m.	Bus and vans return to hotel; bus/van transport will be provided to Atlanta Hartsfield airport on Friday morning	

**Closed-toe shoes or boots are recommended. Bring hats and sunscreen. Water will be provided throughout the tour.*

The Centennial Garden on the Tifton Campus

New hybrid of native Indian Pink (Spigelia marilandica).

ORAL ABSTRACTS

O-01

Sources of genetic variation in breeding materials, and how they can be enhanced

Jeff Bennetzen | University of Georgia | maize@uga.edu

Advances in the quality, durability and yield of crops have been an outcome of selective mating and progeny testing by farmers and plant breeders for thousands of years. The continued success of this traditional selection strategy is a testimony to the high level of diversity in most crops. Much of this diversity is derived from the unusually high level of genome instability in flowering plants, particularly in the generation of new genes and new genetic regulation. My lab has been among those that have characterized many of these genome-change processes, at levels of both the mechanisms and rates of change. Current crop improvement strategies have greatly accelerated and made more precise the use of traditional tools for breeding and selection, but have done little to change the level or nature of useful genetic variation. However, several recent technical and conceptual advances now suggest strategies for generating exceptional improvements in the availability of valuable genetic diversity. These advances include greater (and more controlled) use of relatives of wild crops, more directed and efficient generation of pre-selected genetic change, and the employment of other organisms in the environment (especially the microbiome) to improve crop performance. Each of these three strategies will be discussed and demonstrated using examples from the Bennetzen laboratory.

O-02

NIFA: Unlocking novel wild alleles in cultivated peanut to increase disease resistance and productivity

Soraya Leal-Bertioli | University of Georgia | sorayab@uga.edu
Tom Stalker, North Carolina State University
Corley Holbrook, USDA-ARS, Tifton
Scott Jackson, University of Georgia
Peggy Ozias-Akins, University of Georgia
David Bertioli, University of Georgia

The peanut crop suffers from numerous pests and diseases. Development and adoption of resistant varieties is the most effective way to control disease and reduce yield losses. Peanut has very low genetic diversity, which led us to conclude that genetic potential in the cultivated genotypes was near reaching its limit and new alleles from crop wild relatives were needed. Wild species are a source of strong resistance alleles, but have undesirable agronomic traits, such as small seeds and spreading habit, a disincentive to their use in breeding. We have identified genomic regions that harbor disease resistances in wild species as the first step of implementation of marker-assisted selection that can speed the introgression of wild disease resistances and the elimination of linkage drag. The foundation for this project was laid over 18 years ago with the realization of the complexity of peanut genetics and the creation of diploid populations to start to understand genetics under reduced complexity. Over the years, genetic resources, plant materials, information and genome sequence of the diploid progenitors and the cultivated peanut allows us to efficiently use wild alleles for the improvement of the peanut crop, with emphasis on disease resistance. This has only been possible with the conversion of three elements: (1) free access to species from the USDA germplasm bank (2) knowledge of potential of wild species and of methods to introgress alleles into the tetraploid species (3) genome sequence of the wild progenitors and the cultigen. We aim to create advanced lines with introgression of wild species with resistance to late leaf spot and nematode, and the establishment of a bank of wild derived synthetic allotetraploids. These materials will be deposited in the USDA National Plant Germplasm System for use in breeding programs.

O-03
NIFA: Merging breeding and gene editing: Lessons from tomato

Zachary Lippman | Cold Spring Harbor Laboratory | Lippman@cshl.edu
Samuel Hutton, University of Florida

A major challenge in modern agriculture is to find new approaches to expedite breeding and make its outcomes more predictable. Revolutions in the breeding of many crops point to a recurring theme: selection for beneficial genetic variation in the universal florigen flowering pathway, which includes the flowering hormone florigen and its antagonist antiflorigen. A prominent example is the classical antiflorigen *self pruning* (sp) mutant of tomato, which provided compact 'determinate' growth that enabled large-scale field production for both processing and fresh-market production. We found that induced mutations in components of the tomato florigen pathway can be exploited to quantitatively modify plant architecture and yield. In this pre-breeding project, we introgressed mutant alleles from our "florigen pathway toolkit" into large-round and cherry type tomato inbreds to assess the impact on fresh market tomato production, with the goal of identifying specific alleles and allelic combinations that improve yield. Field-based evaluations of shoot architecture and yield components for a collection of single and higher order mutant combinations in both homozygous and heterozygous states revealed clear trends towards improved productivity, with the magnitude of effects varying with genetic background. In parallel, we have used CRISPR/Cas9 gene editing to expand our toolkit to customize tomato for various agronomic conditions.

O-04
NIFA: Robotic field measurements for plant breeding and crop management

George Kantor | Carnegie Mellon University | kantor@ri.cmu.edu

The robotic technologies of mobility, sensing, analysis, and manipulation are rapidly emerging as useful tools for agriculture. In this talk, I will present some recent work my group has done to address these problems, including the development vehicles that can autonomously navigate agricultural environments, and the use of imaging, modeling, and deep learning to measure agricultural parameters in the field. I will also discuss how we have combined the resulting tools for applications to problems such as phenotyping for plant breeding and yield prediction for production.

O-05
NIFA: Breeding for food safety

Allen Van Deynze | University of California- Davis | avandeynze@ucdavis.edu
Maeli Melotto, University of California-Davis
Michelle Jay-Russell, University of California-Davis

The demand for nutritious and safe food will likely increase as the human population is expected to reach 9.1 billion by 2050 along with increasing urbanization. Healthy eating of fresh fruits and vegetables is part of an integrated strategy to decrease the risk of serious diseases. More than 9 million foodborne illnesses in the United States are estimated to be caused by major pathogens each year and 51% has been attributed to plant commodities. Leafy vegetables are associated with the majority of illnesses (2.2 million; 22%). A conference was held June 5-6, 2019 at Davis. The workshop goals were to 1) Connect plant scientists, breeders, extension specialists, food safety experts to discuss collaborative efforts and multidisciplinary approaches geared towards eliminating the occurrence of human pathogens in crop production systems and 2) Identify knowledge gaps, innovative strategies, and research priorities in this emerging field of breeding for crop safety. Sixty-five plant scientists, breeders, extension specialists, food safety experts discussed collaborative efforts and multidisciplinary approaches geared towards eradicating the occurrence of human pathogens in crop production systems. The conference included plenary talks, panel discussion, and break-out sessions. There was overwhelming support for advancing research towards breeding crop with the goal of increasing the safety of food supply chain. Short to medium term efforts were identified as follows: a) Continue foundational research to create crucial knowledge of plant interactions with human pathogens and contamination of food with mycotoxins and allergens b) Initiate pre-breeding strategies to validate existent genetic variability, robustness, and heritability of target traits. The organizing committee and moderators of the breakout groups, with input of all attendees and breakout group reports, will provide recommendations moving forward in a form of white paper, to be made available widely to reach audiences across disciplines.

O-06

NIFA: Transdisciplinary plant phenomics and unmanned aerial system phenotyping for maize crop improvement

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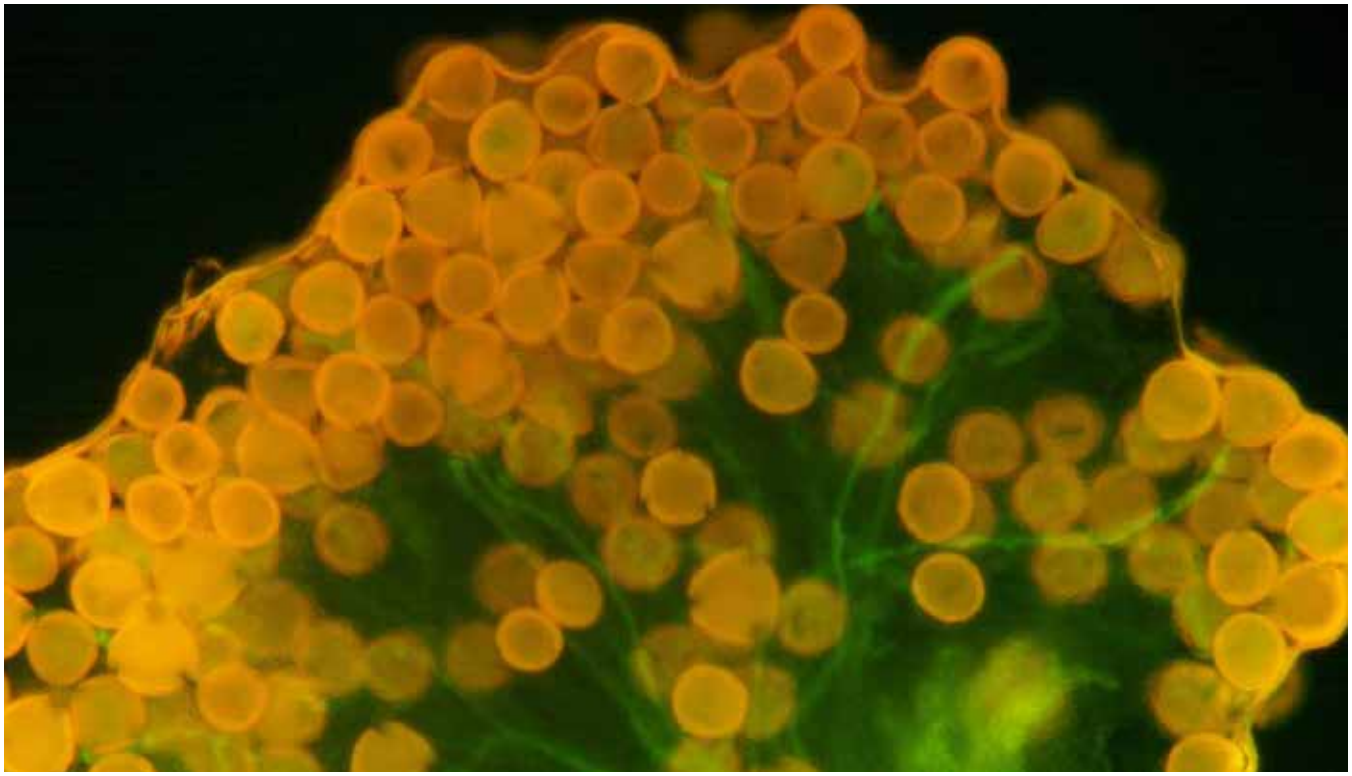
Use of unmanned aerial systems (UAS, aka drones) in high throughput field phenotyping has largely focused on measuring routine traits faster or better. While this research has been beneficial, more exciting opportunities for crop improvement exist in measuring features that can accurately predict end products such as yield; traits not previously feasible to measure manually, novel image features, and temporal image features through the growing season. Over three years, near weekly UAS flights were conducted on the Texas maize (*Zea mays* L.) Genomes to Fields (G2F, www.genomes2fields.org) GxE field experiment with both rotary and fixed wing aircraft, capturing RGB and multispectral imagery. In 2017, 250 diverse hybrids grown in three different management conditions (two replicates) were used to evaluate UAS abilities to estimate plant height, growth curves and feature-based yield predictions. Temporal height and vegetation index pipelines were among the first developed and these extracted phenotypes have shown to be repeatable. Height, growth curves and vegetation index phenotypes could correctly predict the top 10% yielding genotypes in our experiments, even a month before harvesting. Such insights could speed up breeding decisions and increase the number of genotypes feasible to screen. We are striving to improve predictions by incorporating other previously unmeasurable predictive features. Two important community resources have been made available through this project; 1) R code on Github (plotshpcreate.R) to help researchers generate shapefiles from their fieldbooks and 2) the first complete seasons dataset of UAS information for others to develop and test feature extraction algorithms (https://doi.org/ 10.25739/4ext-5e97). This USDA-NIFA-AFRI enabled project has already shown that UAS can be a useful and predictive tool for applied plant breeding. Resources and information developed will be instrumental in implementing phenomic selection; additionally, by identifying novel UAS features, we may identify relevant new biological phenomena to be explored though subsequent fundamental research.



Pollen tube growth on the stigma of a self-pollinated Abelia x grandiflora (400x).

O-07

NIFA: Facilitating the increased use of genetic resources: Custom core collections and genomic prediction with carrot as a model crop

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Germplasm collections are underutilized because of the difficulty breeders have in identifying relevant accessions for specific traits or environments. To efficiently use the diversity present in large germplasm collections, breeders often identify a subset of accessions that represent the larger collection. Methods to identify these subsets, called core collections, do not consistently capture functional diversity, and breeders would benefit from methods that help create custom core collections using existing data from variety trials or breeding programs. The rapid development of genetic and genomic technologies in recent years has led to opportunities for using genomic information for screening and selection at a level that has not been possible until recently. Carrot is a good model crop to develop methodology because it has an unusually high amount of genomic information available for a non-commodity crop, including a complete genome sequence. Making use of high-density genomic data and existing phenotypic data from a collection of 433 domesticated carrot (*Daucus carota* L.) accessions, we tested whether it is possible to develop custom subsets of accessions for specific breeding purposes. We found that for this collection, representative strategies were effective in developing core collections that capture the diversity of the collection, but they were no better than random sampling, likely because the collection itself is not strongly subdivided. Custom strategies generated subsets that differed from the total collection with altered genetic, geographic, and phenotypic compositions. When used as training populations for genomic prediction of the other accessions in the collection, however, these custom cores did not produce a substantial improvement over traditional core collections. Increasing the size of the core did improve prediction accuracy, suggesting that it is possible to improve the usefulness of core collections by identifying custom subsets that are large enough to represent the functional genetic diversity present in the collection.

O-08

NIFA: Genomics-enabled chromosome engineering for alien introgression and genome characterization in wheat

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The limited genetic variability of the wheat genome has increasingly become a bottleneck in wheat improvement. The polyploid origin of wheat had left tremendous genetic variation in its ancestors and relatives, which can be brought back to the wheat genome by chromosome engineering. Thus, the wheat genome can be enriched and diversified by harnessing the genetic variation of its ancestors and relatives. Recent advances in genomics have provided great potential to improve the efficacy and throughput of chromosome engineering in alien introgression and genome studies. Here we report our research progress toward the enrichment and understanding of the wheat B genome, whose ancestor remains obscure, by genomics-enabled chromosome engineering and comparative genome analysis. We incorporated the genes for resistance to rusts, scab, tan spot, and Septoria nodorum blotch, and those for tolerance to salt and waterlogging from *Aegilops speltoides* (2n = 2x = 14, SS) and *Thinopyrum elongatum* (2n = 2x = 14, EE) into wheat and produced over one thousand B-S and B-E recombinants by *ph1b*-induced homoeologous recombination. In addition, we constructed composite bin maps of the B genome based on B-S and B-E recombination and wheat 90K SNP assay, and developed a unique physical framework useful for further study of the B genome and its potential ancestors. Also, we determined the nucleotide position of the *ph1b* deletion and developed *ph1b*-specific DNA markers, which were not available before. They are extremely useful in *ph1b*-mediated gene introgression and genome study. Moreover, we found that *Ae. speltoides* was involved in the origin of the wheat B genome, but should not be considered an exclusive donor. The B genome might have a polyphyletic origin with multiple ancestors. Therefore, homoeologous recombination-based chromosome engineering enriches and diversifies the wheat genome, and facilitates genome studies of wheat and its relatives, especially in the genomics era.

O-09

NIFA: Opportunity is knocking - a white paper on establishing an organic winter wheat breeding pipeline in the Great Plains

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This presentation will provide an overview of opportunities and challenges of establishing a successful organic winter wheat breeding pipeline in the Great Plains. The presenter is from Heartland Plant Innovations (HPI), a private company that provides Advanced Plant Breeding Services to plant science industries. In 2018, Heartland Plant Innovations (HPI) was awarded an AFRI conference grant (# 2019-67013-28961) to plan and host an "Organic Wheat Conference." This event, held in January 2019, brought together key regional supply chain stakeholders to discuss the industry challenges and opportunities and identify the organic breeding needs for Winter Wheat in the Great Plains. 80 key industry representatives actively engaged in the organic wheat market supply chain attended and participated in the discussions. The conference objectives were to 1) Bring together key regional supply chain stakeholders to discuss the challenges and opportunity per industry segment; 2) Assess the feasibility of developing an independent breeding pipeline that delivers locally-adapted organic wheat varieties; 3) Develop a concise list of breeding targets and traits; and 4) Establish a strategy to build an organic breeding pipeline. The conference proceedings were summarized in an industry wide white paper entitled *Opportunity is Knocking: Establishing an Organic Winter Wheat Pipeline* in the Great Plains. It highlights priorities for breeding varieties to optimize organic wheat production and the impact of varieties developed for organic wheat production. It also reveals results of a producer survey conducted prior to the conference.

O-10

NIFA: Optimizing the convenience, nutrition, and taste of yellow dry beans (*Phaseolus vulgaris L.*) to promote pulse consumption in the U.S.

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Dry beans (*Phaseolus vulgaris* L.) are rich in key nutrients deficient in American diets, including dietary fiber, iron, and potassium, but would benefit from further nutritional optimization. Consumption of dry beans is low in the U.S., which may be due to unmet consumer expectations for convenience and taste. The yellow bean market class is largely unknown to Americans and has many attributes consumers demand. The goal of this project is to develop yellow bean varieties for U.S. markets with improved convenience (fast cooking), nutrition (iron bioavailability), and taste (texture, flavor) to reduce barriers to dry bean consumption. To address this goal, a yellow bean diversity panel was assembled with 308 genotypes including landraces, breeding lines, and varieties from around the world. Cooking time evaluation of the panel revealed numerous genotypes that cooked in under 20 minutes. The fastest Can44, from the International Center for Tropical Agriculture, Colombia, cooked in less than 15 minutes. In addition, a recombinant inbred line population of 244 lines developed from a cross between a fast cooking yellow (Ervilha) and a slow cooking yellow (PI527538) was grown in Michigan for two years and evaluated for cooking time, flavor, and texture. Cooking times ranged from 18 to 40 minutes, and flavor variability was characterized within the population. In regard to nutritional attributes, *in vitro* assays revealed some fast cooking yellow bean genotypes have high iron bioavailability. This finding was validated in an *in vivo* animal (*Gallus gallus*) feeding trial. Over the course of the 6 week experiment, animals fed yellow bean diets (especially Manteca type) had significantly ($p \leq 0.05$) higher total body hemoglobin iron than animals fed a white or red kidney bean diet. This work serves as the foundation in the development of fast cooking, nutritious, and appealing yellow bean varieties for U.S. consumers.

O-11
Plant breeding: A lifetime passion

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As a Seed Research Management professional during my lifetime, I have often been involved in business prioritization exercises which resulted in a reduction of crop scope and a cessation of plant breeding for "minor" crops. As more and more "minor" crops become orphaned, improvement in these crops slows or stops. These crops provide an opportunity for professional plant breeders to take up a "hobby" of breeding in their free time. I have been breeding ornamental peppers as a hobby for 40 years. I enjoyed the hands-on engagement in my first true love, plant breeding, during my lifetime of management. I cultivated this project with an eye toward my retirement years. I am now retired and relish the opportunity to continue my passion for plant breeding. Although modern technologies are powerful tools for plant breeding, remarkable improvements in a crop can be achieved with old-fashioned but persistent long-term selection. I will discuss my 40 years of breeding peppers and a more recent initiative in popcorn breeding. Hopefully, like-minded breeders with a passion for their science will see that a sideline of "hobby" breeding can be low-cost, rewarding and help prepare them to continue their passion into retirement.

O-12
The application of machine learning to trait prediction and the underlying genetic architecture of complex traits

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Changes in the regulation of gene expression can play an important role in phenotypic variation and evolution. Thus, gene expression, as measured by transcriptomes, can be considered a bridge between the genotype and phenotype. Complex traits typically involve many genes, each of which may have small effects on phenotypic variation. Recent studies have shown that noncoding variants affect phenotypic variation, presumably via gene regulation. In this study, we used transcriptome data from early developmental stage tissues and machine learning to create transcriptome-based predictive models to predict adult traits in common bean and maize. The predictive accuracies were as high as 0.93 for seed weight in common bean and 0.83 for flowering time in maize, estimated from cross-validations in different prediction methods. Transcriptome based prediction closely matched predictive accuracies from genomic best linear unbiased prediction (GBLUP) and, in some cases, outperformed GBLUP. The importance of genes were ranked based on the order of their elimination using recursive feature elimination. We found that the 500 most important genes in the predictive model were significantly enriched in GO categories were known to be involved in the regulation of a specific trait, further supporting that variation in gene expression plays a role in the phenotypic variation. We further identified expression quantitative trait loci (eQTLs) for genes and performed association analysis between the eQTLs and traits. We found significant correlations between the importance of genes in transcriptome-based prediction and the significance of their eQTLs in the association analysis. Our study showed that adult phenotypes can be predicted with early stage transcriptome and provided evidences to support that phenotypic variations might arise from noncoding variations affecting gene expression through complex cis- and/or trans-regulation networks.

O-13
Editing the complex sugarcane genome

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Genome editing tools such as CRISPR/Cas9 have been employed in several crops. They enable precise targeting and introduction of double strand DNA breaks which are proceeded by cellular repair mechanisms, such as NHEJ or HDR, critical in endogenous gene editing or correction. Highly efficient NHEJ generates an abundance of random insertions and deletions (indels). Frameshift mutations associated with these indels of unspecified size and sequence might result in loss of function phenotypes of agronomic importance. Gain of function mutations, on the other hand, generally require precise nucleotide editing in the target gene and replacement of inferior alleles. This can be accomplished with the aid of a homologous repair template and the cellular HDR mechanism. We present a highly efficient HDR mediated precision nucleotide editing in multiple alleles of the acetolactate synthase (ALS) gene in the highly polyploid sugarcane which confer herbicide resistance. Faithful transmission of superior ALS alleles with introduced target mutations at 574 and/or 653 amino acid locations to vegetative progenies was confirmed with amplicon sequencing using Sanger chain termination, PacBio SMRT sequencing and evaluation of herbicide resistance.

O-14
Doubled haploid technology and utilization in plant breeding

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Doubled haploid technology is very critical in plant breeding. Here we briefly introduce the benefits of doubled haploids and common practices in creating, identifying, and doubling haploids as we as caring for doubled haploids.

O-15
Achieving apomixis in sorghum

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O-16
Robot-assisted and machine learning-enabled in-field high throughput plant phenotyping

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High throughput plant phenotyping (HTPP), measuring traits and assessing plant development and performance, has become a rapidly evolving focus area in agriculture, but remains a major bottleneck in crop improvement. In particular, phenotyping platform development and data analytics are two main challenges in field-based high throughput plant phenotyping. UGA B-SAIL has been focusing on the following two areas: 1) robotic system integration and development; 2) data analytics using computer vision and machine learning. In the first area, we have developed a multi-tier HTPP platforms including a) a ground-based GPhenoVision system consisting of a high-clearance tractor and multiple high resolution phenotyping imaging sensors and customized image acquisition software, b) unmanned aerial systems that integrate customized image acquisition for much higher throughput than ground systems, quantifying plant height and canopy growth rate, biotic and abiotic stresses, initiation and progression of flowering, and c) unmanned ground vehicles that can autonomously navigate between rows with centimeter accuracy while acquiring LiDAR, thermal and RGB images. In the second area, we have developed machine learning based data analytics to extract phenotypic traits from 3D point cloud and 2D imagery. For instance, we have developed algorithms for 3D cotton boll mapping, internode distance measurement, and branching pattern characterization. In addition, deep convolutional neural networks have been used to detect various organs or sub-plant regions in images including seedlings, flowers, cotton bolls, and inter-nodes. Accurate detection results can be used for tracking and counting fruit and yield estimation.

O-17
Trait mapping in non-model crops: Challenges and successes

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With the advent of next-generation sequencing technologies, trait mapping in non-model crops has greatly increased in efficiency. Even in species with a dearth of genomic resources, including those that lack a reference genome, genotyping-by-sequencing (GBS) can provide large numbers of robust single nucleotide polymorphism (SNP) markers. Early pipelines for the analysis of GBS data, however, were developed for application in diploid species and had limitations in the type of reads that could be analyzed. We therefore developed UGbS-Flex, a flexible pipeline that can use single-end as well as paired-end reads and which has been successfully applied in species with different ploidy levels and breeding systems. Using GBS-derived SNP markers, we have developed genetic maps in a range of non-model monocot crops, including finger millet, seashore paspalum and switchgrass. The latter two are obligate outcrossing species, where mapping was further complicated by a lack of knowledge on the linkage phase of markers. The robust maps are being used to aid in the validation of genome assemblies and for the mapping of morphological and expression traits.

O-18
Optimal mating in *Pinus taeda*

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Fikret Isik, North Carolina State University

Loblolly pine (*Pinus taeda*) is the most important tree crop in the US, planted over 25 million acres in the south. The Tree Improvement Program at North Carolina State University manages the genetic improvement of Loblolly pine. Loblolly pine has a high genetic load and suffers greatly from inbreeding depression. It is a challenge to balance two important but contrasting goals of capturing as much genetic gain as possible while managing short- and long- term inbreeding. While methods and algorithms for animal breeding are well-established, an efficient algorithm suited to this species remains elusive. Developing an algorithm to design mating that optimizes genetic gain whilst putting constraints on relatedness is imperative for loblolly pine breeding. Towards this goal, we have adopted evolutionary genetic algorithms for optimized mating design and breeding. PineBreed is an optimization algorithm developed that can utilize pedigree-based relationships to create optimal mating list for breeding. Modified differential evolution algorithms have been applied to create mating lists that can be realized to give maximum return of genetic gain in future progeny while minimizing the increase in average co-ancestry in the population. Using the PineBreed software and optimizing the mating list from 964 monoecious loblolly pine tree candidates, resulted in 35% increase in genetic gain and no inbred progeny. The completion of this study will see the development of a suite of software that is able to not only utilize genetic relationships from pedigree but also utilize genomic relationships derived from SNP markers. The framework and methods adapted for loblolly pine breeding have relevance to breeding of other monoecies species as well.

O-19
FDA's role in supporting plant biotechnology including genome editing

Susan Mayne | CFSAN | FDA

Bulldog 805 Alfalfa Inter-seeded in Tift. 44 Bermudagrass

O-20
GICRS: Bringing UGA-developed varieties to the marketplace

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Surveys have reported that many companies find it difficult to conduct business operations with universities. These challenges include the development of license agreements with marketing organizations for new university-developed cultivars. At the University of Georgia (UGA) we attempted to overcome some of these challenges by the creation of a virtual business named Georgia's Integrated Cultivar Release System (GICRS). This virtual business consists of four separate units; the UGA-Institute of Plant Breeding, Genetics, and Genomics (UGA-IPBGG), the UGA Research Foundation (UGARF), the Georgia Seed Development (GSD), and the Georgia Crop Improvement Association (GCIA). The UGA-IPBGG serves as the research and development unit in the business, UGARF is the owner of the intellectual property (cultivar) and develops the license agreements, GSD serves as the production arm of GICRS and increases the breeder seed or plant material for the licensee and the GCIA provides the quality control and auditing for the business. We believe that GICRS serves as an effective bridge for taking new UGA-developed cultivars from the plant breeder and delivering them to regional, national, and international turfgrass producers, plant nurseries, and seed companies.

O-21
Don't forget to follow and complete the scientific process

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Research programs that follow and complete the scientific process usually have the most impact. Impact is so important today for additional funding and for personal satisfaction and encouragement that one's efforts are making a difference. Parts of the scientific process are more enjoyable to complete than other parts. Asking the right questions to develop a hypothesis and designing the experiment to provide reliable answers are very important. Over the years I have found that conducting the experiment is one of the easiest and most enjoyable parts of the process. It is important to keep data analyses current. Then there is interpretation and summarization of the data which some of us would rather delay completing. Peer review of our research can be both intimidating and educational. However, I have always felt that one should feel confident in submitting research for peer review if one followed the scientific process. Publishing the scientific information is not the end of the scientific process. I believe that one must 'sell' your research so that others will use your product(s), apply your techniques, and/or use your research to branch out into new areas of science.

O-22
Exploring plant height plasticity observed in natural field environments

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Plant phenotypes are determined by genetics, environment, and their interactions. Phenotypic plasticity describes that a genotype behaves differently when exposed to different environments. When multiple genotypes are showing different levels of phenotypic plasticity, genotype by environmental interactions (G x E) are present. Unraveling G x E is crucial to understanding plant local adaptability, which can be utilized in breeding, and provide new solutions in times of climate change. Recently, we established a joint genomic regression analysis (JGRA) framework to dissect the complex flowering time plasticity observed in natural environments by leveraging an explicit environmental index. In this study, we hypothesized that plant height G x E interactions can be unraveled and explained in a similar manner. The objectives were to 1) uncover the patterns of sorghum plant height plasticity in diverse environments; 2) predict performance in new environments; 3) identify and dissect the genetic determinants to explain the observed G x E interactions. Our results showed that varied degree of plasticity in plant height of sorghum lines could be explained, modeled, and predicted with a biologically meaningful environmental index. High prediction accuracy was achieved by using this environmental index. The effects of three height QTLs changed dynamically across environments, contributing to the observed G x E. In conclusion, by combining environmental and genomic components, we were able to explain and predict sorghum plant height under natural field conditions.

O-23
Plant breeding for future food systems

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Crops and cropping systems have evolved over centuries. A grand challenge for plant breeders is often stated as meeting the food, feed, and fiber needs of a rapidly growing population. However, that simple call-to-action is no longer sufficient. Future generations will require a wider diversity of food products that more completely meet nutritional needs. Those crops will need to be produced in systems that sustain and improve the environment and planet adding challenges to the breeding process. Future plant breeders will find value in understanding ethnobotany and characterizing and harnessing new species and germplasm. Overcoming the lottery of segregation and recombination via gene-editing will accelerate production of cultivars and utilization of germplasm. Advanced phenotyping approaches will support variety development and crop deployment across landscapes. The path to future systems involves complex interactions of human preferences, governmental policy, marketing and supply chains, as well as breeding-related research. Development of varieties with novel characteristics will be a critical component of achieving a vision for our future sustainable planet.

O-24
Reflections on 38 years of corn breeding and diversity

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Many changes have occurred during a 38 year career in corn breeding. Breeding programs have evolved from conventional breeding methods with smaller, more autonomous, locally based efforts and changed into large, complex multidisciplinary systems focused on marker assisted breeding and other new technologies. These new systems require high levels of coordination and timing, and create greater efficiencies and potential gain. Skill sets and opportunities have also changed with the growing processes. The need to maintain genetic diversity has remained a constant, and is vital to the health of any large breeding program in order to continue genetic gain. I will review some of the changes during my career and discuss some opportunities and hurdles for diversity efforts. The challenges of creating high value diverse lines can be large, but the rewards can be great and are essential to continued long term gains.

O-25
Genomics-assisted breeding in potato

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As a PhD student and postdoc, I had the opportunity to develop new methods and software for genomic selection. When I joined the faculty at UW-Madison in 2013 and became a potato breeder, one of my main goals was to implement genomic selection. In 2018 we achieved this objective, and I will describe several advances for using genome-wide markers in autotetraploids that were made along the way. I will also describe how we are using new computational tools for tetraploid linkage analysis to discover and track haplotypes in the breeding program.

O-26
Exploring a shared organ shape regulatory network in three solanaceous crops

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Shape of harvested organs in crop species is important for ease of harvest, processing, and shipping, and can limit supply in vegetables and other horticultural crops. Mounting evidence indicates ovate family protein (OFP) and Tonneau1 recruiting motif (TRM) genes interact to regulate organ shape similarly across plant species. We sought orthologous genes regulating the shape of multiple organs in multiple species, beginning with the harvested organs of crops in the family Solanaceae, which includes the tomato model organism for fleshy fruit development. Following a candidate gene approach, we performed marker-trait association tests with organ shape genes known from species including Arabidopsis and tomato on a population of F2 pepper plants segregating for fruit shape (n=178) and fruit weight (n=181), and a population of F2 potato plants segregating for fruit (n=155) and tuber (n=209) shape. We found a significant ($p<2x10^{-16}$) association between potato SlOFP20 ortholog marker genotype and tuber shape. Using comparative genomics, we identified a likely deletion allele with an organ-lengthening effect analogous to the large deletion of the tomato SlOFP20 promoter. However, pepper orthologs of SlOFP20, SlOvate, and SlWUS were unassociated with fruit shape in our population. Instead, markers around another Ovate-associated TRM ortholog were significantly ($p=7.48x10^{-16}$) associated with pepper fruit shape. This suggests potential conservation of the TRM-OFP network as central to organ shape development across crop species. Progeny tests are ongoing to validate this gene's effect, along with genomic analyses to further explore functional genomic diversity in early vegetable domesticates

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O-27
My mother is also my father: Tales of inbreeding and redemption through the eyes of a potato

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For over a century, potato breeders have fought against the constraints imposed by tetraploidy and asexual reproduction. Instead of continuing to push against these roadblocks, we have decided to transform potato into a more malleable system. By converting the crop into a diploid in which inbred-hybrid cultivars are grown from true seed, we expect to dramatically enhance potato breeding efficiency. Using germplasm from cultivated and wild relatives, we are able to create diploids via parthenogenesis and overcome self-incompatibility. The most common manifestation of inbreeding depression is poor fertility. Through brute force pollination efforts, we have generated recombinant inbred lines. Hybrids express impressive vigor for foliage, fertility and tuber production. In a parallel project, we are investigating methods to optimize seed production and seedling vigor.

O-28
Breeding for flavor: Field and kitchen co-selection

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Plant breeders are often forced to shelve innovations because they are not seen as a "right" for the marketplace. As a result, many of us make conservative pairings of parents and prioritize commodity aesthetics. By engaging chefs early in the selection process, we can gain new insight into the functionality and potential of our crops — and find value in diversity that would otherwise be thrown away. I'll share a participatory model that was discovered in discarding traditional rubrics for butternut squash and how we are applying this model to crops that fit new uses in the kitchen, reduce waste and improve sustainability.

O-29
Herbaceous ornamental plant breeding at UGA

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The University of Georgia has had an herbaceous ornamental plant introduction program for many years that basically operated as 1) finding novel plants and 2) introducing them. In 2011 I was tasked with the development of a formal herbaceous ornamental plant breeding program. Genera evaluated in the program so far include Abutilon, Agapanthus, Baptisia, Dissotis, Helianthus, Heliopsis, Hibiscus, Kniphofia, Pavonia, Stokesia, Thermopsis, and Tibouchina. Research methods have included traditional breeding (intra- and interspecific hybrids), ploidy manipulation (all the way up to 16x), and mutagenesis. An overview of the program and work with plants in the Malvaceae will be discussed.

O-30
Pecan tree breeding at the University of Georgia

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Pecan (*Carya illinoinensis*), is a native North American crop that is grown throughout the southern United States. Pecan is one of Georgia's most valuable horticultural crops, and Georgia is the leading pecan producing state. The pecan scab fungus (*Venturia effusa*) is the most economically damaging pathogen of pecan in the humid southeastern U.S. The development of resistant cultivars with commercial nut quality is the major focus of the UGA pecan breeding program, one of only two breeding programs in the nation. Pecan trees are large and long-lived trees with a juvenile period of 5-10 years. These characteristics, in combination with a high degree of herterozygosity maintained through dichogamy, have limited genetic studies in this crop. Consequently, the genetic control of most important traits, including disease resistance and nut quality, are poorly understood. Effective phenotypic selection and testing methods are therefore paramount in the development of new cultivars. This talk will focus on the collaboration that has been developed between the breeding program and pecan producers and nurserymen in the testing and release of new cultivars.

New orchard of 'Avalon' pecan, a new scab-resistant release from the University of Georgia.

O-31
Starting from scratch: 10 years of peach breeding program at Clemson University

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Environmental challenges, changes in production systems and human preferences are driving the need for development and release of new peach cultivars for sustainable production. The South Carolina peach industry is the second largest producer of fresh market peaches in the United States, after California. Peaches in SC are produced on ~7,000 ha with an annual gross income of $80M. Most of the cultivars grown in the Southeastern US are developed in breeding programs that differ in environmental conditions, such as CA, emphasizing the need for new improved cultivars suited for our conditions. The peach breeding program at Clemson University was re-established in 2008, after 25 years of dormancy, to develop high quality, disease resistant peach varieties adapted to environmental conditions specific to Southeastern US. The emphasis of the program is on combining high quality and consistent productivity with improved resistance to bacterial spot and brown rot and with nutritional composition and abiotic stress tolerance being the latest focus. To accomplish this goal, both traditional and molecular breeding approaches are utilized. Sources of new and improved traits were sought via characterization and utilization of the peach genetic diversity and development and utilization of genomic technology to improve breeding efficiency. The program has been actively involved in development and application of modern technological tools in breeding programs (www.rosbreed.org; www.rosaceae.org) and 10 years of progress will be presented.

O-32
Identifying fire blight resistance/susceptibility loci in apple for breeding use

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Breeding for resistance offers a long-term solution to fire blight, a devastating bacterial disease (caused by *Erwinia amylovora*) in apple. Most resistance alleles at fire blight quantitative trait loci (FB QTLs) were characterized in diverse *Malus* species with poor fruit quality, reducing breeding utility. The objective of this study was to identify FB QTLs in a pedigree-connected apple reference germplasm set that provides allelic representation of important breeding parents (IBPs) in three US public apple scion breeding programs. Twenty-seven IBPs were represented in a replicated planting of 556 individuals with Honeycrisp being the most highly represented IBP. Seedlings and progenitors were genotyped using the International RosBREED SNP (single nucleotide polymorphism) Consortium Apple 8K Infinium® array. Multiple actively-growing shoots per tree (~3 trees/individual) were inoculated with *E. amylovora* 153n in 2016 and 2017. Response for each inoculated shoot was quantified as proportion of current season's shoot length that was blighted (SLB). Seedling responses ranged from highly susceptible to highly resistant and were relatively consistent between years (ρ= 0.75; p-value $<1\times10^{-4}$). Best linear unbiased predictions (BLUPs), adjusted by the overall SLB mean, were estimated for seedling effects within and across years. Adjusted BLUP values ranged from 0.04 to 0.97 SLB and were used as phenotypic values in FB QTL analyses, which were conducted using FlexQTL™ software. FB QTLs were identified on chromosomes 6, 7, 8, and 15, accounting for approximately 42% of phenotypic variation. Honeycrisp half-sib families showed segregation for the major-effect FB QTL on chromosome 6. This FB QTL region was further characterized for its haplotypes, revealing resistance haplotypes of varying effects derived from multiple IBPs including Enterprise, Honeycrisp, and Minnewashta. FB QTL discovery and haplotype characterization are enabling development of predictive DNA tests for use in selection of high-quality, resistant apple cultivars.

Digging USDA-ARS peanut breeding lines for harvest.

O-33
Design optimization in field experiments

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Design of field experiments to support field-based breeding research is often conducted using informal and ad hoc approaches that are based more on traditions and perceptions than on anything related to optimization theory. As such, many field-based breeding experiments are under-powered and unable to provide statistical significance, e.g. they may have insufficient replication or insufficient mechanisms of error control. Alternatively, they may be over-powered and wasteful of resources, e.g. more replication than necessary. Most researchers struggle with the decision between keeping a small and simple experiment that may end up under-powered versus a larger and more complex experiment that requires more effort and resources. This often creates a push-pull decision process between cost and statistical power, or the ability to detect true treatment mean differences. Without any definitive guidelines, this final design is little more than a guessing game. The simplest definitive approach to making this decision is to have some predictive idea of both the cost and expected power of hypothetical experiments of various sizes and designs. The presentation will show how numerical values for both cost and statistical power can be generated for a range of designs and used to choose an "optimal" design that maximizes the chances of a successful experiment within the cost limitations of the grant or project.

O-34
Importance and impact of cotton breeding in the U.S.

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O-35

The peculiar genetics of peanut - breeding with a segmental allotetraploid

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Cultivated peanut (*Arachis hypogaea* L.; genome type AABB 2n = 4x =40) is an allotetraploid with closely related subgenomes and well-defined ancestors (*A. duranensis* and *A. ipaënsis*, which contributed the A and B subgenomes respectively). The polyploid origin is very recent, less than 10,000 years ago, and the subgenomes have remained substantially distinct and intact. However, during meiosis, chromosomes from different subgenomes occasionally do interact and exchange genetic information. These genetic interactions often result in the transformation of genome structure from the expected AABB to AAAA or BBBB. Some of these transformations, that presumably occurred shortly after polyploidy, became fixed in all cultivated peanuts, resulting in a loss of alleles for the peanut crop. Furthermore, these genome transformations are continual in every peanut lineage, representing a continual ratchet-like loss of alleles. This highlights the special possibilities of using lineage recombination to restore the ancestral "fixed hybrid vigour" inherent in the AABB genome state. Alleles lost in in all cultivated peanut germplasm can be replaced using new allotetraploid hybrids derived from wild species.

