National Association of Plant Breeders

NAPB

Improving Plants to Improve Lives

Annual Meeting 2023

July 16–20, Greenville, SC

Clemson University

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Ksenija Gasic (Clemson)

Todd Campbell (USDA-ARS)

Subcommittee chairs

Conference planning	Victoria Artigliere (Clemson)
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Pre-conference program	Ksenija Gasic (Clemson)
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Student engagement	Christopher Saski (Clemson)
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Co-chairs of 2024 NAPB meeting	J.D. Rossouw (Bayer), Martin Bohn (UIUC)
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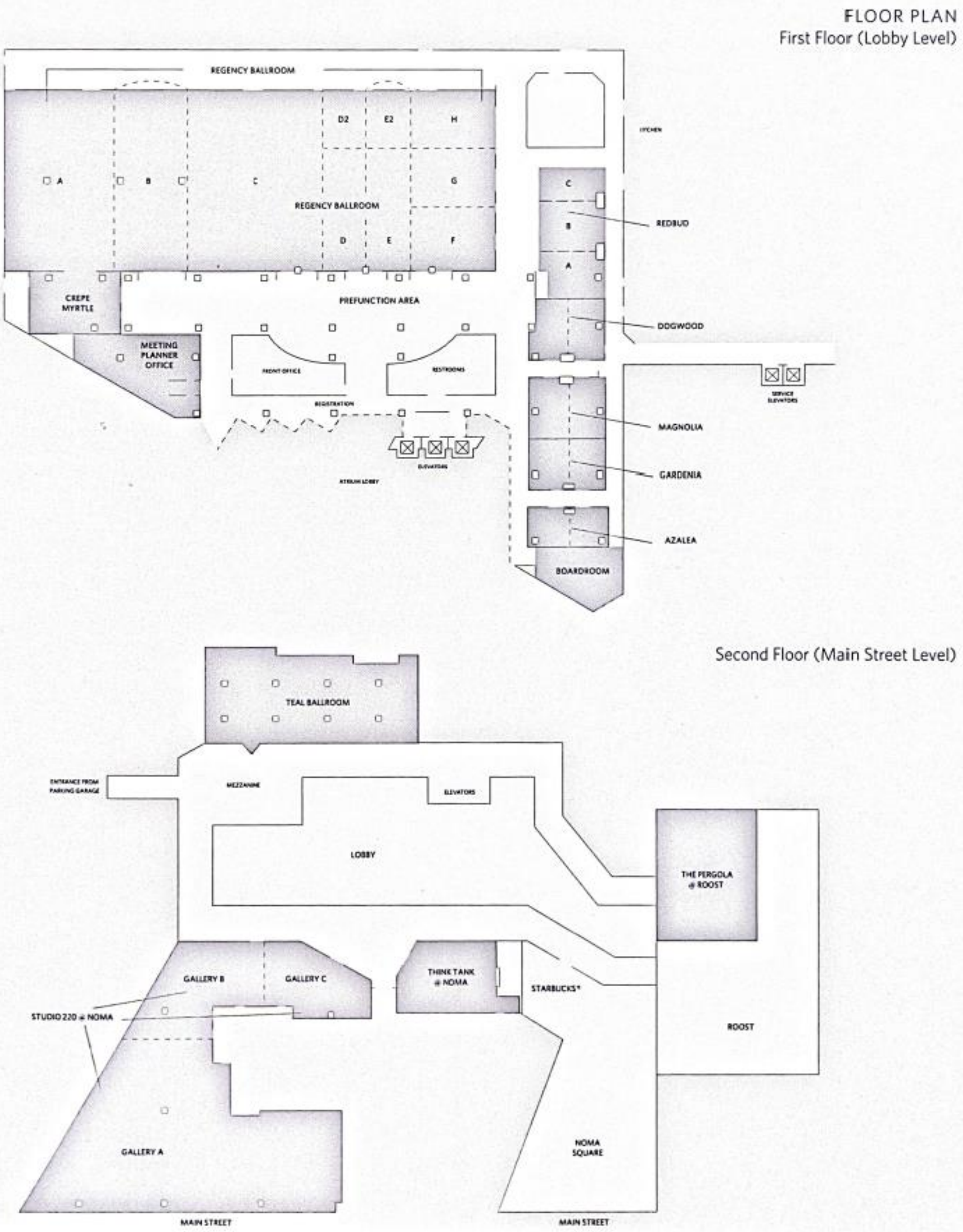
Poster sessions	Valerio Hoyos-Villegas (McGill)
Soft skills workshop	Masha Trenhaile (Bayer), Klaus Koehler (Corteva)
Breeders Tools workshop	Dorrie Main (WSU), Trevor Rife (Clemson), Moira Sheehan (Cornell)
NAPB committees/working groups	Kevin Falk, Mala Ganiger, Gurleen Kaur, Allen van Deynze, Plant and Environmental Sciences faculty, postdocs, and Graduate Student Association members (Foster Kangben, Harleen Kaur, Shalini Etukuri, Sonia Salaria, Daniela Moreno, Linus Schmitz, Mohit Goyal)