Arachis hypogea, runner-type peanut pods at optimum maturity for harvest.

Summer color on new UGA Abelia hybrids.

NIFA ABSTRACTS

The UGA release "Titan®."

N-01
NIFA: Developing genomic tools to facilitate breeding of highbush blueberry for anthracnose fruit rot resistance

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Anthracnose fruit rot is the most destructive and widespread fruit disease of blueberries across the United States, impacting both yield and overall fruit quality. The primary goal of this project is to develop a more cost effective and environmentally conscious solution for anthracnose fruit rot. The proposed research will not only permit us to gain valuable insight into the underlying genetics of anthracnose fruit resistance, but develop molecular markers that will enable breeding programs to release superior cultivars that are resistant to anthracnose fruit rot for the US industry. This work is supported by AFRI Foundational Plant Breeding for Agricultural Production Program (A1141) grant #2017-07723 From the USDA National Institute of Food and Agriculture.

N-02
NIFA: Wheat yield and quality improvement via testing of new semi-dwarf alleles

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The inverse relationship between height and yield in wheat has been well characterized since the introduction of high-yielding semi-dwarf wheat during the Green Revolution. Most modern semi-dwarf wheat is the result of a mutation in the *Reduced Height (Rht)* gene which inhibits the plant's ability to respond to Gibberellic Acid (GA). The two most common mutations used in wheat breeding programs are *Rht-B1b* and *Rht-D1b*, both of which result in a premature stop codon near the N terminus. Using EMS mutagenesis we have created novel *Rht* alleles with a range of functionality in hexaploid and durum wheat. We are evaluating the impact of each allele on plant growth and development, as well as yield and grain quality. We are also developing lines which carry multiple mutations in order to investigate additive effects of the gene. This work will greatly increase the allelic diversity of the *Rht* gene in wheat, as well as provide useful genotypes to optimize wheat yield and quality in many different environments. This work is funded by Agriculture and Food Research Initiative Competitive Grant 2019-67014-29199 from the USDA National Institute of Food and Agriculture.

N-03

NIFA: Prebiotic carbohydrate enriched lentil cultivars to combat obesity, malnutrition, and climate change

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Lentil, "poor man's meat," is an important staple crop in many parts of the world, particularly South Asia and Africa. In addition to protein and minerals, lentil is rich in prebiotic carbohydrates, which support a healthy digestive system and have been linked to the prevention of chronic illness, including obesity, overweight, micronutrient deficiency, type II diabetes, and cancer. Also, certain prebiotic carbohydrates play a role in abiotic stress tolerance (heat, cold, and salinity) in plants. Consequently, biofortification of prebiotic carbohydrates in lentil is an essential target for nutrigenomic breeding efforts, both to promote human health and develop cultivars resistant to climate change. This breeding effort can be accelerated through genomic-assisted breeding and selection. However, genetic markers have yet to be identified for prebiotic carbohydrates in lentil. To meet this need, this seed grant characterized the type and concentration of prebiotic carbohydrates in two lentil association mapping populations. Ongoing study results reveal the following prebiotic carbohydrate ranges per 100g of lentil: sorbitol (38-3631mg), mannitol (0.3-300mg), raffinose+stachyose (2.8-10.1g), and verbascose+kestose (1.6-9.7g). A genome-wide association study will be conducted on these populations using genome-by-sequencing data and the phenotypic data to identify quantitative trait loci for prebiotic carbohydrates in lentil.

N-04

NIFA: Genetic and genomic approaches for American chestnut (*Castanea dentata*) restoration

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American chestnut (*Castanea dentata*) was once the most economically and ecologically important hardwood species in the United States, but was functionally extirpated from its native range in the early part of the 20th century by an exotic fungal pathogen – *Cryphonectria parasitica*. While chestnut survives in the wild through re-sprouting from uninfected roots, these new stems are invariably re-infected with blight. Two approaches to developing blight resistant chestnut populations for species restoration are currently in progress. First, The American Chestnut Foundation (TACF) has introgressed blight resistance alleles from Chinese chestnut (*Castanea mollissima*) into American chestnut. This began by identifying rare flowering trees in the forest and breeding them with Chinese chestnuts, subsequently backcrossing these F1's to American chestnut over three generations, and intercrossing the resulting BC3 trees to produce a segregating population for selection, further intercrossing, and reforestation. We have developed as accurate genomic selection model to accelerate selection of these backcross populations, which will yield a cohort of elite, blight resistant germplasm morphologically identical to native chestnuts. Second, TACF and collaborators at SUNY – Syracuse have developed American chestnut lines expressing a wheat oxalate oxidase (OxO) transgene that show levels of resistance comparable to that of Chinese chestnut. Federal regulatory approval is currently being sought to use these trees for restoration. However, crossing the transgenic founder lines with wild germplasm will be required to produce diverse, locally adapted reforestation populations. To this end, we are using genome resequencing coupled with modern population genomic tools to comprehensively characterize the neutral and adaptive processes that impinge on local adaptation in remaining wild American chestnut populations, which will guide further breeding to both increase the effective population size and improve local adaptation of these blight resistant cultivars.

N-05

NIFA: Positive correlation between A3 subunit of glycinin and firmness of tofu made from soybeans grown in three locations over two years

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Producing desirable firmness is important in manufacturing tofu from soybeans. However, which component among the soybean storage proteins that is mostly responsible for determining tofu firmness is not fully understood. This study's objective was to identify the correlations between seed protein sub-units and the firmness of tofu made from soybeans planted in three locations over two years.Twenty-two soybean Plant Introductions from the USDA Soybean Germplasm Collection and eight check varieties were planted in Mississippi, Virginia and Missouri in 2017 and 2018. For each genotype, pressed tofu and filled tofu were made in duplicate. The textural parameters were measured by a texture analyzer. Percentages of 7S, 11S, 11S+7S, A_3 subunit and ratio of 11S/7S were calculated after SDS-polyacrylamide gel electrophoresis. Phytic acid, Ca^{2+} and Mg^{2+} were determined. Pearson's correlation coefficients between seed components and tofu firmness were calculated. Across locations over two years, A3 subunit content was strongly correlated with filled tofu firmness (r= 0.82, p0.0001) and pressed tofu firmness (r= 0.83, p0.0001). 7S content did not show any correlations with tofu firmness for both pressed tofu and filled tofu. 11S content correlated with filled tofu firmness (r=0.70, p0.001) and pressed tofu firmness (r=0.53, p0.01). No correlations were found between total (7S+11S) content and tofu firmness. 11S/7S ratio only exhibited moderate correlations with filled tofu firmness (r=0.47, p0.05). For pressed tofu, firmness was found to negatively correlate with the tofu yield (r=-0.78, p0.001). Locations and years showed no significant variations for tofu firmness. Phytic acid, Ca^{2+} and Mg^{2+} content did not significantly correlate with the firmness of tofu.The current study confirmed the validity of using A_3 peptide as a biomarker in soybean breeding or as a criterion for estimating tofu firmness in both tofu manufacturing and food-grade soybean trade.

N-06

NIFA: CRISPR-based genome editing of grain size regulators for novel variation to increase wheat genetic yield potential

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IWYP's overarching goal is to increase wheat yield by 50% in 20 years, demanding an increase of the annual genetic yield gain from ~1% to 1.7%. This quantum gain in genetic yield will require the development of breakthrough approaches and novel genetic resources for wheat improvement. This NIFA-IWYP project aims to develop an improved CRISPR/Cas9 system, create edit mutations for grain-size and grain-number candidate genes, and characterize the phenotype effect of the mutations. We have made significant progress in the development of three *Agrobacterium*-delivered CRISPR/Cas9 systems and two types of guide RNA cassettes, one for targeting single genes with two guide RNAs and the second one for targeting multiple genes with up to eight guide RNAs. An advantage of these *Agrobacterium*-delivered systems is a requirement of a small number of transformation events to recover desired mutations in T1 or T2 generations. Using these CRISPR/Cas9 systems, we have generated 17 CRISPR constructs targeting 16 genes for wheat transformation, obtained 74 mutations derived from 4 constructs for four grain-regulatory genes, 63% of which are due to deletions larger than 20 bp. We have characterized five mutations from the *TaCKX2-1*, *TaGLW7*, and *TaGW2* for grain number and grain size. Under the greenhouse conditions, a 1,160-bp deletion in *TaCKX2-D1* and 5-bp deletion in *TaGLW7-D* could increase grain number up to 140% and 121%, respectively. A 10-bp deletion in *TaGLW7-A*, a 17-bp deletion in *TaGW2-A*, and a 1-bp deletion in *TaGW2-D* increased grain size to 108%, 107%, and 113%, respectively. We are combining the mutations from homoeologous loci and selecting transgene-free mutants, which can be used as novel germplasm for breeding high grain yield.

N-07

NIFA: Dissecting the sea wheatgrass genome to transfer biotic stress resistance and abiotic stress tolerance into wheat

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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 $J_1J_1J_2J_2$), 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 the solid stem) in SWG. Our long-term goal is to broaden the wheat genetic basis and develop SWG-derived novel germplasm that will contribute to a more sustainable wheat industry. This NIFA-funded project includes two objectives: (1) to develop a draft SWG genome assembly for genome-specific markers; and (2) to construct an SWG chromosome library in wheat consisting of 14 wheat-SWG addition lines. We have developed a draft assembly of the SWG genome and 127 SWG-specific markers using the assembly and established a GISH procedure to distinguish the two subgenomes. A total of 55 wheat plants carrying one or two SWG chromosomes have been selected by genotyping large backcross populations and a complete set of 14 wheat-SWG chromosome addition lines have been identified using GISH analysis of the plants. In addition, we localized several agriculturally important traits to SWG chromosomes, including the solid stem to chromosome $3J_1$, waterlogging tolerance to $1J_1$, and WSMV resistance to $2J_1$. With these results, we are one step closer to our goal to transfer the biotic stress resistance and abiotic stress tolerance from SWG to wheat.

N-08

NIFA: Physiological and transcriptomic characterization of superior waterlogging tolerance in the sea wheatgrass-derived germplasm of wheat

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Waterlogging is an increasing threat to world and US agriculture as climate change projects more floods. The primary effect of waterlogging comes from the hypoxic stress to root growth and development. Very little is known about the physiological mechanisms underlying waterlogging tolerance in dryland crops like wheat. We recently identified superior waterlogging tolerance in sea wheatgrass (SWG; *Thinopyrum junceiforme*), a distant relative of wheat and a relatively untapped source for wheat improvement. Our long-term goal is to understand the genetic mechanisms mediating hypoxia response and to improve waterlogging tolerance in the dryland cereals. This NIFA-funded project includes two objectives: 1) determine the morphological and physiological features of the SWG-derived waterlogging tolerance, and 2) identify hypoxic response genes and pathways by profiling the waterlogging tolerance-dependent root transcriptomes. Comparative analysis of the wheat parent and wheat-SWG amphiploid indicated that the formation of aerenchyma and barrier to radial oxygen loss may not contribute significantly to the waterlogging tolerance, but the continuous formation of adventitious roots and longer survival of the root tips are linked to the SWG-derived waterlogging tolerance. We are currently analyzing the transcriptomes to identify genes and pathways that are associated with the waterlogging tolerance.

N-09

NIFA: Spectral reflectance indices for indirect selection and genomic prediction of grain yield in US Pacific Northwest winter wheat

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Spectral reflectance indices (SRI) from high-throughput phenotyping platforms are promising tools for selection of lines with high yield potential. The objectives of this study were to evaluate the potential of using SRI to select grain yield of Pacific Northwest winter wheat lines and assess the effect of including SRI measurements as fixed effects on the accuracy of genomic prediction (GP) model for yield. A total of five SRIs were measured for winter wheat breeding lines from the Washington State University (WSU) Wheat Breeding program planted in 2017 and 2018 in Lind, and Pullman, WA; and in Pendleton, OR. SRI across three developmental stages showed low to moderate broad-sense heritability and genetic correlations with yield. Relative selection efficiency was highest for Normalized Difference Red Edge-2 (NDRE-2) at heading (0.74). A ridge regression model for independent predictions was assessed using 11,089 genotyping-by- sequencing (GBS)-derived single nucleotide polymorphism (SNP) markers and over 16,800 phenotypic datapoints. Using three SRI (Normalized difference vegetative index (NDVI), simple ratio (SR), and normalized water index (NWI-1)) as fixed effects in the model resulted to an over-all increase in accuracy compared to when no fixed effect was used across datasets (0.25 vs. 0.01). Including all three SRI resulted to 7-32% increase in accuracy compared to when using only two or a single trait as fixed effect in the prediction model. Our results demonstrated the potential of using SRI as proxy measurements for yield and for improving GP accuracy to increase genetic gains in the WSU Winter Wheat Breeding program.

Newly developed UGA wheat variety GA16E39 with high yield potential, resistant to stripe and leaf rust, Hessian fly insect and soil borne mosaic virus.

N-10

NIFA: Genetically-informed envirotyping tools to better match test and target environments

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Our profile regression methods provide key tools for better matching of test environment types to target production environments. Traditional regression analyses that attempt to fit main effects and interactions of increasing order to complex datasets quickly become unwieldy. Instead, our inference is based on clusters representing covariate patterns. We use semi-parametric approaches that discretize a multi-dimensional risk surface into cells, also called clusters, having similar risks. These clusters represent groups of individuals that share common characteristics, leading to similar risk profiles. Heterogeneity is thus broken down by augmenting the model with an underlying latent structure that partitions the observations into more homogeneous subgroups or clusters. PReMiuM profile regression is a statistical modeling framework that is inherently suitable for modeling highly correlated data. PReMiuM profiling can be used to examine patterns of genotype (or variety) and weather variates and relate these patterns to crop yield. Two key components are implemented in a unified Bayesian approach: 1) A profile assignment sub-model (which assigns profiles to clusters), which utilizes advanced Dirichlet process mixture-modeling techniques to group the exposure into clusters, allowing the number of clusters to vary and 2) A response sub-model which links clusters of exposure profiles to outcomes of interest, taking into account relevant confounders. Our analysis workflow thus enables breeders to exploit genotype-environment interactions — for value-added traits, for specific environments, and for germplasm exchange across networks of smallholders who share similar envirotypes even if they are not physically adjacent. Our method has the potential to weight by a combination of climate variates that optimally predict the target production environment, enables future development of genotype-by-environment-informed breeding schemes, and allows for data analysis methods that benefit both large producers and smallholders. We use simulations to illustrate method performance. All code and analyses are open source and public. 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.

N-11
NIFA: Dispensable genes in maize – their role in heterosis, specific combining ability, and accuracy of genomic prediction of hybrid performance

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Breeding procedures in maize are designed to efficiently identify inbred line combinations, which form hybrids with improved agronomic performance in target environments. Genomic prediction of hybrid performance has the potential to dramatically increase genetic improvement by both increasing selection intensity and speeding up breeding cycles. No information is yet available of how dispensable genes (i.e., genic copy number and present absent genes) and their interaction with the environment affect the accuracy of genomic prediction in maize and what role they play in the expression of heterosis. We hypothesize that the accuracy of genomic hybrid prediction models constructed with single nucleotide polymorphisms (SNPs) tightly linked to known present/absence variation (PAV) and copy number variation (CNV) will be higher than the accuracy of genomic hybrid prediction models built without such SNPs, and that the interaction between dispensable genes and the environment might substantially contribute to the variation of agronomically important traits. Six inbreds representative of the genetic diversity in contemporary elite germplasm were crossed in a diallel fashion to develop segregation populations with a total of 375 recombinant inbred lines (RILs). We are in the process of identifying SNP, PAVs, and CNVs in the parental inbreds and overlaying dense SNP, PAV, and CNV markers onto RILs. 400 F_1 hybrids derived from the 375 RILs are currently evaluated for their agronomic performance for the first season at eight locations in Illinois and Minnesota. Breeding companies Bayer, Beck's Hybrids, Corteva, and Syngenta are supporting this effort. We envision that the results obtained in this project will shed light on the contribution of genic copy number variation to heterosis in maize, and ultimately explore genomic selection methodology for improvement of hybrid performance for agronomically important traits, such as grain yield or tolerance to high plant density.

N-12
NIFA: Towards genomic selection in forest trees

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The Conifer SNP Consortium met a key milestone in the development of the Axiom 50K application array for loblolly pine (Pita50K). A list of 642,000 probe sequences was delivered to Thermo Fisher for prediction of marker quality. This pipeline delivered a number of quality metrics for each probe, which were aggregated into a single index score for each marker. A screening array was fabricated with the top 423K probes. In order to empirically validate these probes, a diverse panel of 392 diploid loblolly pine samples, as well as 36 haploid megagametophytes, were assayed. A total of 84,852 SNP were selected for downstream analysis. The genetic data revealed a highly skewed allele frequency distribution, with a mean below 0.1. Three main criteria were used for variant selection. 1) SNP with minimal heterozygosity on the haploid samples, 2) SNP with intermediate minor allele frequency ($q > 0.05$) and displaying three genotype clusters, 3) SNP with genotype ratios in Hardy-Weinberg equilibrium. This SNP selection process resulted in 46,439 markers for inclusion on the application Pita50K array. The Pita50K is being manufactured and will be ready for large scale genotyping by the forest tree breeding community in September 2019 to jumpstart genomic selection in forest trees.

White clover shows off its new colors.

N-13
NIFA: Breeding for soft seeded non shattering hairy vetch (*Vicia villosa L.*)

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Hairy vetch (*Vicia villosa* L.) is a major leguminous cover crop utilized in the United States. The high incidence of hard seed in the species is a limitation to farmer acceptance of this species. Furthermore, economic viability of seed production of this crop is hampered by the high incidence of shatter in the species. We report here on the initial phases of a program to develop soft-seeded non-shattering hairy vetch. This program has a two-pronged approach that includes 1) breeding for soft seed and non-shattering hairy vetch and 2) determining underlying genes for hard seed and shattering in hairy vetch. So far, in the project rapid phenotyping assays have been developed and evaluated. Two GWAS seed production evaluation nurseries were established and are under evaluation in Texas and Oregon. Efforts are underway to create a hairy vetch reference assembly. A rapid inexpensive PCR-SSR-amplicon genotyping assay has been developed for routine genotyping to assist in the program. A first cycle of phenotypic selection for soft-seeded hairy vetch is in progress.

An example of the genetic diversity in the peanut germplasm collection.

N-14

NIFA: Coordinated Adaptive Phenotyping (CAPs) for improving soil water acquisition and utilization

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Water deficit stress is responsible for more crop loss than any other abiotic or biotic stress. Since 1964, losses in national average cereal production due to drought were approximately 10%. One solution to mitigate the losses associated with crop water deficit stress is breeding for traits that provide increased resilience to water scarcity. This approach has been challenging partly due to the inability to identify and quantify the correct suite of traits needed to provide agronomic water stress resilience. Approaches have largely attempted to identify traits which provide general adaptability to all water deficit scenarios as well as focusing either on below or above ground traits. This solution is unlikely due to the heterogeneity in regional hydrologic conditions. Our team is developing a novel research approach aimed to establish a multi-stage phenotyping pipeline focused on the combination of below and above ground trait selection. This will enhance germplasm resistance to several key desiccation vulnerability scenarios (DVS) which are consistent with the hydrologic and agronomic management practices in the Southern United States. Preliminary results demonstrate several pertinent above and below ground traits which must be considered to avoid making assumptions about genotypic water use strategies. By quantifying the coordination and functioning of these traits, inference can be made about the adaptability of these particular traits for a given DVS. After one year of work, we present preliminary results from greenhouse screening of 38 peanut genotypes and report on the next steps to characterize several lines in the field which displayed disparate response to water stress in the greenhouse.

N-15
NIFA: Transcriptomics and metabolomics to identify drivers of seed composition in oat

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The "central dogma" of molecular biology defines how genes impart phenotypes via the subsequent processes of transcription, translation, and metabolism. Can these intermediate layers of 'omic data be leveraged in order to improve prediction of phenotypes for plant breeding? We are testing this using transcriptomic and metabolomic data in order to understand and predict nutritional quality traits in oat (*Avena sativa*). Oats are widely appreciated for their healthful nutritional profile consisting of soluble fiber (beta-glucan) and a variety of health-promoting metabolites such as avenanthramides and poly-unsaturated fatty acids. We seek to accelerate breeding for these traits by discovering their genetic and metabolic architecture. First, we are characterizing the metabolome and transcriptome of a 378-line oat diversity panel. We are using these data to develop network-informed genomic prediction models that are being tested with a population of elite lines assembled from the breeding programs of the University of Minnesota, South Dakota State University, and the University of Wisconsin. In parallel, we are developing an oat mutant population in the background of the reference genome GS-7 breeding line. We will use this collection to screen for mutations in candidate genes that we identify from studying the other two populations. The mutants that we identify will be used for two purposes: to test our functional hypotheses and as sources of novel alleles for modifying seed composition through breeding. By testing our predictions in these three populations, we will evaluate whether transcriptomic and metabolomic data can augment genomic prediction in order to improve prediction accuracy between different populations.

N-16
NIFA: Characterizing the USDA peanut core collection through genotype and phenotype information

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The US core peanut collection is a diverse set of 831 *Arachis hypogaea* (cultivated peanut) accessions, developed by Corley Holbrook, William Anderson, and Roy Pittman (Holbrook et al., 1995). To improve the use of this collection by breeders, the entire core has been genotyped. This data, combined with image analysis of the seeds from each accession and 2 years of phenotype data collected in 2013 and 2015, will provide a valuable resource to peanut breeders. To further enhance the value of the data, one plant from each accession was sampled then grown to maturity for seed, enabling single seed descent. A subset of accessions was selected for biological replicates, to test for heterogeneous and mixed accessions. These biological replicates were grown only to seedling stage. As part of this genotyping project and the earlier phenotyping project, the existing 742 accessions have been grown out for seed increases and are available from the Plant Genetic Resources Conservation Unit in Griffin, Georgia. All data from this project and the earlier phenotyping project will be, or is now available at PeanutBase.org. This project was supported by the Agriculture and Food Research Initiative Competitive Grant no. 2017-07777, co-funded by the USDA National Institute of Food and Agriculture and the National Peanut Board.

N-17
NIFA: Novel delivery systems for gene editing in plant cells

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One of the fundamental challenges for gene editing is the delivery of select molecules into the target cells. For gene delivery to animal cells, researchers have developed large libraries of delivery agents in an effort to identify structural trends that improve the efficiency of gene delivery, a process that has not been done for plant systems. Here, we develop a database for DNA delivery in a model onion system using a particle bombardment-mediated approach. Our initial library uses a series of amines to bind the DNA to the gold micro-particles. Promising amines are then systematically modified to identify structural trends that improve delivery efficiency. As part of developing this library, we have implemented a double-barreled biolistic testing system, which allows the use of an internal control in each shot, thus significantly reducing the effect of sample variability. By comparing the pristine and modified amines in our library to spermidine, the industry standard, within each sample, we were able to streamline our screening and analysis. The goal of this project is to reveal the effect of structural-property relationships of the delivery agents on delivery efficiency and establish an improved platform for plant cell gene editing.

N-18
NIFA: Has selection reduced GxE for productivity in inbreds derived from the Iowa Stiff Stalk Synthetic population?

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Plant breeders have utilized selection to maximize productivity of economically important crops grown across diverse environments. To ensure dependable plant growth and productivity in farmers' fields, breeders evaluate the stability of plant performance across a range of environments and select stable hybrids. The goals of this study were 1) identify environmental stability of unselected, old, and more recently released inbreds derived from the Iowa Stiff Stalk Synthetic (BSSS) population and 2) evaluate how estimates of stability can be refined using climatic data. A set of hybrids was generated by crossing 102 inbred lines derived from BSSS (which varied in release date and selection level) by tester DK3IIH6. Hybrids were evaluated in a total of 6,032 plots across 31 environments as part of the GenomesToFields Initiative using a RCBD with two field replications for two years. Stability was estimated using two environmental indices with Finlay-Wilkinson linear regressions; (1) performance-based using the average hybrid performance in each location; and (2) environmentally-based, using average hybrid photothermal time at flowering for each environment. Slope and mean squared error (MSE) estimates were extracted from both regressions. Breeders typically aim for high performing, stable genotypes that have minimal MSE (type III stability) and demonstrate a slope of 1 (type II) across growing environments. Slope and MSE estimates from both indices suggest an increase in type II and decrease in type III with selected lines being more stable than unselected and recently released lines being, on average, more stable than older lines. When comparing values' significant difference from a slope of 1 and MSE of 0, the environmentally-based index identified 40% of hybrids as stable, while the performance-based identified 36% of the hybrids as stable. Future work will focus on identifying key environmental factors to estimate performance stability and ultimately assist breeders with evaluations across environments.

Tomato diversity found in semi domesticated germplasm. Credit Alexis Ramos, PBGG UGA.

N-19

NIFA: Advancing resistance to *Fusarium* wilt of tomato through the pyramiding of available and novel resistance genes

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Tomato (*Solanum lycopersicum*) is one of the most important vegetables in the U.S., valued at over $2.0 billion annually. However, tomato production is increasingly threatened by Fusarium wilt race 3 (Fol3) caused the soil-borne fungus *Fusarium oxysporum* f. sp. *lycopersici*. Fumigation has traditionally been used to help manage soilborne diseases including fusarium wilt, but the phase-out of methyl bromide has left the industry with less effective replacements, and cultural control methods are inadequate. Although host resistance to *Fol3* through the *I-3* gene is the most effective management strategy, producers often choose to grow susceptible cultivars due to the association of *I-3* with detrimental traits, including increased bacterial spot sensitivity and reduced fruit size. Our goal is to remedy these problems by reducing the *I-3* introgression to eliminate linkage drag, pyramiding multiple *Fol3* resistance genes to promote greater durability of resistance, and assessing the genetic diversity of *Fol3* strains from throughout the U.S. and abroad to guide the deployment of resistance alleles. In order to address potential linkage-drag effects, we reduced the *I-3* introgression from 5 Mb to approximately 120 Kb through successive recombinant screening and crossing efforts and evaluated this reduced introgression for its effects on bacterial spot sensitivity and fruit size. The reduced introgression was found to result in significantly less bacterial spot and larger fruit size than the original introgression, and it has no effect compared with *Fol3* susceptibility. To promote greater durability of resistance, we are seeking to identify novel *Fol3* resistance loci from *S. pennellii* and pyramid these with available genes in a commercial background. We are also investigating *Fol3* isolates from Florida and abroad to identify potential changes in virulence patterns and characterize genetic diversity. Together, these efforts will support the development of improved *Fol3* resistant cultivars and more durable resistance against this pathogen.

N-20

NIFA: Functional dissection of chickpea (*Cicer arietinum L.*) stay-green phenotype associated with an ortholog of Mendel's I gene for cotyledon color: Implications for crop production and nutritional quality

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"Stay-green" crop phenotypes have been shown to impact drought tolerance and nutritional content of several crops. We aimed to genetically describe and functionally dissect the particular stay-green phenomenon found in chickpeas with a green cotyledon color of mature dry seed and investigate its potential use for improvement of chickpea environmental adaptations and nutritional value. We examined 40 stay-green accessions and a set of 29 BC2F4-5 stay-green introgression lines using a stay-green donor parent ICC16340 and two Indian elite cultivars (KAK2, JGK1) as recurrent parents. Genetic studies of segregating populations indicated that the green cotyledon trait is controlled by a single recessive gene that is invariantly associated with the delayed degreening (extended chlorophyll retention). We found that the chickpea ortholog of Mendel's I locus of garden pea, encoding a STG protein as very likely to underlie the persistently green cotyledon color phenotype of chickpea. Further sequence characterization of this chickpea ortholog CaStGR1 revealed the presence of five different molecular variants (alleles), each of which is likely a loss-of-function of the chickpea protein (CaStGR1) involved in chlorophyll catabolism. We tested the wild type and green cotyledon lines for components of adaptations to dry environments and traits linked to agronomic performance in different experimental systems and different levels of water availability. We found that the plant processes linked to disrupted CaStGR1 gene did not functionality affect transpiration efficiency or water usage. Photosynthetic pigments in leaves and grains, including provitaminogenic carotenoids important for human nutrition, were 2-3 fold higher in the stay-green type. Agronomic performance did not appear to be correlated with the presence/absence of the stay-green allele. We conclude that allelic variation in chickpea CaStGR1 does not compromise traits linked to environmental adaptation and agronomic performance, and is a promising genetic technology for bio-fortification of provitaminogenic carotenoids in chickpea.

N-21

NIFA: Developing hard winter wheat germplasm with new resistance to multiple arthropods using primary synthetics and exome capture

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This research project was funded by USDA-NIFA Foundation program with award# 2019-67013-29172. We have identified primary synthetic lines with new resistance to greenbug, hessian fly and wheat curl mite and will transfer the pest resistance simultaneously into an adapted wheat cultivar TAM 114 using marker-assisted backcrossing, doubled haploid and other techniques. We have harvested an average of 100 BC1F1 seeds from each of the 10 crosses. All seeds will be germinated in August and then be used to develop doubled haploid to obtain homozygous resistant lines. We have selected 48 lines (43 primary synthetics plus 5 cultivars) and extracted DNA samples for exome capture assay. Genic SNPs will be developed and validated for the prediction of multiple pest resistance. Germplasm lines with multiple resistance confirmed by both linked genic SNPs and phenotyping under the adapted genetic background will be available to other wheat breeders.

N-22

NIFA: High-throughput in-field phenotyping systems to accelerate breeding of climate-resilient vegetable crops

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By the year 2050 the world's population is projected to increase to about 10 billion people; with a corresponding demand on increased agricultural output by 70%. At the same time, climate change is expected to decrease crop yields and increase extreme weather events. Plant breeders are pressured to accelerate the rate of new crop cultivar development that can produce more food under extreme weather conditions. In plant breeding trials, the most difficult task is phenotyping each genotype to find breeding traits relevant to important members of the Solanaceae family of vegetable crops (i.e., tomato, pepper, eggplant, potato) such as day of first green fruit, total yield, and plant height and width. The current labor-, cost- and time-intensive manual methods of evaluating (phenotyping) traits in field-grown crop plants are a major bottleneck that slows progress. New technologies such as high-resolution, digital cameras, time of flight cameras, and infrared sensors have made it possible to automate many of the phenotype measurements that breeders currently are making manually. A novel design for an automated high-throughput phenotyping system for the Solanaceae family of vegetable crops (i.e., tomato, pepper, eggplant, potato) has been created at the University of California, Davis. This system is unique in that it captures very high-resolution proximal images of each plant in a breeding trial from multiple viewpoints and is capable of creating photorealistic true 3D imagery. The sensor platform carries an array of 18 true color and infrared cameras. Camera array image acquisition is geo-referenced and synchronized to allow automated genotype registration. The sensor platform also carries multiple time-of-flight cameras and infrared canopy temperature sensors. The data collected is used to find phenotypic features comparable to traits that plant breeders manually collect to predict which tomato and pepper genotypes perform best under normal and drought conditions.

N-23
NIFA: Pyramiding QTLs/genes from multiple donors to enhance salt tolerance in rice

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Salinity is a major abiotic constraint that affects rice production worldwide. Since rice is highly sensitive to salinity at both seedling and reproductive stages, development of salt tolerant varieties is necessary to continue rice farming in salt affected areas. However, the major bottleneck is the narrow genetic base of US germplasm. Using several exotic salt tolerant donor, we successfully developed salt tolerant breeding lines, which are now being evaluated for agronomic traits including yield in replicated field trials. The QTLs for seedling stage and reproductive stage tolerance have been mapped in four and two mapping populations, respectively. Since the level of salt tolerance needs further improvement, this project aims to identify and stack the superior alleles of the QTLs/genes from multiple donors. To accomplish this goal, we are making crosses between salt tolerant introgression lines carrying the salt tolerant QTLs to introgress multiple QTLs to several high yielding US varieties. Several mini-multi-parent advanced generation inter-cross populations are being developed to accumulate superior alleles from multiple donors. Our preliminary evaluation indicated substantial improvement of salt tolerance in selected breeding lines. While advancing these populations, plants with desirable agronomic traits are selected for multiplication and salinity screening. We analyzed whole genome sequences of two donor germplasm (Pokkali and Nona Bokra) and three salt susceptible varieties (Bengal, Cocodrie, and IR64) and identified the polymorphic SNPs and InDels differentiating these two groups. This information will be integrated with the RNA-Seq data of the parents and selected salt tolerant breeding lines to identify the superior salt tolerant alleles from donor germplasms. The advanced breeding lines with enhanced salt tolerance and the genomic resources developed in this project will accelerate development of climate resilient rice varieties and elucidation of the molecular basis of complex salt tolerance mechanisms operating in rice.

N-24
NIFA: Identifying functional variation in complex plant genomes

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The objective of this project is to test the hypothesis that DNA sequence variation in regions of accessible chromatin and in coding sequences of transcribed genes can be used to build predictive models of the genetic basis of phenotypic variation in loblolly pine (*Pinus taeda*), the most-planted commercial timber tree species in the US. Assay for Transposase-Accessible Chromatin – sequencing (ATAC-seq) and Micrococcal Nuclease – sequencing (MNase-seq) have been used to identify regions of the pine genome that are accessible to soluble factors in intact nuclei, and may therefore be coding sequences or sequences involved in gene regulation. The extent of chromatin accessibility, as estimated by the depth of sequencing coverage, varies widely across the genome. As yet there is little evidence to support a strong relationship between depth of sequencing coverage and functional significance, so additional criteria may be required to identify functionally-important regions. The comparision of positions of regions of accessible chromatin relative to gene models in the current pine genome annotation identifies a subset of regions associated with annotated genes, but this overlapping subset is a small fraction of the total sets either of gene models or of accessible chromatin regions. Identification of functional genes not represented in previous hybrid-capture sequencing experiments, as well as putative regulatory regions of the genome outside of transcribed regions of genes, is the current focus of research. After identification of a set of likely regulatory and coding regions, a targeted-sequencing experiment will be conducted to obtain the genotype data required to test the overall hypothesis.

N-25
NIFA: Joint linkage analysis and selection in autotetraploid potato & blueberry

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Molecular breeding is a powerful approach to improving traits with a positive impact on the sustainability of US agriculture. Progress in autotetraploid crops, such as potato, blueberry, and alfalfa, has lagged behind diploid species due to fewer computational resources for genetic analysis. Despite significant advances in the past five years, a major obstacle remains: the ability to estimate genetic effects across multiple populations through joint linkage analysis. This project will develop computational tools to address this need and apply them toward public cultivar development. For Objective 1, two software packages will be developed and tested via simulation: the first uses genome-wide markers to infer parental identity-by-descent probabilities, and the second regresses phenotype data on these probabilities to estimate genetic effects. For Objective 2, the software will be applied to five connected F1 populations from the University of Wisconsin potato breeding program. A number of economically important traits will be studied, including periderm maturity or "skin set," which is critical to maintaining healthy, marketable tubers during storage. For Objective 3, the software will be applied to seven connected F1 populations from the University of Florida blueberry breeding program. The target of the blueberry research is resistance to anthracnose because it is an emerging, devastating disease for which a molecular breeding strategy is sorely needed. We have selected a few traits to focus on during this project, but the methods and software can be used to improve any trait and will allow breeders to more efficiently develop new varieties that benefit producers, consumers, and the environment.

N-26
NIFA: Functional validation of candidate genes for resistance against Hessian fly and their applications in wheat breeding

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Hessian fly, Mayetiola destructor Say, is one of the most destructive pests of common wheat in the U.S. and worldwide, and the biotype Great Plains (GP) is most prevalent in the southern Great Plains. Two dozen genes for resistance against wheat diseases have been cloned, allowing us to have better understanding of the molecular genetic mechanisms of wheat-disease interactions and more effective and efficient utilization of the resistance genes in wheat breeding. However, no gene has been cloned for resistance against any insect herbivores in wheat. In this study, we initially mapped a major resistance gene for the Hessian fly biotype GP on the short arm of chromosome 1A in a Duster x Billings doubled haploid (DH) population. Then we have screened 4,500 individual $F_{2:3}$ plants for recombinant events and narrowed down the targeted region to 169 kb where only three candidate genes exist according to the International Wheat Genome Sequencing Consortium (IWGSC) Chinese Spring (CS) genomic sequence. We have sequenced each of these three candidate genes from Duster and Billings and identified allelic variation between the two alleles. Furthermore, we have carried out transgenic complementation through over-expression of the Duster resistance allele into susceptible wheat cultivars and also transformed CARISPR-CAS9-based gene editing constructs into Duster to validate the function of the candidate genes. We will develop diagnostic markers for the cloned gene to accelerate its deployment in aphid resistance improvement in collaboration with wheat breeders in Oklahoma, Nebraska, and Kansas.

N-27
NIFA: Exploring the genetic basis of yield in a biparental wheat population

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An alternative approach to directly analyzing the genetic basis of a highly polygenic trait like yield is to break it down into components and analyze their genetic bases. Phenotypes related to the amount of grain produced by a plant, the size and shape of grains, and the rate of plant development were collected in a 348-line biparental RIL population across two years in three locations in North Carolina and Georgia. Estimates of yield from head rows was collected from one location, along with yield from larger plots of selected genotypes. Genotyping with high-density GBS markers and KASP markers for causative polymorphisms identified known variants (including *RhtD1, PpdD1, TaGW2, WAPO1,* and *B1*) and novel QTL associated with variation for all phenotypes. Most significant variants were associated with multiple phenotypes, with associations being consistent with knowledge about underlying genetic pathways (eg, variation in flowering time genes impacted both flowering time and spikelet number). Within the set of phenotypes collected in a given environment, the relative proportion of genetic variance explained by given variants increased or decreased across phenotypes, suggesting strong allele-by-environment interactions. To validate the yield-component approach, the effects on yield of selected known yield component variants in the biparental population were estimated in diverse germplasm, and found to be significant in an environment-specific manner.

N-28
NIFA: Integrating genomic data and physiological measurements to identify fast growing, drought-tolerant loblolly pine varieties

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The southeastern U.S. is known as the world's "wood basket", supplying 12% of the world's wood products and 19% of its pulp and paper. These forests contain one-third of the entire forest carbon in the contiguous U.S. Commercially, loblolly pine (*Pinus taeda* L.) is the most important species in the region. Much of the past focus of tree improvement programs has been on improved growth and disease resistance. As temperatures increase and droughts become more frequent and severe, drought resistance and water use efficiency (WUE) have become important characteristics to consider. We will develop biomarkers (stable isotope discrimination as a measure of WUE and A/Ci curve points as a measure of photosynthetic efficiency) and molecular markers that can be used by cooperative tree improvement programs, to assist with breeding of loblolly pine with improved WUE, photosynthetic efficiency, survival and growth. In turn, this will insure a continued wood supply, employment in the wood products industry and forests for recreation and ecosystem services. Through a collaboration with the Western Gulf Forest Tree Improvement Program (WGFTIP), we have access to and growth and survival data from three progeny tests located along a precipitation gradient in East Texas and will use them for association analyses. We collected foliage from one of the tests as well as the 61 parents involved in the crosses. We plan to genotype and phenotype the progeny and the parents to identify SNPs that will be of value to the WGFTIP. As part of the previously funded PINEMAP project, we discovered ~2.8 million SNPs through exome sequencing. A subset of these markers and SNPs discovered in other projects have been used to develop an ~50K loblolly pine SNP array available to the community. In addition to genotyping these SNPs, we will develop ~1000 additional SNPs that are of particular interest due to being found in drought response genes, especially if the SNPs have been identified in trees from the Western Gulf region. Some genes will be chosen after being identified as differentially expressed in an RNA-Seq experiment and others were identified as genes of interest in the PINEMAP project.

N-29

NIFA: Resequencing putative recombinants to identify genes impacting malic and citric acid concentrations in cranberry fruit

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We have identified Mendelian loci which impact malic and citric content in American cranberry (*Vaccinium macrocarpon*) fruit using GBS. Malic and citric acids are the primary contributors to the acidity in cranberry fruit, which is quantified as titratable acidity (TA), in terms of citric acid equivalents (CAE). Commercially grown cranberries have an average TA of 2.3-3.0% CAE, about five-fold higher than in other fruits, such as blueberry. Malic acid concentrations in commercial cultivars range from 6 to 8 mg/g FW while citric acid concentrations range from 8 to 11 mg/g FW. Two germplasm accessions were identified with reduced TA, resulting from low citric acid (≈ 1 mg/g) and low malic acid (≈ 3 mg/g) levels. QTL analysis, using GBS for SNP marker discovery, has helped identify low acid alleles for citric acid on Chr1 and for malic acid on Chr4. Genomic regions for these two loci have been defined to within ≤1 Mb regions. The current reference genome, using GridION long read sequence technology, provided an assembly of 487 Mb in size across 124 contigs, with a N50 contig length of 15 Mb, the longest contig spanning 37 Mb. Using MAKER, 36,364 genes were predicted to be in the current reference genome, with 477 predicted genes in the malic acid region and 197 predicted genes in the citric acid region. GBS however provides limited SNP and INDEL variant information, leaving only 604 informative variants within the malic acid region and 240 informative variants within the citric acid region. We have resequenced putative recombinants using Illumina short read technology to provide a higher resolution of variation in the genomic regions associated with these traits and to facilitate discovery of the causative variants.

N-30

NIFA: Generating genotype-informed yield prediction models for NextGen breeders based on low cost nitrate sensors

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Phenotype is a function of genotype (G) and environment (E), however, different genotypes respond differently to different environments. To accurately predict phenotype, it is necessary to understand both the roles of genotype and environment on phenotype, and the influences of interactions between genotype and environment (GxE) on phenotype. The primary driver of GxE interactions is year-to-year weather variability, which is intensified by current climate change. Year-to-year variability has large effects on soil processes including water and nitrogen availability. However, a shortage of high-resolution soil and *in planta* N data has limited our ability to understand and predict N dynamics and their influences on phenotypes. This also impedes the understanding of GxE, particularly under lower N input management practices with fewer negative environmental consequences. Our team has developed an innovative Micro-Electro-Mechanical Systems (MEMS)-based nitrate sensor for both soil and plants to generate data from yield trials of hybrids with known genotypes in multiple, well-defined environments. This sensor operates on the principle of ion selective field-effect transistors (ISFETs) that have been widely used for continuous sensing of different ions. As initial studies, in 2017 and 2018 we grew 12 hybrids in replicated plots at Ames, IA to determine sensor accuracy, the number of sensors required per plant as well as the number of sensed plants required to accurately model crop and soil N dynamics. Our improved understanding of sensors and the sensor-based Agricultural Production Systems sIMulator (APSIM) model calibrations developed in these studies were used to design our 2019 experiment. In 2019, twenty-five hybrids were planted in 5 locations across Iowa in 3 replicated plots with the goal of replacing destructive measurements with sensors data to inform APSIM calibration for all 25 hybrids. Results from 2017-2019 will be used to test predictive ability of the genotype-enable crop model.

N-31
NIFA: An unmanned aerial system (UAS) for hyperspectral measurements of solar-induced chlorophyll fluorescence and surface reflectance to improve crop monitoring

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Sun-induced chlorophyll fluorescence (SIF) and the photochemical reflectance index (PRI) are both functionally related to photosynthesis and highly sensitive to crop stress. These measurements could potentially revolutionize crop monitoring via remote sensing, which conventionally relies on greenness-based indices such as the normalized difference vegetation index (NDVI). However, few studies have explicitly explored their individual unique and complementary strength for real-time crop monitoring. Moreover, no mobile platforms are available to acquire sufficiently high temporal and spatial resolution measurements of both SIF and PRI to understand the mechanisms regulating crop responses to heat/water stress. Here, we present the development of a novel Unmanned Aerial System (UAS) designed to measure visible and near-infrared surface reflectance, SIF and RGB images. Onboard the DJI Matrice 600 Pro equipped with D-RTK GNSS, the UAS is capable of GPS positioning with <1m precision. A bifurcated, cosine-corrected fiber optic is rotated using dual servo motors to transmit incoming and outgoing irradiance to two spectrometers: 1) Ocean Optics FLAME acquiring hyperspectral surface reflectance from 400-900nm (visible to near-infrared, ~1 nm spectral resolution), and 2) Ocean Optics QE-Pro acquiring far-red SIF from 730-780nm. During scanning, the servo arm doubles as a dual-axis gimbal to stabilize the fiber with ±1.1 degree accuracy (~0.15 nm spectral resolution). Flight information, live video, and images of the latest acquired spectra are monitored by the pilot via the DJI GO mobile app. The UAS is designed as a mobile version of a ground-based tower system which continuously records SIF, surface reflectance, solar radiation, temperature, and humidity, enabling cross-validation. The UAS was deployed at a maize field in upstate New York beginning July 2019. Ground validation of the systems will be performed using canopy gas exchange from an adjacent eddy covariance tower and ground measurements of leaf-level photosynthetic gas exchange, chlorophyll fluorescence, leaf water potential, and soil moisture. This project will provide the first comprehensive ground validation of remotely sensed seasonal and diurnal SIF-PRI dynamics from leaf to canopy.

N-32
NIFA: From gene to global hydroclimatic controls on hybrid performance predictability

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Sustained increases of crop yield in the Midwest USA are produced by the development of better and more stable genotypes coupled with the introduction of improved technological developments, management practices, and resources availability. However, the occurrence of extreme hydrometeorological and climate events (EHCEs) may affect negatively these trends. So far, the geospatial extent of these effects on genotype responses are unclearly identified and consequently such effects across scales is poorly understood. This research aims to create a conceptual model to geospatially identify the areas where the intensity of water deficits challenges our abilities to predict phenotypic responses. The Genomes to Fields (G2F) project have monitored environmental variables through more than 100 weather stations since 2014 across the USA. In such locations a wealth of multidimensional, discontinuous and heterogenous data are also collected from multiple sources (i.e., remote and proximal sensing and various monitoring networks). We explored the potential of machine learning techniques to integrate multi-dimensional database to predict phenotypes across scales. For describing environmental similarities among environments we focused on environmental/hydroclimate variables (i.e., precipitation, wind speed and direction, temperature, etc.). We integrate Artificial Neural Networks and kriging interpolations to take advantage of the spatiotemporal proximity between G2F data and publicly available data. Results of this technique evidence an improvement on precipitation and temperature estimates of 20% in locations when data from other sources is used as input. On the other hand, genome molecular markers were used for modeling genetic similarities between genotypes via the general and the specific combining ability components. We will present contribution of data, from different sources, across the experimental areas of the G2F project in areas with and without water deficits resultant from dry spells. Also, we will show the effects in predictive ability by increasing (double) the number of environments (location-by-year combination) for calibrating models.

N-33
NIFA: CRISPR/Cas9-mediated genome editing toward improving the quality of seed oil in peanut

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Natural mutations that occurred in the coding region of fatty acid desaturase (FAD2) genes, have provided evidence that the increase of oleic acid content in peanut seeds have added commercial value. The accumulation of oleic acid by natural mutations was a result of reduced *FAD2* gene activity that catalyzes the conversion of oleic acid to linoleic acid. Mutations induced by CRISPR/Cas9-mediated genome editing in *FAD2* genes also could lead to the increase of oleic acid, but genome editing has not been applied to peanut yet. In this project, several CRISPR/Cas9 constructs have been designed to induce Indel or point mutations (C to T) in the coding region and to regulate transcription in the promoter region of peanut *FAD2A* and *FAD2B* genes simultaneously. The functionality of these constructs was validated in peanut through protoplast transfection, leaf infiltration, and hairy root transformation. Our results showed various *FAD2* edits via deletion, insertion and cysteine conversion to thymine. Up to 28% of tested cells or tissues contained targeted mono-allelic or bi-allelic chromosome mutations at three test sites. The mutations induced by gene editing might result in increased oleic acid content, although phenotypic data need to be assessed. Furthermore, we have developed peanut protoplast, leaf infiltration and hairy root systems, as well as constructs that can be used for routine genome editing in peanut.

N-34
NIFA: Generating *Salvia hispanica* genomic resources

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Recent studies correlate high saturated fatty acid (SFA) and low polyunsaturated fatty acid (PUFA) diet with cardiovascular diseases, diabetes, obesity, and high blood pressure. These studies sparked interest in the general population to shift to a healthier lifestyle. *Salvia hispanica* L. (commonly known as chia) is gaining popularity worldwide and specially in USA as a healthy oil and food supplement due to its high PUFA, protein, fiber, and antioxidant content. Despite these benefits and its growing public demand, limited gene sequence information is currently available in public databases and no breeding efforts have yet been directed towards improving the currently cultivated varieties. There are several known key traits suitable for improving both the nutritional qualities and the crop yield. However, they are distributed among different accessions. Breeding for these traits is often complex and requires multiple generations to stabilize traits because they are often controlled by multiple genes. The objectives of this project are 1) to sequence the genomes of two domesticated and one wild type *S. hispanica* accessions and generate molecular markers for the various desirable traits. To date, we sequenced the full 372Mbp genome of 'pinta' cultivar (the most commonly grown commercial variety) using a combination of PacBio, Illumina, and Hi-C platforms and assembled the sequences to six chromosome-scale scaffolds. Currently, we are phenotyping two large F2 populations derived from a cross between two domesticated cultivars (pinta x tropical) and a cross between wild type and domesticated cultivar (wild x tropical). The availability of genomic and phenotypic data from the segregating populations will enable discovery of markers associated with the desirable agronomic traits. Genetic markers will greatly facilitate and speed-up the future breeding efforts aimed at developing cultivars with high yield and improved nutritional qualities tailored towards the global efforts of reducing diseases through healthy diets.

N-35

NIFA: Crosses between genetically distant parents generate novel epi-alleles in commercial grapevine cultivar Cabernet Sauvignon

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It is expected that 50-81% of grapevine's growing acreage in the USA will fall out of production due to weather changes by 2040. This demands the breeding of varieties more resilient to periods of environmental stress. Epigenetic priming has been proposed as a system to produce locally adapted cultivars. However, most grape cultivars are crosses between distantly related parents, making them highly heterozygotic. This is of particular importance for epigenome-focused explorations, since previous studies in model organisms have highlighted the importance of cis-genetic variation in epigenome diversity. Moreover, little is known of the effect that trans-genetic effects, such as those induced by the interaction of two genomes from genetically distant parents. To understand the how heterozygosity influences DNA methylation, the leaf methylomes of Cabernet Sauvignon (CS), and its parents, Sauvignon Blanc (SB) and Cabernet Franc (CF), were sequenced using a Whole Genome Bisulfite Sequencing (WGBS) approach. WGBS reads were then mapped to diploid phase assemblies of Cabernet Sauvignon and its two parents generated using PacBio sequencing. Analysis of CpG methylation shows that: 1) within-cultivar epigenetic diversity is higher in CS than in its parents, 2) 24% of methylated sites are shared between all cultivars, 3) CS shares more methylated CpG sites with both of its parents (22% with CF and 24% with SB) than SB with CF (2.4%), and 4) 26% of the methylated CpG sites are cultivar-specific. Taken collectively, our results suggest that, although part of parent specific DNA methylation is inherited, the interactions between the genomes from two distant parents induces a significant number of novel epialleles. Overall, deep characterization of the DNA methylation profiles of highly heterozygous genomes will lead to a better understanding of the potential contribution of epigenetic mechanisms towards the regulation of cultivar specific alleles in grapevine.

N-36

NIFA: Emerging opportunities for pulse production: Genetics, phenomics, and integrated pest management

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Pulse crops, which include chickpeas, dry beans and peas, and lentils, have served as cornerstones of sustainable agricultural production and human nutrition for thousands of years. The NIFA funded conference "Emerging Opportunities for Pulse Production: Genetics, Phenomics, and Integrated Pest Management" was held June 24-25, 2019 at Washington State University, Pullman, WA. Approximately 60 participants represented seven countries, 14 universities, multiple federal and international research centers, and various private sectors including national grower organizations, farmers cooperatives, seed companies, and producers. The primary goal was to develop transdisciplinary research and facilitate knowledge and technology transfer among the pulse research community. The first day included a Keynote presentation titled "Breeding for the Pulse Value Chain" and facilitated concurrent breakout sessions on 1. Genetics, genomics, phenomics and breeding, and 2. Disease and weed control and integrated pest management. These were followed by moderated panel discussions on 1. Enabling technologies to improve pulse production, and 2. Cooperative disease screening, oral presentations on root diseases and control of flowering time in pulses, and poster presentations by graduate students. The second day included field tours of pea, lentil, and chickpea evaluation and breeding trials, and research plots established to examine effects of autumn sown crops on soil microbe populations. Field tours were followed by oral presentations on harnessing crop diversity for pulse breeding and gene editing technologies for pulse crops, and a final session on future steps to improve coordination among pulse researchers. There was great consensus on developing standardized methods to evaluate disease resistance and establishing a national laboratory for pulse genotyping. Determining the rotational value of pulse crops was consistently identified as a high impact transdisciplinary research effort requiring the expertise of conference participants along with additional capacity in economics and soil, air, and water resource management.

N-37
NIFA: 3D and precision soybean phenotypes from temporal UAS imagery of yield trials

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We present two distinct types of processing pipelines for RGB and Multispectral images acquired from unmanned aerial systems (UAS) over soybean breeding plots. From temporal RGB images the crop field was reconstructed in 3D by image-based modeling. Algorithms were combined to compute canopy volume per plot and and validated with above ground measurement of biomass. Within-plot height variation was quantified to improve the biomass correlations. The results confirm the adequacy of the approach for selection of temporal biomass growth dynamics. We also developed a second processing pipeline that consists of 1) Crop Image Extraction (CIE 2.0) and 2) Vegetation Indices Derivation (VID 1.0). CIE extracts multispectral and RGB composite images enabling hundreds to thousands of plot scale images to be analyzed. Outputs from CIE are inputs for VID, where image calibration, band algorithms and other user-defined helper functions can be used to evaluate replicate plot-scale image clips and quantify canopy coverage, color, biomass and other phenotypes with an estimate of accuracy. Quantitative genetic properties of these phenotypes will be presented.

N-38
NIFA: Confirmation, validation and deployment of a QTL on 6BL underlying tiller number

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Plant tiller number, defined as the number of tillers that produce a fertile spike with seeds, is associated with important impacts on grain yield in wheat. Increased tiller number has been associated with increases in yield potential in wheat in response to various environmental resources and competition levels. A quantitative trait loci (QTL), QTn.mst-6B associated with increased tiller number was identified in three recombinant inbred line (RIL) hexaploid spring wheat populations on chromosome 6B. *QTn.mst-6B* was associated with increased tiller number, specifically an increase in early tiller number (ETN) defined as the number of vegetative tillers produced before stem elongation at Zadoks 31 stage. Increased ETN resulted in increased yield in reduced competition and irrigated environments. This study focuses on the fine mapping and validation of the high tiller number allele at *QTn.mst-6B*. Heterogenous inbred families (HIF) derived from two bi-parental crosses were used to map *QTn.mst-6B*. Current fine mapping suggests a chromosome region between 156 Mb and 310 Mb on the short arm of 6B (IWGSC RefSeq v1.0). Potential candidate gene *TraesCS6B02G191800* has been identified at 226 Mb to 226 Mb (IWGSC RefSeq v1.0) and is the orthologous gene to *MONOCULM1* (*MOC1*.) in Rice (*Oryza sativa*), responsible for development and outgrowth of plant tiller buds.

N-39
NIFA: Proximal and remote sensing techniques for phenotyping agronomic and performance traits in pulses

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Pulses such as dry pea and chickpea are specialty crops that serve as key rotational crops and enhance soil health. In addition, some of these pulse crops can be grown as winter crops with enhanced productivity. Pulse breeding programs are focusing on the development of stress tolerant, high yielding varieties. In this study, high-throughput phenotyping techniques were evaluated to assess key agronomic and performance traits in dry pea and chickpea breeding programs. Visible (RGB) and multispectral imaging systems (proximal and aerial) were used to monitor flowering; while tractor-integrated light detection and ranging (LiDAR) system and unmanned aerial system-based RGB imaging sensor were used to monitor plant height. In general, high correlation coefficient up to 0.95 can be achieved for flower detection, depending on image resolution, sensor type, flower size, background, and image processing method. LiDAR- and digital surface model (derived from RGB data) based methods rendered similar correlation coefficients with manually measured plant height, especially in dry pea. We anticipate that the sensing methods can contribute towards accelerating the pulse crop breeding efforts with improved throughput, objectivity, and accuracy in phenotyping. This work was funded by the Agriculture and Food Research Initiative competitive grant # 2017-67021-26252 (accession no. 1011741) of the USDA National Institute of Food and Agriculture.

N-40
NIFA: Utilizing genomic-signals of eco-geographic adaptation from wild relatives to improve wheat

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Wild relatives of wheat are adapted to a wide range of climatic conditions and proved to be a rich source of allelic diversity for trait improvement. To select *Aegilops tauschii* (diploid wild ancestor of the wheat D genome) accessions for breeding, we combined next-generation sequencing (NGS) of 137 individuals with historic environmental data from the accession's collection sites. Using these data, we identified climate-adaptive SNPs that help Ae. tauschii to adapt to water-limiting and high temperature environments. A subset of *21 Ae. tauschii* accessions was used to develop octaploid wheat that was crossed with six cultivars from Kansas. A total of 351 $BC_1F_{3:5}$ introgression lines generated from these crosses were sequenced, and introgressed regions were identified based on the identity by descent (IBD) regions shared between wheat and *Ae. tauschii*. Using the reference panel of *Ae. tauschii* we were able to infer that introgression lines had single or multiple IBD segments from *Ae. tauschii* accessions of diverse geographical distribution. *Ae. tauschii*-derived wheat lines were grown for two seasons under irrigated (IR) and non-irrigated (NI) conditions, and phenotyped for major agronomic and drought adaptive traits. The latter traits were assessed using the UAV-based phenotyping platforms by collecting image data with hyperspectral, thermal and RGB cameras. The yield of 60 *Ae. tauschii*-derived lines under IR and NI conditions was equal to or higher than that of best checks in the experiment. The relative yield under NI and IR conditions of nearly half of the lines in the population was higher than that of the best-performing checks, suggesting that *Ae. tauschii* introgressions can substantially improve yield stability under water limiting conditions. Our results indicate that introgression of *Ae. tauschii* alleles into wheat following their prioritization based on the correlation with climatic factors can help to accelerate the development of climate resilient wheat varieties.

N-41
NIFA: Genomic breeding of blackberry for improved firmness and postharvest quality

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Blackberries are considered one of the most difficult fruits to ship due to their susceptibility to many conditions that reduce marketability, shelf life, and fruit quality. The improvement of fruit firmness is an important objective in the University of Arkansas (UA) blackberry breeding program, as firm fruit generally perform better for many postharvest quality parameters. A dramatic advance in firmness was achieved with the discovery of very distinct 'crispy' texture in a handful of breeding selections. These crispy selections are considerably more firm than other UA breeding selections and cultivars and experience significantly less red drupelet reversion, a problematic postharvest physiological disorder where blackberries harvested when completely black and full ripe develop red discoloration following cold storage. Crispy-textured blackberries have the potential to increase the profitability of the US blackberry industry because of their superior postharvest performance and resistance to red drupelet reversion. However, the underlying biology of crispy texture is not understood and the trait has been difficult to recover in crosses between crispy and non-crispy selections. The USDA-NIFA AFRI Plant Breeding for Agricultural Production program has funded new research on the genetics of fruit firmness and red drupelet reversion to facilitate marker-assisted selection for texture in the UA fruit breeding program and expedite the process of developing new crispy blackberry cultivars with enhanced firmness and superior postharvest performance. During the summer of 2019, we phenotyped a panel of over 300 tetraploid breeding selections for firmness and red drupelet reversion. This winter, we will genotype the panel with 20,000 target capture probes and conduct genome-wide association mapping. We are also measuring the temporal sequence of cell wall disassembly events and changes in gene expression in developing blackberries with soft, firm, and crispy texture and developing a biparental mapping population segregating for fruit texture.

N-42
NIFA: Development of waxy sorghum breeding lines for diverse food, feed, and fermentation applications

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The purpose of this FASE research is to substantially improve waxy grain sorghum [*Sorghum bicolor* (L.) Moench] germplasm based upon extensive pilot studies and feedback from commercial end users of materials previously publicly released by PI Yerka. The waxy trait is a high-value endosperm trait associated with high digestibility, rapid fermentation into ethanol, and improved baking properties due to high-amylopectin (low amylose) starch content. Nevertheless, our industry collaborators have identified additional agronomic and grain quality traits that would improve its commercial value, expand production into additional regions, and help open underexplored, high-value domestic markets. Published studies on waxy sorghum have focused on classical breeding using older inbred lines, or QTL mapping with limited genome coverage or sequence read depths, and cannot be used to inform more modern, genomic prediction approaches to breeding. We will use a set of biparental populations, derived from publicly-available elite hybrid parents, as a training population for genomic prediction model development. We will integrate marker information from PI Yerka's new waxy sorghum MAGIC population having additional target traits of interest, and use the F2 to F5 generations following pyramiding to validate the GP models. This approach will enable us to rapidly, and for minimal cost, develop high-dimensional markers and GP methods for improving waxy sorghum. Our partners include Richardson Seeds, NuLife Market, the USDA-ARS, and ICRISAT (India) to ensure end user acceptability and domestic and international impact. In addition, Benson Hill Biosystems is generously providing cost-free use of their new Breed software for data management and GP support throughout the project.

N-43
NIFA: Diversification of cropping systems: Adaptational genomic selection in maize

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Plant breeding has led to remarkable improvements in crop productivity, but further innovations in artificial selection are crucial to creating the next-generation of climate-adapted cultivars that will sustain the needs of society. In order to capitalize on a broader array of diversity and mine alleles from germplasm that is inaccessible due to maladaptation, our project aims to establish a framework for rapidly adapting exotic populations to novel environments. Using maize as a target crop and model system, this work builds off of unique germplasm resources, emerging knowledge on the genetic basis of flowering phenology and advances in genotyping and genomic selection methodology. Field trials are currently underway to simultaneously select for early flowering time and construct models to predict the flowering time of individuals for a long-day, temperate environment (target environment) in a short-day, subtropical environment (off-season nursery) where genomic selection will be implemented. In addition, exploratory analysis of genomic features underlying environmental adaptation are being performed with an eye toward enhancing the proposed "adaptational genomic selection" approach. It is anticipated that this translational research project will demonstrate a new pathway for capitalizing on diverse germplasm collections and lead to new developments in genomic-assisted plant breeding.

N-44
NIFA: Breeding pepper for mechanical harvesting

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The long-term goal of this project is to develop green chile peppers amenable to mechanical harvesting. The critical need is to reduce labor costs associated with harvesting for processed peppers, essential for sustainability of the US industry and a growing market worldwide. Our supporting objectives formulate a systems approach combining genomics, biology, plant breeding and mechanical harvesting. They include: 1) Characterize and introgress a novel fruit destemming trait in jalapeños and New Mexico type green chile breeding lines. 2) Develop and apply DNA markers to introgress and determine the inheritance of traits important for mechanical harvesting. 3) Evaluate advanced jalapeño and New Mexico type green chile breeding lines for mechanical harvesting in multistate trials and define harvester settings. The outcomes of this work include improved germplasm and harvester settings for mechanical harvesting and DNA markers for associated traits such as destemming, determinacy and fruit quality. The results will likely extend to other pepper germplasm and may extend to other vegetables. We are working closely with an established harvester company, growers, seed companies and processors. Results from field trials, selections and marker analyses will be presented.

N-45
NIFA: Wheat yield prediction and advanced selection methodologies through field-based high-throughput phenotyping with UAVs

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To realize a new level of yield potential, breeding programs must increase the rate of genetic gain by evaluating larger populations, making more accurate selections, and decreasing the length of the breeding cycle. We are applying novel developments in remote sensing with unmanned aerial vehicles (UAVs) combined with deep learning to score complex traits and implement yield prediction and advanced selection methodology directly within breeding programs. To make more accurate yield predictions across environments we are focused on combining genomic prediction and physiological modeling. Recently we have implemented physiological evaluation of crop growth and yield components together with breeding nurseries evaluated across South Asia field trials. These component models are being developed using crop growth models to assess physiological prediction when using genomic information along with high-throughput phenotyping.

N-46
NIFA: Enhancing bread making performance of triticale

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In an effort to systematically tackle the final barrier to triticale meeting its full potential as a bread making grain crop, we are leveraging the knowledge gained on the genetic basis of wheat grain quality to improve bread making performance of triticale. This effort consists of three phases, beginning with the yield and quality evaluation of near isogenic lines each carrying different cytologically engineered 1R chromosomes in eight cultivars. These engineered chromosomes contain interstitial segments of wheat chromatin resulting in the removal of *Sec1* and *Sec3* loci which are detrimental to baking quality and carry beneficial alleles of *Glu1* and *Glu3* in different combinations in each chromosome. While these engineered chromosomes were associated with an overall yield reduction of 29%, this effect was chromosome and background specific, with a chromosome in two backgrounds having no yield penalty compared to the cultivar control. Additionally, these chromosome were associated with enhanced bread making perforce, increasing mixing stability by 3.8 fold and loaf volume by up to 46%. The second phase involved screening over 200 lines from around the world for grain yield potential and with rapid tests of grain quality including hardness, protein content and SDS sedimentation. These tests yielded a wide variation for hardness index, from 32 to 103, protein content from 9.4-13.8% and SDS sedimentation values from 29% to 106% of those observed in bread wheat. The third phase involves marker assisted selection of genes for grain quality from wheat. The primary targets are the beneficial 2* allele of *Glu-A1*, the Bx7 overexpressing allele of *Glu-B1* and the high grain protein content gene, *GPC-B1*. The objective of this effort is the development of a high yield potential triticale that combines a good bread making background, selected engineered 1R chromosomes and known wheat alleles for improved protein, hardness and gluten strength.

N-47

NIFA: High temperature stress tolerance analysis of blueberry species *V. corymbosum* and *V. darrowii*

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Experience of extreme heat waves is becoming common in recent years including Europe and North America. High chill blueberry (*Vaccinium corymbosum* L.) is a temperate fruit crop noted for desirable fruit quality. However, highbush cultivars are being subjected to higher summer temperatures, as well as the increased consumer demand, has blueberry production expanding to almost all continents with varying climates. With the warming climate in temperate zones northern highbush blueberry will likely require higher heat tolerance. *V. darrowii*, a diploid evergreen subtropical blueberry species native to the southern gulf coast may offer heat tolerance. In this study we are analyzing gene expression differences among two divergent diploid, blueberry, *V. darrowii* vs. *V. corymbosum*, species. Plants were exposed to 45°C for a nine-hour period. Using Illumina sequencing transcriptomes, unigenes, differentially expressed genes and predominant pathways involved were identified. The information obtained from this project can be a resource for further genetic improvements in blueberries and other small fruits.

N-48

NIFA: SNP marker discovery in a *Vaccinium* diversity panel

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The genus *Vaccinium* includes one of the highly coveted small fruits, 'blueberry'. Blueberries are recently domesticated plants with the cultivation history of about 100 years. Due to its recent domestication history, many economically useful traits of blueberry have not been fully exploited. Conventional blueberry breeding is a slow process, requiring 3-4 years to evaluate the useful phenotypic traits on a progeny. The molecular breeding approach would overcome this problem by providing the means to select elite parents for crossing as well as to screen the progenies for economically valuable traits in early seeding stage. However, an extensive set of PCR based markers to cover the widely diverse blueberry genotype is still lacking. To develop single nucleotide polymorphic (SNPs) markers, we re-sequenced 29 blueberry accessions and cultivars including 19 diploids, 7 tetraploids, and 3 hexaploids from 18 *Vaccinium* species. The genome of each accession was sequenced to an average coverage of 20-60X using Illumina HiSeqX. Subsequently, Illumina reads were mapped to a blueberry reference genome, and variant positions along the genome were identified. After removing insertion-deletion variants (InDels), the SNPs with alternate alleles, e.g. [A/G], between at least two genotypes out of 29, a total of 22 million SNP markers were retained. The 100bp flanking sequences of SNP loci were extracted from the genome and aligned (BLAST) to a comprehensive blueberry transcriptome database to obtain a list of 1.7 million SNPs in the exonic regions. Thirty-six randomly selected markers from the list of 1.7 million SNPs were experimentally tested in a panel of 44 blueberry commercial cultivars using Kompetitive allele-specific PCR (KASP). Of the 36 tested markers, 33 (91.7%) were polymorphic and validated. A subset of these markers will be used for cultivar and true to type plant identification that can be used by blueberry propagators and breeders.

N-49

NIFA: New genomic resources for octoploid strawberry enable mapping and genomic prediction of fruit quality and photoperiod-insensitive flowering

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Garden strawberry (*Fragaria × ananassa*) is an octoploid (2n = 8x = 56) hybrid of two distinct New World species. Traditional reliance on the diploid (2n = 2x = 14) woodland strawberry genome for octoploid genetic studies required complex approaches for disentangling subgenomic origins, and hindered genomic approaches toward identifying specific genes controlling fruit quality and other horticultural traits. This problem was solved by the publication of the first chromosome-scale, subgenome-resolved reference assembly of *F. × ananassa cultivar* 'Camarosa' genome. We identified 45M disomic, subgenome-specific DNA variants in strawberry from whole-genome shotgun (WGS) sequences of 145 geographically diverse wild and cultivated octoploids uniquely mapped against the Camarosa v1.0 genome. Using this information, we designed 2M subgenome-anchored marker probes representing nearly 100% of 108,087 genes, and developed the 850K and 50K FanaSNP arrays, permitting end-to-end physical coverage of the octoploid genome and high-density genetic mapping wild and domesticated populations. These resources are being applied to forward-genetic and genomic prediction studies of horticulturally important strawberry traits, including photoperiod-insensitive flowering and fruit quality. We used genome-wide association (GWA) and haplotype-sharing analyses to pinpoint the physical locations of perpetual flowering (PF), a dominant gene controlling day-neutral flowering, to a 200-kb region on chromosome 4-4. This has enabled the design of kompetitive allele specific PCR (KASP) assays for day-neutral breeding, and allele-specific CRISPR guide RNAs for editing candidate genes in the region. Studies are underway to support genomic prediction of fruit quality related traits, including measurements of firmness, shelf-life, volatiles, anthocyanins, acidity, and soluble solids in populations derived from diverse heirloom hybrids and commercial cultivars.

New UGA release 'RubyCrisp' (Ga.8-1-338) with novel red color next to traditional bronze and black colored muscadine grapes.

N-50

NIFA: Identification of a candidate gene for a QTL for spikelet number per spike on wheat chromosome arm 7AL by high-resolution genetic mapping

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A better understanding of the genes controlling differences in wheat grain yield components can accelerate the improvements required to satisfy future food demands. In this study, we identified a promising candidate gene underlying a quantitative trait locus (QTL) on wheat chromosome arm 7AL regulating spikelet number per spike (SNS). We used large heterogeneous inbred families (> 10,000 plants) from two crosses to map the 7AL QTL to an 87-kb region (674,019,191– 674,106,327 bp, RefSeq v1.0) containing two complete and two partial genes. In this region, we found three major haplotypes that were designated as H1, H2 and H3. The H2 haplotype contributed the high-SNS allele in both H1 × H2 and H2 × H3 segregating populations. The ancestral H3 haplotype is frequent in wild emmer (48%) but rare (~1%) in cultivated wheats. By contrast, the H1 and H2 haplotypes became predominant in modern cultivated durum and common wheat, respectively. Among the four candidate genes, only TraesCS7A02G481600 showed a non-synonymous polymorphism that differentiated H2 from the other two haplotypes. This gene, designated here as WHEAT ORTHOLOG OF APO1 (WAPO1), is an ortholog of the rice gene ABERRANT PANICLE ORGANIZATION 1 (APO1), which affects spikelet number. Taken together, the high-resolution genetic map, the association between polymorphisms in the different mapping populations with differences in SNS, and the known role of orthologous genes in other grass species suggest that WAPO-A1 is the most likely candidate gene for the 7AL SNS QTL among the four genes identified in the candidate gene region.

N-51

NIFA: Deploying desirable fiber quality mutants in the gene pool of upland cotton

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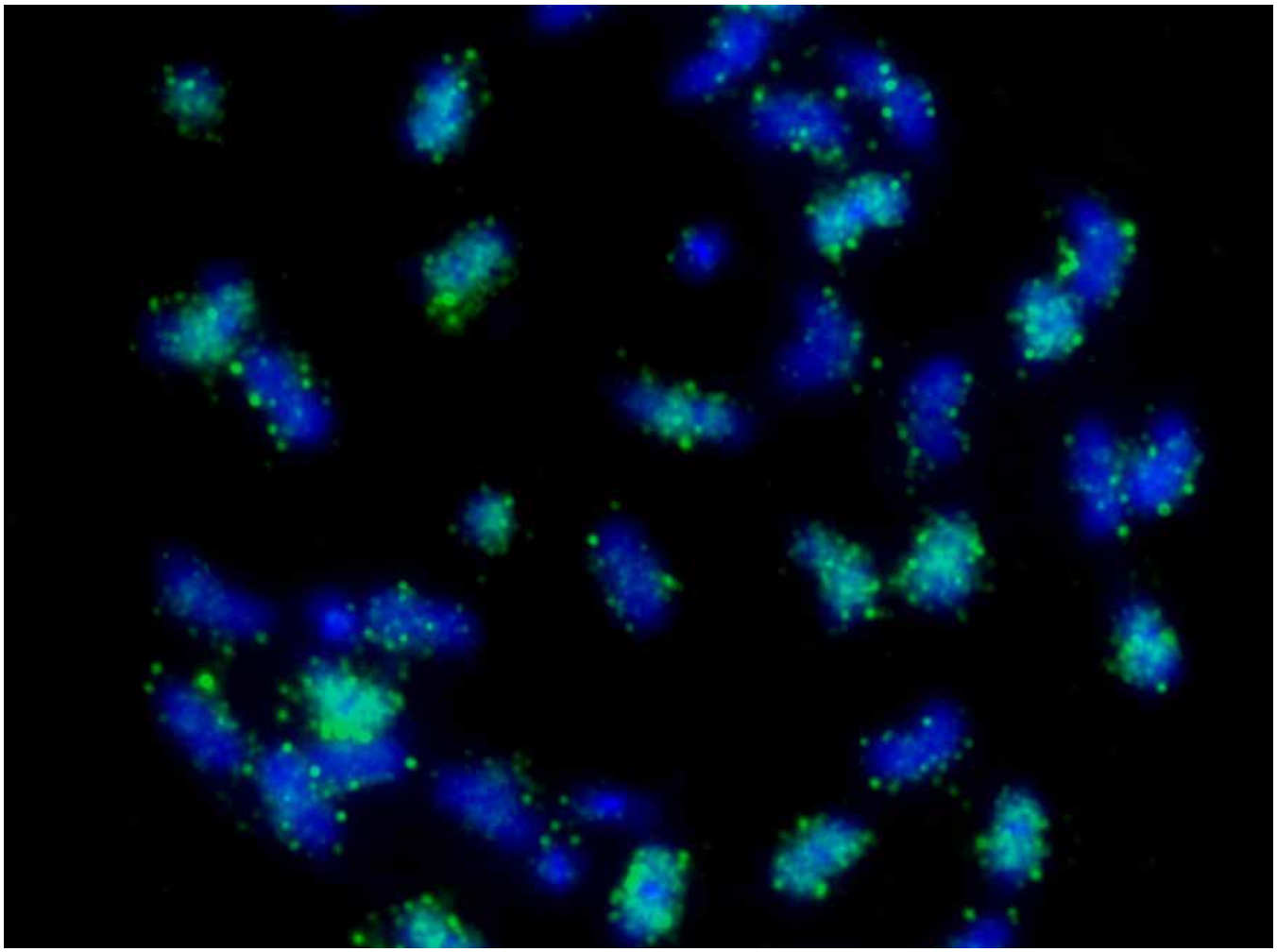
This standard research proposal addresses utilization of novel induced mutants to enrich genetic diversity and accelerate breeding progress in one of the most economically important and genetically vulnerable major US crops, cotton. This research is founded on the discovery that screening of large mutant populations identified lines conferring striking fiber quality improvements, for which a subset have been validated in 5 years of testing in their native background and two additional backgrounds. Moreover, pyramiding of multiple mutants by intercrossing resulted in superior levels of one fiber quality component (fiber length) and showed correlated improvements of other components. The proposed research includes development and evaluation of trait-focused populations that pyramid multiple mutants to attain superior levels of additional key fiber quality components, genetic mapping of fiber mutants conferring striking phenotypes to quantify their individual and interactive phenotypic effects and identify diagnostic DNA markers, intercrossing among superior lines from multiple-mutant populations to investigate scope for continuing genetic gains, and investigating the impact of mutant-derived fiber quality improvements on yield components. Integrative analyses will test a recent hypothesis about the nature of cotton fiber quality QTLs, and provide a framework for deployment in mainstream cotton breeding of lines selected from the study populations, accompanied by diagnostic DNA markers to facilitate their manipulation. Partnership between a plant breeder and a genome biologist will integrate training in field-based breeding with effective utilization of genomic data and tools toward mitigating genetic vulnerability of cotton, in a manner that is also applicable to many other crops.



FISH of a fragment of FIDEL, one of the most abundant LTR retrotransposons in the peanut genome.

N-52

NIFA: CRISPR-based precision breeding in wheat

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Gene editing (GE) has emerged as a disruptive technology that can be used to generate novel variation in the genomic regions affecting major agronomic traits. Our 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 used wheat orthologs of genes that were shown to affect yield component traits in various crops to select targets for gene editing. The gene editing pipeline based on the Cas9 and Cpf1 nucleases was established for wheat. For eighteen genes, the Cas9 and Cpf1 constructs were designed and successfully tested for editing efficiency using the protoplast assay and next-generation sequencing. GE plants were obtained for majority of these genes in spring and winter wheat. The phenotypic effects of GE on yield component traits were confirmed for several genes, and phenotyping of remaining GE plants is underway. Wheat lines combining several edited genes were created by crossing single-gene mutants or by the modification of multiple genes and their homoeologs using a multiplex GE construct. The latter was shown can be facilitated by CRISPR/Cas9 activity maintained across generations. For example, GE showed that TaGW2 gene homoeologs' effects are dosage-dependent and cultivar-specific with 16-20% increase in grain weight and size in triple-genome mutants. The GE variants of the seed size increasing gene transferred to other wheat cultivars showed similar phenotypic effects. An approach for high-efficiency gene editing and inter-cultivar trait transfer was established using a wheat line expressing Cas9 at the high level. In our project, we successfully demonstrated that GE technology can be used for creating novel variation in the genes that directly control yield component traits thereby building new genomic and biotechnological tools and resources for accelerating wheat improvement.

N-53

NIFA: Breeding of phytoglycogen-type sweet corn traits based on ISA2 deficiency rather than the standard ISA1 deficiency

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The genetic basis of a major sector of the commercial sweet corn crop is highly limited because it relies solely on the mutation *su1-Ref* and essentially a single haplotype over the entire short arm of chromosome 4. To overcome potential genetic bottlenecks, this project seeks to create phytoglycogen-accumulation phenotypes typical of *su1-Ref* lines using independent *su1* alleles or mutations in other loci that encode functions related to that of su1. su1 and isa2 encode isoamylase (ISA)-homologs, ISA1 and ISA2, respectively, involved in determining ρ(1ϕ) branch linkage location and frequency in the amylopectin component of starch granules. Changes in ISA activity in *su1-Ref* mutants alter polysaccharide structure so that the soluble polymer phytoglycogen forms instead of a substantial portion of what would normally become granular amylopectin. ISA1 and ISA2 interact directly in a complex that exhibits ISA activity. The null mutation isa2-339 previously was reported not to condition phytoglycogen accumulation in the W64A background, indicating ISA1 alone can support ISA activity and normal amylopectin levels. *isa2-339* was introgressed into inbred Ia453-Su1, derived from Purdue Bantam and Bantam Evergreen sweet corn hybrids and conversion of *su1-Ref* to wild type *Su1*. In contrast to W64A, isa2-339 caused a classical phytoglycogen-type sweet corn phenotype in Ia453-Su1. Genomic sequencing confirmed the *su1* locus was wild type in the *isa2-339* mutant version of Ia453-Su1. Thus, genetic polymorphism outside of *su1* determines whether or not ISA2 is required for normal amylopectin biosynthesis, offering the potential to breed sweet corn based on *isa2* rather than *su1*. The entire suite of starch biosynthetic genes in Ia453 has been sequenced to investigate the basis of this functional variation, and those data will be reported. Finally, comparison of genomic sequences confirmed that *su1-Ref* arose only once in a single haplotype and has been maintained essentially intact without intergenic recombination since.