CONFERENCE CHECK-IN

DAY	TIME
Saturday	5:00 pm – 7:00 pm
Sunday	7:00 am – 9:00 am 5:00 pm – 7:00 pm
Monday	7:00 am – 9:00 am 5:00 pm – 7:00 pm
Tuesday	6:30 am – 9:00 am 5:00 pm – 7:00 pm
Wednesday	7:00 am – 9:00 am

Clemson highlights 1: Aerial snapshot of Clemson University main campus

Hyatt Regency Floor Plan



NAPB 2023 MEETING AGENDA

SUNDAY, JULY 16

WHEN	WHAT
8:00 am – 3:00 pm	**Graduate Student Soft Skills Workshop**, *Regency F, G & H*
8:00 am – 12:00 pm	**Breeding Tools Workshop** *Redbud*
1:00 pm – 4:00 pm	**Breeding Tools – hands on session** **BIMS -** *Teal* **Delta Breed –** *Redbud*
1:00 pm – 5:00 pm	**NIFA-AFRI Plant Breeding Project Directors Session** *Regency B, C, D, D2, E & E2*
2:45 pm – 3:05 pm	**Break**
6:00 pm – 9:00 pm	**Opening Session and Reception** Keynote Speaker: Hanna Raskin *Regency B, C, D, D2, E & E2*

Clemson highlights 2: Biosystem Research Complex at Clemson University houses several plant breeding laboratories.

MONDAY, JULY 17

WHEN	WHAT
6:30 am – 7:45 am	**Borlaug scholar and George Washington Carver scholar breakfast** *Studio 220 NOMA*
8:00 am – 9:30 am	General Session - 1 **The Crossroads of Food and Agriculture in the Southeast** Session Chair, Stephen Kresovich *Regency B, C, D, D2, E & E2*
8:00 am – 8:20 am	**Peter Coclanis** "The Ambiguities of Innovation: Agricultural Patterns and Processes in the Southeast, c1600-c1950"
8:20 am – 8:40 am	**BJ Dennis** "Seeds for Communities"
8:40 am – 9:00 am	**Glenn Roberts** "40 Days to Green Pizza from Where?"
9:00 am – 9:20 am	**Sandra Branham** "Genomics-enabled vegetable breeding for production in the Southeastern US"
9:30 am – 10:00 am	**Borlaug and GW Carver Scholar introductions** *Regency B, C, D, D2, E & E2*
10:00 am – 10:15 am	**Awardee Talk – Clayton Carley** 2022 PhD – First Place "Knowing Nodulation, Let's Dig In!" *Regency B, C, D, D2, E & E2*
10:15 am – 10:45 am	**Break**
10:15 am – 12.00 pm	**Poster Session 1 - Odd Numbered Posters** *Crepe Myrtle Regency A2*
12.00 pm – 1.00 pm	**Lunch – Speed Networking** *Regency B, C, D, D2, E & E2*

1:00 pm – 1:30 pm	**Awardee Talk - Jim Anderson** 2022 Public Sector Impact Award *Regency B, C, D, D2, E & E2*
1:30 pm – 2:45 pm	General Session - 2 **Culinary-driven Plant Breeding** Session Chair, Sandra Branham *Regency B, C, D, D2, E & E2*
1:30 pm – 1:50 pm	**Lane Selman** “Culinary Breeding Network: How working with chefs can impact your breeding program”
1:50 pm – 2:10 pm	**Michael Mazourek** “The Art of Vegetable Breeding”
2:10 pm – 2:30 pm	**Julie Dawson** “Connecting local food systems to regional plant breeding through flavor”
2:30 pm – 2:45 pm	**Awardee Talk – Sarah Jones** 2022 PhD – Second Place “Multi-modal phenotyping for drought tolerance breeding in soybean”
2:45 am – 3:15 am	**Break**
2:45 pm – 4:30 pm	**Poster Session 2 - Even Numbered Posters** *Crepe Myrtle Regency A2*
4:30 pm – 6:30 pm	**PBCC Session** *Regency B, C, D, D2, E & E2*
6:00 pm – 9:00 pm	**Graduate Student and Early Career Mixer** *Studio 220 NOMA*
Evening	**Dinner on your own**