N-54

NIFA: QTL for ammonium tolerance in spring wheats under different N forms and CO_2 levels

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The atmospheric CO2 concentrations anticipated during the coming decades pose a threat to global food security. As CO2 rises, grain yield and protein yield decline in wheat, depending on its relative dependence on nitrate (NO_3^-) and ammonium (NH_4^+) as nitrogen sources. To understand the genetic basis of biomass production in response to nitrogen forms and elevated CO_2, we performed a genome-wide association (GWA) analysis of 875 spring wheat accessions from the National Small Grain Core collection grown at ambient CO_2 in a nutrient solution containing either nitrate or ammonium as a sole nitrogen source. We identified QTLs for biomass production during the early tillering stage that were significant in at least four out of six environments in the GWA analysis. We validated these QTLs in a panel of six bi-parental mapping populations, with a common female parent, at a 750 ppm CO_2 concentration. The loci identified and validated in this study should prove useful in breeding food crops that meet the challenges of climate change.

N-55
NIFA: Robot-assisted and machine learning-enabled in-field high throughput plant phenotyping

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High throughput plant phenotyping (HTPP), measuring traits and assessing plant development and performance, has become a rapidly evolving focus area in agriculture, but remains a major bottleneck in crop improvement. In particular, phenotyping platform development and data analytics are two main challenges in field-based high throughput plant phenotyping. UGA B-SAIL has been focusing on the following two areas: 1) robotic system integration and development; 2) data analytics using computer vision and machine learning. In the first area, we have developed a multi-tier HTPP platforms including a) a ground-based GPhenoVision system consisting of a high-clearance tractor and multiple high resolution phenotyping imaging sensors and customized image acquisition software, b) unmanned aerial systems that integrate customized image acquisition for much higher throughput than ground systems, quantifying plant height and canopy growth rate, biotic and abiotic stresses, initiation and progression of flowering, and c) unmanned ground vehicles that can autonomously navigate between rows with centimeter accuracy while acquiring LiDAR, thermal and RGB images. In the second area, we have developed machine learning based data analytics to extract phenotypic traits from 3D point cloud and 2D imagery. For instance, we have developed algorithms for 3D cotton boll mapping, internode distance measurement, and branching pattern characterization. In addition, deep convolutional neural networks have been used to detect various organs or sub-plant regions in images including seedlings, flowers, cotton bolls, and inter-nodes. Accurate detection results can be used for tracking and counting fruit and yield estimation.

N-56
NIFA: Gene stacking to generate multi-disease resistant lettuce

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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. These studies are the logical progression of our lettuce molecular genetics and breeding program; it builds upon our germplasm collection with genetically characterized loci, the genome sequence of multiple lines of wild and cultivated lettuce, representative collections of pathogen isolates, and experience with and access to the technologies required. We have currently mapped 52 phenotypic loci that confer resistance in lettuce to ten diseases. We are cloning major genes for resistance to *Bremia lactucae* (downy mildew) and *Verticillium dahliae* (Verticllium wilt) and refining gene editing technology for lettuce, with the long term goals of generating gene stacks to combine resistance genes and releasing 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, genome editing, and the availability of lettuce genome sequences. This involves high-resolution mapping of resistance phenotypes and validation of candidate genes by targeted knock-outs. Germplasm is being 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 more durable disease resistance.

N-57

NIFA: Using high-throughput sequencing to characterize the genetic and genomic architecture of brown stem rot resistance in soybean

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NIFA: Breeding for pathogen resistance is an important objective to improve and protect yield. Brown stem rot (BSR), caused by the fungus *Phialophora gregata*, reduces soybean yield by as much as 38%. To date, three dominant BSR resistance genes have been identified: *Rbs1*, *Rbs2,* and *Rbs3*. However, the gene networks regulating defense responses to BSR remain unknown and the mapped location of all three loci is large and undefined. Identifying resistant germplasm by genotyping or phenotyping remains difficult due to complexities of soybean/*P. gregata* interactions. Therefore, the overarching goal of this postdoctoral research project was to characterize the genetic and genomic architecture of BSR resistance. To identify and characterize downstream defense genes, gene networks, and candidate resistance genes, RNA-seq of *P. gregata*-infected and mock-infected tissues of resistant (*Rbs1*, *Rbs2,* or *Rbs3*) and susceptible soybean genotypes was conducted. Preliminary analysis has revealed that one week after infection, there is little overlap in differentially expressed genes between each resistant genotype. Further analyses will identify candidate genes for *Rbs1*, *Rbs2,* and *Rbs3* mediated resistance. Virus induced gene silencing (VIGS) has been used to characterize the genes and gene networks important in resistance. VIGS constructs were designed to target five clusters of receptor like proteins (RLPs) located within the three known *Rbs* loci. Silencing the RLPs in resistant genotypes resulted in susceptibility to *P. gregata*, further validating their role in resistance. These results will increase the efficiency of identifying and developing cultivars with one or more BSR resistance genes, ultimately reducing yield loss due to BSR in soybean.

Stacking leaf coloration traits in white clover converts it from a lawn weed to an ornamental groundcover.

Interspecific hybrids in peanut – Arachis (duranensis x ipaensis) x hypogaea.

POSTER ABSTRACTS

P-01

Integrating genomic selection and accelerated generation advancement to improve genetic gain in a winter wheat breeding program

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Winter wheat (*Triticum aestivum* L.) is a cold-hardy crop with higher yield potential compared to its spring counterpart, which makes it more desirable to Ontario farmers. Given its economic importance, it is imperative that new selection methods, including genomic selection (GS), are introduced to allow for the rapid selection of value-added traits and the development of commercial cultivars. The objectives of this experiment are to examine the feasibility of integrating genomic selection with an accelerated generation-advancement population development strategy in a winter wheat breeding program and to determine the accuracy of predicting the performance of optimal winter wheat lines for advancement to the advanced and elite yield trials. Genotypes in the advanced and elite yield trials will be used as the training set to train GS models to predict performance of the genotypes in the preliminary yield trials (the testing set). A number of traits with varying expected heritability estimates are evaluated, including grain yield, kernel hardness and kernel weight, to examine the suitability of various prediction models chosen. Prediction accuracy of each model will be tested as the correlation between predicted and observed values for each trait. Overall, this will examine the possibility of increasing annual genetic gain and decreasing the selection time period prior to rigorous testing for commercial release, resulting in tremendous benefits to winter wheat breeding programs.

P-02

Mapping QTLs for 15 morpho-metric traits in *Arabidopsis thaliana* using Col-0 × Don-0 population

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Genome wide QTL mapping was conducted in *Arabidopsis thaliana* using F_2 mapping population (Col-0 × Don-0) and SNPs markers. It was found that selected ecotypes of *Arabidopsis thaliana* i.e. Col-0 and Don-0 were different at morphological and molecular level. Total five linkage groups were obtained with number of SNPs per linkage group varied from 45 to 59. Single locus analysis detected a total of 36 QTLs for 15 traits with number of QTLs per trait ranging from one (root length, root dry biomass, cauline leaf width, number of internode and internode distance) to seven (for bolting days). Phenotypic variance explained (PVE) and logarithm of the odds ratio (LOD) of these 36 QTLs found upto 38.17% and 6.26 respectively. Further, two locus analysis identified one main effect QTL (M-QTL) and four epistatic QTLs (E-QTLs). Five major QTLs (PVE >15.0%) may found to be useful for fine mapping to identify genes associated with respective traits, and also for development of specialized population through marker assisted selection. Major QTLs could be utilized to characterize the genes through fine mapping and map based cloning. The identification of additive and dominant effect QTLs and desirable alleles of each of above mentioned traits would also be important for future research.

P-03

A connected half-sib family training population for genomic prediction in barley

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Genomic prediction accuracy is affected by population size, trait heritability, relatedness of training and validation populations, marker density, and genetic architecture. Nested-association mapping (NAM) populations have advantages in many of these features compared to biparental families and may be an effective strategy for increasing prediction accuracy. The classic NAM design was modified to create a two-row spring malting barley population of 1341 F3:F4 lines in seven families that was phenotyped for heading date, plant height, leaf rust, spot blotch, pre-harvest sprouting, and grain protein. Multiplexing founder lines allowed genotyping-by-sequencing markers to be projected to low-plex progeny. Population structure and size enabled quantitative trait loci (QTL) detection with genome-wide association analyses for height, leaf rust, pre-harvest sprouting, and spot blotch. Prediction accuracies were assessed using cross-validation strategies that included or omitted population structure. Across-family prediction accuracy (0.607-0.811) was improved by including population structure and surpassed within-family prediction accuracy. Reductions in marker density (70-80%) and training population size (25-50%) did not cause significant loss of prediction accuracy. Addition of fixed marker effects from genome-wide association studies had minimal impact on prediction accuracy in the full training population but improved accuracy in reduced training populations. Within-family prediction for traits highly influenced by population structure can be improved by adding half-sibs and some full-sibs to the training population.

P-04

Mapping quantitative trait loci (QTL) associated with flavonoid in tomato (*Solanum lycopersicum L.*)

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Flavonoids are a group of plant secondary metabolites which are reported to provide health benefits through antioxidant effects. Based on human dietary values, flavonoids include anthocyanins and five other subclasses. Anthocyanins in tomato plants and fruits are relatively uncommon but have been introgressed from its wild accessions into the cultivated tomato. Little is known about the genes responsible for the biosynthesis of anthocyanin in tomato, although three genes linked to synthesis. The inheritance and segregation pattern of these genes are still unknown, and there may be other genes involved in anthocyanin synthesis in tomato. We were interested to identify the QTL associated with anthocyanin content in tomato. To achieve this objective, a backcross population BC_1 (NC 16267) of 250 individuals was developed from the parents – NC 74CAP (purple) x Ailsa Craig (green) and grown at the Mountain Horticultural Crops Research and Extension Center (MHCREC), Mills River, NC. The resulting BC1S1 population was grown at the Mountain Research Station (MRS), Waynesville, NC adopting completely randomized design (CRD) with two replications. Anthocyanins content in both generations were quantified using high performance liquid chromatography (HPLC). QTL-seq approach was adopted by performing Next – Generation Sequencing of Bulk Segregant Analysis (NGS – BSA) of the DNA bulk from low and high anthocyanin containing individual plants from BC1 population. Five QTL were identified on chromosome 1, 2, 4, and 7 responsible for anthocyanin content in tomato. However, we declare only four QTL in chromosome 1, 2, and 4 to be novel as the one located in chromosome 7 is not investigated whether to be the same QTL as previously reported or a novel one. These QTLs located on chromosome 1, 2, and 4 may be informative to explain the genetic control of anthocyanin biosynthesis in tomato and to manipulate its content by breeding.

P-05

Identification and genetic diversity of a protein kinase gene in two maize-teosinte introgression near isogenic lines (NILs)

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Maize is an agriculturally important crop worldwide that plays a role in global food security. One of the many threats to this crop is *U. maydis*, a basidiomycete fungus that produces various symptoms in maize and causes significant yield loss annually. Teosinte has been shown to be resistant to several pathogens and may be a source for resistance to *U. maydis*. Using the 100 maize-teosinte near-isogenic introgression lines (NILs) composed of maize (B73) and a teosinte species (*Zea parviglumis*), we identified two Nils (0068 and 1068) that were resistant to U. maydis and had a teosinte introgression (3.6 Mbp and 3.9 Mbp, respectively) on the short arm of maize chromosome 9. This indicated that the teosinte introgressed region was likely responsible for the resistance. Further analysis of these of NILs 0068 and 1068 showed a high level of resistance to *U. maydis* that is quantitatively controlled. Gene specific primers from B73 were used to PCR amplify one of seven potential protein kinase gene from Nil 0068 and 1068, and then the genetic diversity of the amplified products was analyzed using a neighbor-joining phylogenetic tree to identify the protein kinase genes that are potentially responsible for the resistance against *U. maydis* observed in the two NILs. I PCR amplified gene #1 determining that it indeed was a protein kinase. A phylogenetic tree was generated. It had a nucleotide identity of 45.7% to 99.63% percent indicating high genetic diversity among gene #1 in both NILs. They were grouped together on the same clades indicating that although protein kinase gene #1 is divergent in both NILs, they are evolving in a similar manner.

P-06

An MKK3 allele affects seed dormancy at physiological maturity in common barley varieties (*Hordeum vulgare*)

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In many crops an appreciable level of dormancy is tolerated, however, the process and economics of malting inherently applies selection pressure for nondormant varieties and, as a result, elevates varieties to production level that have little or no innate dormancy. Reduced dormancy has resulted in increased susceptibility of malt varieties to preharvest sprouting, which is the precocious germination of grain while still on the ear. Preharvest Sprouting (PHS) reduces grain quality, making the barley no longer suitable for malting. This has a large negative economic impact on farmers that then must sell their barley as feed. Much of the observed variation in PHS resistance is genetic with previous reports indicating that the *HvMKK3*, *HvQsd1* and the *HvMFT* genes play important roles. Thus, our research project's goal is to identify and explore genes impacting PHS among commonly grown Northern Great Plains malting barley varieties. One hundred fifteen barley varieties were grown over two years (x3 reps each year) and PHS susceptibility was assessed. About 110 of the varieties were genotyped by direct sequencing of *HvMKK3*, *HvQsd1*, and *HvMFT*. We observed four *HvMKK3* alleles, two *HvQsd1* alleles and two *HvMFT* alleles. Our results indicate at least one *HvMKK3* mutation is associated with a large increase in PHS susceptibility in multiple popular malting varieties. Furthermore, the previously described *HvQsd1* mutation, F214L, is associated with increased PHS resistance in This set of varieties. Variation in *HvMFT* was not observed to be significantly associated with PHS as each mutant allele was found in only a single variety. To better characterize effects of the novel *HvMKK3* allele and known Qsd1 alleles in Northern Great Plains malting barley, four varieties from the previous analysis were chosen based on their genotyping, yield, product quality, and PHS scores, to create barley bi-parental populations. The results of this study indicate potential to breed for a specific window of high seed dormancy that quickly degenerates after harvest.

P-07

Validation of vegetation indices for use in winter wheat (*Triticum aestivum*) genomic selection

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The development of high throughput phenotyping systems has resulted in an influx of phenotypic data for breeding programs. Vegetation indices form the basis of many high throughput phenotyping systems, as they have been shown to be highly correlated with desirable plant characteristics. The optimal use of this data is not yet known and several workflows are being explored for how best to utilize the increase in phenotypic and genotypic information. Before these systems can be used to the best of their capabilities, it is essential to identify and validate which plant characteristics are being measured and their underlying genetic architecture. Here we show that in winter wheat (Triticum aestivum) the strong correlation between different vegetation indices and grain yield is reflected in the relationship between the marker effects for these phenotype. The polygenic genetic architecture of the vegetation indices also shows that the best approach for modeling of these phenotypes is whole genome prediction models that can be applied in genomic selection.

P-08

Identification and characterization of novel *Rht-1* alleles for wheat plant growth and end use quality

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The inverse relationship between wheat plant height and yield has resulted in the widespread development of semi-dwarf wheat varieties since the 1960s. This relationship was initially discovered through the introduction of mutant forms of the *Reduced Height* (*Rht-1*) gene. There are two commonly used semi-dwarfing mutant alleles, *Rht-B1b* and *Rht-D1b*. Both introduce a premature stop codon near the N terminus of the gene. The resultant plant is 20% shorter than the tall wildtype and yields 5-7% greater. However, *Rht-B1b* and *Rht-D1b* are also associated with decreased grain protein content, reduced emergence under arid conditions, and there is limited allelic diversity. Furthermore, despite significant research regarding the impact of the semi-dwarfing alleles on plant growth and development, much less is known regarding their impact on bread baking and end use quality. Using EMS mutagenesis, we have identified and characterized 16 novel *Rht-1* alleles with a range of functionality. We are evaluating the impact of each mutation individually, as well as in combination to investigate the additive effects of the alleles. We have also determined that although the semi-dwarfing alleles reduce total grain protein content (2%), they increase dough mixing strength (33%) by impacting gluten protein composition. This work is increasing the allelic diversity of *Rht-1* in wheat, as well as creating useful genotypes to optimize wheat grain yield and quality in a wide range of environments. This work is funded by Agriculture and Food Research Initiative Competitive Grant 2017-67014-26190 from the USDA National Institute of Food and Agriculture.

P-09

Pear rootstock breeding program at Washington State University

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The Pacific Northwest (Washington, Oregon and California) accounts for over 95% of national pear production; however, the industry is economically stagnant which is reflected in the decreasing market presence of pears in the face of other competitive fruit crops, such as apple. Over the last 50 years, apple production has been revolutionized through the release of numerous dwarfing apple rootstocks, which reduce labor inputs and management costs, thereby increasing profitability. By contrast, the pear industry remains bereft of dwarfing and precocious rootstocks – a critical need to revive the industry and enable modern, high-density, profitable production. In 2015, the Washington State University pear rootstock breeding program was initiated with the overarching aim of producing dwarfing and precocious rootstocks that are suited especially for the Pacific Northwest. Collection of germplasm (i.e., crossing parents) began in 2009. Currently, the program consists of approximately 700 seedling trees (from biparental crosses) in phase 1 assessment and about 1,000 seedlings in the greenhouse. The "phase 1" rootstock seedlings were evaluated for general horticultural traits, including height and branch angle. In 2018, these seedlings were grafted with a standard scion cultivar to determine their dwarfing potential in the following years. The availability of genomics resources including a 70K *Pyrus* SNP array is enabling high-resolution genotyping. Work is currently underway to construct high-resolution genetic maps of the "phase 1" biparental families for future marker-trait association of important rootstock traits. Additionally, several dwarf and dwarfing markers for apple and pear reported in the literature will be validated for their applicability and reliability in the WSU pear rootstock breeding germplasm.

P-10

Identification and confirmation of an allele from Danbaekkong (PI619083) for increasing seed protein content in soybean

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Soybean meal is the largest source of animal protein feed due to the high protein concentration and availability. The study of the genetic control of seed protein is essential for the development of new cultivars with higher protein. Our previous research using a bi-parental population and GWAS approach identified a QTL from Danbaekkong on chromosome (Chr) 20 that increases 3-4% of seed protein. In the present study, we aimed to fine map the QTL and develop functional SNP markers to select for the high protein allele from Danbaekkong. QTL mapping in a bi-parental population, GWAS and sequencing analyses identified a deletion region in Danbaekkong on Chr 20 responsible for increased seed protein and KASP markers were developed. To validate this high protein allele, we developed 10 elite F5-derived populations consisting of 960 RILs using a parent derived from Danbaekkong. RILs were genotyped using the KASP assays and seed composition of these RILs was analyzed using NIR. Results indicated that the allele from Danbaekkong explained 68-76% of the phenotypic variation and could increase 3.4 to 3.8 % of total seed protein content across populations. Correlation coefficients indicated a negative relationship between protein and oil content. The results show that the marker is very effective in making selection of the Danbaekkong allele for high protein content. The next step is to assess the influence of the high protein allele on yield and balance the increase of protein content with acceptable levels of oil content.

P-11

Genome-wide association study of pecan scab resistance in a provenance collection

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Pecan (*Carya illinoinensis*) is a species native to North America and the United States is currently the largest global producer of pecans. Natural pecan scab infections, caused by the fungal pathogen *Venturia effusa*, result in foliar lesions, defoliation and decreases in nut yield and quality. Current management practices include hedging, spraying fungicides with different modes of action and planting scab resistant cultivars. However, multiple applications are needed during the growing season to cover the entire canopy surface increasing production costs and the effectiveness of certain fungicides against scab is declining. The objective of this study is to identify the genetic mechanisms associated with pecan scab resistance from diverse germplasm evaluated in the field. The pecan provenance collection consists of over 800 trees that represent the natural range of variation for the species in the United States and Mexico. Scab susceptibility ratings were collected from the provenance collection orchard located in Byron, GA for three years. Genotyping-by-sequencing (GBS) approaches were used for genome-wide association studies including assessment of various statistical models to identify additive components for scab resistance. Single nucleotide polymorphisms (SNPs) in genes associated with biotic stress responses and pathogen resistance mechanisms were identified. Ongoing experiments include evaluating gene expression of susceptible and resistance trees prior to and after scab infections using RNA-Seq approaches and quantitative RT-PCR. The identification of genetic loci associated with pecan scab resistance will provide insights on the genetics of pecan scab resistance and contribute to the pyramiding of resistance genes aimed at developing enhanced cultivars that combine multiple scab resistance genes through genomics-based selection approaches.

P-12

Viability of inbred yield trial replacing preliminary hybrid yield trial in scaled commercial breeding program

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Corn (*Zea mays* L.) hybrid yield trials, traditionally, has been the dominate method for evaluating and selecting best hybrids during the past nearly 100 years. Based on time series studies, since the 1930s, the parental inbreds and hybrids yields have been increasing nearly in parallel, with only a modest increase in heterosis yield. Meanwhile, there has been an increased correlation between inbreds and hybrids. We tested the viability of replacing preliminary hybrid yield trials with inbred yield trials, in our current commercial breeding system. Results showed a positive correlation of 0.37 and 0.39, between yields of S3 inbreds and testcrosses in a preliminary yield trial, and 0.56 and 0.61 between finished inbreds and testcrosses in an elite yield trial. We find that there is a respectable probability of finding potential commercializable hybrids in inbred yield trials. However, based on our testing system, an inbred yield trial costs more than a testcross yield trial, an increase of $21 per entry. Additionally, the low vigor of inbreds aggravates the border effect, and distorts yield data accuracy. Our conclusion is that replacing preliminary hybrid yield trials with inbred yield trials is a solid concept, but not economically viable at this time with our current system. We expect these results to be helpful for breeders to comprehensively assess the idea of replacing preliminary hybrid yield trials with inbred yield trials.

P-13

Predicted genetic gains from introgressing chromosome segments from exotic germplasm into an elite soybean cultivar

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Broadening the diversity of cultivated soybean [*Glycine max* (L.) Merrill] through introgression of exotic germplasm has been difficult. Our objectives were to 1) determine if introgressing specific chromosome segments (instead of quantitative trait locus alleles) from exotic soybean germplasm has potential for improving an elite cultivar, and 2) identify strategies to introgress and pyramid exotic chromosome segments into an elite cultivar. We estimated genomewide marker effects for yield and other traits in seven crosses between the elite line IA3023 and seven soybean plant introductions (PIs). We then predicted genetic gains from having ≤2 targeted recombinations per linkage group. When introgression was modeled for yield while controlling maturity in the seven PI × IA3023 populations, the predicted yield was 8 to 25% over the yield of IA3023. Correlated changes in maturity, seed traits, lodging, and plant height were generally small but were in the favorable direction. In contrast, selecting the best recombinant inbred (without targeted recombination) in each of the PI × IA3023 populations led to negative or minimal yield gains over IA3023. In one PI × IA3023 population, introgressing and pyramiding only two linkage groups from recombinant inbreds into IA3023 was predicted to achieve an 8% yield gain over IA3023 without sacrificing the performance of other traits. The probability of inheriting intact chromosomes was high enough to allow introgression and pyramiding of chromosome segments in 5-6 generations. Overall, our study suggested that introgressing specific chromosome segments is an effective way to introduce exotic soybean germplasm into an elite cultivar.

P-14

Genome assembly of five Stiff Stalk inbreds: PHJ40, LH145, PHB47, NKH8431, & B84

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Our team has a goal of developing and acquiring resources to support maize research in elite genetic backgrounds that are efficient research tools and that facilitate technology transfer. The Stiff Stalk heterotic pool is a cornerstone of commercial U.S. cornbelt dent hybrids. B73 – the inbred chosen for the current reference genome – is an influential founder in this group. B14, B37, and B84 are additional influential Stiff Stalk Synthetic founder inbreds, and companies have internally developed additional lines within this heterotic group. We constructed whole-genome reference-guided assemblies of five Stiff Stalk ex-PVP and public inbred lines. LH145 represents the B14 founder group, and PHB47 represents the B37 founder group. B84 is found in multiple commercial pedigrees and is related to the B73 group. PHJ40 is an early Stiff Stalk type developed by Pioneer Hi-Bred. NKH8431 was Northup King's recombination of B73 and B14 based germplasm for early maturity. Genomes were sequenced using PacBio, assembled using MECAT, polished using QUIVER, and pseudochromosomes were generated using reference-guided assembly relative to the B73 version 4 genome. Misjoins were mitigated by breaking and reassembling the sequences, and Illumina sequencing was used to correct SNPs and indels. The project is being finalized, but example assembly statistics for PHB47 and PHJ40 exemplify results of the project. The PHB47 genome was assembled into 3841 contigs and 940 scaffolds, resulting in 2155.6 Mb of assembled sequence space. The PHJ40 genome was assembled into 1547 scaffolds consisting of 4250 contigs, resulting in 2126.8 Mb of assembled sequence. Annotation supports that >96% of the B73 version 4 annotated primary transcripts are present in these assemblies. Details on the sequencing process and outcomes will be described. In addition, the genetic relationships among inbreds will be presented and the association with phenological information will be described to support their utilization in research programs.

P-15

Estimating of genomic prediction for *Pythium myriotylum* in lines common bean in two environmental evaluated

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Pythium myriotylum is a soil pathogen that causes serious damage to common bean production. *Pythium* is among the pathogens causing the disease termed root rot. In this study, a panel of 218 root rot (RR) lines was developed and evaluated in the greenhouse for *Pythium* and in the field for plant vigor, number plant germinated and seed weight. The results show positive and significant correlations between greenhouse and field evaluations, as well as high heritabilities (0.71 - 0.94) of evaluated traits. All samples were genotyped by GBS and 15,004 SNPs were identified. In GWAS analysis, we did not observe significant SNPs with evaluated phenotypes, indicating absence of major resistance genes. However, high genomic prediction accuracy was found for *Pythium*, plant vigor and related traits calculated, using RKHS genomic prediction algorithm. The prediction accuracies of traits ranged between 70 and 80%, the highest being the general root rot disease score estimated from combined field and greenhouse data. In addition, using the greenhouse data as a training population good predictions of field phenotypes were obtained. Genomic prediction is shown to be a useful tool in the estimation of the behavior of the phenotype for *Pythium* and related traits, especially in the evaluations carried out in different environments.

P-16

Marker-assisted introgression of *Gn1a* and *WFP* increased primary branching and grain number in rice

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The major quantitative trait loci (QTLs) *WEALTHY FARMER'S PANICLE (WFP)* and *Grain number 1a (Gn1a)* controls the number of primary branches per panicle and grain number of rice, respectively, and hence has the potential to dramatically improve rice yields. A strategic approach based on marker-assisted backcrossing (MABC) was used to introgress these two major QTLs from ST12 into 14 rice cultivars that are preferentially cultivated by farmers in different rice growing regions for their adaptive traits and good grain qualities. DNA markers located less than 5 cM upstream and downstream of *WFP* and *Gn1a*, and that can discriminate between genotypes of the breeding materials for the target loci were used for the MABC. Foreground and recombinant selection were performed from BC_2F_1 when 87.5% of the donor background genome has been recovered. Preliminary investigation into the genetic effects of WFP on a BC_2F_1 population derived from the cross between one of the recipient cultivar, NERICA1 and ST12 showed that plants heterozygous for the WFP^{ST12} allele have an average of 17 primary branches per panicle, which is 54% higher than the average 11 primary branches per panicle of plants homozygous for the $WFP^{NERICA1}$ allele. This increase in the number of primary branches per panicle consequently increased the grain number per panicle by 29%. Similarly, plants that are heterozygous for the $Gn1a^{ST12}$ allele recorded a 36% increase in grain number compared to those that are homozygous for the $Gn1a^{NERICA1}$ allele. No significant differences in the 100-grain weight were observed between plants with homozygous $ST12^{WFP}$ or $NERICA1^{WFP}$ allele, and between plants with homozygous $ST12^{Gn1a}$ or $NERICA1^{Gn1a}$ allele. Comparative results were also observed in the early breeding lines derived from the 13 remaining recipient lines. Efforts are currently underway to pyramid *WFP* and *Gn1a* into each of the recipient lines.

P-17

TN15-5007, a new high yielding soybean cultivar with ultra-high meal protein

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The conventional (non-GM) soybean [Glycine max (L.) Merrill] line TN15-5007 was released by University of Tennessee Agricultural Research in 2019 as a new cultivar based on high seed yield potential in Tennessee and the southern region of USA. The objective of its development was to create a high yielding cultivar with high meal protein. Soybean germplasm line TN15-5007 was developed from one of 3,500 single plants, of which 40 were selected to carry forward as plant rows. Progeny rows were selected based on adapted maturity, lodging resistance, disease resistance, and pod density and were entered in yield tests in 2015 through 2018. TN15-5007 has white flowers and gray pubescence. The plants show good resistance to lodging. The pods have a tan pod coat, and the seeds are yellow with smooth seed coats. The seed size is approximately 12.7 grams per hundred seeds, which was equal to that of Ellis in the 2018 USDA Uniform Test. In that test, TN15-5007 matured two days earlier than Ellis, matured equal to that of AG 46X7, one day earlier than AG 4835, and one day later than AG 4632 indicating that the relative maturity of TN15-5007 is approximately 4.7 to 4.8, which is highly desirable for producers in Tennessee and the Mid-South region. Soybean line TN15-5007 is resistant to stem canker, Diaporthe phaseolorum (Cooke & Ellis) Sacc. var. caulivora K.L. Athow & R.M. TN15-5007 produced 436 g kg-1 protein and 213 g kg-1 oil on a dry weight basis and produced a very high 505 g kg-1 meal protein in the 2018 Southern Uniform Test.

P-18

Root architecture traits variability in southern highbush blueberry breeding population

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Southern highbush blueberry (*Vaccinium corymbosum* interspecific hybrids) have shallow, fine, fibrous, and highly branched root system. They prefer to grow in soil with high organic matter, low pH, and enough water and aeration. Due to its strict soil requirements, soil amendment is often needed and thus results in a high cost investment. Breeding root system architecture (RSA) to improve plants' adaptability to sandy soils can be a solution. The SHB breeding population in the University of Florida blueberry breeding program is highly diversified in terms of yield, fruit quality and plant architecture. The objective of this project is to screen the genetic variability of RSA in the breeding population. The population used in the experiment was generated through 70 controlled crosses of 108 selected parents which was made in February 2017. Each family had five individuals and three of them were phenotyped after four months of growth. Total biomass of shoots and roots of each sample was used as covariate in linear mixed model equations to analyze different root traits such as total root length, maximum root depth, average root diameter, the number of tips, and root volume. Our results showed significant variability among root architecture traits in the breeding population. Among all of the traits, average root diameter had the highest heritability (0.79). The heritability of other traits was range from 0.31 to 0.47. Based on the pairwise genetically correlation (bivariate analysis), we found most of traits were significantly correlated to each other. For example, the average root diameter was negatively correlated with specific root length, root tissue density, the number of tips, and maximum root depth, but was positively related to the root volume and biomass of both root and shoot. These correlations and heritabilities estimates can guide selections in breeding ideal root architecture in future.

P-19

Identification of candidate genes for resistance to lettuce downy mildew using RenSeq k-mer association studies

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Downy mildew (DM), caused by Bremia lactucae, is the most important foliar disease of lettuce worldwide. The use of resistant varieties carrying dominant genes (Dm genes) is the most effective method for controlling this disease; however, pathogen variability has led to the rapid defeat of individual resistance genes. Many resistances have been introgressed from wild species by repeated backcrosses to cultivated lettuce resulting in numerous near-isogenic lines (NILs). Segregating populations derived from these NILs were used to genetically map resistance genes against several Bremia isolates. Most of the resistances were conferred by single dominant genes that were mapped to individual loci in the lettuce reference genome. Resistance gene enrichment sequencing (RenSeq) allowed the identification of numerous NBS-LRR sequences from these NILs and from multiple lettuce cultivars carrying known Dm genes. These, in combination with phenotypic data from these lines was used for Kmer-association mapping, which allowed the identification of several candidate genes for known and new Dm genes. Knowledge of resistance genes at the sequence level provides the foundation for engineering resistance cultivars carrying multiple Dm genes by using genome editing leading to more durable resistance to multiple isolates of lettuce DM.

P-20

A value-added soybean variety increases the inclusion rate of shrimp diet

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Inclusion of high-quality soybean meal in Pacific white shrimp (*Litopenaeus vannamei*) feed as a replacement for fishmeal could increase the affordability, availability, and sustainability of high-protein feed sources for shrimp production. Soybean meal has beneficial high protein content and amino acids, but also contains anti-nutritional trypsin inhibitors (TI) and raffinose family oligosaccharides (RFOs), which could potentially negatively affect the growth of the animal. The objective of this study was to determine the effect of various inclusion rates of soybean meal from the variety V12 on shrimp survival, average weight gains, and feed conversion rate. V12 is low in anti-nutritional TI and RFOs, high in crude protein, and high in beneficial sucrose carbohydrates and was included in the shrimp diet at rates of 25, 45, 65, and 80%. These experimental diets were compared to a fishmeal control and a treatment containing 80% soy protein concentrate (SPC). Each diet was replicated in three tanks with water quality monitored during the six-week feeding trial. No significant differences were found among the diets for either shrimp survival percentage or individual average weight gains, although diets containing 45% soybean meal and 80% soy protein concentrate were similar to the control for survival, and diets containing up to 65% soybean meal were similar to the control for average weight gains. A significantly higher feed conversion rate was observed for the 80% soybean meal diet compared to the control and all other diets. The results indicate that inclusion rates of up to 65% soybean meal may provide shrimp production results similar to those of fishmeal. Larger-scale studies in the future could clarify these results and determine the optimal soybean meal inclusion rate so producers can improve their production practices and become more profitable.

P-21

QTL mapping of winter dormancy and spring emergence in two switchgrass F1 populations: Lowland x lowland and lowland x upland

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Switchgrass (*Panicum virgatum*) is a perennial warm season grass utilized as a forage and biofuel production. Its growth is influenced by the changes in the length of photoperiod and temperature. Switchgrass becomes dormant in winter and regrow in spring. Planting semi-dormant genotypes in southern locations with mild winters can potentially increase biomass yield through extension of growth period. Finding QTLs associated with winter dormancy and spring emergence can reduce breeding cycle through marker assisted selection. In this study we performed QTL mapping in two pseudo-testcross F1 populations derived from Lowland x Lowland (AP13 x B6) and Lowland x Upland (B6 x VS16) crosses. Populations of 285 and 227 F1 progenies in AP13 x B6 and B6 x VS16 populations, respectively, being evaluated in the field for two seasons. A total number of 42, 43, and 42 QTLs were identified for fall regrowth height (FRH), normalized difference vegetation index (NDVI), and spring emergence (SE), respectively, in both populations. Percent variance explained (PVE) by the QTLs ranged from 3.5 – 31.9% for FRH, 3.4 – 31.3 % for NDVI, and 3.5 – 53.9% for SE. The additive genetic effects of individual QTL ranged from -8.39 – 10.61 for FRH, -0.11 – 0.09 for NDVI, and -5.84 – 1.60 for SE. Higher number of QTLs was discovered in Lowland x Upland population, suggesting accumulation of more traits controlling genes in the population. There was a medium level of broad-sense heritability (H^2) for FRH (0.55 – 0.64) and NDVI (0.32 – 0.61), and a small to medium H^2 for SE (0.14 – 0.56), proving that the traits can be used in a selection of genotype with improved performance. QTLs with large effect will be used in future work of selecting the semi-dormant and extended growth period genotypes.

P-22

Identification of freeze tolerance associated QTL in zoysiagrass

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Zoysiagrass (*Zoysia spp.*), a relatively low input warm season turf; has grown in popularity within the southern United States since its introduction in the 1880's. This primarily vegetatively propagated turf was one of the first grasses well suited for the southeastern U.S. due to its low input requirements, and wide general tolerance to a variety of abiotic stresses. However, since the introduction of the freeze tolerant cultivar 'Meyer' during the 1950's, little progress has been made to advance the winter hardiness of zoysiagrass, a factor that limits further spread of the species north of the transition zone. In order to push commercialization of zoysiagrass further north, breeding efforts stand to benefit considerably from a greater knowledge base behind the physiology of winter hardiness and freeze tolerance. The goal of this research was to investigate the physiologic and metabolic components of freeze tolerance in zoysiagrass to facilitate selection of freeze tolerant zoysiagrass cultivars. Thirty-five putative QTL regions were identified for cold acclimation and freezing tolerance traits using a SNP-based high-density genetic map of *Zoysia japonica*. When partitioned by trait, twenty-seven regions of interest were identified for surviving green tissue, and twenty-four regions were identified for regrowth across multiple environments. Across five chromosomes, eight regions of interest overlapped with previously identified QTL associated with winter injury on chromosomes 1, 5, 8, 12, 13, and 19. Within these regions of interest, sequence alignment analysis revealed genes that have been previously determined to be associated with abiotic stress response, particularly freezing stress, including polygalacturonase, WRKY and aspartyl protease. Following further validation, these overlapping QTL of interest and their associated markers may be utilized in future breeding efforts to incorporate freezing tolerance into elite zoysiagrass germplasm for the development of a broader pool of cultivars capable of thriving in regions north of the transition zone.

P-23

Genome-wide association and fine mapping of *bgm-1* gene and other QTLs for resistance to Bean Golden Yellow Mosaic Virus in dry beans

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Bean Golden Yellow Mosaic Virus (BGYMV) (family *Geminiviridae*) is a begomovirus vectored by Bemisia tabaci (Gennadius) whitefly that causes severe yield losses (40 to 100%) in common bean. The most effective control of BGYMV is to combine genetic resistances in the host. Two SCAR markers developed 25 years ago have been used for marker-assisted selection (MAS) programs for BGYMV resistance. The marker SR2 is linked to the bgm-1 gene on chromosome Pv03 and SW12 marker with a quantitative trait locus (QTL) on Pv04. Our objective was to improve MAS for BGYMV. QTL analysis was applied in two biparental recombinant inbred populations, DOR364/XAN176 and DOR476/SEL1309, and genome-wide association studies (GWAS) were conducted on a panel of 415 breeding lines developed by the International Center for Tropical Agriculture (CIAT) and a panel of 120 select lines/cultivars developed for abiotic stress evaluations (BASE 120 panel). Linkage mapping revealed bgm-1 on Pv03 and three QTL for BGYMV resistance on chromosomes Pv04, Pv07 and Pv08 with phenotypic variation explained between 10 to 33 percent. GWAS revealed significant SNPs associated with bgm-1 and the same QTL on Pv04, Pv07, and Pv08, and a novel QTL on Pv09. Two candidate genes for bgm-1 were identified, both related to Geminivirus resistance. An indel marker was developed from one candidate gene and evaluated on multiple bean genotypes by melting temperature (Tm)-shift method. This marker was completely correlated with BGYMV resistance across more than 700 genotypes. These results enhance our understanding of the genetic mechanisms of resistance to BGYMV and provide improved MAS for resistance to BGYMV in common bean breeding programs.

Sorghum seeds are being prepared for viability testing which will be used to determine the health of germplasm conserved in the USDA National Plant Germplasm System.

P-24

Combining ability of new maize lines for yield and aflatoxin resistance

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Pre-harvest aflatoxin contamination caused by the fungus *Aspergillus flavus* is a common problem in maize production in the Southeast USA, resulting in significant economic losses. Genetic resistance to *A. flavus* infection and aflatoxin accumulation would minimize risks to growers. Seventeen inbred lines from five different pedigrees were developed in our breeding program with good agronomic traits and low aflatoxin. A line by tester (Design II) crossing experiment was conducted, in which these 17 lines were used as males, each crossed onto six female testers. The hybrids were planted in replicated trials at Tifton, GA in 2014 and 2015. All top ears were inoculated with *A. flavus* isolate NRRL 3357 using the side-needle technique 14 d after silking. Ears were harvested 60 d after silking, dried at 40°C, and aflatoxin was quantified using the Vicam Afla-test procedure. Grain yields were measured in separate replicated trials using a two-row plot combine. Agronomic traits such as ear height, plant height, days to anthesis, days to silking, and lodging were also measured. Among testers, LH210 had positive general combining ability (GCA) for grain yield in both years, and LH195 had positive GCA for grain yield in 2015. Among males, GT1209 and GT1309 showed marginally significant positive GCA for yield. Among testers, LH132 and LH195 showed negative GCA for aflatoxin, indicating that these testers tended to produce hybrids with lower aflatoxin levels. GT1203, GT1204, GT1214, and GT1326 had significant negative GCA for aflatoxin in 2014 and were numerically negative in 2015. Within years, specific combining ability (SCA) contributed a larger proportion of the genetic variance for aflatoxin than GCA, and genotype by environment interaction was apparent across years. Hybrids with high yield and low aflatoxin were identified and included LH210 × GT1214 and LH195 × GT1329. Some experimental hybrids had yields comparable to commercial checks.

P-25

Evaluating the effectiveness and efficiency of introgression of important economical features of *Vaccinium elliottii* into Southern Highbush Blueberry

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The native blueberry *Vaccinium elliottii*, found in North Florida, presents multiple traits that could benefit blueberry production in the Southern United States. This species possesses highly desirable traits in today's industry, such as a high sugar content and a characteristically pleasant aroma. *Vaccinium elliottii* also presents a short bloom to ripe period and adaptations to upland sandy soils, which could possibly affect the earliness of new cultivars and improve adaptation to well drained sandy soils. For a successful introgression, characteristics such as direction of crosses, viability of seeds obtained, and genotype compatibility need to be investigated. Therefore, the main objective of this study was to understand the best way to perform interspecific crosses between SHB and *V. elliottii*. This study was comprised of 11 combinations of biparental reciprocal crosses between 11 unique tetraploid *V. elliottii* and 11 SHB genotypes. Percentage of fruit set, number of seeds per pollinated flower, and germination ratio were measured in order to evaluate the success of the crosses. Based on our results, the cross direction for SHB and *V. elliottii* interspecific hybridization did not have any significant effect on the traits measured. However, this study allowed us to verify the specific capacity of combination among genotypes, since some of the combinations used presented significantly better results in fruit set, seeds per pollinated flower, and seed germination when compared to other combinations. We identified the genotypes and crosses that preformed best and yielded a higher amount of seeds per pollinated flower. These genotypes were propagated for future hybridization into the Blueberry Breeding Program at the University of Florida.

P-26

FDA's voluntary plant biotechnology consultation program eases pathway to marketplace

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The U.S. Food and Drug Administration (FDA) is committed to helping foster innovation in plant biotechnology by working with developers to ensure that foods developed through the use of biotechnology meet the FDA's rigorous safety standards. The FDA's voluntary premarket Plant Biotechnology Consultation Program provides developers the opportunity to engage with the FDA to help navigate the appropriate regulatory pathways and bring safe, innovative plant-based products to market. The program provides individualized advice from the agency's knowledgeable biotech and food safety experts. To date, FDA has completed consultations on food from more than 180 varieties, including a genome-edited soybean variety. FDA encourages developers of innovative products to utilize our voluntary consultation process as an efficient tool to help ensure the safety of products derived through plant biotechnology, to instill public confidence in the use of such technologies and avoid unnecessary barriers to future innovations that could have potential health or other benefits.

P-27

Identification and validation of QTL associated with malting quality traits in two winter barley doubled haploid populations

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Demand for malting quality winter barley has dramatically increased in recent years in the Eastern United States. Currently, there is a lack of commercially available cultivars that farmers can access. This has caused issues for maltsters trying to source locally grown, high quality malting barley. To address this problem, Virginia Tech has initiated an effort to develop malting quality winter barley varieties by crossing well-adapted Virginia feed barley breeding material to good quality malting barley lines from Europe and the Western US. The number of advanced lines in the program has far exceeded our ability to phenotype for important malting quality characteristics (i.e. beta-glucan, enzyme activity, malt extract). Therefore, marker assisted selection is needed to screen for malting quality traits in breeding populations to more efficiently utilize phenotyping resources. Two VA feed x European/Western US malt doubled haploid mapping populations were developed in order to identify high throughput predictive markers associated with improve malting quality relevant to this breeding program. Both populations were grown in Blacksburg and Warsaw, Virginia in 2018-2019 and 2019-2020, genotyped with a public Illumina 50,000 SNP array, phenotyped for malting traits by the USDA-ARS Cereal Crops Research Unit in Madison, Wisconsin, and QTL mapping was performed in ICIMAPPING and r/qtl. A total of eleven putative QTL were identified in a population of 150 doubled haploids derived from the cross Endeavor/VA09B-34. One QTL in particular on chromosome 5H near the telomere was consistently associated with >50% of the phenotypic variance for FAN, beta-glucan, alpha-amylase, wort protein, and as much as 42% for malt extract. The second validation population of 205 individuals (Violetta/VA09B-34) is still under investigation.

P-28

Saliency-driven robotic network for spatio-temporal plant phenotyping

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This work presents the design, architecture (hardware and software) and deployment of a multi-robot system for row crop field data collection and data processing. Data collected from the platform can be used for various plant science research themes. The research would benefit a broad spectrum of the agricultural community. The proposed system has been deployed in a soybean research farm at Iowa State University for testing and validation. This work is funded by the Agriculture and Food Research Initiative 2017-67021-25965 of the USDA National Institute of Food and Agriculture.

P-29

Improving the genetic variation in hexaploid spring wheat through the introgression of durum wheat yield component QTL alleles on 2BL and 3BL

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Hexaploid bread wheat and tetraploid durum wheat have been cultivated in similar geographic areas for approximately 10,000 years. The crossing barrier caused by ploidy difference suggests that different favorable alleles for yield-related traits may have accumulated in the two crops. Previous work allowed identification of favorable alleles at six quantitative trait loci (QTL) from durum wheat in a recombinant inbred line (RIL) population from a cross of Mountrail durum wheat and Choteau spring wheat. The purpose of this study was to determine the impact of six durum wheat alleles at yield component QTL in several hexaploid spring wheat backgrounds. Three spring bread wheat cultivars were crossed with six hexaploid lines derived from the original Choteau/Mountrail cross to generate recombinant inbred lines (RIL). Heterozygous RIL, containing both the durum wheat allele and the bread wheat allele, were identified for each of the QTL. A population consisting of near-isogenic lines (NIL) for the six introgressed QTLs were grown in five environments under irrigated and dryland conditions in Montana in 2017 and 2018. A durum wheat allele QTL on chromosome 3B, *QGw.mst-3B*, resulted in increased kernel weight in all five environments. The introgressed durum QTL alleles caused pleiotropic interactions among yield component traits. Favorable alleles for yield components were often associated with physiological traits. Environment significantly impacted the stability of introgressed QTL on yield components for four of the six QTL. Genetic background also influenced the impact of durum allele for the four yield component QTL with significant main effects. Results suggest that alleles from durum wheat may be useful for yield improvement of hexaploid spring wheat. However, interrelationships of yield components, pleiotropic interactions, and environment will impact the value of durum wheat alleles in hexaploid wheat backgrounds.

P-30
Phenotyping and breeding for blueberry aroma

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For years consumers have complained about the poor flavor in modern supermarket fruit. Recently, efforts have been undertaken in different crops to better understand the complexity of fruit flavor. Besides sugar and acid, each fruit species has unique volatile compounds which results in the suite of nuanced flavor sometimes called aroma. Volatiles can be quantified analytically, however this process is laborious and requires expensive instruments such as a gas chromatography mass spectrometer (GC-MS). Berry aroma can also be quantified by a trained individual, such as a plant breeder, similar to many other phenotypic characteristics. This study focuses on southern highbush blueberries (*Vaccinium corymbosum*). We aim to use the human derived aroma value to estimate the heritability of aroma in blueberry breeding populations. Thirteen blueberry genotypes with aroma were phenotypically identified in the University of Florida breeding populations. Crosses were made to generate twenty-five full-sib populations with both aromatic and non-aromatic parents. Berries from 795 individual plants within the twenty-five families were phenotypically evaluated for aroma in spring 2019. Aroma scores ranged from 0-5 where 5= the strongest aroma ever experienced in a blueberry and 0= non-aromatic fruit with low flavor but still discernable sugar and acid. The most aromatic parent's average score was 3.81 and the six least aromatic parents all averaged 0. With an extensive pedigree record, we computed the numerator relationship matrix and extracted the pairwise relationship of the evaluated genotypes. We combined such information in a linear mixed model equation (animal model) and estimated the variance components and breeding values. Breeding values ranged from -0.95 to 1.42. The narrow sense heritability of aroma was 0.35. This estimate is consistent with other fruit quality heritability estimates for southern highbush blueberry. Our results illustrate that breeding for aroma can be systematically screened for as a target for genetic improvements.

P-31
Phenomic prediction of maize grain yield from near-infrared reflectance spectroscopy of kernels

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High-throughput phenotyping technologies, which can generate large volumes of data at low costs, may be used to indirectly predict yield. Here, we explore this concept, using high-throughput phenotype information from Fourier Transformed near-infrared reflectance spectroscopy (NIRS) of harvested kernels to predict parental grain yield in maize (Zea mays L.). A dataset of 2,563 kernel samples from diversity panel hybrid testcrosses were scanned using NIRS, including 3,076 wavenumbers (bands) in the range of 4,000-10,000 cm-1. Corresponding grain yield for each sample was used to train predictive models using three types of statistical learning: (a) partial least square regression (PLSR), (b) NIRS best linear unbiased predictor (NIRS BLUP) and (c) functional regression. Our results found that the spectral data were a useful tool to predict maize grain yield, and showed promising results for evaluating genetically independent breeding populations. All model types were successful, but the functional regression followed by the PLSR model resulted in the best phenotypic predictions. Pearson's correlations exceeded 0.7 in many cases, both within random cross validation and on independent breeding trials. Across the breeding trials, the functional regression models performed best. High correlations between predicted and observed values, even in cases where yield estimates were not accurate, demonstrated value for grain NIRS in ranking varieties yield relative to one another. More research in this area will provide better understanding how NIRS and other phenomic technology can be used in predicting phenotypes in breeding programs and identifying biological phenomenon underlying these correlated relationships.

P-32
Mapping a new disease resistance locus in an F1 progeny derived from two grape wild relatives

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Linkage maps and QTL analysis have become essential tools for the positional cloning of agronomically important genes and for marker-assisted selection. In this study, two North American grape species, *Vitis rupestris* and *Vitis riparia*, and their 294 F^1 progeny were used to construct parental linkage maps and to perform QTL analysis for downy mildew resistance. Marker discovery was accomplished by genotyping-by-sequencing (GBS), and resulted in 348,888 single nucleotide polymorphism (SNP) markers. Of these, 11,063 informative markers (3.17% of original SNP dataset) were retained after filtering for various quality parameters and missing data. A two-way pseudo-testcross strategy was followed for map construction using JoinMap5.0. The 1,115 and 1,177 significant markers (threshold LOD ≥ 14) for *V. riparia* and *V. rupestris* were grouped into 19 linkage groups covering 1657.4 and 1401.3 cM of genetic distances with an average marker interval of 1.486 and 1.19 cM, respectively. Maps were validated by pinpointing a single significant QTL determining maleness at chromosome 2 in the genetic background of the *V. riparia* male parent. Phenotype data for leaf downy mildew resistance were collected with both *in vitro* and natural inoculation of 86 and 136 F1 progeny, respectively. With both methods, QTL analysis for reduced leaf area coverage by mildew lead to a significant peak at chromosome 10 in *V. rupestris* explaining 15-45% of the phenotypic variance. For *in vitro* inoculation, a significant QTL was detected for reduced disease intensity at chromosome 8 of *V. riparia* also, explaining 15% of the variance. These are the first SNP-based high-density linkage maps of these native North American grape species. The maps are expected to serve as an important resource for breeding modern varieties for environment-friendly grape cultivation.

P-33
Hyperspectral phenotyping of legume physiology

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Hyperspectral sensing in the visible through shortwave infrared (VSWIR) portion of the spectrum has been demonstrated to provide significant information on the structural and functional properties of vegetation, resulting in powerful techniques to discern species differences, characterize crop nutrient or water stress, and quantify the density of foliage in agricultural fields. Modern machine-learning techniques allow for the entire set of spectral bands, on the order of hundreds with modern field and airborne spectrometers, to be used to develop models that can simultaneously retrieve a variety of foliar chemical compounds and hydrological and structural states. The application of these techniques, in the context of leaf-level measurements of VSWIR reflectance, or more complicated remote airborne surveys, has the potential to revolutionize high-throughput methods to phenotype germplasm that optimizes yield, resource-use efficiencies, or alternate objectives related to disease resistance or biomass accumulation, for example. Here we focus on breeding trials for a set of warm-season legumes, conducted in both greenhouse and field settings, and spanning a set of diverse genotypes providing a range of adaptation to drought and yield potential in the context of semi-arid climate cultivation. At the leaf-level, a large set of spectral reflectance measurements spanning 400-2500 nanometers were made for plants across various growth stages in field experiments that induced severe drought, along with sampling for relevant trait values. Here we will discuss the development and performance of algorithms for a range of leaf traits related to gas exchange, leaf structure, hydrological status, nutrient contents and stable isotope discrimination, along with their relationships to drought resistance and yield.

P-34

Identification of QTL for storage root α- and β-amylase activity in sweet potato at harvest and during storage

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The activity of α-and β-amylases in storage roots is one of the major factors determining sweet potato sweetness, texture and end-user preference. Due to the hexaploid nature and high heterogeneity of sweet potato, little has been known about the genetic architecture of amylase activity and the candidate genes determining amylase variation in sweet potato. In the present study, α- and β-amylase activity of 248 genotypes in a bi-parental population derived from the cross of Tanzania x Beauregard (TB) was measured at harvest and during post-harvest storage replicated in two years. A high density genetic map with 14813 SNP markers was developed using hidden Markov models. Moderate positive linear correlations ($r = \sim 0.40\text{-}0.65$ $p < 0.001$) between pairs of 2016 and 2017 β-amylase activity for uncured, cured and stored storage roots were observed. Correlations for β-amylase activity in 2016 and 2017 for each treatment were ~ 0.6 $p < 0.001$. Broad sense heritabilities were very high at 77% and 91% for α- and β-amylase activity, respectively. We identified four QTL each for α- and β-amylase activity explaining 61.7% and 72.4% of the total phenotypic variation, respectively. QTL for β-amylase were observed on linkage group (LG) 3 and 9, and explained 25.1 % and 21.3% of the phenotypic variation, respectively. A QTL on LG 13 at 79.68 cM explained 54.4% of the phenotypic variation for βamylase. Using the sweet potato genome browser and NCBI resource we observed that the QTL on LG 3 for α- and β-amylase were co-located with α- amylase like and β-amylase annotated genes involved in starch and sucrose metabolism. This study has provided a better understanding of the genetic architecture of α-and β-amylase activity in a bi-parental mapping population and candidate α-and β-amylase genes are proposed for diagnostic marker development in the next step.

P-35

Understanding genetic resistance to bacterial wilt in tomatoes

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Resistance to bacterial wilt caused by *Ralstonia solanacearum* in certain tomato lines used today is a very desirable trait with several unknowns. As a soil borne bacterial disease, there are not many consistently effective methods for controlling and managing this disease in the field. This problem makes developing a good resistant tomato line the most ideal solution. Existing resistance can vary widely across field locations, temperatures, and bacterial strains. Combined with the less desirable horticultural traits that usually come with bacterial wilt resistance, there is a great interest for better understanding how resistance works, and how to improve not only for resistance, but for fruit quality as well. In this study, RNA-Seq analysis provided a comprehensive look at changing gene expression in the resistant HI 7998 line compared to the susceptible NC359 line. These changes in gene expression levels give a more detailed look at what genes and gene types play an important role in conferring resistance. An in-depth look at tomato line NC11212, the progeny of a cross between contrasting susceptible and resistant lines, also gives more insight into linked traits associated with resistance and a detailed quantitative trait loci (QTL) analysis for North Carolina resistant lines. A better understanding of how tomato lines covey resistance in the U.S. will help in breeding better bacterial wilt resistant tomato lines suited for U.S. tomato production quicker and more effectively

P-36
Feasibility of genomic prediction in peach for brown rot tolerance

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DNA-informed breeding has become conventional for Rosaceae crops. Using the trait associated markers breeders can precisely select desirable individuals using marker assisted selection (MAS). MAS works best when few genes of major effect are controlling the trait of interest and is less efficient in complex traits for which many genes across genome are contributing to the phenotype. To overcome that limitation genome-scale predictions (GP) are being explored in fruit breeding. GP uses whole genome markers to predict the breeding values for each individual and thus can facilitate rapid parental/seedling selection. Brown rot, caused by *Monilinia* spp., is one the most important pre- and postharvest diseases worldwide. Tolerance to *Monilinia* spp. in peach is polygenic, controlled by multiple genes with small effect. The objective of this study was to assess the feasibility of GP in peach for brown rot tolerance. Twenty-six cultivars /advanced selections and 140 progenies, representing 10 breeding families, with 'Bolinha' source of resistance were phenotyped for fruit response to brown rot, using wounded(W) and non-wounded (NW) disease assays in 2015 and 2016. High-density genotyping was performed with the newly developed 16K peach SNP array. Genomic best linear unbiased prediction (GBLUP) method was used to predict genomic estimated breeding values (GEBVs). Heritability for each treatment (W and NW) in each year ranged from 0.39-0.70 (NW_2015: 0.70, NW_2016: 0.48, W_2015: 0.57, W_2016: 0.39). Predictive ability, estimated as the correlation of true and predicted phenotypes, ranged from 0.55 (W_2016) to 0.91 (NW_2015). Overall, the predictive ability achieved in this study supports the feasibility of genomic prediction in breeding for tolerance to brown rot in peach.

P-37
Cloning and characterization of genes affecting kernel weight on chromosome arm 2BS

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This research project is part of the WheatCAP funded by USDA-NIFA-IWYP with award# 2017-67007-25939. We identified a major QTL for kernel weight from a popular hard red winter wheat cultivar TAM 111 and will study underlining candidate genes for this major locus. We are working to develop a large population from several heterogeneous families. At the same time, we are also transferring this locus into five CIMMYT spring wheat lines. We have harvested BC2F1 seeds and will make another round of backcrossing then using doubled haploid to fix the loci in the backgrounds of CIMMYT lines.

P-38
Discovering a deletion on chromosome 16 associated with high sucrose in soybean seeds

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Soybeans are among the most economically important crops, and are grown at a large scale worldwide. Last year, 90.1 million acres of soybeans were planted in the United States— more than any other crop. One of the primary uses of soybeans is for animal feed. Approximately five percent of a soybean seed is comprised of sucrose, and this is desirable in animal feed as it is a source of easily metabolized energy. A high sucrose/low oil mutant line, G15FN-54, was derived from G00-3213 seeds that were irradiated with 25 Gray Units. This fast neutron mutant line was crossed to elite variety Benning, the population was advanced, and phenotypic data was taken on F2 seeds. NIR was performed, and demonstrates a range of high sucrose values in the F2 population. The individuals with high sucrose also had a low oil content. The phenotype of G15FN-54 was confirmed with HPLC wet chemistry. Through comparative genomic hybridization, three large deletions were located. Whole genome sequencing confirmed this. Thirty-six candidate genes were identified in these three deletions. From the results of a bulked segregant analysis, it was determined that the deletion on chromosome 16 was responsible for the high sucrose/low oil phenotype. It accounts for 22% of overall sucrose variation and 36% of total oil variation. Although there are other known high sucrose genes, they are in different regions of the genome than the deletion found on chromosome 16. Mutants with high sucrose content are valuable resources for breeding soybeans with improved seed composition.

P-39
Genetic parameters for agronomic traits in a reference alfalfa population

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Alfalfa (*Medicago sativa* L.) is the most-grown cool season perennial forage legume in the world. In the U.S., alfalfa is grown on approximately 6.7 million hectares with an estimated crop value of US$9 billion; however, alfalfa production has not been recently reported in Florida. The objectives of this study were: i) create a reference alfalfa population following a factorial mating design; ii) phenotype the population for agronomic traits at the plot/family level; iii) estimate variance components and genetic parameters using mixed models. For the mating design, a single plant per genotype was selected (plant vigor and biomass production) from a variety trial run from 2014 to 2016 in Citra, FL. Six genotypes with known adaptation in Florida (breeding lines from UF's former breeding program and 'Bulldog805') were used as male parents and crossed to 27 females following a factorial design. A total of 145 full-sib and 36 half-sib families were used for the field phenotyping experiment. The experiment was designed as a row-column (14x32) with augmented representation of three controls (Bulldog805, 'FL99' and an advanced breeding line from UF). Bulldog805 was planted as border for each experimental unit, and 20 seedlings were manually transplanted in the center of each plot for all families and controls. Borders were mowed before phenotyping for these traits: plant height, foliar disease ratings, flowering percentage and dry matter yield. Data was analyzed using linear mixed models in R and ASReml. Variance component estimates were used to calculate narrow-sense heritability (h^2). Narrow-sense heritability by harvest ranged from 0.25 to 0.50 for flowering, 0.07 to 0.27 for plant height, 0.04 to 0.33 for foliar diseases, and 0.14 to 0.33 for dry matter yield. Narrow-sense heritability across all harvests were 0.22 for flowering, 0.13 for plant height, 0.089 for foliar diseases, and 0.28 for dry matter yield. These results show great potential to develop alfalfa cultivars with improved biomass yield for subtropical environments. The phenotypic data collected in this study will be used in genomic prediction models in the future.

P-40
Capturing extensive allelic variation through a pangenome approach

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Short read whole genome sequencing (WGS) has become a common practice when attempting to capture genetic diversity in crop plants. Yet, due to crop genome complexity, simple read alignment may result in erroneous detection of short polymorphisms (i.e. SNPs and small InDels) and misses altogether the larger structural variations. An alternative approach is to first de-novo assemble short reads into contigs for every genotype and compare contigs to a reference genome. This approach overcomes most of the challenges of capturing genomic diversity, but still leaves a major fraction of unmapped contigs. We present here our "pan-genome" approach where multiple chromosome-level genomes are compared all to all, producing a broad diversity database. Comparing contigs of new genotypes to the complete pan-genome greatly increases the fraction of mapped contigs and thus the broad allelic diversity is described per locus. We describe here the results of several full genome assemblies, chromosome level comparisons and contig mapping of dozens of genotypes towards capturing the broad allelic diversity in crops such as maize, soy and cotton.

P-41
Detecting resistance alleles in Upland Cotton (*G. hirsutum*) to the Cotton Leaf Curl Virus

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Cotton Leaf Curl Virus (CLCuV), the causative agent for Cotton Leaf Curl Disease (CLCuD), first appeared in Multan, Pakistan in the 1980s. The Multan strain of the virus was mitigated with resistant varieties until the early 2000s, when the new Burewala strain overcame resistance previously bred into cotton varieties. The disease stunts growth of the plant and prevents the production of flowers and therefore cotton fibers. CLCV causes an estimated loss of 2 to 3 million bales of lint in Pakistan. Whitefly is the CLCuV vector and is a pest on many crops and ornamentals. The disease has also been reported in neighboring countries, i.e. India and China, and it is the potential threat in all countries where whitefly is prevalent causing concern that the virus will move into unaffected countries before resistance can be bred. Currently development of resistant lines depends on screening each generation in Pakistan. DNA markers would allow development of resistant varieties without field screening in Pakistan each generation. By making F2 mapping populations from crosses between a resistant line from one of two different sources and a non-resistant line, we used quantitative trait loci (QTL) mapping to identify single nucleotide polymorphism (SNP) markers associated with CLCuD resistance trait. The study used SNP markers obtained using CottonSNP63K array data and phenotypic data from the F2 populations. Genetic linkage mapping and QTL mapping identified SNP markers associated with resistance. SNP markers were identified for each F2 population, but the SNPs for each were from different chromosomes, indicating the resistance may be due to different alleles in the two resistance sources. Future directions will strive to validate the QTLs through additional F2 populations and SNP assays created from validated SNPs. SNP assays will be used for marker assisted selection and eliminate the need to field screen every generation.

P-42

Validation of quantitative trait loci associated with freeze tolerance in St. Augustinegrass across two populations

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St. Augustinegrass (*Stenotaphrum secundatum* (Walt.) Kuntz) is a warm-season turfgrass commonly used in home lawns in the southern United States. A lack of freeze tolerance has limited the spread of St. Augustinegrass further north into the transition zone. 'Raleigh', released in the early 1980s, is still the industry's standard for cold tolerance. Despite the identification of freeze tolerant germplasm, limited progress has been made in increasing the available pool of freeze tolerant cultivars for the species. In order to elucidate the genetic control of freeze tolerance, previous research developed a SSR-based linkage map for a 'Raleigh' by 'Seville' (RxS) mapping population. The map was used in conjunction with field and lab-based freezing data and identified multiple QTL on linkage groups 1, 2, 3 and 4. A linkage map of 2871 SNPs has since become available for this previously-studied population. The objectives of the present study were to 1) improve the resolution of the previously identified freeze tolerance QTL and 2) validate these QTL in a separate population. A 126 SSRs linkage map of a F1 population of 'Raleigh' (RxR) was developed and freeze tests yielded data on surviving green tissue and regrowth. Composite interval mapping of least-squares means was used for the analysis of both populations and the significance thresholds were determined through permutation. The RxS population yielded 42 QTL with significant QTL identified in each linkage group. QTL for spring green-up and winterkill were co-localized on linkage groups 8 and 9. In the RxR population, four significant QTL were identified on linkage groups 1, 3, 5 and 9, which align with the previously identified QTL. Several of these QTL could be used as potential targets for marker assisted selection, reducing the need for multi-year field evaluations.

P-43

Analyzing the effects of Rht-A1 missense mutations in durum wheat (*Triticum turgidum* spp. *durum*)

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Incorporation of semi-dwarfing alleles of the reduced height (*Rht*) gene into hexaploid wheat (*Triticum aestivum*) varieties led to increased yield during the Green Revolution. *Rht-B1b* and *Rht-D1b* reduce stem elongation and increase productive tillers by reducing the plant's receptiveness to gibberellic acid. *Rht-B1b* and *Rht-D1b* are the most widely used semi-dwarfing alleles and are present in most modern wheat varieties. *Rht-A1* is expressed in stem tissue at comparable levels to *Rht-B1* and *Rht-D1*, but no *Rht-A1* yield enhancing alleles have been identified. Much research has focused on the effects of *Rht-B1b* and *Rht-D1b* in hexaploid wheat, but less is known about the impact of Rht alleles in durum wheat (*Triticum turgidum* ssp. durum). This projects goal is to expand the range of plant height that can be targeted with one or a combination of *Rht* alleles by identifying useful allelic variation for *Rht-A1* in durum wheat. An EMS mutagenized population of a standard height durum was screened for plant height variation and for *Rht-A1* mutations. We identified two *Rht-A1* missense mutations with low SIFT values and reduced plant height. Plants containing the *Rht-A1* mutations were crossed with both standard height and semi-dwarf durum parents to test the impact of each *Rht-A* allele on plant height and yield in the presence or absence of *Rht-B1b*. We anticipate finding that the *Rht-A1* mutations will confer a less severe semi-dwarf phenotype than *Rht-B1b*, and the addition of the *Rht-A1* missense allele to *Rht-B1b* will result in reduced plant height. One objective is to identify an *Rht* allele or combination of *Rht* alleles that produce plants taller than current semi-dwarf varieties and shorter than full-height varieties. Such allele(s) could be integrated into durum breeding programs that produce varieties for moisture limited Northern Great Plains climates where *Rht-B1b* semi-dwarf varieties are too short.

P-44

From genomes to fields: Understanding genotype-by-environment interactions in maize hybrids

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Plant breeding programs are often faced with challenges in making initial selections among breeding materials based on evaluation in a single environment, with the ultimate goal of creating new varieties that will later be planted across multiple, more diverse conditions. In some cases, genotypes that initially seemed very promising are observed to vary dramatically for important agronomic traits across diverse environments. Genotype-by-Environment interactions (GxE) underlie relative differences in performance across environments but are difficult to predict without understanding how genotypes respond to specific environmental covariates. Recent advances in genomics and prediction modeling have accelerated the ability to perform selections using genomic data, but little has been done to incorporate environmental data into such modeling. Including environmental variables in G×E analysis often results in issues with multicollinearity, caused by presence of large numbers of predictors that are often highly correlated, each of which only explains a small amount of variance. Development of methods to incorporate both genomic and environmental data into genomic prediction models should provide ability to predict genotypic performance in specific new environments. Using publicly available data for 1,919 maize hybrids spread across multiple locations over three years in North America, we explore GxE modeling using a mixed models approach incorporating high density DNA marker data and weather covariates. Using these data, we gain a clearer insight of what GxE means in context of plant development and response to fluctuating environmental conditions, and explore the possibility of predicting hybrid phenotypes in previously untested environments.

P-45

Identification and genetic characterization of new sources of Tomato Yellow Leaf Curl Virus resistance from *Solanum pimpinellifolium*

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Tomato yellow leaf curl virus (TYLCV) is a highly significant threat to tomato production in the United States and other tropical and subtropical regions in the world. TYLCV is spread by the sweet potato whitefly (*Bemisia tabaci*), and current management practices include the use of resistant cultivars and/or insecticide treatments to control whiteflies. Genetic resistance against TYLCV is considered a more cost-effective and environment-friendly compared to the chemical control of whiteflies. We recently identified three *Solanum pimpinellifolium* accessions (LA2093, LA2102, and LA2173) with high levels of resistance to TYLCV under natural disease pressure in a field trial in north Florida. Further testing under controlled TYLCV inoculations using viruliferous whiteflies confirmed strong TYLCV resistance in all three accessions. To identify the genetic loci responsible for TYLCV resistance, a recombinant inbred line (RIL) population derived from a cross between NC EBR-1 and LA2093 was phenotypically characterized. The quantitative trait loci (QTL) analysis of the RIL population identified a single major QTL (LOD score >13) on chromosome 6 which was responsible for TYLCV resistance. Interestingly, the physical location of this QTL encompassed that of the Ty-1/Ty3 alleles from *S. chilense*, suggesting either further allelic diversity at the Ty-1/Ty-3 locus or a new Ty gene located within this region. Further genetic characterization of the three *S. pimpinellifolium* accessions was conducted by developing interspecific F_2 populations from cross of each accession with a susceptible tomato inbred, Fla. 8059. The pooled DNA of highly resistant and the highly susceptible plants from each F2 population were also subjected to sequencing-based bulked segregant analysis (BSA). The latest results of BSA, QTL mapping, and genetic characterization of the newly identified TYLCV resistance sources will be presented.

Cotton is still king! Photo by Peng Wah Chee

P-46

Prospects of genomic prediction using training population design in an interspecific soybean NAM panel

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Agronomically important traits generally have complex genetic architecture, where many genes, each one with a small additive effect controls the trait. Genomic prediction has been designed to increase genetic gain and efficiency in plant breeding programs. The objective of this study was to evaluate the training population design on prediction accuracy of genomic prediction models in wild soybean-derived materials. We used a soybean NAM panel containing three *G. max* x *Glycine soja* families evaluated in multi-environment. Three training population designs were used, a) Within family: predictions were made exclusively within each family. b) Leave one family out: each family is predicted using a training set that contains the other two families. c) Across all families: all the individuals from the three families were randomly assigned to either the training or validation set. As in previous studies, training population size showed a strong relationship with accuracy; Increasing the training population size from 50 to 300 individuals improved prediction accuracy from 0.49 to 0.77 (57% increase) across all traits, with little increment in average between 300 and 390 individuals (1%). Marker density had little impact on the prediction accuracy across traits, with a significant increment in prediction accuracy up to 1423 markers (18.5%). Across all families, design had higher prediction accuracies for all the traits compared with Leave one family out and Within family design, with prediction accuracies ranged from moderate (0.55) to high (0.75) across traits. The NAM panel containing interspecific crosses, successfully predict grain yield, maturity, oil and protein. Our results showed encouraging prediction accuracies for grain yield (0.55-0.73), which is impressive from crosses originated from half-wild soybean materials. In conclusion, training population strategies where population size and multiple families were maximized (Across all design) produce robust prediction accuracies for yield, maturity, protein, and oil. Genomic predictions might also accelerate genetic gain in pre-breeding efforts using wild soybeans.

P-47

Qualitative analysis of Pima and Upland Cotton in the National Cotton Germplasm Collection

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Quantitative phenotypic traits such as yield and fiber quality are variable across environments and may also be controlled by epistatic and pleiotropic effects. Contrastingly, qualitative morphological traits are relatively stable across normal growing environments and commonly used to evaluate genetic diversity. In the past two decades, molecular markers in genome mapping have largely superseded phenotypic surveys, however, qualitatively inherited traits continue to be used as sources for A) descriptors in cataloging accessions of germplasm collections, B) obtaining plant variety protection status, and C) germplasm registration. To date, several cotton qualitative reviews have been published, and the current research focuses on comparative analysis of morphological traits of Upland Cotton (*Gossypium hirsutum*) and Pima Cotton (*Gossypium barbadense*). Recently, the USDA-ARS Crop Germplasm Research Unit in College Station, TX updated previous disparate descriptor schemes with a standardized rating scale that encompasses the diversity observed across *Gossypium* species. A large portion of the National Cotton Germplasm Collection has been evaluated under this standardized scheme and was analyzed here. A distribution and clustering analysis of categorical data using the collected standardized scores of 37 traits/descriptors, such as leaf hairs, boll nectaries, and seed type, among others, was performed. The traits evaluated have been collected over the last 6 years by the USDA-ARS at College Station, Texas, USA; Tecoman, Colima, Mexico; and Liberia, Costa Rica. The results allowed us to investigate the distribution of phenotypic traits and sets of clusters establishing similarities and dissimilarities across the evaluated dataset.

P-48

Cultivar, trait and management system selection to improve soft-red winter wheat productivity in the Eastern US

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Wheat growing regions and seasons are diverse, mandating different varietal adaptation and management practices. Grain yield is the primary target for soft red winter (SRW) wheat, due to lower protein content requirements. The growing season for SRW wheat in the eastern US takes up to 9 months under variable environments, highlighting the importance of variety and management. In this study, we present the results of a two-year field-based investigation of yield response of 30 wheat lines to different nitrogen treatment. We dissected yield components in 30 lines. For five out of the 30 lines we performed in-tissue nitrogen analysis. Nitrogen (N) treatments were two levels of 0 kg N ha^{-1} and 112 kg N ha^{-1}. On average, application of 112 kg N increased phytomass by 23% at heading, anthesis, and maturity, enhanced fertile tiller numbers by 16%, and increased grain yield by 18% that coincided with a 26% increase in grain numbers per unit area. While grain number increased, individual kernel weight was not affected by N treatment. Phytomass N concentration was 37% higher at anthesis, and 34% greater at physiological maturity, respectively, in high-N treatment than in low-N treatment. At maturity, high-N grain N concentration contained 10% more N than low-N treatment. N in the grains, nitrogen harvest index, was lower (36% of total) in high-N than in low-N (40% of total) treatment, which indicated plants did not increase the in-grain utilization of N. The 18% higher grain yield with 112 kg N treatment, therefore, occurred without considerable change in grain N content. Increasing tiller numbers and grain numbers for SRW wheat are the targeted traits for increasing grain yield under N management, with less emphasis on utilization of N in grains because N content is not critically influential for marketability of soft wheat grains.

P-49

Dissecting the genomic regions conferring resistance to frogeye leaf spot of soybean using a genome-wide association analysis

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Frogeye leaf spot (FLS, *Cercospora sojina* K. Hara) is a foliar fungal disease of soybean [*Glycine max* (L.) Merr] that affects yield in every growing region. Genetic resistance effectively controls FLS. The Soybean Genetics Committee has recognized three genes involved in FLS resistance. Of these genes, Rcs3 is widely used because it has provided resistance to *C. sojina* for over 30 years. To understand the diversity of resistance alleles and mine novel genes conferring resistance to FLS, a genome wide association study (GWAS) was done using a panel of 294 diverse accessions, 35 ancestral lines, and 6 check cultivars. Four replicates of the panel have been evaluated for their reaction to race 8 of C. sojina in the greenhouse on the University of Georgia Griffin campus. The association panel was genotyped with the SoySNP50K Beadchip and a GWAS was performed using a compressed mixed linear model in R. Genetic variation in reactions to C. sojina was observed among the genotypes. The GWAS identified four significant SNPs ($p < 0.000001$) at one locus on chromosome 11 which were associated with resistance to FLS. The four SNPs spanned a 1.15 kb region and are harbored within the gene model Glyma.11g230400, a leucine-rich repeat receptor-like protein kinase gene. Accessions with all four favorable SNPs had over 50% reduction in disease severity compared to those with unfavorable SNPs. Twenty-four accessions with the favorable haplotype showed no symptoms. Three of these lines, including the Rcs1 source 'Lincoln' are a part of the 35 ancestral soybean lines that account for 95% of the parentage of North American soybean germplasm. A validation study will be carried out using selected breeding lines to confirm the QTL and candidate gene. The genomic regions and germplasm identified can be used by breeders to improve frogeye leaf spot resistance in soybean.

P-50

Fine mapping of powdery mildew resistance gene *Pm54* in soft red winter wheat (*Triticum aestivum* L.)

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Powdery mildew, caused by the obligate biotroph *Blumeria graminis* (DC) Speer f. spp. tritici emend. E. J. Marchal (*Bgt*), is an important disease-causing increasing damage in USA wheat (*Triticum aestivum* L.) production regions. A major QTL on chromosome 6BL linked to powdery mildew resistance was reported by Hao et al. (2015). They identified the cultivar AGS2000 as a source of a new resistant powdery mildew gene, designated as *Pm54*. A recent genome-wide association study in southern soft red winter wheat conducted by Sarinelli (2017), discovered and validated several powdery mildew resistance genes. In the study, the 6BL QTL was associated with a marker (SNP) at position 695,007,016 bp. Thus, the interval containing the 6BL QTL linked to the powdery mildew gene Pm54 is being targeted for fine mapping in a recombinant inbred line population derived from the cross between the susceptible and the resistant cultivars LA95135 and AGS2000, respectively. First, we screened 256 recombinant inbred lines (LA population) under greenhouse and growth chamber conditions. We used the isolate "NCF-D-1-1" of *Blumeria graminis* f. sp. *tritici* to induce uniform and strong epidemics. Disease severity was scored on a scale of 0 – 4 (0=resistant and 4= susceptible). LA95135 showed moderate to susceptible reaction while the AGS2000 moderate to resistant reaction. The progeny segregated in a ratio of 3:1 (resistant:susceptible) indicating the presence of 2 genes in the LA population. Second, we exploited exome capture data to discover new polymorphisms for marker saturation in a 10 Mbp region flanking the Pm54 locus. We were able to identify 135 annotated genes and 396 new polymorphisms (SNPs) between LA95135 and AGS2000. We selected two SNPs every 1 Mbp and a total of 20 KASP assays were developed to genotype the LA population. Based on the genotypic and phenotypic results, we identified three genes annotated as disease resistance proteins (RPM1) located nearby to the reported Pm54 gene as the possible cause of the resistance displayed in AGS2000. Further work will be done to identify and valid the polymorphism underlying the Pm54 resistance allele.

P-51

A novel allele underlying resistance to soybean cyst nematode (*Heterodera glycines*) in soybean PI 567488 B

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Soybean cyst nematode (SCN) is the most devastating pest of soybean production in the U.S. Currently, breeders have mainly exploited two major resistance alleles at Rhg1 and Rhg4 loci in Peking and PI 88788 to develop SCN resistant cultivars. However, overusing these resistant sources has led some SCN populations have overcome *Rhg1* and *Rhg4* derived resistance. Therefore, it is critical to identify new resistant source, different with Peking and PI 88788 resistance. Our greenhouse screening tests revealed that PI 567488 B was found to be resistant to multiple SCN populations including SCN race 3 but did not carry resistance allele at *Rhg1* and *Rhg4* loci. We conducted quantitative trait loci (QTL) study to discover the resistance loci in PI 567488 B. Two F2:3 populations derived from two crosses: Lee x PI 567488B (Pop1) and Hutcheson x PI 567488B (Pop2) using 12 replications per one in a greenhouse and genotyped using the SoySNP6K Infinium Chip. The integrated map of 982 common polymorphic SNPs between two populations were constructed. Composite interval mapping identified two significant QTLs on Chromosome (Chr) 10, conferring SCN race 3 (HG Type 5) resistance. Although two populations did not map same QTL on Chr 10 but two QTLs located around 50 cM away and the QTL in Pop2 had higher LOD score than Pop1. Compared with previous QTL mapping studies, this locus may overlap with a region in PI 567516 C, but based on haplotype analysis, PI 567488 B might carry different resistance allele with PI 567516 C at Chr 10.