TUESDAY, JULY 18

WHEN	WHAT
6:30 am	**Breakfast** *Grab and go breakfast set out in prefunction area*
7:00 am – 4:00 pm	**Local tours, Clemson University Research and Education Centers** *Buses depart from hotel*
1:00 pm – 3:00 pm	**Lunch** *Madren open pavilion*
6:00 pm – 9:00 pm	**Diversity, Equity, and Inclusion Program/Dinner** Session Chairs, Sandra Branham and Julian Nixon **Julian Nixon and Rushawnda Olden** “Leadership and Beyond: How the South Carolina 4-H Pinckney Leadership Program helps youth develop cross-cutting skills that will help them influence their communities as stronger leaders, positive role models, and engaged citizens“ **Greetchen Díaz-Muñoz** “Culturally-relevant approaches for K-12 education“ **Marceline Egnin** “Educating and Training of the Next Generation of Plant Breeders under The Tuskegee University iBREED Program“ **Kenai McFadden** “Cultivating Diversity: Empowering high school students to steward the future“ *Regency B, C, D, D2, E & E2*

WEDNESDAY, JULY 19

WHEN	WHAT
7:00 am – 8:00 am	**Breakfast** *Prefunction area*
8:00 am – 8:30 am	**Awardee Talk - Edwin Grote** 2022 Private Sector Impact Award *Regency B, C, D, D2, E & E2*
8:30 pm – 9:45 pm	General Session - 3 **Participatory Plant Breeding** Session Chair, Jenna Hershberger *Regency B, C, D, D2, E & E2*
8:30 am – 8:50 am	**Lisa Kissing Kucek** “Participatory plant breeding introduction and case studies in small grains and cover crops”
8:50 am – 9:05 am	**Nicolas Enjalbert** “PPB digitalization with SeedLinked + Case studies from early to late breeding stages”
9:05 am – 9:20 am	**Solveig Hanson** “Case studies: Participatory plant breeding for flavor in beet and participatory vegetable variety trialing”
9:20 am – 9:30 am	**Panel Discussion** “Can digitalization make participatory plant breeding the norm?”
9:30 am – 9:45 am	**Awardee Talk – Autumn Brown** 2022 MS – Second Place “Phenotypic and Genotypic Characterization of Hemp (*Cannabis sativa L.)* Fiber Traits”
9:45 am – 10:15 am	**Break – Picture**

10:15 am – 10:45 am	**Awardee Talk - Marcio Resende** 2022 Early Career Award *Regency B, C, D, D2, E & E2*
10:45 am – 11:15 am	**Awardee Talk - Fernando Gonzalez** 2022 Lifetime Achievement Award *Regency B, C, D, D2, E & E2*
11:15 am – 12:00 pm	**Plant Breeding Listening Session** Opening Remarks: Christian Tobias John Lovell “Plant breeding innovation” *Regency B, C, D, D2, E & E2*
12:00 pm – 1:00 pm	**Lunch – Speed Networking** *Regency B, C, D, D2, E & E2*
1:00 pm – 2:15 pm	General Session - 4 **Plant Breeding Innovation** Session Chair, Christopher Saski *Regency B, C, D, D2, E & E2*
1:00 pm – 1:20 pm	**Manny Saluja** “Genome editing driving the future of plant breeding”
1:20 pm – 1:40 pm	**Lolita Mathew** “Elimination of Pungency in Allotetraploid *Brassica juncea* Through Gene Editing of the Multicopy Myrosinase Gene Family and Commercialization of ConsciousTM Greens”
1:40 pm – 2:00 pm	**Christopher Saski** “Improvements in somatic regeneration and plant architecture in upland cotton”
2:00 pm – 2:30 pm	**Round Table Discussion** *Regency B, C, D, D2, E & E2*
2:30 pm – 2:45 pm	**Awardee Talk – Leonardo Volpato** 2022 Early Career – First Place “Digital Phenotyping to Measure Agronomic Traits in Plant Breeding”