P-52

Crop growth model calibration and simulation of 12 maize hybrids

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Crop modeling approaches that combine environmental parameters, management, and maize hybrid properties have been described to predict genotype by environment interactions. Plant breeders have the potential to be greatly supported by crop models. However, large-scale application of crop modeling in plant breeding is severely limited by labor and cost required to measure cultivar-specific crop-model parameters. The use of crop models in plant breeding has primarily been for identifying and improving specific physiological traits. In most studies, varieties are classified into maturity groups to generate generic cultivar calibrations for a maturity range. The majority of cultivar specific parameters are assumed to be synonymous among cultivars. Our objective was to fully calibrate 12 commonly grown central corn belt hybrids to determine which cultivar-specific parameters differentiate these hybrids and determine if differences in yield, phenology, biomass accumulation and partitioning, and nitrogen uptake of specific tissues can be accurately simulated from a limited set of parameters. In this experiment, the APSIM (Agricultural Production Systems sIMulator) maize model version 7.10 was calibrated for 12 hybrids grown widely throughout the Genomes To Fields Initiative by empirically estimating hybrid-specific model coefficients from field experiments in 2017. Calibrations for the 12 hybrids were then tested on observational data collected from 2018 where the same field experiment was conducted in two environments. This allowed us to evaluate how hybrid calibrations based on just one year of observational data performed. Calibrations were then improved by integrating 2018 observations and a sensitivity analysis was performed. Following calibration, simulations of crop growth were conducted and a difference between hybrids was clearly expressed in traits such as biomass accumulation, partitioning among organs, and nitrogen uptake.

P-53
Marker *easA* indicates ergot alkaloid toxicity in tall fescue

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Tall fescue is a perennial cool season grass widely grown in the United States and Europe for livestock grazing and hay production. Tall fescue owes its hardiness and persistence to a symbiotic relationship with an endophyte fungus (*Neotyphodium coenophialum*). The endophyte confers insect resistance and drought tolerance; however, it can also be toxic to mammals. Endophyte toxicity in tall fescue, fescue toxicosis, affects grazing cattle and pregnant horses and is caused by an ergot alkaloid (ergovaline). Fescue toxicosis can lead to many health issues such as reproduction problems, weight loss and vasoconstriction. Therefore, identification of the toxin in tall fescue is essential. There are currently immunochemistry methods that can be used to identify toxic plant material. However, a DNA marker for ergovaline may offer a more efficient method. Different candidate markers were developed based on sequencing known genes in the alkaloid biosynthesis pathways such as chanoclavine-I aldehyde reductase, lipoprotein-releasing system transmembrane protein, and lipoprotein-releasing system ATP-binding protein. EAS is the gene that has been identified for the toxic ergot alkaloids. The marker easA was identified based upon the sequence data from the EAS locus. PCR was performed with this marker on 35 accessions of tall fescue including toxic and nontoxic varieties. Based on the results, this marker has been shown to characterize fungal DNA extracted from tall fescue as toxic. The identification of the easA primer will allow for more efficient screening of tall fescue for toxicity.

P-54
RNA-seq analysis of a soybean serine hydroxymethyltranferase mutant responding to infection by the soybean cyst nematode *Heterodera glycines*

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Soybean cyst nematode (SCN, *Heterodera glycines* Ichinohe) is the major pathogen of soybean (*Glycine max* (L.) Merr.) causing over $1 billion in yield losses annually in the United States. Planting SCN-resistant soybean cultivars combined with rotation of non-host crops has been the core strategy to control SCN population densities in the field. Resistance of all currently available soybean varieties is derived from two major QTL, rhg1 (on chromosome 18) and Rhg4 (on chromosome 8). In some soybean cultivars, rhg1 is sufficient to provide resistance whereas other cultivars such as Forrest require both rhg1 and Rhg4. Rhg4 encodes for a cytosolic serine hydroxymethyltransferase (GmSHMT8), but its function in SCN resistance remains unclear. In this study, we conducted a transcriptome analysis of the resistant cultivar Forrest and a Forrest SHMT mutant upon infection with SCN. RNA-seq analysis revealed a series of gene expression changes uniquely expressed in Forrest. The differentially regulated genes uncovered in this study not only shed light on the function of SHMT-mediated resistance, but also serve as a valuable resource to identify novel genes that might be involved in SCN resistance in soybean.

P-55

Characterizing a rice diversity panel with a 7K SNP chip and flowering time evaluation

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Rice (*Oryza sativa* L.) is an essential food crop with demands for increased yield, providing the daily caloric intake of over 50% of the world's growing population. Flowering is one of the most sensitive stages of rice growth and is highly variable among varieties and across environments. In Texas, farmers often desire early flowering varieties as these can avoid peak temperatures of the summer months and give sufficient time for the ratoon crop to mature before the cold temperatures of winter begin. Using a diversity panel of 208 accessions, a genome-wide association study (GWAS) for days to flowering successfully employed the Cornell-IR LD Rice Array (C7AIR) to identify key loci contributing to this trait over the 2017 growing season. The C7AIR contains 7,098 markers and is designed to detect genome-wide polymorphism within and between the five subpopulations of Oryza sativa (*indica, aus, aromatic, tropical japonica,* and *temperate japonica*) as well as between *O. sativa* and *O. glaberrima*, *O. rufipogon* and *O. nivara*. During the 2017 season 6 significant loci were identified that contribute to days to flowering. Of these 6 loci, 1 co-localized with Hd3a and RFT1, 2 previously described flowering time genes. Due to strong impact of environmental factors on flowering, this model was run again with solar radiation as a covariate. This increased the significance of QTL; however, these loci did not co-locate with previously described genes or with any significant loci identified in the basic model. The GWAS results can be further validated using gene editing to better enable future efforts to rapidly develop early flowering rice varieties.

P-56

Genetic diversity and population structure of *Rhododendron canescens*, a native azalea for urban landscaping

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Rhododendron canescens is a deciduous azalea native to the southeastern United States that is used in landscaping because of its ornamental qualities. A genotyping-by-sequencing approach was taken to characterize the genetic structure and diversity of a *R. canescens* germplasm collection. Single nucleotide polymorphisms (SNPs) were identified by two software platforms, STACKS and GBS-SNP-CROP. Three distinct *R. canescens* populations were detected by STRUCTURE analysis with GBS-SNP-CROP data, while two populations were distinguished using STACKS data. Principal component analysis with data from either SNP pipeline supported the presence of three populations. Statistical results indicated that there was low genetic differentiation between the populations, but relatively high genetic diversity within populations. The inbreeding coefficient of the *R. canescens* accessions was low, which would be expected with an outcrossing species. These results suggest that there may be a significant level of gene flow between populations of *R. canescens*.

P-57

Identifying new uses and plant breeding targets for nutritional benefit in feeding animals

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Previous studies have identified normal-oleic peanuts as a suitable and economical broiler feed ingredient. However, no studies to date have examined the use of high-oleic (HO) peanut cultivars as a feed ingredient for laying hens and determined the impact of feeding HO peanuts on performance and egg nutritive qualities. This project aimed to examine the use of HO peanuts as a feed ingredient for layer hens to determine the effect on performance, egg lipid chemistry, and quality of the eggs produced. It was found that there were no significant differences in hen performance or egg quality as measured by USDA grade quality, egg albumen height, or egg Haugh unit between the treatment groups. But there were significant differences in many beneficial traits of interest fed the peanut diet, including lower egg weights, greater palmitic and stearic acid, lower trans-fat and yellower egg yolks. All egg protein extracts from all treatments at each time point were non-reactive with rabbit anti-peanut agglutinin antibodies. The results of the study indicate that HO peanuts could be used to produce beneficial traits in poultry. As an important commodity crop in the southeastern United States, production areas closely overlap those of the poultry industry and could be of economic advantage to producers while providing a potential health benefit to the consumer with improved egg nutrition. As results are promising and of great interest to the poultry industry, this is a unique opportunity to target nutritional profiles of the commodity via plant breeding in a collaborative manner to optimize the HO, protein, and fat components in the peanut for additional use in feeding animals.

A. hypogaea subsp fastigiata var fastigiata cultivar IAC-Tatu

P-58

Purifying selection of deleterious alleles and hitchhiking effects on micronutrients during maize domestication and improvement processes

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Maize is not only an important crop species but also represents a promising system for population genetics research. The incremental demands for the human diet, animal feed, and industrial feedstock require the yield and quality of maize to be continuously enhanced. During the processes of maize domestication and improvement, deleterious alleles, likely affecting fitness and yield, have been purged to keep their low allele frequencies in the population, a process known as purifying selection. The effects of purifying selection on maize quality traits such as the compositions of micronutrients, however, have been less explored, especially under different nitrogen conditions. Public data indicated that some of the compositions of micronutrients in kernels are declining during the past serval decades. Based on this observation, we hypothesized that beneficial alleles for micronutrients might have been selected against unintentionally, likely due to the hitchhiking effect if they are in linkage disequilibrium with the deleterious alleles. To address this hypothesis, we conducted largescale field experiments using the maize diversity panel under two nitrogen conditions (N+ and N-) with two replications. We collected micronutrients and other phenotypic traits using highthroughput phenotyping approaches. Then, we performed genome-wide complex trait Bayesian analysis to estimate parameters of genetic architectures using genome-wide SNPs including putative deleterious SNPs. Results from this study will help in understanding the purifying selection for deleterious alleles and their effects on micronutrients, and eventually for maize improvement.

P-59

Fine-mapping *d4* and *Br1* in pearl millet

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Pearl millet (*Cenchrus americanus* (L.) Morrone) is a highly nutritious staple crop to sub-Saharan Africa and India. Grown on marginal lands with poor soil and under drought-prone conditions, it thrives where other crops often fail. Despite its importance, pearl millet has been dubbed an "orphan crop" as it has been neglected by researchers, thus, hindering breeding efforts. Dwarfism has been highly sought after in several crops, as shorter plant heights reduce lodging and hence yield loss. Multiple dwarfing genes have been identified in pearl millet, such as *d4* and the widely used *d2*, which was previously cloned in our lab. *d4*, in its homozygous recessive state, exhibits an extreme dwarf phenotype, unattractive to farmers. However, it was observed that the *d4* gene, when present in lines that had bristled panicles, resulted in a semi-dwarf phenotype. The bristling gene, *Br1*, is dominant and produces awn-like structures on the panicle. Since the semi-dwarf phenotype, conditioned by the homozygous recessive *d4* mutation and homozygous dominant or heterozygous *Br1*, has an intermediate height attractive to farmers, it is of interest to fine-map both *d4* and *Br1*. A d4 candidate gene with a missing exon in the *d4* mutant allele has been identified. The *Br1* interval is being narrowed down by designing new markers based on comparative approaches and genotyping-by-sequencing (GBS) data. Fine-mapping these genes would not only help researchers better understand the molecular basis of pearl millet plant height but also help breeders create semi-dwarf cultivars with less yield loss to better feed those who rely on it.

P-60

Development of molecular breeding resources for increased grain pro-vitamin A carotenoids in sorghum

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Sorghum bicolor serves as a dietary staple for over 500 million people in developing countries, where vitamin A deficiency, is one of the most prevalent public health problems. To successfully use nutritionally enhanced crops to ameliorate micronutrient deficiencies, a better understanding of the biochemical pathway and its regulation its required. In this regard, a panel of 400 sorghum accessions was evaluated for carotenoid content and composition through high-performance liquid chromatography. Subsequently, a genome wide association study (GWAS) based of genotype by sequence data, was performed to elucidate the genetic basics of this traits. In parallel a pathway level analysis was employed to test association in genes involved in carotenoids or precursors biosynthetic pathways. The GWAS found 13 QTLs associated with β-carotene, 29 with Zeaxanthin and none for Lutein, after multiple test correction. The pathway level analysis detected six QTLs for β-carotene, three for Zeaxanthin, and none for Lutein. Several QTLs detected in the GWAS were located within 100kb of genes involved in the geranyl geranyl pyrophosphate biosynthesis pathway as well as carotenoid biosynthesis genes such as, carotene epsilon monooxygenase, β-ring hydroxylase, zeaxanthin epoxidase and phytoene synthase. The pathway level analysis detected QTLs within geranyl geranyl phyrophosphate biosynthesis genes as well as the carotenoid pathway genes: zeaxanthin epoxidase and β-carotene dioxygenase.

P-61

Hemibiotrofic and necrotrofic resistance to *Colletotrichum acutatum* and *C. gloeosporioides* in a biparental population of *Fragaria* × *ananassa*

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Anthracnose diseases of the octoploid strawberry (*Fragaria* x *ananassa*) are rotting diseases caused by fungal pathogens of the *Colletotrichum* genus. These diseases have complex lifecycles with a hemibiotrophic stage in the leaves and a necrotrophic stage in other tissues. In addition, several strains have resistance to multiple fungicides. *C. gloeosporioides* and *C. acutatum*, causal agents of Anthracnose Crown Rot (ACR) and Fruit Rot (AFR), respectively, cause significant losses in the Southeastern US. The resistance to the necrotrophic phase is well known, but there is little information for resistance to the hemibiotrophic infection (HBI) and no QTL(s) have been identified. A biparental population comprised of 286 F1 progenies was generated from the cross of NCSU germplasm material NCS 10-080 (susceptible to HBI) and NCS 10-147 (resistant to HBI). The population was maintained *in vitro* condition and explants were used for a series of studies. In 2017, two replicates of the population were planted in the fall and evaluated during the summer of 2018 for ACR resistance, a second set of the population was planted in fall 2018 and evaluated in spring 2019 for AFR resistance. Using AUDPC, resistance to the necrotrophic stage was observed approaching normal distributed and some individuals are highly resistant to ACR or AFR. There was no fruit production in the 12 individuals that are highly resistant to ACR. A third and fourth set of the population were evaluated for HBI for both pathogens in a phytotron. Using photo image analysis, the sporulation area on infected leaves revealed that HBI was detected in the population and the distribution was normal. The population is undergoing reduced representation sequencing. Quality filtering of sequence data, genotype and dosage calling, linkage map construction and QTL analysis will be performed using NGS-Composer, GBSapp, MAPpoly-R and QTLPoly-R software, respectively.

P-62
Developing profitable canola germplasms in the Southeast region

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Canola (*Brassica napus* L.) seeds produce over 40% of vegetable oil rich in oleic acid that is considered a healthy monounsaturated fatty acid. After crushing to extract its oil, canola meal is still valuable for livestock feeding because of its high content of proteins with desirable amino acid composition and minimal amount of the undesirable glucosinolates. During the period between 1991 and 2019, the canola oil domestic production increased from 36 to 1764 million pounds and U.S. import from 815 to 4,176 million pounds, indicating the greater gap between the domestic demand and the production currently. In an effort to expanding canola growing acreage more widely, winter canola growth has been evaluated during the winter season to identify the potential value of canola production and to improve existing germplasms with more profitable traits such as winter hardiness, disease resistance, early maturation, and high oil/oleic acid contents. A collection of canola germplasms representing most of the canola growing regions worldwide have been grown in Pee Dee REC of Clemson University located in Florence, SC. Preliminary study shows that the improvement of winter canola production is possible in the area of study as potential canola varieties have been identified with beneficial traits such as winter hardiness, early maturation, and white mold resistance, allowing us searching for canola varieties that can sustain under the SE environment toward development of highly profitable winter canola cultivars.

P-63
Harnessing the wild side to improve wheat curl mite resistance

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Genetic diversity is the foundation for crop breeding. When genetic diversity is scarce, we can return to the source of origin to explore wild relatives as donors of novel sources of diversity. *Aegilops tauschii* is the donor of the D genome of the cultivated bread wheat. It has been used as a valuable source of novel genes for many economically important traits such as pest and disease resistance. Wheat curl mite (WCM) is a threating pest for wheat, mainly because of vectoring wheat streak mosaic virus. To date, 4 genes have been reported against WCM (Cmc1-Cmc4). The objective of this study was to characterize a diverse panel of *Ae. tauschii* accessions against WCM and identify resistance alleles that can be used to breed wheat against WCM. We tested 234 accessions that included 109 from lineage 1 (spp. *tauschii*) and 125 from lineage 2 (spp. *strangulata*). WCM phenotyping was performed under controlled conditions using the WCM biotype 1. Six plants for each accession were tested 14 days after exposing the plants with infested straw. Phenotypic response to WCM was recorded using a 0 to 4 scale, where 0 was resistant (R) and 1-4 different levels of susceptibility (S). Genotyping-by-sequencing data was used to perform GWAS in order to map genomic regions associated with WCM resistance. Lineage 1 resulted in 71 S and 38 R accessions, while lineage 2 presented 119 S and 6 R. Strong population structure was identified within the accessions, consistent with the lineages. GWAS analysis resulted in a major QTL on chromosome 6S, corresponding with three haplotypes, where no haplotype was exclusively associated with the resistance phenotype. This study identified genomic regions involved in resistance to WCM in wild wheat. Further analysis of these regions will reveal if they are novel or already present in cultivated wheat varieties.

P-64

High-throughput sequence based genotyping for wheat quality genes

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The quality of products produced from wheat flour depends largely on gluten proteins. Gluten proteins are comprised of several classes of proteins, including the high-molecular weight (HMW) glutenins, the low molecular weight glutenins, and the gliadins. HMW glutenin proteins form inter- and intra-molecular bonds to create a large matrix that gives rise to the strength and extensibility of the dough and the final product. Not all HMW glutenin alleles play well in the matrix and thus result in poor quality products. Therefore, breeding programs must continually monitor the quality of lines to ensure consumer acceptance. Given that HMW glutenins are major determinants of the end-use quality and the most widely characterized, wheat breeding programs often use gel or PCR markers to select for the preferred alleles. In this research, we used the extensive sequence information from the 10+ Wheat Genome Project and whole genome sequencing of 98 CIMMYT wheat varieties to identify nucleotide differences between HMW glutenin alleles. These differences were captured as k-mers and an association analysis identified k-mers that were diagnostic for the alleles. These diagnostic k-mers were then built into a bioinformatics pipeline that searched sequencing data of breeding lines to determine the HMW glutenin alleles present in each line. This approach has the potential to offer a low cost, high-throughput sequence based alternative to gel methods of gluten genotyping in breeding programs.

P-65

Modelling for ambiguous SNP calls in allotetraploid peanut

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Cultivated peanut is an allotetraploid crop with highly similar A and B sub-genomes coupled with large genome size of around 2.7 Gbps. Accurate genotyping of allotetraploid peanut is challenging due to alignment ambiguities caused by homoeology leading to an excess of heterozygous calls. In this study we propose an allotetraploid specific method that carefully assesses the strength of the A and B alignments to estimate the genotype of a sequenced individual at a single locus in a homoeologous region. The paired end reads derived from targeted resequencing were merged using a custom read merger and then aligned to the A and B genome targets separately using the Burrows Wheeler Aligner. The log likelihoods of each alignment were computed using quality scores and assuming independence of nucleotides and equally likely substitutions. The alignments and their posterior probabilities were used to estimate a flexible sequencing error model. The recalibrated error model is then used to estimate, via Monte Carlo sampling, the likelihood of all n reads aligned to the SNP region given the genotype. Then, the genotype that maximizes the likelihood is reported as the estimated genotype. In providing this tool, we hope to benefit plant breeding programs by genotyping allotetraploids with greater accuracy and thereby better revealing the true variations among genotypes.

P-66

AGHmatrix 1.0: R package to build genetic relationship matrices for diploid and autopolyploid species using pedigree, genomic, or both

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Understand the relatedness between genotypes is key in plant breeding programs. By estimating how the individuals covary in a population, breeders can calculate genetics parameters of the population (e.g. inbreeding, heritability, and effective population size), predict breeding values, and guide the selection of promising individuals. Different software can be used to obtain such estimate for diploid species. However, there is a lack of specialized software addressing autopolyploid crops (e.g. blueberry, potato, and alfalfa). Relatedness can be estimated based on genealogical records and/or molecular information. If based on genealogical records, accounting for double-reduction – an autopolyploid meiotic phenomenon – leads to better breeding values estimates. If based on molecular information, the genomic relationship matrix computation needs to accommodate a higher number of genotypic classes (or probabilities). The *AGHmatrix* software implements different ways to compute genetic relationships. Using genealogical records, it is possible to compute the numerator relationship matrix assuming ploidy level and double-reduction proportion for additive effects and, if diploid, also for dominance effects. Using diploid SNP data, it is possible to compute two distinct methods for additive effects and two others for dominance effects. Using autopolyploid SNP data, it is possible to compute one for additive effects, one for dominance, and one for full-autopolyploid effects. The software also has internal functions to organize the input and to double-check errors. It includes a user-friendly tutorial. Initially handling only pedigree data, now, its new version allows the use of SNP data to build realized relationship matrices for any even ploidy level. With this expansion, the breeder community has a novel tool to make useful inferences about the genetic parameters in autopolyploids and move towards genomic selection and association (e.g. K+Q-GWAS). The software is freely available at *https://CRAN.R-project.org/package=AGHmatrix*.

P-67

QTL analysis of a yellow *Phaseolus vulgaris* recombinant inbred line population for a fast cooking, flavorful, and flourishing future of dry beans

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Dry beans are a nutrient-rich food with diverse culinary attributes, but dry bean consumption in the United States remains low due in part to their often long cooking times and the preconceived notions held by consumers regarding their flavor. Cooking time and sensory quality are two important traits considered when consumers choose whether to purchase dry beans and which dry bean products to purchase. However, the process of evaluating germplasm for these consumer-valued traits is costly in time and resources, which limits the ability of breeders to incorporate these traits in their programs. This study uses QTL analysis to contribute to the growing understanding of the genetic control of cooking time and to lay the foundation for sensory quality improvement in dry bean breeding programs. In this study, a yellow dry bean (*Phaseolus vulgaris* L.) recombinant inbred line population of 244 genotypes including parents Ervilha and PI527538 were grown in Entrican, Michigan for two years. The population was evaluated for cooking time, flavor characteristics, and texture. Cooking times ranged from approximately 18 to 40 minutes. A trained sensory panel determined flavor and texture profiles of cooked samples using 5-point attribute intensity scales. The genotypes exhibited a range of attribute intensities with beany flavor having the largest range from 1.38-4.13. A genotyping-by-sequencing approach with an ApeKI digest was used to genotype the parents and RILs. QTL mapping of cooking time, flavor profiles, and texture identifies genomic regions influencing these traits. This information will enable breeders to target faster cooking times and specific sensory profiles in their programs, as well as allow for selection on agronomic traits without sacrificing desirable cooking time and flavor. By addressing the barriers these traits pose, dry bean consumption and their suitability in new food products might improve allowing increased access to their associated nutritional benefits.

P-68

Molecular breeding of nitrogen use efficiency in sweet corn

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Almost half of nationally distributed fresh market sweet corn is grown in the southeastern United States (USDA NASS, 2016). In order to maximize yield in sweet corn production systems, nitrogenous (N) fertilizers are routinely applied in large quantities. N fertilizers are produced using the Haber-Bosch process, relying heavily on fossil fuels and representing one of the largest costs to agricultural systems. To safeguard yields, farmers over apply N fertilizers (Ng et al., 2016). The remaining N leaches into nearby ecosystems, creating environmental and health problems (Stoner, 2011). Towards the ultimate goal of improving productivity and sustainability in Florida agriculture, we aim to increase the nitrogen use efficiency (NUE) in FL sweet corn varieties for commercial production. A crucial first step in this process is to assess available germplasm for natural variability of NUE and related traits. A diversity panel of sweet corn has been screened for top-performing breeding material. Plant N has been assessed at three different growth stages and trait heritability has been estimated. NUE has complex genetics and is resource intensive to evaluate. Hence, traditional breeding results in slow genetic gains. In order to accelerate NUE breeding, we plan to expand our information about the genetic mechanism controlling NUE and to incorporate this genetic and molecular information into the breeding process. We are currently sequencing the entire genome of all lines in the diversity panel and phenotypic data from this screen will be used to perform a genome-wide association study to identify key genes responsible for high NUE. These results are expected to guide specific introgression of beneficial alleles and accelerate genetic gain in the breeding program.

P-69

Identification of the key carotenoid biosynthesis pathway genes impacting tomato fruit lycopene content

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Tomato (*Solanum lycopersicum* L.) is the most economically important horticultural commodity in the U.S., and is rich in vitamins A and C, fiber, essential minerals, and several health-promoting antioxidants including lycopene, a dietary antioxidant carotenoid which contributes to tomato red color and reduces the risks of cancer, cardiovascular disease and diabetes. The lycopene content in tomatoes is largely under genetic control and varies greatly among genotypes. Analysis of gene expression levels in the carotenoid biosynthesis pathway may provide genetic information to maximize tomato fruit lycopene content. In the present study, forty-six high lycopene tomato breeding lines with different genetic backgrounds were collected worldwide, representing a wide spectrum of lycopene concentration. These lines were grown to maturity in the same greenhouse at the same time, and fruits of six different developmental stages (i.e., immature green, mature green, breaker, orange, pink, and ripe) were harvested. Real-time RT-PCR is underway to quantify the expression levels of the complete carotenoid biosynthesis pathway genes individually at different developmental stages, relative to lycopene and beta-carotene –content. Our preliminary data showed that breaker and orange/pink stages are critical to lycopene production. Some lines have shown unique gene expression and lycopene characteristics and will be further examined at different fruit maturity stages. Earlier maturity stages of interesting lines may provide an indication as to which genes are most critical. By linking the gene expression patterns to fruit lycopene content during ripening, we expect to identify which carotenoid biosynthesis pathway genes most impact tomato fruit lycopene content. This information will be used to improve fruit lycopene content in tomato breeding and gene editing.

P-70

Characterization and molecular mapping of stripe rust resistance in a winter wheat doubled haploid population

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The majority of global wheat (*Triticum aestivum* L.) production is susceptible to the stripe rust pathogen (*Puccinia striifromis* f. sp. *tritici*) and new stripe rust races are evolving more rapidly than in the past, causing farmers to lose more yield due to the disease. A combination of all-stage resistance and high-temperature adult plant (HTAP) resistance in new cultivars will either provide complete resistance or reduce disease damage, thus providing a greater overall level of protection. A doubled haploid population (n=204) developed from a cross between winter wheat cultivars 'Hatcher' and 'Denali' was developed and characterized for response to stripe rust during 2018 and 2019 at Fort Collins, CO and Rossville, KS. A high-density genetic linkage map consisting of 3,150 single nucleotide polymorphism markers was used to identify markers linked to quantitative trait loci (QTLs) for stripe rust resistance in this population. Four stripe rust resistance QTL for infection type (IT) (*QYr.coh-2B, QYr.coh-3A, QYr.coh-3B and QYr.coh-5A*) and one resistance QTL for disease severity (*QYr.coh-2D*) were found to contribute to decreasing stripe rust damage. Among the resistance QTL for IT, *QYr.coh-3A* was detected at Rossville in 2018 and 2019 and at Fort Collins in 2019. A separate analysis for the two ratings, before and after higher temperatures occurred in Rossville in 2019, was done and confirmed that *QYr.coh-3A* provides HTAP resistance and *QYr.coh-3A* is expected to be a major-effect *QTL.QYr.coh-2B, QYr.coh-3B,* and *QYr.coh-5A* are likely the same as previously mapped loci in other studies, but *QYr.coh-3A* is likely a new adult-plant resistance QTL that provides HTAP resistance to stripe rust. Flanking markers for all the identified QTL, especially *QYr.coh-3A*, will be useful to develop resistant wheat cultivars.

P-71

Developing robust SNP marker assays to introgress semi-indeterminate trait into determinate soybean for improvement of soybean yield

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Soybean (*Glycine max* (L.) Merrill) has three developmental patterns called growth habits: determinate, semi-determinate, and indeterminate. Northern soybean varieties (early maturity groups) typically have indeterminate growth habit, while southern soybean varieties (late maturity groups) have determinate growth habit. Growth habit is regulated by two genes, Dt1 and Dt2, with recessive epistatic interaction at these loci. Introgression of semi-determinate growth habit into determinate soybean might help improve soybean yield in the southern U.S. However, it is difficult to differentiate semi-determinate and determinate soybean under field conditions. Development of robust SNP marker assays for these genes would assist introgression of semi-determinate growth habit into soybean varieties in late maturity groups. From previous reports, we identified SNP markers at the Dt1 and Dt2 loci from the Gmax_275_v2.0 soybean genome assembly and developed KASP marker assays. The SNP marker assays were used to genotype 779 plants of two F3:4 populations derived from the crosses of G00-3880 × LD09-30454 and Woodruff × LD09-30454, which segregate for growth habit. The individuals from the two populations were phenotyped for growth habit post-harvest as well. Two KASP markers, named GSM744 and GSM740, consistently gave correct allele calls on parental Dt1 and Dt2 loci, respectively. Association analysis of these two SNP markers with the growth habit phenotypes indicated a correlation coefficient of 0.7 ($p < 0.001$). This level of correlation indicates that these SNP markers are effective in identifying the growth habit of soybean. These markers will aid introgression of indeterminate growth habit into soybean varieties in late maturity groups.

P-72

CRISPR-Cas editing and hairy root evaluation of gene targets to obtain low phytate soybean

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Phytate (InsP6) is a strong chelator of cations important for nutrition, and therefore considered an antinutritional factor. Phytate is abundant in soybean seeds since plays number of regulatory roles, but also limit the availability of some essential nutrients and decrease the nutritional value of the seeds. The generation of low phytic acid soybean can overcome these limitations. This study has been conducted to develop a soybean low in phytate by CRISPR-Cas9 But first, it is necessary to evaluate if the systems will work, through the evaluation of Targets, candidate genes, besides the enzymes SpCas9 and Cpf1. Candidate genes were chosen, and targets identified based on their target/off-target scores > 0.6. Vectors were constructed in two different configurations to compare the efficiency of a conventional system, with separate promoters for each component, vs a simplified system with a single promoter for all components. The guide RNAs were synthesized and incorporated into the vectors using NEBuilder assembly. The basic vector codes for Cas9 from *Streptococcus pyogenes* or Cpf1 from *Moraxella bovoculi* under the control of GmUbi3 promoter. It also contains a GFP cassette to aid in the detection of the transformed roots. Seeds of soybean variety 'Jack' were germinated and 4-day-old cotyledons were excised and inoculated with *Agrobacterium rhizogenes* K599 previously transformed with each vector; cotyledons were cocultivated for 4 days and then transferred to growth medium with antibiotic (Timentin 500mg/L).DNA was extracted from those roots positive for GFP, and PCR amplicons around the target sites were sequenced sequencing. The editing efficiency was evaluated by the Web-tool, TIDE and Synthego. The results showed that the targets worked and will help in choosing the most efficient system. That cassette will be transferred to a vector suitable for transformation by biolistics to obtain stably transformed soybean plants with low phytic acid, without losing important agronomic characteristics.

P-73

Depicting the genetic control and the relationship among yield related traits in blueberry

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Phenotypic variation for quantitative traits results from the expression of multiple regions on the genome. Breeding these traits is challenging since environmental effects can highly affect their expression. However, the phenotypic expression decomposition of these traits can highly contribute to the understand and to improve breeding. The objective of this study was to determine the genetic variation, heritability and relationships among fruit-set (FS) and fruit-quality (FQ) related traits, in order to depict yield and generate information towards selection for blueberry (*Vaccinium corymbosum*). For this, a population of 400 genotypes, was evaluated for FS (flower bud density; number of flowers, number of green fruits, number of ripe fruits) and for FQ related traits (weight, and fruit diameter). All measurements were obtained considering three repetitions. FS traits were measured as an average of three random branches per plant. FQ traits were obtained from 25 fully mature berries. Linear mixed models using pedigree information were used in order to estimate variance components and heritability, correlation tests were performed among all traits, and genotypes were ranked considering the information generated. Heritability ranged from 0.2 to 0.5 across traits. All FS traits presented positive and significant correlation (>0.6). Number of buds (BN) and total number of ripe fruits (NRF) were highly correlated (0.7). Meaning that selection can be performed early in the season considering BN with high impacts on the NRF, consequently, on yield. The information generated here can help understanding the architecture and expression of yield related traits, and be used to help genotype selection, accelerating and improving cultivar release.

P-74

Improving selection towards machine harvesting in blueberries

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Machine harvesting (MH) blueberry is faster and less costly. Among the key traits for the blueberry plant to be suitable for MH are concentration of production (narrow window of harvest), fruit firmness, bush architecture, and detachment strength (DS - delta between the detachment force required to dislodge green fruit versus the force required to harvest ripe fruits). Peduncle and pedicel (PDL and PDC) length may also interfere in MH by allowing, or not allowing, for an easier separation of individual berries. During MH blueberries are dropped via agitation of the plant, while mature fruit separates from the PDL and PDC junction, green fruits are kept in the plant. Tight clusters could affect this by not allowing for the agitation to release the ripe berries as one, releasing the whole raceme (not favorable for packing). In order to verify if the PDL and PDC have an effect on MH we evaluated the effect of these traits on detachment strength. We measured PDL and PDC for a population of 400 genotypes managed commercially since 2014. For each genotype a total of 15 peduncles were taken, five for each biological replicate. All pedicels presented on the peduncle were measured. Least square means were obtained for each trait and Pearson correlation tests performed to verify the association between the PDL and PDC with DS. A genotype rank was obtained indicating possible selections, suggesting genotypes more adapted to MH. To generate information about variance components and heritability of the traits, pedigree information was used. The information generated in this study can be used to direct selection towards MH in the University of Florida blueberry breeding program.

P-75

Differentiation length and berry size as yield-component traits for Southern Highbush Blueberry

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Yield assessment is notably complex as it involves the analysis of several different traits and is subject to variability based on environmental conditions. The investigation of genetic and selectable traits that provide breeders with an accurate projection of yield for a particular cultivar is thus extremely valuable. In grasses and forage plants like alfalfa, raceme length is a commonly studied yield-component trait which is subject to polygenic control. Raceme length shows a high correlation with number of floral buds and seed size, which deem it a highly informative quality to be considered for indirect selection to increase yield. However, research of analogous traits is limited for woody perennial species, such as blueberry. In the present study, the number of ripe fruits (NRF), fruit diameter (FD), and differentiation length (DL), i.e. the distance from the apical meristem of a fruiting shoot to the most distal opened flower, were measured in an University of Florida (UF) breeding population, comprising 400 genotypes of Southern Highbush Blueberry (*Vaccinium* spp.). The objective is to establish the possible effect of DL and FD on yield. Empirical best linear unbiased estimations (eBLUEs) were obtained for each trait and Pearson correlation tests were performed to verify the association between DL and FD with NRF and, by inference, with yield. Genotypes were ranked for selection based on the results obtained for DL and FD. Our results revealed a positive and significant correlation between DL and NRF, indicating that DL may be classified as a yield-component trait for blueberry, and measurements of DL can help guide selection. Heritability was estimated using pedigree information to dissect the genetic control of DL and FD. The information generated in this study can help to direct the selection process in the UF blueberry breeding program, considering the increase of yield.

P-76
Increasing future blueberry variety compatibility with machine harvest

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Blueberry (*Vaccinium* spp.) is an important high value specialty crop, with both consumption and production increasing exponentially over the last decade. The largest producer of Blueberries globally is the United States (US), but due to the high labor cost of harvesting US growers are at a global disadvantage. Mechanical harvesting is needed in order to maintain a competitive position in the industry, and work is needed to provide growers with varieties optimized for mechanical harvesting. Traits such fruit firmness (FF) and detachment strength (DS - delta between the detachment force required to dislodge green fruit versus the one required to harvest ripe fruit) are of great importance for MH. Because it is desired that only the ripe fruits are collected during harvest, and that fruits are firm to support the drop from the top of the bushes onto the machine catchers without injury. Our goal is to generate information to direct selection of genotypes that will present features compatible with mechanical harvesting. For this, we evaluated DS and FF in a University of Florida breeding population comprising 400 genotypes. All measurements were taken from 25 fruits obtained for three biological replicates. For DS, measurements were taken for both the green and ripe conditions, the delta between the DS for ripe and green fruits was used in the statistical analyses. Least square means were obtained for all genotypes and used to rank genotypes based on both traits; and a projection of selection was obtained. The heritability of both traits was estimated using pedigree information. The information generated in this study can be used to help direct the selection process in the UF blueberry breeding program towards the development of varieties that could be marketed commercially as mechanical harvest specialty varieties.

P-77
Genetic and molecular analysis of *Aegilops tauschii*-derived resistance to yellow rust

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Yellow or stripe rust caused by *Puccinia striiformis* f.sp. *tritici* is one of the devastating fungal diseases of wheat, causing yield losses up to 40% in susceptible wheat cultivars. With the emergence of new, aggressive stripe rust races that are adapted to warmer temperatures, there is need to identify new sources of resistance. *Aegilops tauschii* (2n=2x=14, DD), the D-genome donor of hexaploid wheat, *Triticum aestivum* L. (2n=6x=42, AABBDD) is a rich source of disease resistance genes to rust diseases as well as other foliar diseases. At Wheat Genetics Resource Center (WGRC), eight out of 40 core *Aegilops tauschii* accessions were screened for resistance to five stripe rust isolates at two-leaf stage under controlled conditions. Out of these eight accessions, TA2474 displayed high levels of resistance to four out of five stripe rust isolates examined and TA1694 displayed moderate to high susceptibility to all five isolates. For the genetic and molecular dissection of the stripe rust resistance present in accession TA2474, we developed two reciprocal diploid populations - TA1694 X TA2474 and TA2474 X TA1694, and used the isolate *YR18.1.1.1* for disease evaluation. A total of 208 F_2 individuals of TA1694 X TA2474 segregated in 143 resistant and 65 susceptible, and 247 F_2 individuals from the reciprocal cross segregated in 178 resistant and 69 susceptible. The phenotyping result indicates there is a single locus conferring the resistance. For initial mapping, we employed Bulked segregant RNA-seq (BSR-seq) with two resistant and two susceptible bulks from the two F_2 populations.

P-78

Yellow Bean Collection (*Phaseolus vulgaris L.*) – genotypic diversity of cooking time and iron bioavailability

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Dry beans (*Phaseolus vulgaris* L.) are grown and consumed worldwide, serving as a dietary staple and an important source of protein and minerals in Africa and Latin America. However, long cooking times poses a barrier to bean consumption, and the bioavailability of iron from beans is generally low despite the high iron concentration. Bean germplasm within some yellow bean market classes have been identified to be fast cooking and high in iron bioavailability. To further understand the value of yellow beans for cooking time and iron nutrition, the Yellow Bean Collection (YBC) was assembled with 308 genotypes collected from across the world. Genotyping-by-Sequencing identified 52,622 single nucleotide polymorphisms (SNPs) among 296 genotypes. A PCA analysis using those markers classified approximately 175 genotypes as Andeans, 73 as Middle Americans, and 48 as admixtures. The YBC was planted in a randomized-complete block design with two field replicates at the Michigan State University Montcalm Research Farm near Entrican, MI, USA in 2018. Raw seeds were soaked in distilled water for 12 hours prior to determining the cooking time with automated Mattson pin-drop device. A 4.7-fold difference in cooking time was observed among the genotypes in the YBC. Iron bioavailability in cooked whole seeds was expressed as Caco-2 cell ferritin formation (ng ferritin / mg total cell protein) relative to a white kidney bean control (cv. Snowdon) run with each bioassay. Analysis on a subset of 60 fast-, medium-, and slow-cooking genotypes in each PC group revealed that fast cooking yellow beans from the Manteca and Mayocoba market classes in the Andean gene pool have improved iron bioavailability.

P-79

Prospects and progress in novel bioenergy grass (*Tripidium* spp.) breeding for temperate climates

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High biomass accumulation within the genus *Tripidium* spp. (Erianthus spp., *Saccharum* spp.) has been documented, but has a limited breeding history. Several new interspecific Tripidium hybrids (*Tripidium ravennae* and *T. arundinaceum*) were developed and planted into comparative feedstock trials in 2016. Evaluations examined biomass yield, cytogenetics, plant fertility and compositional analyses relative to Miscanthus ×*giganteus* (Anderss.). Dry biomass yields varied as a function of year and accession increasing each year and ranged from 3.4 – 10.6, 8.6 – 37.3, and 23.7 – 60.6 Mg/ha for *Tripidium* compared to 2.3, 16.2 and 27.9 Mg/ha for M. ×giganteus in 2016, 2017 and 2018 respectively. Cytological and cytometry based evidence revealed the accessions to be tetraploid (isoploid) with 2n = 4x = 40 (5.06 pg) supporting interspecific hybridity of the offspring. Flowering and reproductive characters varied considerably with some accessions producing fewer observed offspring than M. ×*giganteus*. The *Tripidium* hybrids varied significantly for inflorescence number, height and dates of peak anthesis ranging from the end of September through November. Variations in yield and compositional analyses for all carbohydrates contributed to variations in theoretical ethanol yields ranging from 10,181 to 27,546 L/ha for *Tripidium* accessions compared to 13,095 L/ha for M. ×*giganteus*. Relative feed value for winter-harvested *Tripidium* accessions varied from 52.8 - 60.0% compared to M. ×*giganteus* with 45.4%. The biomass yield, hardiness and compositional assets of these new Tripidium hybrids are promising and warrant further research and development of *Tripidium* as a temperate bioenergy crop.

P-80
A survey of hybrid ploidy from interspecific crosses in *Vaccinium* species

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Interspecific hybridization functions to increase the genetic diversity of a population. Interspecific hybridization in the cultivated blueberry (*Vaccinium corymbosum* L. spp, 4x, and *V. virgatum* Aiton. 6x) serves dual purposes of alleviating inbreeding depression and infusing the population with key attributes for expanding blueberry production, including increased berry firmness for harvest mechanization, plant architecture, adaptation to higher pH soils, aroma, and skin and flesh color. While species introgression into the cultivated blueberry is made difficult through ploidy variation between species and across sections, hybridization between *Vaccinium* species of varying ploidy levels is often made possible through unreduced gametes. This study determined the DNA content of interspecific hybrids resulting from *Vaccinium* species of varying ploidy levels. Selecting 204 clonally replicated complex *Vaccinium* hybrids of the NC State blueberry breeding program and control species, dormant bud tissues were collected in triplicate. While the ploidy level of progenies from 6X × 6X, 4X × 4X and 2X × 2X are predictable, the ploidy level of progenies of interspecfic crosses with differing ploidy levels is less predictable. Nuclei were extracted and stained with propidium iodide and DNA content was measured using a Partec PA-II flow cytometer. Samples were compared to 2C DNA content means of known diploids at 1.14 pg, tetraploids at 2.40 pg, and hexaploids at 3.63 pg. Twenty-eight pentaploid hybrids were identified with 2C-value means of 2.98 pg. The pentaploid 2C-value was significantly different from either hexaploid or tetraploid ($p<0.001$). Through determining the 2C-value in addition to knowledge of pedigree history, this study gives insight into the fertility of F1s across *Vaccinium* species as well as unreduced gamete potential in selected species. Understanding the capacity to breed across *Vaccinium* species/sections and the probable offspring ploidy thereof, furthers hybridization and introgression of novel native traits.

P-81
Genetic survey of historic Pee Dee cotton germplasm

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The Pee Dee Cotton Germplasm Enhancement Program in Florence, SC, encompasses over 100 years of breeding and genetics for the improvement of Upland cotton. The objectives of this study are: 1) to identify changes in allele frequency over the history of the program; and 2) to characterize the relationship and relatedness between 95 selected genotypes. Breeders leading the program have placed a specific emphasis on the elusive goal of coupling satisfactory lint yield with exceptional fiber quality over the course of 8 breeding cycles, as well as maintaining and improving genetic diversity. We hypothesize that although key alleles from founding genotypes in this program are fixed across breeding cycles, changing focus over time and introduction of new material have resulted in differences between breeding groups. To test our hypothesis, the Cotton 63K SNP Array was employed to develop a genetic fingerprint for each of 95 genotypes. We are evaluating a number of different SNP filtering criteria to form a core set of markers for population structure analysis, including principal component analysis and clustering techniques. Our results suggest the materials in the Pee Dee Program are indeed diverse and can be distinguished with the 63K array. In a preliminary analysis using 18,664 markers following filtering, the proportion of identical-by-state alleles ranges from 0.527 to 0.969, averaging 0.669, and the number of sub-populations (K) inferred is 7 or 8, with group membership differing from the predicted 8 breeding groups. This study will provide the basis for future work in marker-trait association.

2018 Advanced yield trials of the UGA soybean breeding program.

P-82

Reverse genetic screening to identify mutations in candidate genes involved in carbohydrate metabolism in soybean seeds

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Most of the soybean produced in the USA goes to animal agriculture. Soybean is an excellent source of protein, oil and carbohydrates. Of US-produced soybean meal, approximately 67% is consumed by poultry. With advances in plant breeding and molecular biology, the oil, protein and carbohydrates in soybean seed can be modified to enhance functionality. Soluble carbohydrates in soybean consist of sucrose, raffinose and stachyose. Raffinose and stachyose are referred to as raffinose family oligosaccharides (RFOs). The RFOs are derived from sucrose and are considered antinutritional carbohydrates, whereas sucrose is a nutritionally useful component in human or animal diets. Consumption of soybean seed products with low levels of RFOs increases metabolizable energy efficiency in chickens. Through the application of a reverse genetic technique, known as TILLInG (Targeting Induced Local Lesions In Genomes), unique chemically induced mutations that have the potential to alter gene function can be identified within target genes. One of the goals of this project is to identify allelic variation for carbohydrate composition. Chemical mutagenesis via N-nitroso-N-methylurea (NMU) was used to create new alleles. NMU induces single-nucleotide polymorphism (SNP) mutations across the genome. Our method makes this more affordable by surveying the available diversity in the population using next-generation sequencing, then isolating the desired mutant individuals by genotyping with a custom SNP marker. For this approximately 5,000 M2 families in the Williams 82 background were used. A mutant allele of RS3 (RAFFINOSE SYNTHASE3) was identified, a false positive was discarded. The population is still being screened for additional targets.

P-83
Seed hardness phenotyping, genetics and breeding in hairy vetch (*Vicia villosa*)

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Hairy vetch is a versatile winter legume with value as both a forage and cover crop. Hairy vetch has the capacity for symbiotic nitrogen fixation, broad adaptability, winter hardiness, vigorous growth habit and can contribute organic matter to the soil. Seed hardness affects the ability of the seed to uptake water and imbibe prior to germination, and is therefore an important trait in hairy vetch breeding. Hard seeded cultivars are useful as forages while soft seeded cultivars are useful as cover crops. Phenotyping methods to quantify the level of seed hardness developed include optimization of the incubation period of un-germinated seeds in sulphuric acid. A numerical scale was used to determine seed hardness of multiple germplasm sources including the soft seeded cultivar 'AU Merit' and NF21, a hard seeded breeding line. A total of 90 to 180 seeds were evaluated per cultivar, and a range of seed hardness was identified per entry. The plants with the most seed hardness were inter-mated for one cycle and the amount of seed hardness in the resulting half-sib families increased 18 to 48%. The correlation between seed hardness and seed size is being explored in multiple GRIN accessions. F1 progenies from a cross between AU Merit and NF21 were generated and will be genotyped using genotyping-by-sequencing (GBS) for genetic linkage map construction and identification of QTL for seed hardness and other seed traits. RNA sequencing of multiple hairy vetch tissues (leaves, flowers, immature pods, seed coats and cotyledons) of plants generated from soft and hard seeds of a single genotypes was used to identify candidate genes that are expressed at higher levels in seed coat tissues. Understanding the genetic mechanisms underlying soft vs. hard seed development in hairy vetch can facilitate breeding applications aimed at developing enhanced hairy vetch cultivars for use as a forage and as a cover crop.

P-84
Cover crop breeding: Releasing regional varieties through a collaborative effort

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Cover crops are planted between cash crops to prevent soil erosion, improve soil health and moisture, suppress weeds, and provide resources for beneficial organisms such as pollinators. If the cover crop is a legume it also fixes nitrogen, decreasing the amount of fertilizer needed for the cash crop. Cover crops can benefit all agricultural systems, but they especially important for organic farmers. Until 2015 very little effort had been put into developing better cultivars for cover crop use. In 2015, a skilled group of ecologists, plant breeders, agronomists and soil scientists from different institutions came together to start a project that will release regionally adapted varieties of hairy vetch (*Vicia villosa*), Austrian winter pea (*Pisum sativum*), and crimson clover (*Trifolium incarnatum*). We use traditional, participatory, and marker-assisted methods to select plants that will deliver good soil coverage, high biomass content and other specific traits depending on the species. Come to the poster to learn more about cover crops, our selection criteria, the breeding pipeline, and preliminary data.

P-85

Black pod peanut shell extracts reduce In vitro *Aspergillus parasiticus* growth

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Peanut (*Arachis hypogaea* L.) is one of the food crops affected by aflatoxin, a mycotoxin produced by *Aspergillus* spp. Aflatoxins are one of the most potent naturally occurring carcinogens known. Due to the great human health risk associated with aflatoxin, economic costs are incurred in food systems to prevent aflatoxin from reaching consumers. Attempts to identify an *Aspergillus* or aflatoxin resistant peanut have been unsuccessful partly due to the large environmental effect on toxin development. However, the benefits of a resistant or tolerant peanut cultivar would be enormous for farmers, the peanut processing industry and consumers. Thus, there is a need to continue searching for a cultivar that could reduce Aspergillus growth or aflatoxin contamination. University of Florida breeding research results with landrace "Vaina Negro" (Black pod in English) has led to the hypothesis that it could be tolerant to aflatoxin based on the chemical composition of its shell as compared to the shell of commercial peanut genotypes. Methanol extracted compounds of the landrace and commercial peanuts were added to Czapek's agar. Media was inoculated with *Aspergillus parasiticus* and plates were scanned in a daily basis for 10 days with an Epson flatbed scanner beginning three days after inoculation. Scans were analyzed using the WinCam® pixel color classification software. Media containing landrace extracts reduced growth and growth rate in a 60% when compared to the media with no peanut shell extracts and in 40% when compared to the commercial cultivar ($p<.0001$). These results show that the compounds present in the landrace have an effect on *Aspergillus* growth. A reduced growth of the fungus could result in a reduced risk for infection that leads to reduction of aflatoxin levels thus providing some level of tolerance to these peanuts.

A selection of cultivated and wild peanuts. The three peanuts in the top of the frame are cultivated by the Caiabí from the Ilha Grande, Mato Grosso, Brazil. At the left of the frame is Tatu, a heritage variety from Brazil. At the bottom of the frame are three wild species Arachis duranensis, A. stenosperma and A. cardenasii.

P-86

Characterizing a peanut chromosome segment substitution line population using high throughput phenotyping

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Currently, high throughput genomics aided breeding is being tested in peanut research. This has been facilitated by the recent development of high quality genomic resources, a phenomenal feat considering the genetic heritage of cultivated peanut. Its recent polyploidization, self-pollinating breeding system, and domestication bottleneck have resulted in a crop with reduced diversity. To harness polymorphism from its wild relatives, a chromosome segment substitution line (CSSL) population was created via the tetraploid route to interspecific hybridization. The 58K and 48K peanut Affymetrix SNP chips were used to characterize the genetic makeup of the population. To associate the genotypic differences with specific traits, phenotype data was manually collected in 2017. In 2018, field based high throughput phenotyping (HTP) techniques were deployed to alleviate some of the drawbacks of manual phenotyping such as labor and time intensiveness. Sensors mounted on an unmanned aerial vehicle (UAV) were used to acquire data on various vegetative indices as well as canopy temperature. A combination of aerial imaging and manual scoring showed that CSSL 100, CSSL 84, CSSL 111 and CSSL 15 had remarkably low tomato spotted wilt virus (TSWV) incidence, a devastating disease in South Georgia. CSSL 100, CSSL 84, and CSSL 111 also performed well under early leaf spot (ELS) pressure. The vegetative indices strongly correlated with the disease scores, indicating that aerial phenotyping is a reliable way of selecting under disease pressure. In addition to being potentially resistant to foliar diseases, the latter three lines also had high plot pod yields comparable to the cultivated check Tifguard. Using a CSSL population, this study has enabled us to propose that chromosome segments from peanut wild relatives may be a potential source of valuable agronomic traits.

P-87

Identification of a polymorphism within the *Rosa multiflora Rdr1A* gene conferring resistance to multiple races of *Diplocarpon rosae* W. in tetraploid garden roses (*Rosa* x *hybrida*)

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Black spot, caused by *Diplocarpon rosae*, is one of the most serious foliar diseases of landscape roses that reduces the marketability and weakens the plants against winter survival. Genetic resistance to black spot (BS) exists and race specific resistance is a good target to implement marker-assisted selection (MAS). High-density Single Nucleotide Polymorphism (SNP) based genetic maps were created for the female parent of a tetraploid cross between 'CA60' and 'Singing in the Rain' using Genotyping-By-Sequencing (GBS) following a two-way pseudo-testcross strategy. The female linkage map was generated based on 227 individuals and included 31 linkage groups, 1055 markers, with a length of 1980 cM. Race specific resistance to four *D. rosae* races (5, 7, 10, 14) was evaluated using a detached leaf assay. Black spot resistance was also evaluated under natural infection in the field. Resistance to races 5, 10 and 14 of *D. rosae* and field resistance co-located on chromosome 1. A unique sequence of 32 bp in exon 4 of the *muRdr1A* gene was identified in 'CA60' that co-segregates with *D. rosae* resistance. Two diagnostic markers, a presence/absence marker and an INDEL marker, specific to this sequence were designed and validated in the mapping population and a backcross population derived from 'CA60'. The robustness of the two markers were also tested against a collection 577 elite roses. Resistance to D. rosae race 7 mapped to a different location on chromosome 1.

P-88

Analysis of effects of Trifluoromethanesulfonamide on sorghum inbreds and their derived hybrids

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Commercial hybrid seed production in sorghum is facilitated through cytoplasmic male sterility (CMS) systems. This system is depended on the tedious process of development of male-sterile seed parents which impedes improvement of new seed parent lines. Mechanisms to reduce the number of lines that require sterilization would be beneficial. Determination of the value of a potential new seed parent requires testcross hybrid evaluations but due to male fertility of these lines, conventional methods of cross-pollination are inadequate to generate the hybrid seed required for testing. A chemical gametocide, Trifluoromethanesulfonamide (TFMSA) was tested to assess its potential applicability to generate testcross hybrid seed. Specifically, the effect of TFMSA on inbred line productivity and its derived hybrids is assessed. In summer 2018, foliar applications of 25 mg of TFMSA and deionized water were made prior to flowering to a select set of white-seeded male-fertile B-lines and their corresponding male-sterile A-lines versions respectively. The bagged panicles were then pollinated using two red-seeded R-lines (R.08306 and R.07178), to produce hybrid seed. Harvested seed panicle parameters included panicle length, panicle weight, seed weight, test weight and percent germination. Seed production on the TFMSA treated B-lines had reduced seed weights compared to the corresponding male-sterile A-lines, but seed production was sufficient for testcross hybrid evaluations of B-lines. These hybrids are planted in a multi-location replicated yield trial in South Texas in summer 2019. Parameters such as uniformity, plant height, maturity, percent self-pollination, and yield will be evaluated to compare the derived hybrids.

P-89

Can Pima cotton be produced in South Carolina?

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Pima cotton (*Gossypium barbadense* L.) in the United States is currently produced in California, Arizona, New Mexico, and Texas, and is more valuable than traditional Upland cotton (*Gossypium hirsutum* L.) due to its superior fiber quality. In this study, we hypothesize that Pima cotton can be produced economically in South Carolina when managed for earliness. The main objectives of this study were to identify accessions with acceptable adaptation, agronomic performance, and fiber quality characteristics when produced under SC growing conditions, and to determine how these Pima accessions respond to different management practices such as irrigation and planting date. These objectives were carried out through separate two-year field trials established at the PDREC in Florence, SC. The first trial compared the fiber quality and yield performance of 44 Pima accessions, four commercial Pima checks, and two elite Upland checks. Fiber quality samples collected after harvest were also ginned by two different ginning methods to determine the impact on fiber quality. The second trial evaluated the fiber quality and yield performance of four Pima accessions and DP 1646B2XF grown under dryland and irrigated conditions when planted on three different dates, Late-April, Mid-May, and Late-May. As expected, the Upland checks were superior in yield, with DP 1646B2XF averaging 1143 lbs lint/ac. and PHY 444WRF averaging 852 lbs lint/ac., and most Pima accessions had longer, stronger fibers than the Upland checks in this trial. The results of the management trial show lint yields for all Pima accessions were at least 50% lower than DP 1646B2XF and gin turnout was also lower for Pima accessions (38.4-42.3%) than DP 1646B2XF (45.4%). Supplemental irrigation increased gin turnout slightly, but had no significant impact on final lint yield. Through this study, we hope to identify accessions and management practices for a Pima breeding program targeted for South Carolina.

P-90

Use of Oxford nanopore genome sequencing technology towards diagnostic marker development and dissection of disease resistance in sweet corn

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Georgia and Florida make up almost 75% of the total fresh market sweet corn acreage in the Southeastern (SE) U.S. Southern and Northern Corn Leaf blight are foliar diseases caused by closely related ascomycete fungi, *Bipolaris maydis* and *Exserohilum turcicum* that threaten yield losses every year. Developing resistant cultivars requires both introgression of resistant germplasm and understanding how fungal pathogens adapt and evolve to cope with pest control management strategies. Here, we present a systematic screen of diverse sweet corn germplasm for corn leaf blight resistance. This project emphasizes the importance of field plot design and inoculation procedures for an accurate readout of disease resistance. This information will serve as the basis for quantitative genetic studies aimed at dissecting quantitative disease resistance. Additionally, the *de novo* long read assemblies of two fungal isolates are presented: *A B. maydis* isolate from Live Oak, Florida and a *E. turcicum* isolate belonging to highly virulent race 23N. This sequencing project highlights the combined power of Illumina and Nanopore technologies to quickly generate cost-efficient, accurate, and near-complete *de novo* assemblies of microbial pathogens. Characterization of fungal populations inform breeding of resistant germplasm specifically adapted to growing region in the SE. Initial stages of marker development for both fungal and maize populations are explored for molecular diagnostic testing. Ultimately this information will accelerate introgression into elite sweet corn lines well adapted to the SE with quantitative disease resistance.

P-91

Evaluating TOMI for foliar pathogen in Pacific Northwest

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TOMI (Tomato Organic Management and Improvement) Project is a multistate, interdisciplinary project developing an integrated approach to manage foliar pathogens while allowing growers to deliver tomatoes to farmers. TOMI aims to meet the needs of organic growers by focusing on three main concepts; 1. Selecting Improved tomato varieties in organic systems, 2. Facilitating expression of induced systemic resistance, 3. Identifying effective organic fungicides and biopesticides. OSU Vegetable Breeding Program focused on the first concept, selecting improved tomato varieties in organic systems. The objectives were to select new indeterminate organic tomatoes, and quantify stability of genotype performance across variable environments. The experimental material was screened alongside commercial varieties in IN, NC, OR, and WI over four years. The year 2019 was the last year for TOMI I, Vegetable breeding program TOMI field trial contained 16 F3 families and 4 checks of Indeterminate Tomato Varieties. Tomato varieties were evaluated for defoliation from Early Blight (*Alternaria solani*) and Late Blight (*Phythophotora infestans*) once every week. Fruit was harvested once first ripe was observed weekly, and data was only collected for second, third, and fourth week. Fruit was sorted into marketable and unmarketable recording weight and number for each plot. Two lines, IN 1736 and one NCSU 1720, had the highest number of marketable fruits compared to unmarketable fruit. IN 1761, IN 1723, and OR 1764 lines had the highest marketable compared to unmarketable weight. Wisconsin and NCSU selected lines were more susceptible to early blight throughout field trial. Oregon lines had the least amount disease severity from both early blight and late bright throughout the four weeks. Fruit tasting was performed for all the tomato varieties, 2 OR, 1 NSCU and 1 WI lines had good tasting rating overall. Seed was saved from the best performing field plots from each site, IN, NC, OR and WI, and seed will be used for another round of crossing and selfing in 2020.

P-92

Evaluation of self-compatibility in 10 highbush blueberry cultivars by controlled crossing in greenhouse

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Self-incompatibility (SI) is the condition where pollen grains of one plant cannot fertilize the ovule(s) of the same plant to produce a viable embryo(s). SI in the plant species is under strict genetic control. Although the mechanism of self-fertility greatly varies across most flowering plants, a large number of shared structural similarities exists among them. The SI in blueberries varies from partially self-fertile (Highbush blueberries) to complete self-incompatible (low-bush blueberries). To achieve a higher pollination rate, and hence a higher fruit production, blueberry growers are required to grow patches of different cultivars in their field and complement the pollination process with several beehives to provide enough pollinators. Introduction of the self-fertility trait in the blueberry cultivar will reduce the production cost to growers by eliminating the obligatory outcrossing conditions. In this project, we studied the variation in self- and cross-fertility in four Northern Highbush, four Southern Highbush cultivars, and two advance selection lines at NC State University. A set of ~ 100 flowers from each genotype was hand pollinated with the pollen of the same plant while another set of ~100 flowers was pollinated with the pollen from a different cultivar. The self-fertility score for each cultivar was determined in terms of percentage of successful fruit set, fruit weight, fruit size, and the number of seed development. Our initial analysis shows that the Northern Highbush cultivar 'Duke' is highly self-fertile with the self/cross ratio of 1.14, 0.87, and 0.92 for each of percentage fruit set, fruit size, and fruit weight, respectively. Similarly, the advance selection line 'NC3104' of the Southern Highbush blueberry was performed better than other cultivars with the self /cross ratio of 0.70, 1.01, and 0.93 for the percentage fruit set, fruit size, and fruit weight, respectively.

P-93

Characterizing value-added QTL from wild soybean for enhancement of germplasm resources

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Current U.S. soybean (*Glycine max* (L.) Merill) cultivars have relatively low genomic variation which could constrain genetic improvement for grain yield, seed quality, and other agronomic traits. In both public and private soybean breeding programs, the introgression of wild soybean (*Glycine soja* Siebold & Zucc.) genes has been utilized to incorporate novel genetic diversity. In our study, the soybean cultivar Osage was crossed with a wild soybean line, PI593983, which was then advanced to create a recombinant inbred line (RIL) population for quantitative trait loci (QTL) mapping of seed composition traits. Two seed compositional QTLs were identified by linkage analysis to be associated with protein and oil content. The objective of this research is to identify candidate genes controlling protein and oil content corresponding to two soybean QTLs. In 2018, approximately 3,500 single RIL soybean plants, corresponding to two residual heterozygote lines for the two QTL, were examined by multiplexed Next-Gen PlexSeq, a next generation sequencing analysis. Twenty-eight SNPs were used to select 120 near-isogenic lines which were unique recombinants for the QTLs of interest. A greenhouse study with these 120 recombinant residual heterozygote derived near isogenic lines (RHD-NILs) was conducted during the winter and spring of 2018. Seed were examined via near-infrared spectroscopy (NIRS) using a DA 7250 Perten for prediction of protein and oil content. In 2019, 120 RHD-NILs were planted in hill plots at two locations (Columbia, MO and Novelty, MO), with two replications in a randomized complete block design. Using the 6K BeadChip array, candidate genes for protein and oil will be identified. Wild soybean genes can be a powerful resource for enhancing soybean cultivars and germplasm resources.

P-94

Gene expression profiling of heat stress tolerance in blueberries

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Blueberries, an increasingly popular super food with numerous health benefits requires specific temperature conditions for optimal growth. Extreme temperatures and rapidly changing climate's pose a threat to all plants, but those with narrow temperature thresholds, like blueberries, will be drastically affected without human intervention. Prolonged exposure to elevated temperatures reduces fruit production by stunting or killing blueberry plants. Some species of blueberries are more temperature tolerant than others, identifying phenotypes and genes associated with heat stress tolerance is an initial step to understand plant molecular mechanisms involved in tolerance to harsh temperature conditions. As of now, limited literature is available on identifying genes associated with heat stress tolerance through mRNA sequencing in blueberries. Many commercially available blueberries are derived from multiple species. In this study we are focusing on divergent diploid species. *V. darrowii* an evergreen southern shrub and *V.corymbosum* a deciduous northern highbush. Treatment conditions and sampling time points were determined using commercial varieties with mixed genetic backgrounds. Catalase concentration, stomata, and chloroplast integrity were assessed as indicators of successful stress. Based upon these results two *V.corymbosum* and two *V.darrowii* plants were exposed to 45°C over a 9 hour period, and leaf samples were collected at 0,6 and 9hrs. Illumina sequencing Yielded 99,093 and 109,193 total assembled genes respectively, both species share high metabolic pathway enzyme and protein processing in endoplasmic reticulum gene enrichment pathway activity. Uniquely, *V.corymbosum* has more expressed gene enrichment pathways and a higher number of expressed genes than *V.darrowii* which has fewer differentially expressed genes but more biosynthesis pathway activities.

P-95

Adaptation to agro-climatic conditions fashions grain characteristics of Ethiopian sorghum landraces

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Sorghum is a significant source of nutrients for people living in drought-affected areas of the world. The crop, unlike other major cereals, has a naked kernel which is vulnerable to biotic and abiotic conditions. This study was based on the hypothesis that grain physicochemical characteristics confer to the fitness of sorghum adaptation to diverse bioclimatic conditions existent in the country. The objective of this study was to assess the association of grain physicochemical parameters of the diverse Ethiopian sorghum landraces with genotypic factors and, bioclimatic conditions from where these landraces originated. The study utilized 369 Ethiopian sorghum landraces genotyped using Genotyping By Sequencing (GBS) and evaluated for different physicochemical characteristics, directly and indirectly, using Near Infrared Spectrometry (NIRS). After Bonferroni correction for multiple tests, Spearman correlation analysis between principal components (PCs) of NIR and bioclimatic factors revealed significant ($P<0.01$) association related to levels and variability of both temperature and precipitation. These associated PCs were also found to significantly ($P<0.01$) be correlated to presence or absence of tannin in the kernel, endosperm virtuousness, and hundred seed weight. Some of the genetic loci associated with grain physicochemical attributes were also found to be associated to bioclimatic factors. The bioclimatic factors exerted their influence likely through either direct selection pressure on kernel characteristics or, by affecting the length of the growing season and, overall photosynthetic efficiency of the crop. The result may be used for the improvement of kernel quality.

P-96

A high-throughput method for flavor phenotyping using metabolomic selection

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Although a staple in cuisines globally, commercial fruit varieties have become considerably less flavorful. Due to the cost and difficulty associated with flavor phenotyping, many breeding programs have long been barred from selecting for this complex trait. To address this issue, we leveraged targeted metabolomics of diverse tomato and blueberry accessions and their corresponding consumer flavor panel ratings to create statistical and machine learning models that can predict sensory perceptions of fruit flavor. Using these models, a breeding program can assess the flavor rating for a large number of varieties, which is traditionally limited by the low-throughput and high cost of consumer sensory panels. The ability to predict consumer ratings of liking, texture, sweet, sour, salty, bitter, umami, and flavor intensity was evaluated by a 10-fold cross-validation and the accuracies of 17 different models are assessed. The best performing models were used to infer the sugars, acids, and volatiles that contribute most to each flavor attribute. The prediction accuracies were high for most attributes in both blueberries and tomatoes. We hope these models will encourage the selection of more flavorful fruit varieties by helping breeders to assess flavor attributes at the breeding program scale.

P-97

A suite of CRISPR/Cas9 based gene editing tools tailored for switchgrass genetics

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CRISPR/Cas9 technology has become the genome editing tool of choice in almost all kingdoms of life, including protists, fungi, animals and plants. Our aim is to develop an efficient and predictable gene editing system for switchgrass (*Panicum virgatum* L.). Switchgrass has been recognized as an important biomass resource of fermentable mixed sugars that can yield biofuels and other value-added chemicals and biomaterials. Being able to fine-tune switchgrass metabolic capabilities via CRISPR/Cas9 gene editing would be extremely useful to exploit its potential. However, switchgrass is an allotetraploid. Furthermore, its two subgenomes show extensive gene duplication, which makes the identification of unique gene-specific targets very challenging. Fortunately, since CRISPR/Cas9 system was first described, a suite of Cas9/Cfp1 proteins with diverse size, activity, recognition target site and trans-activating crRNA (scaffolds) have been characterized. By exploiting the wide range of target specificities of the available Cas9/Cfp1 proteins, we are developing a platform that will allow editing any gene of interest in switchgrass. The ultimate goal is to ensure the editing of all copies in the switchgrass genome. As a first step, we have tested five different Cas9/Cfp1 proteins (SpCas9, SaCas9, St1Cas9, Mb3Cpf1, and AsCfp1) in embryogenic rice calli from Taipei-309, aiming to transfer the knowledge acquired in the rice model system into switchgrass. Also, all protein combinations are being tested both at 37°C (optimal temperature for most Cas9/Cfp1 proteins) and 27°C (optimal temperature for tissue culture) to assess rate of editing under standard tissue culture conditions. Our preliminary results suggest that St1Cas9 protein at both 27°C and 37°C yields the best editing efficiency and these are the chosen conditions that we will further explore in switchgrass.

P-98

Integrating crop modeling into genome wide family prediction in alfalfa (*Medicago sativa*)

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Alfalfa is the most grown perennial forage legume in the world because of its high yield potential and forage quality, stress tolerance capability, and biological nitrogen fixation ability. Forage production must be increased by the next few decades to meet up the demand for beef and livestock production. Forages are one of the most important crops in Florida. However, alfalfa production has not been reported in the state possibly due to the lack of adapted germplasm. The aim of our research is to construct GWFP (genome-wide family prediction) models incorporating genomic and crop growth model (CGMs) data to predict the performance of alfalfa breeding lines for complex traits and make selections aiming at cultivar development. Conventional breeding takes a long period of time to release perennial cultivars. The GWFP approach incorporates statistical, genomic and computational tools to accelerate cultivar development. To imply this, we are creating a large and genetically diverse alfalfa training population. In addition, we are applying CGMs to represent the impact of the functional relationship between plant physiology and environmental condition. It will help us to explain the impact of G×E and a certain type of additive gene effects on the expressed phenotype. The CROPGRO perennial forage model (PFM), which has been recently updated for alfalfa, is being used in our research. The combination of GWFP and CGMs would potentially enable us to predict the performance of complex traits accurately, resulting in substantial increases in genetic gain rates, by early selection in a perennial crop.

P-99

Understanding ploidy levels in the *Abelia* genus

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Abelia is a genus of flowering woody shrubs with high ornamental value. Few species and cultivars are available commercially and these are mostly sports of *Abelia xgrandiflora*. Despite the diversity of the genus, no genetic information is available and most ploidy levels are unknown. The aim of this study is to estimate ploidy levels and genome sizes by flow cytometry in the species *Abelia chinensis* (three accessions), *Abelia engleriana, Abelia floribunda, Abelia xgrandiflora, Abelia schumanii* and *Abelia serrata*, the hybrids 99-1-1 (*A. chinensis* x A. 'Edward Goucher'), 99-6-7 (A. 'Edward Goucher' x *A. chinensis*), and 99-6-11 (A. 'Edward Goucher' x *A. chinensis*), and the cultivars A. 'Edward Goucher' (*A. chinensis* x *A. schumannii*), A. 'Francis Mason' (sport of *A. xgrandiflora*) and A. 'Raspberry Profusion' (A. 'Edward Goucher' x *A. chinensis*). A CyFlow© Ploidy Analyser (Sysmex TM) was used to evaluate genome size with propidium iodide as a stain. Genome size and ploidy levels were estimated using *Raphanus sativus* 'Saxa' and *A. xgrandiflora*, respectively. *A. engleriana*, two accessions of *A. chinensis*, A. 'Francis Mason', *A. xgrandiflora, A. schumannii, A. serrata,* and the hybrids 99-1-1, 99-6-7, and 99-6-11 have a genome size of approximately 0.89 to 0.93 pg of DNA and the same ploidy level as A. xgrandiflora. (2n=4x=32). One accession of A. chinensis presented inconclusive results. Abelia floribunda has a genome size two times larger, approximately 1.92pg of DNA, and stomata significantly larger than the other *Abelia* species, with exception of *A. engleriana*, suggesting a ploidy level greater than 4x. This needs to be confirmed with chromosome counts.

P-100

QTL discovery for resistance to a devastating sweet potato pathogen: Combating *Fusarium oxysporum f.* sp. *batatas* at the frontlines

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Vascular wilts are devastating pathogens in numerous high value crops around the world. At this time, a wilt of banana caused by *Fusarium oxysporum* f. sp. *cubense* is likely the most commonly known due to its impacts on the popular banana variety, 'Cavendish.' It severely threatens the immediate and, potentially, long term trajectory of the banana industry as we know it. Alternatively, in sweet potatoes, (*Ipomoea batatas*) Fusarium wilt (*Fusarium oxysporum* f. sp. *batatas* (FOB)) has been of little concern to farmers in recent memory. This lapse in awareness is owed almost wholly to backcrosses with resistant lines discovered in the 1970s, followed by stringent disease screening of varieties intended for release. As evidenced by the current state of the banana industry, sweet potato researchers must stay vigilant in developing diverse sources of resistance to FOB in case the pathogen overcomes current resistance mechanisms. In recent years additional funding sources, decreased sequencing costs, and advances in bioinformatics have allowed for an expanded role and focus on genomic studies in sweet potato and its relatives. Amidst this opportunity we developed this study using genotyping by sequencing (GBS) to identify single nucleotide polymorphisms with the goal of discovering quantitative trait loci (QTL) responsible for resistance to FOB. The mapping population used consists of 413 genotypes from a cross between a resistant line ('Covington') and a susceptible line ('NCDM04-0001'). Seven separate experiments were conducted under controlled greenhouse conditions. After analysis of the combined data, our results to date have uncovered two QTL responsible for 14% and 10% of observed variation in FOB infection among our mapping population. With supplementary statistical analysis we expect to uncover additional QTL allowing us to further explain our results. Going forward we intend to use these results to expedite the selection of FOB resistant sweet potato germplasm.

P-101

Towards a methodology to improve somatic embryogenesis and transformation efficiency in switchgrass (*Panicum virgatum* L.): Overexpression of *baby boom* and *Wuschel2* Genes

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Genetic transformation of switchgrass (*Panicum virgatum* L.) is important in the incorporation of value-added traits, especially those leading to production of lignocellulose-derived biofuel. This process can take between 18 and 31 weeks starting from callus induction until regeneration of a transgenic plant. The overexpression of transcription factors *Baby Boom* (*Bbm*) and *Wuschel2* (*Wus2*) is a method to improve monocot transformation. *BBm* and *Wus2* stimulate the rapid development of embryogenic callus from embryogenic and non-embryogenic tissue, improving the efficiency of transformation. Looking for readily available explant tissue, leaves and culms from switchgrass *in vitro* grown plants were evaluated in terms of the efficacy to form callus. Callus formation was observed from culms, specifically in the area spanning from the proximal end (culm-root junction) to the middle zone of the distal region. Five culture medium for callus induction were tested. Two weeks later, between 2.2 and 7.41% of the culm´s surface was capable of forming callus. Medium based on N6/B5 salts and vitamins induced a better response. Callus type I is predominant (79.48%) regarding type II (20.5%). Additional helper plasmid in Agrobacterium can improve the efficiency of transformation. Extra copies of vir E and G genes will be included in LBA4404 strain by transforming with helper plasmid pCH32. Transformation of Agrobacterium with pAS1305, which contains *GusPlus* marker gene and *Arabitol dehydrogenase* as selectable marker, would allow us to evaluate the efficiency of transformation in leaves and culms. To overexpress Bbm and Wus2, plasmids were constructed that contain those genes from *Zea mays*, regulated by plant promoters ZmUbipro and OsE1F5pro, which have high and low levels of expression, respectively. Once *BBm* and *Wus2* induce regeneration, their continued expression is detrimental. Therefore, desiccation-inducible CRE mediated excision was included to allow for excision of the cassette containing *Bbm* and *Wus2* before regeneration of plants.

P-102

Developing a cost-effective strategy for implementing genomic selection in a soybean breeding program

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A successful breeding strategy for prediction of soybean yield that is based on resource allocation will open many opportunities for enhancing productivity in soybean breeding programs. Genomic selection (GS) has great potential to increase the efficiency of plant breeding and is already successful in most private and animal breeding programs. Recently, genomic selection methodologies have catalyzed the reorganization of plant breeding programs thus increasing their genetic gains while reducing time and cost. While GS has great potential to increase the efficiency of plant breeding, breeders are still struggling to identify the best strategy to deploy genomic selection in a conventional breeding program. Making decisions on plant breeding programs require plant breeders to be able to test different breeding strategies. However, it is difficult for plant breeders to determine an optimal breeding strategy considering all crucial factors affecting crop genetic improvement. The objective of this study was to evaluate expected genetic gain for alternative breeding strategies enabled by genomic selection. We will present our work on developing breeding strategies using stochastic simulations to integrate genomic selection into a soybean breeding program considering problems related to resource allocation and rapid cycling.

P-103

Developing a Solo papaya for South Florida

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Papaya is one of the most popular tropical fruits worldwide, and a valuable component of South Florida's diverse agricultural economy. The recent deregulation of University of Florida's papaya ringspot virus (PRSV)-resistant line, X17-2, has stimulated increasing interest from local growers. With a source of PRSV resistance available, the breeding program at University of Florida is now free to target other traits key to the success of a new papaya cultivar. In particular, we aim to develop new papaya varieties combining PRSV resistance and solo-type fruit characteristics, along with strong agronomic performance in South Florida's subtropical climate. Fruit quality targets include high soluble solids (> 12%), single-serving size (< 675 g per fruit), a pear shape, and an exquisite aroma devoid of off-flavors. An early objective of our program is to identify accessions for use as parents in pursuit of this ideotype. Towards this end, we have conducted a preliminary survey of twenty-one papaya accessions planted at the Tropical Research and Education Center (TREC) in Homestead, Florida in spring 2017. Throughout summer and fall of 2018, we collected field measurements and fruit samples for the characterization of both agronomic and fruit quality traits including plant height, fruits per tree, fruit weight, total soluble solids, titratable acidity, and aroma. Through this study, we have identified several promising accessions for further characterization and use in our breeding program.

P-104
GRID: A python package for aerial high-throughput phenotyping

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Aerial images have the potential for high throughput phenotyping agricultural experimental fields. Currently, the image analysis relies on either intensive framing manually, or tools requiring stringent structures. We developed a python package, GRID (GReenfield Image Decoder) to overcome these challenges. GRID has a graphical user interface to crop area of interest. Users can see the instant graphic results of tuning parameters such as number clustered objects, degree of noise reduction, and cutoff to balance overall and local structure. With map file, GRID automatically connects plot identifications to the recognized imagery plots. For each plot. the output includes the vertical and horizontal coordinates, the total number of pixels, average NDVI (normalized difference vegetation index based on either near Infrared or regular RGB (red-green-blue) sensors. With GRID, users are completely liberated from manually drawing plot edges, or lines to define the image structure. The GRID executable file, user manual, tutorials, and example datasets are freely available at http://zzlab.net/GRID

P-105
Combining high-throughput phenotyping and GWAS to reveal temporal genetic variation in soybean biomass

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Traditionally, genetic mapping treats plant`s phenotypic traits as static points (i.e. measure once in the growing season). As a consequence, information regarding plant functioning and activation of genes and interacting gene networks at different stages of plant development and in responses to an environmental stimulus are lost. Biomass accumulation is a dynamic process that progressively occurs throughout plant development. High-throughput phenotyping (HTP) enables the screening of thousands of genotypes in multi-location field trials relatively effortless, making it possible to track biomass accumulation from images of the same experimental plot throughout the course of its life cycle. The objectives of this study are to develop an HTP methodology for soybean biomass phenotyping and to reveal the quantitative properties of temporal biomass accumulation in the context of growth analysis and dynamic trait dissection. For that, a random subset of 32 families from the SoyNAM panel, resulting in 384 lines, were grown in field trials in three environments. Weekly destructive biomass measurements of a small set of the panel were taken, as well as unmanned aerial platform-based multi-spectral imaging of the field up to 78 days after planting. The images were used to derive different reflectance vegetation indices and canopy coverage values to predict biomass accumulation. We used principal components analysis for all imagery features for dimensionality-reduction and selected the 8 first components in a linear model to predict biomass for each environment. We performed a 10-fold cross validation using ordinary least squares (OLS) to estimate the parameters. The average root mean square error (RMSE) for the 10-fold cross validation was 38.7, 115.6 and 112 for each environment. We estimated biomass for all the plots and we are performing a random regression for biomass accumulation over time.