2:45 pm – 3:15 pm	**Break**
3:15 pm – 4:45 pm	**NAPB Business Meeting and Awards** *Regency B, C, D, D2, E & E2*
5:30 pm – 6:30 pm	**Pre-dinner Mixer with Beverage Station** *Prefunction Area*
6:30 pm – 7:00 pm	**Awardee Talk - Peter Bretting, USDA-ARS** 2022 Friends of Plant Breeding Award *Regency B, C, D, D2, E & E2*
7:00 pm – 10:00 pm	**Banquet** *Regency B, C, D, D2, E & E2*

Clemson highlights 3: Robert Muldrow Cooper Library at Clemson University

THURSDAY, JULY 20

WHEN	WHAT
6:30 am	**Breakfast** *Grab and go breakfast set out in prefunction area*
7:00 am – 5:00 pm	**TitanFarms (Peach and Vegetable production) and W.P. Rawl (Vegetable production)**

Clemson highlights 4: Tillman Hall representing the clock tower at Clemson.

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SPEAKER BIOS

Benjamin BJ Dennis

Born and raised in Charleston, SC, personal chef and caterer Benjamin “BJ” Dennis infuses the flavors and culture of the Lowcountry into his Gullah Geechee cuisine, bringing a new taste to an ever- expanding culinary palate of the south. What differentiates Chef BJ’s food from his contemporaries in “southern” cooking is the homage he pays to the Gullah Geechee culture, brought to the Americas by West Africans, and disseminated along the West Indies and the American South. Dennis infuses the techniques of his ancestors, learned from four years of study in St. Thomas, as well as the lessons of his grandparents about eating from the land, to create fresh interpretations of local dishes focusing on in-season, locally sourced vegetables and seafood. Recent trips to Trinidad and Tobago, Haiti, Barbados, Dominica, U.S. Virgin Islands, Angola, Bahamas, Benin, Togo, Senegal, Gambia, and Cameroon has brought his work full circle. Dennis is connecting the people and cultures of the African diaspora through food and bringing back a true taste of Gullah Geechee culture.

Christopher Saski

Chris is an Associate Professor in the Department of Plant and Environmental Sciences at Clemson University. He holds both a B.S and Ph.D. from Clemson University in microbiology and genetics, respectively. His expertise is in systems genetics and functional genomics in crop and weed species. Chris’s research at Clemson University is focused on linking genome structure with function to advance crop breeding, productivity, horticultural traits, and resilience to abiotic/biotic stresses. His current projects are mainly directed at crop improvement using systems-level gene discovery techniques and genome editing/engineering to improve or enhance crop performance.

Glenn Roberts

Glenn Roberts founded Anson Mills in 1998 in Charleston, South Carolina, to rematriate lost foods of the 18th and 19d' century Southern Pantry. Today Anson Mills grows and produces artisan organic landrace grain, legume, and oil seed ingredients for chefs and home cooks worldwide and provides culinary research support for pastry chefs, bakers, brewers, and distillers through Anson Mills Research Lab. Anson Mills provides pro bono seed biosecurity for the growing community of Southern organic place based identity preserved landrace crop farmers. Glenn is a recipient of the USA Artisan of the Year and National Pathfinder Awards and a founding member of the Carolina Gold Rice Foundation.

Greetchen Díaz-Muñoz

Dr. Greetchen Díaz-Muñoz is a scientist, educator, communicator and advocate of diversity and inclusion in the careers of science, technology, engineering and mathematics (STEM). Throughout her professional career, Greetchen has participated in countless initiatives in Puerto Rico, the United States and beyond, including the creation of projects and collaborations in science education, communication, outreach and public policy. Greetchen, is currently the Director of the Science Education Program and Community Partnerships at non-profit Ciencia Puerto Rico (CienciaPR). At CienciaPR, Greetchen founded the "Borinqueña" blog, focused on empowering Hispanic women and girls in STEM, and the first Girl's in STEM Ambassadors Program in Puerto Rico, Seeds of Success. Greetchen's role in elevating underrepresented groups in STEM also include her contributions at the PuertoRico Science, Technology and Research Trust, the Puerto Rico Society of Microbiologists, the American Society for Microbiology, and the American Association for the Advancement of Science, as one of their IF/THEN Ambassadors. Her work and projects has received numerous awards and honors from various organizations, and has been featured on a diversity of local and international media outlets.