P-106

Haplotype maps for the genetic dissection of parallel selection response to flowering time in a multiparent maize population

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Genetic diversity is fundamental to environmental adaptation and breeding for crop improvement. However, capitalizing on diverse germplasm is challenging because polygenic maladaptive phenotypes must be purged in order to uncover the genetic merit of an individual in a target environment. This can result in the loss of beneficial alleles that are strongly linked to unfavorable alleles. Therefore, understanding the genomic response to selection for adaptational traits is crucial for overcoming genetic barriers to crop improvement. We created a Tropical Synthetic (TropicS) population of maize from seven tropical inbred lines and performed parallel selection for early flowering time across a latitudinal transect (eight locations spanning from Puerto Rico to Wisconsin) for two generations. During each generation of selection and at each location, 384 individuals from the extreme tails in flowering time were genotyped via genotyping-by-sequencing (~12,000 total samples). Founder data was used to perform imputation with MACH (Li et al. 2010) and to infer ancestral haplotypes using RABBIT (Zheng et al. 2015). Simulation analysis was used to determine the accuracy of imputation and ancestral haplotype inference showing a success rate of greater than 82% across 25,000 markers. Reconstruction of founder haplotype blocks for each of the 12,000 samples will be used to explore patterns of recombination and determine founder contributions in selected populations. Ultimately, integrating genome-wide imputation, reconstruction of ancestry blocks and tests for selection will provide new insight into the response to selection. These analyses are ongoing and the latest results from this study will be presented.

P-107

Fruit characterization of Ecuadorian *Prunus serotina* subsp. *capuli*

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Prunus serotina (black cherry) is native to America and consists of five subspecies. Black cherry trees are found in forests throughout the U.S. and are known for their high-quality wood. Their fruits are small, with high astringency, making them unsuitable for human consumption. One of the *P. serotina* subspecies, known as subsp. capuli, is endemic to Ecuador and is characterized by larger, juicer, and tastier fruit. They have important nutraceutical values and are available in the Ecuadorian market. However, no commercial varieties of capulies are currently available. In 2016, 45 accessions (genotypes) of capulies collected from three main provinces in Ecuador were characterized for fruit weight and shape, endocarp weight and shape, and °brix. The weight of three replicates of 10 fruits and 10 endocarps of each accession were measured. Diameter and height for five fruits and five endocarps of each accession were measured. °Brix for five individual fruit representatives of each accession were also quantified using a handheld refractometer. The accession PserTU48 had the largest average weight of 4.4 g per fruit and PserCH90 had the smallest average weight of 0.7 g per fruit. PserTU77 had the largest endocarp with an average 0.48 g per fruit and PserCH90 had the smallest with an average 0.17 g per fruit. °Brix was found to be the highest for PserCH112 (30.1) and lowest for PserCH113 (14.4). Strong correlations were observed between fruit and endocarp for weight ($r=0.78$, $P<0.001$), diameter ($r=0.78$, $P<0.001$) and height ($r= 0.79$, $P<0.001$). °Brix was independent of fruit and endocarp height, diameter and weight. This research is an important first step towards determining capuli's potential and adaptability to the Southeastern U.S. and selection of valuable genotypes with commercial characteristics to lay the foundations of their breeding program.

P-108

Major gene for resistance to root-knot nematode sustains yield response under high nematode pressure

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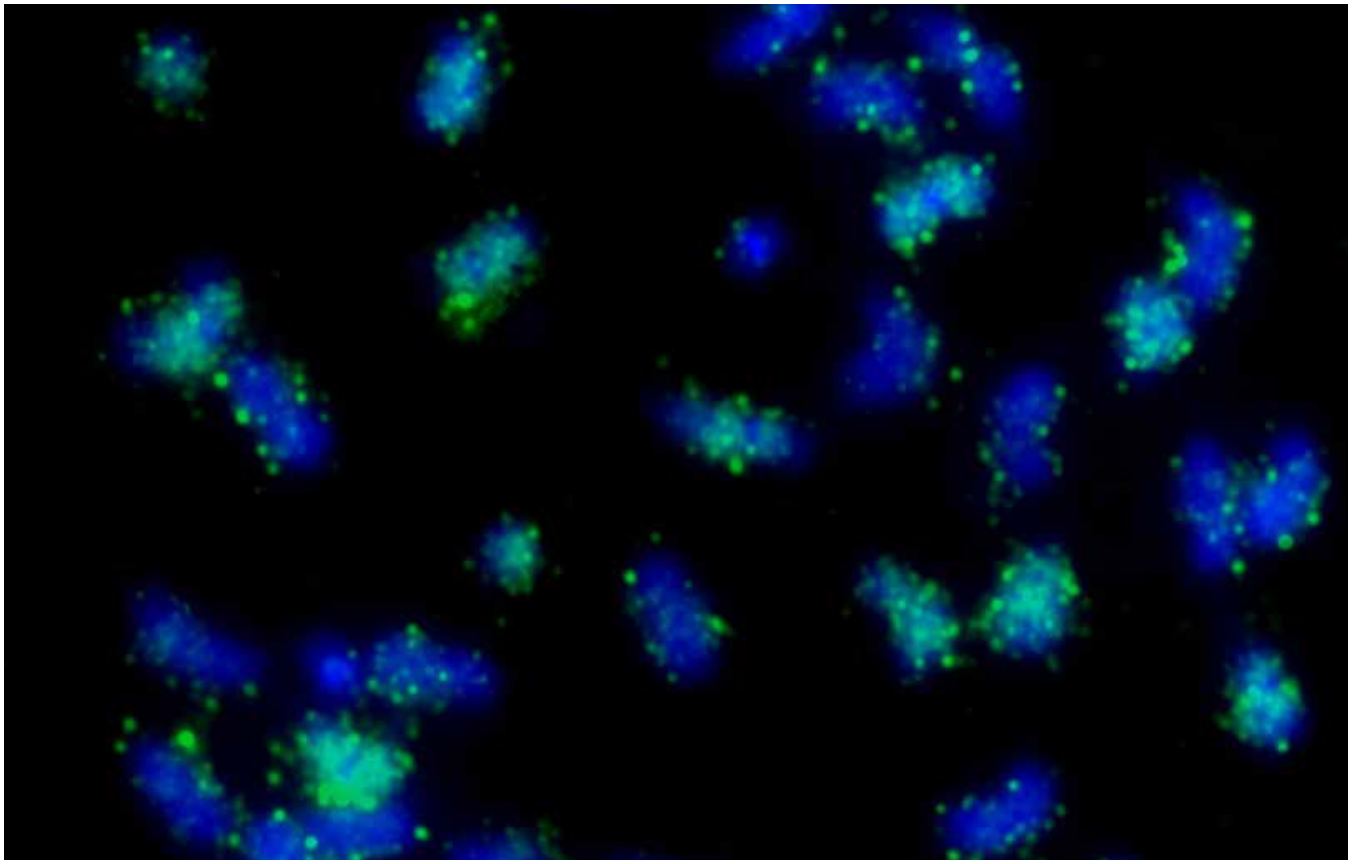
Southern Root-knot nematode (RKN) causes major damage in soybean in Southern United States, resulting in an estimated yield suppression of 12 million bushels in 2017. Besides crop rotation, management relies on the use of resistant cultivars. PI 96354 has been the major source of RKN resistance used in cultivar development. In this study, we evaluated performance of 93 high-yielding elite lines developed at the University of Missouri. The lines were genotyped and phenotyped for RKN resistance, and tested for yield performance at three locations: one RKN-infested and two RKN-free environments, in three replications per location. Under RKN pressure, resistant lines yielded 12.5 bu/ac more than susceptible lines. Resistant and susceptible genotypes did not show significant difference in yield under RKN-free environments. To quantify RKN population density, soil samples were collected at reproductive stage R5 from each yield plot and enumerated for RKN. RKN population densities ranged from 15 to 8,490, with an average of 1,850 juveniles/100cc soil per yield plot. In resistant lines, various RKN pressure did not affect yield. All lines were genotyped using KASP assays to detect QTL located on chromosome 10 and 18. The majority of RKN resistant lines carried the resistance allele on chromosome 10 and none carried the resistance allele on chromosome 18. We conclude that resistance gene/QTL on chromosome 10 is able to secure yield under high RKN infestation for now, although more genes may be required to combat the disease in the future.



FISH of a fragment of FIDEL, one of the most abundant LTR retrotransposons in the peanut genome.

P-109

Evaluation of fruit quality-related traits in a diversity panel of blueberry (*Vaccinium corymbosum*)

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Genetic gain in blueberry (*Vaccinium* spp.) through methods of conventional breeding is unable to keep up with consumer and grower-driven desires for the future of blueberry fruit. New strategies are required to develop advanced breeding methods to accelerate the cultivar development process and capitalize on traits in native *Vaccinium* species. The objectives of this research are to evaluate a diversity panel of 237 clonally replicated tetraploid accessions and cultivars for plant and fruit characteristics and to further genotype the studied accessions for identification of markers associated with the phenotypic traits of interest, a.k.a. genome-wide association mapping (GWAS). Identifying markers associated with key phenotypic traits for population improvement advances blueberry plant breeding by enabling early generation testing for target traits, thus minimizing excess expenditures in bringing undesired progeny to maturity. Phenotypic traits included plant characteristics such as flowering time, fruit ripening time, as well as fruit characteristics like fruit weight (FW), color, firmness, size, texture, percent soluble solids (SS), acidity, pH, and anthocyanin content. A random sample of fruit from each genotype was collected weekly and processed immediately for fresh fruit characteristics from each replicate for a minimum of three weeks. Preliminary data showed that the FW ranged between 0.097 g and 3.211 g; and fruit firmness ranged from 95.32 to 245.67 g/mm2. Fruit firmness had a significant negative correlation to weight, size, SS content, and % acidity ($p<0.0001$). Fruit weight had a significant and negative correlation with both SS content and % acidity, at $p<0.0001$ and $p<0.05$, respectively. While accessions exhibited significant differences in luminescence (*L) and chroma values ($p<0.0001$), these characteristics of fruit color were not correlated with any other phenotypic trait of interest. These preliminary data illustrates the immense variation that exists in our diversity panel.

P-110

Evaluation of wild peanut (*A. ipaënsis* x *A. correntina*) synthetic tetraploid-derived materials to fall armyworm

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Fall armyworm (FAW), *Spodoptera frugiperda*, is an economically devastating, emerging pest in Sub-Saharan Africa. FAW has rapidly spread throughout Africa after it was first reported there in 2016. This pest feeds on more than 80 plant species, including maize, peanut, and sorghum, and it threatens the food security of millions of people in Sub-Saharan Africa who rely on these crops. An integrated pest management strategy including resistant crops is needed to control FAW, since FAW populations developing insecticide resistance have been reported. For peanut, breeding cultivar resistance to FAW is limited by the narrow genetic base of this species. Lynch et al. (1981) identified the wild peanut relative *Arachis correntina* as a donor source of FAW resistance. Our preliminary study supported this finding; the survival rate and development rate of FAW larvae (n = 120) reared on materials derived from crosses with *A. correntina* indicated it as a promising source of resistance. In this study, we tested diploid A. correntina accession 9530 and accession 9548, synthetic tetraploids [A. ipaënsis KG37006 x A. correntina 9530]^{4x} (*IpaCor*), and F_2 plants [*A. hypogaea* x (*A. ipaënsis* KG30076 x *A. correntina* 9530)^{4x}] for FAW resistance to identify priority materials for our breeding program. Replicated thrice (n = 300), 10 FAW larvae are reared on the listed materials and a susceptible control. We measure survival rate, 7- and 14-day larvae weight, days taken to develop from first-instar to pupa, and moth hatch rate. We identified all three synthetic IpaCor tetraploids as well as two *IpaCor* F_2 plants as potential donors of FAW resistance for breeding programs. Differing from the Lynch et al. (1981) study, this resistance appears to be donated from *A. ipaensis* and not *A. correntina*.

P-111

Patterns of LD decay, population structure, and selection signatures in Purdue bred soft red winter wheat population

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Understanding underlying population structure and genomic architecture of breeding germplasm is imperative to design promising breeding program. Small grains breeding program at Purdue University has dedicated resources to develop high-yielding and disease-resistant soft red winter wheat (SRWW) germplasm over the past decades. We genotyped 436 Purdue-bred SRWW lines using genotyping-by-sequencing (GBS) method, and developed ~15,000 single nucleotide polymorphism (SNP) markers. Population structure was studied using STRUCTURE program, showing that there exist four sub-populations within the breeding germplasm. Two North American sub-populations are associated with Truman and progeny of a cross between Indiana lines INW0411 and INW0412. The other two sub-population seems to be derived from exotic lines WHEATEAR and NIANG 7840. Fixation index (F_{ST}) showed signatures of selection for regions that involve *Vrn-A1* and *Fr-A2* in the two North American sub-populations. The sub-population associated with TRUMAN showed selection signature in a region that involves *Glu-D1* locus. We identified significant genomic regions selected in chromosome 2B in all sub-populations. All the sub-populations except the one associated with progeny of INW0411 x INW0412 seem to have been selected for stem rust resistant gene *Sr36*. Further analysis of signature of selection by using hapFLK method identified significant region in chromosome 5B. The region seems to be associated with *Vrn-B1* locus. This study provided an understanding of population structure and genomic regions selected via breeding.

P-112

Heterosis and combining ability for seedling and agronomic traits related to chilling tolerance in sorghum

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Early planting (starting mid-April) helps to extend sorghum growing season in the higher latitude temperate regions. However, average minimum soil temperature of 14.4°C and average minimum air temperature of 8.4°C adversely affects germination, emergence and early seedling growth. Low temperatures also pose serious challenges for the expansion of sorghum in the United States. Cold tolerance is a complex quantitative trait significantly influenced by environment. Hybrids form the backbone of sorghum production in the US. Therefore, it is important to understand the inheritance of seedling and agronomic traits related to cold tolerance and to select the most appropriate parental lines and hybrids with superior heterotic combinations for early planting. A field experiment with two treatments of early (April 15) and regular (May 25) planting was conducted in 2018 at Hays, Kansas. The study included 4 pollinators and 4 seed parents identified for cold tolerance, 27 newly developed hybrids and 3 checks (two lines: RTx430, SQR and one hybrid: Pioneer 87P06) were used to estimate standard heterosis, general and specific combining ability (GCA, SCA). Significant differences were observed among parents, hybrids and their interactions for most of the traits in both early and regular plantings except tiller number and leaf number in early planting. Four parental lines ARCH11170B, ARCH11192B, BTx645 and Redbine58B recorded high per se and GCA for the cold tolerant seedling traits. The hybrid ARCH11192A/ARCH10747-2R recorded high per se with significant heterosis and SCA for emergence percentage, emergence index, days to flowering and grain yield followed by other potential hybrids KS136A/ ARCH10747-2R, KS116A/ARCH10747-1R, KS116A/ARCH10747-2R, ARCH11201A/ ARCH10747-1R. The same field trials will be repeated in 2019 to validate these findings and move towards enhancing the genetic pool in sorghum to tolerant early season cold tolerance.

P-113

Impact of racial structure on genomic prediction of sorghum grain yield

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Marker effects calculated using prediction models can be used to estimate breeding values of genotypes using genome-wide markers. Population structure is an important factor that affects the accuracy of such estimated breeding values. The population structure in sorghum, resulting from genetic and morphological differentiation, has led to distinct racial types which can be classified into five major races (bicolor, caudatum, durra, guinea, and kafir) and their intermediates. To assess the impact of sorghum racial structure and diversity in genomic prediction, we conducted two cross validation (CV) experiments using genomic best linear unbiased prediction (GBLUP) model: CV1; proportional sampling from races, and 2) CV2; sampling from across race (AR) or within race (WR). The sorghum diversity panel with 389 individuals and 224,007 single nucleotide polymorphism markers were used. Grain weight was consistently the best predicted trait across all methods except AR. The prediction accuracy (*r*) for CV1 ranged from 0.52 to 0.69, but declined by 39% and 54% on average for WR and AR methods, respectively. We decomposed the total covariance of each trait in CV1 into expectations due to race and covariance due to individuals within the race. The contribution of race towards CV1 accuracy was large for grain and panicle traits whereas race was a bad predictor of plant height, as expected. Genomic heritabilities were positively correlated (0.63) with mean *r*, and within-subpopulation variance accounted for about 80% of total genetic variance. Prediction accuracy among races with higher proportion of allelic diversity and/or shared alleles is boosted by training population with higher genetic diversity despite poor genomic relationship, whereas genomic relationship outweighed genetic diversity among races with limited diversity and/or presence of unique polymorphisms. Therefore, training population design for a historically diverse and structured population in sorghum requires careful consideration of genetic structure of the testing population.

P-114

Mining QTL for elevated protein and sucrose contents from diverse soybean germplasm

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Soybean is a major source of seed oil and protein, with 60% of the value coming from soybean meal and the remaining 40% from oil. Due to the economic importance of these seed components, seed composition has become an important breeding goal. However, breeding for seed composition is challenging due to the negative relationship of protein with yield, and oil and sucrose content. The objective of this research is to identify the QTL conditioning the protein and sucrose contents. A RIL population derived from G00-3213 and PI594458A was developed and grown at two locations with two reps per locations. NIR results indicated that protein content of the RIL population ranged from 39.6 to 47.15% in Watkinsville, GA and 41.0 to 50.3% at Bossier, LA. Sucrose content ranged from 2.02 to 5.49% in Watkinsville, GA and 0.9 to 4.5% at Bossier, LA. Previously, BSA identified 6 regions conditioning elevated protein, and two for sucrose. After genotyping using the SoySNP6k BeadChips, QTL analysis revealed two significant QTL for protein content at the Watkinsville location and five significant QTL for protein and two for sucrose at the Bossier location. Three oil QTLs were identified across environments on chromosome 5, 10, and 11. The protein QTLs on chromosome 6 and 10 detected at Bossier location, as well as the protein QTL on chromosome 13 detected at the Watkinsville location had also been previously identified with BSA. These results can aid in marker development and introgression of QTL into elite germplasm.

2018 Soybean yield trials of UGA soybean breeding program.

P-115

Characterization of an inducible gene switch for reversible sterility

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Genetic engineering (GE) of plants to display once unachievable phenotypes provides immense capacity to further agricultural production and scientific research. A main concern regarding GE plants is transgene flow to non-engineered plants. One potential way to prevent this altogether is to create sterile plants. However, sterility renders the plants ineffectual for future breeding efforts. A reversible sterility mechanism utilizing inducible gene repression would guard against gene flow while permitting breeding efforts to continue. Previous studies used an ecdysone receptor (EcR) isolated from spruce budworm as a gene expression switch in planta. Here a novel form of the ecdysone receptor (DpEcR) from the non-plant pest Danaus plexippus is presented and analyzed for viability as a gene switch in rice. DpEcR was synthesized, placed in tandem with the rice transcriptional activator RF2a followed by a lexA DNA binding domain, and constitutively expressed. The 8X LexA DNA binding sequence was placed upstream of either the OsE1F5 or 35Smin minimal promoters to express the reporter gene GUSPlus. Two plasmids were cloned with this receptor/activator cassette containing either reporter cassette and transformed into rice calli under hygromycin selection. An ecdysone receptor agonist, methoxyfenozide, was added to the medium of selected rice calli events and calli were stained for GUS expression. A wide variety of phenotypes were observed ranging from the expected response to no response. Once this gene switch is further characterized it can be retooled for applications such as reversible sterility.

P-116

Revealing genetic architecture of physiological efficiencies controlling grain yield in soybean

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Grain yield (*GY*) production can be expressed as the result of three main efficiencies: light interception (*Ei*), radiation use (*RUE*), and harvest index (*HI*). Although dissecting *GY* through these three efficiencies is not entirely new, there is a lack of knowledge about the phenotypic variation, the genetic architecture, and the relative contribution of these three efficiencies on *GY* in soybean. This knowledge gap along with their laborious phenotyping prevents the active consideration of these efficiencies into breeding programs. This study aims to reveal the phenotypic variation, heritability, genetic relationships, genetic architecture, and genomic prediction for *Ei, RUE,* and *HI*. We evaluated a maturity control panel of 383 Recombinant Inbred Lines (RILs) selected from the soybean Nested Association Mapping (SoyNAM) population. Dry matter ground measurements along with canopy coverage (*CC*) from drone imagery were collected in three environments. Light interception was modeled through a logistic curve using *CC* as a proxy. The total above ground biomass collected during the growing season and its respective cumulative light intercepted were used to derive RUE through linear models fitting. Additive-genetic correlations, genome wide association (GWA) and whole genome regressions (WGR) were performed to evaluate the relationship between traits, their association with genomic regions, and the feasibility of predicting these efficiencies through genomic information. Correlations analyses considered three groups: all the data set, top 100, and bottom 100 yielding RILs to determine association as a function of the *GY*. Our results revealed moderate to high phenotypic variation for *Ei, RUE,* and *HI*. Additive-genetic correlation revealed a strong relationship of GY with *HI* and moderate with *RUE* and *Ei* when the whole data set was considered, but negligible contribution of *HI* on *GY* when just the top 100 was analyzed. The GWA analyses showed that *Ei* is associated with three SNPs; two of them located on chromosome 7 and one on chromosome 11 with no previous quantitative trait loci (QTLs) reported for these regions. *RUE* is associated with four SNPs on chromosomes 1, 7, 11, and 18. Some of these QTLs are novel, while others are previously documented for plant architecture and chlorophyll content. Two SNPs positioned on chromosome 13 and 15 with previous QTLs reported for plant height and seed set, weight and abortion were associated with *HI*. WGR showed high predictive ability for *Ei, RUE,* and *HI* with maximum correlation ranging between 0.75 to 0.80. Future improvements in *GY* can be expected through strategies prioritizing *Ei* for short-term results when using high yielding germplasm and *RUE* for medium-long term outcomes. This work is a pioneer attempt to integrate traditional physiological traits into the breeding process in the context of physiological breeding.

P-117
Exploring plant height plasticity observed in natural field environments

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Plant phenotypes are determined by genetics, environment, and their interactions. Phenotypic plasticity describes that a genotype behaves differently when exposed to different environments. When multiple genotypes are showing different levels of phenotypic plasticity, genotype by environmental interactions (G x E) are present. Unraveling G x E is crucial to understanding plant local adaptability, which can be utilized in breeding, and provide new solutions in times of climate change. Recently, we established a joint genomic regression analysis (JGRA) framework to dissect the complex flowering time plasticity observed in natural environments by leveraging an explicit environmental index. In this study, we hypothesized that plant height G x E interactions can be unraveled and explained in a similar manner. The objectives were to 1) uncover the patterns of sorghum plant height plasticity in diverse environments; 2) predict performance in new environments; 3) identify and dissect the genetic determinants to explain the observed G x E interactions. Our results showed that varied degree of plasticity in plant height of sorghum lines could be explained, modeled, and predicted with a biologically meaningful environmental index. High prediction accuracy was achieved by using this environmental index. The effects of three height QTLs changed dynamically across environments, contributing to the observed G x E. In conclusion, by combining environmental and genomic components, we were able to explain and predict sorghum plant height under natural field conditions.

P-118
Exploring a shared organ shape regulatory network in three solanaceous crops

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Shape of harvested organs in crop species is important for ease of harvest, processing, and shipping, and can limit supply in vegetables and other horticultural crops. Mounting evidence indicates ovate family protein (OFP) and Tonneau1 recruiting motif (TRM) genes interact to regulate organ shape similarly across plant species. We sought orthologous genes regulating the shape of multiple organs in multiple species, beginning with the harvested organs of crops in the family Solanaceae, which includes the tomato model organism for fleshy fruit development. Following a candidate gene approach, we performed marker-trait association tests with organ shape genes known from species including Arabidopsis and tomato on a population of F2 pepper plants segregating for fruit shape (n=178) and fruit weight (n=181), and a population of F2 potato plants segregating for fruit (n=155) and tuber (n=209) shape. We found a significant ($p<2x10^{-16}$) association between potato SlOFP20 ortholog marker genotype and tuber shape. Using comparative genomics, we identified a likely deletion allele with an organ-lengthening effect analogous to the large deletion of the tomato SlOFP20 promoter. However, pepper orthologs of SlOFP20, SlOvate, and SlWUS were unassociated with fruit shape in our population. Instead, markers around another Ovate-associated TRM ortholog were significantly ($p=7.48x10^{-16}$) associated with pepper fruit shape. This suggests potential conservation of the TRM-OFP network as central to organ shape development across crop species. Progeny tests are ongoing to validate this gene's effect, along with genomic analyses to further explore functional genomic diversity in early vegetable domesticates.
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P-119
Optimal mating in *Pinus taeda*

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Loblolly pine (*Pinus taeda*) is the most important tree crop in the US, planted over 25 million acres in the south. The Tree Improvement Program at North Carolina State University manages the genetic improvement of Loblolly pine. Loblolly pine has a high genetic load and suffers greatly from inbreeding depression. It is a challenge to balance two important but contrasting goals of capturing as much genetic gain as possible while managing short- and long- term inbreeding. While methods and algorithms for animal breeding are well-established, an efficient algorithm suited to this species remains elusive. Developing an algorithm to design mating that optimizes genetic gain whilst putting constraints on relatedness is imperative for loblolly pine breeding. Towards this goal, we have adopted evolutionary genetic algorithms for optimized mating design and breeding. PineBreed is an optimization algorithm developed that can utilize pedigree-based relationships to create optimal mating list for breeding. Modified differential evolution algorithms have been applied to create mating lists that can be realized to give maximum return of genetic gain in future progeny while minimizing the increase in average co-ancestry in the population. Using the PineBreed software and optimizing the mating list from 964 monoecious loblolly pine tree candidates, resulted in 35% increase in genetic gain and no inbred progeny. The completion of this study will see the development of a suite of software that is able to not only utilize genetic relationships from pedigree but also utilize genomic relationships derived from SNP markers. The framework and methods adapted for loblolly pine breeding have relevance to breeding of other monoecies species as well.

P-120
Utilizing watermelon wild relatives for gummy stem blight resistance

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Gummy stem blight (GSB) is a major pathogen of watermelon globally. GSB is caused by three *Stagonosporopsis* species, *S citrulli, S. caricae,* and *S. cucurbitacearum*. Despite over 50 years of research, little progress has been made towards deploying resistance. The aim of this study is to identify QTL for resistance to GSB in watermelon wild relatives. Three mapping populations have been generated from crosses between elite watermelon cultivars and wild germplasm reported to possess resistance to GSB: 788 [Sugar Baby (*C. lanatus*, susceptible) x PI-189225 (*C. amarus*, resistant)], 792 [PI-526233, (*C. lanatus*, resistant) x Sugar Baby] and ZxD [ZWRM50 (*C. lanatus*, susceptible) x Delagoa (*C. amarus*, resistant)]. The $F_{2:3}$ progeny of the three populations will be inoculated with isolates of S. citrulli and S. caricae known to cause GSB. Population 788 was inoculated using isolate 12178A (*S. citrulli*) and kept at 100% humidity for 48 hours. Disease ratings were taken 7 days after inoculation, using a 0-10 scale. Phenotypic data from 788 shows that the population is segregating for GSB resistance, with the phenotypically extreme members of the population exhibiting resistance levels similar to either resistant or susceptible controls. Two bulks will be created using the 15 most resistant and susceptible plants and sequenced. Resulting reads will be aligned and analyzed in search of SNPs associated with GSB resistance. Identified QTL will be validated using KASP markers in a genetically distinct population. Identification of QTL associated with gummy stem blight resistance will enable marker assisted selection for this import trait.

P-121

Application of pedigree-based analysis (PBA) for QTL mapping in Clemson University peach breeding program

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The use of DNA information can improve selection efficiency through reduced generation intervals, thereby speeding up genetic progress. Identification of quantitative trait loci (QTLs) and development of DNA tests to inform parental and / or seedling selection have recently shown increased application in fruit breeding programs (www.rosbreed.org). Pedigree-based analysis (PBA) is an alternative way of mapping QTLs that uses multiple small populations connected in a pedigree to enhance the identification of important QTLs whose alleles segregate for a trait in or across breeding programs. PBA using FlexQTL™ software has the advantage of predicting QTL allele effects (QQ, Qq, qq) based on available genotypic and phenotypic information. Inconsistent quality of the peach fruit on the market has resulted in peach consumption decrease over the last decade. Thus, the main goal of Clemson University peach breeding program is to develop new cultivars that address consumer demands via utilization of DNA-information to efficiently plan crosses and select individuals with the most desirable traits. A pedigreed population of 351 accessions from the Clemson University peach breeding program was genotyped with 9K SNP array and phenotyped for fruit quality and productivity traits over two seasons. Here we present application of PBA for QTL mapping of two traits: ripening date (RD) and soluble solids concentration (SSC). A major QTL in the same genetic interval for both traits was detected on LG4, with eight SNPs selected for haplotype determination. A total of eight haplotype combinations with significant differences in traits values were identified. Favorable QTL alleles were detected for RD and SSC and a KASP test was developed. The newly developed KASP Ppe Mat/brix DNA test, targeting the major QTLs for RD and SSC is being evaluated for prediction accuracy. The results obtained from FlexQTL and the KASP test development will be presented.

P-122

Dissecting the QTL near the Pb gene on chromosome 15 for resistance to caterpillars in soybean

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Caterpillars are important pests of soybean in the Southern United States and in South America. The use of resistant cultivars can reduce caterpillar damage. Accordingly, a particularly resistant combination of QTLs, known as M and E, is being bred into elite lines. QTL-E is on chromosome 15 and is associated with the *Pb* gene for sharp trichomes. While the gene underlying QTL-M on chromosome 7 appears to be involved with isoflavone metabolism, the mode of action of QTL-E is still unknown. The goal is to identify the gene for *Pb* and elucidate the resistance mechanism of QTL-E. The *Pb* allele from PI227687 was introgressed into Benning, and from Kingwa into Clark and Harosoy. QTL-E segregates with the Pb gene in all three sets of near-isolines, but 50K-SNP-chip genotyping cannot detect a common introgression region. GWAS on a panel of 166 lines consisting of the USDA G. soja core collection plus blunt-tipped genotypes identified a single SNP on chromosome 15. This SNP is within a monomorphic block of markers in the isolines derived from Kingwa, which contains two genes in linkage disequilibrium with the SNP, annotated as GL2 and bHLH transcription factors. Incidentally, these function in the pathway affected by the QTL-M gene. GL2 also regulates trichome shape in arabidopsis. Alternate alleles of a tandem repeat in an intron of GL2 consistently segregate together with sharp trichomes. Confirming the gene responsible for trichome shape will help determine if it is related to the resistance provided by QTL-E.

P-123

Enhancing legume transformation by altering host immune receptor–*Agrobacterium* interactions

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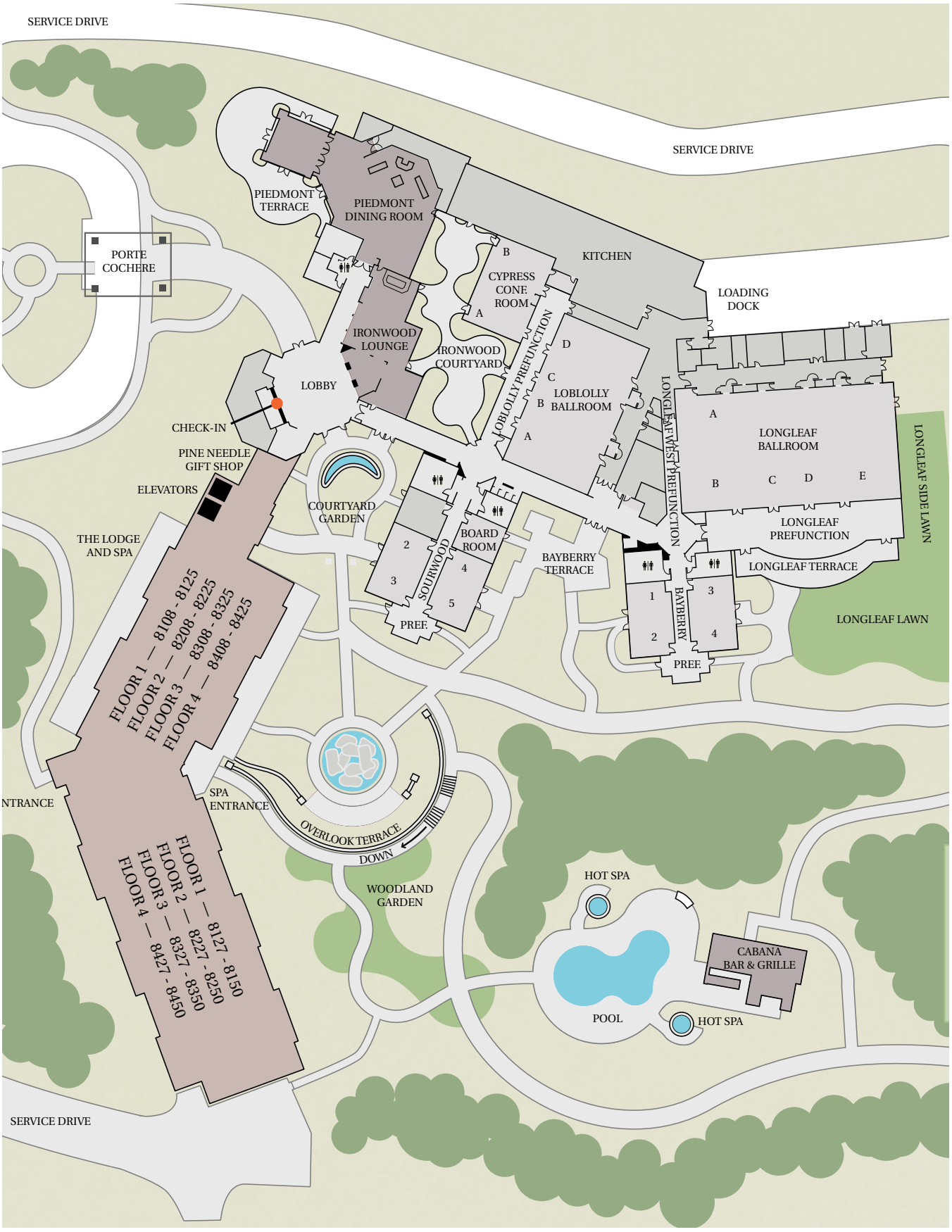
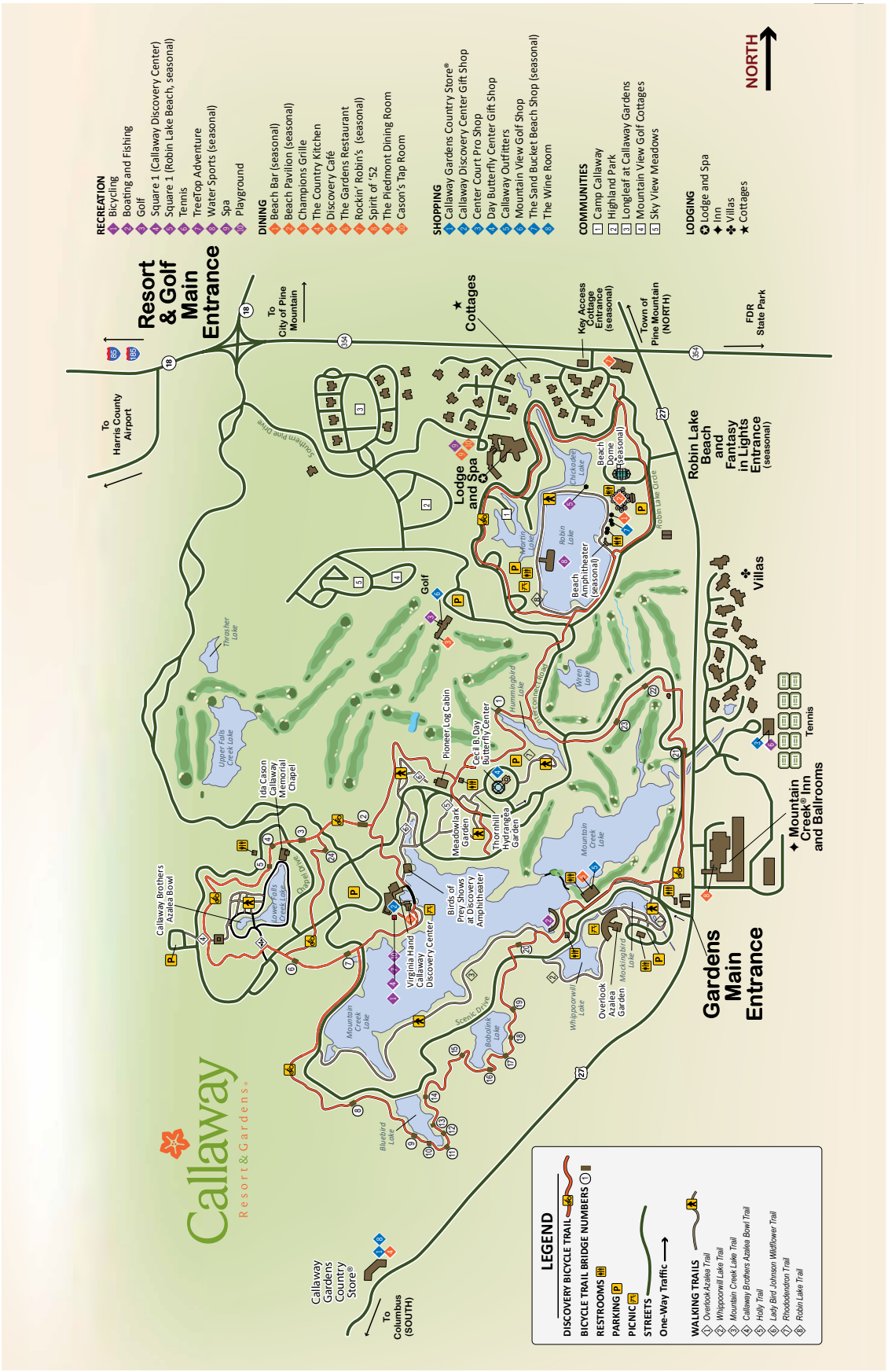
While *Agrobacterium tumefaciens* can deliver DNA to a wide range of plants, most soybean genotypes are recalcitrant to transformation because *Agrobacterium* elicits a hypersensitive response. Evading this host defense response in soybean would facilitate a wider range of soybean genotypes suitable for use in transgenic breeding programs. A search for soybean homologs of known plant-immunity-associated pattern recognition receptors (PRRs) identified a candidate gene, *Glyma.09g216400*, that was present in the *Agrobacterium*-resistant reference genome, but absent in the *Agrobacterium*-susceptible genome. Furthermore, this gene is the most similar homolog in soybean to the arabidopsis Elongation Factor – Thermo unstable receptor (AtEFR), known to restrict transformation in arabidopsis by recognizing the bacterial Elongation Factor – Thermo unstable (EF-Tu) protein of *Agrobacterium*. In addition, while most soybean is incompatible with *Agrobacterium*, most varieties form nodules with other rhizobia. Accordingly, a comparison of bacterial EF-Tu proteins found many changes between these species. Therefore, replacing *Agrobacterium's* EF-Tu with a homolog from compatible rhizobia could allow *Agrobacterium* to go undetected by soybeans possessing Glyma.09g216400, thus allowing *Agrobacterium* to transform most genotypes. Replacing the *Agrobacterium* protein with its ortholog from *Bradyrhizobium* through homologous recombination did not result in resistant genotypes being compatible. However, the new strain also failed to form a compatible interaction with the susceptible genotype, prompting more EF-Tu orthologs to be tested. In addition to testing new strains, future mapping of susceptible by resistant RIL populations, combined with genome-wide association analysis of more than one-hundred genotypes, will aid in identifying additional genetic factors inhibiting *Agrobacterium*-mediated transformation of soybean

CALLAWAY GARDENS CONFERENCE MAP



CALLAWAY GARDENS RESORT MAP



NOTES

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