Hanna Raskin

Hanna Raskin is the editor and publisher of The Food Section, a newsletter covering food and drink across the American South. In its first year, The Food Section was named Best New Business by Local Independent Online News (LION) Publishers, and a Trailblazer by the International Association of Culinary Professionals. Raskin previously served as food editor and chief critic for The Post and Courier in Charleston, South Carolina. Her work has been recognized multiple times by The James Beard Foundation, which in 2017 awarded her its first Local Impact Journalism prize. A past president of the Association of Food Journalists, Raskin serves as the Southern Foodways Alliance's columnist.

John Lovell

Dr. John Lovell leads the Evolutionary Analysis Group at the HudsonAlpha Genome Sequencing Center in Huntsville, Alabama. Before joining HudsonAlpha in 2017, he completed a PhD on the quantitative genetics of drought adaptation in the McKay Lab at Colorado State in 2013. He also completed a postdoc in Tim Sharbel's group at IPK-Gatersleben on plant developmental biology and was an NSF plant genome fellow in Tom Juenger's group at UT Austin from 2014-2017. His research at HudsonAlpha works towards using genomics to better understand biological systems. Currently, his projects are mainly directed at accelerating crop improvement efforts through genomics and using comparative methods to better define candidate genes for agronomically important traits. Dr. Lovell works remotely and lives in Denver, Colorado.

Julie Dawson

Julie Dawson is an Associate Professor in the Department of Plant and Agroecosystem Sciences at the University of Wisconsin-Madison. Research interests include the use of genetic resources in plant breeding for organic systems and methods for participatory selection and variety development. She is also the state Extension specialist for regional food systems and does applied research for growers serving local food markets. She leads a project called the Seed to Kitchen Collaborative, which works with plant breeders to test varieties with farmers, gardeners, chefs, and other culinary professionals.

Julian E. Nixon

Julian E. Nixon has served in higher education as a faculty member, administrator and staff member at both the two-year and four-year levels for more than 18 years. As the CAFLS Director of Diversity & Inclusion, he creates, collaborates and leads initiatives with academic departments, research partners, student organizations, university admissions, campus leadership and community partners that seek to grow, retain and empower underrepresented and underserved populations.

Julian's office provides leadership and guidance for recruiting, outreach and retention for the College of Agriculture, Forestry & Life Sciences. He is a planning administrator for the college's strategic plan for inclusive excellence, and a certified trainer for DEI programming such as the Intercultural Development Inventory and Coming Together For Racial Understanding. His office provides support, DEI training and resources for Clemson Extension as well as the 4-H Pinckney Leadership Program which develops the leadership abilities and awareness of civic engagement for middle school and high school students.

Julian is a co-advisor to MANRRS (Minorities in Agriculture, Natural Resources & Related Sciences) which provides industry connections, internships, conferences and a collegiate STEM community. Julian also provides creative collaboration for grant funded programs such as Training Underrepresented Minority Scholars in Sustainable Management of Plant Diseases, Tigers for Inclusion, Diversity, & Ethics (T.I.D.E.), and Future Leaders Obtaining Research and Extension Career Experiences (F.L.O.R.E.C.E.).

Julian is currently a PhD Candidate in Animal & Veterinary Sciences, an amateur gardener, enthusiastic gamer, and passionate speaker. He currently lives in South Carolina with his wife, daughter, a dog named Tierno and a frog named Toady.

Kenai McFadden

Kenai returned to his home state of South Carolina to serve as the Youth Development Program Director for the Green Heart Project after six years of public health training. He brings with him experiences from Houston, Baltimore, and Atlanta, where he delivered health education programs, pursued a public health degree, practiced as an urban farmer, and communicated about outbreaks. He believes that food is a powerful vehicle for facilitating health behavior change. Kenai loves Charleston so far and enjoys expressing himself through dancing, chess, and roller skating. kenai@greenheartsc.org

Lane Selman

Lane Selman grew up on the citrus farm her Sicilian great-grandparents planted in 1919 on Florida's space coast. She studied Agronomy (BS) and Entomology (MS) at University of Florida before moving to Oregon in 2000. As a Professor of Practice at Oregon State University, Lane manages the marketing and public outreach activities for participatory research projects with organic farmers. In 2011, Lane created the Culinary Breeding Network to build communities of plant breeders, seed growers, farmers, produce buyers, chefs and other stakeholders to improve quality in vegetables and grains. Lane lives in Portland, Oregon.

Lisa Kissing Kucek

Lisa Kissing Kucek is a Research Geneticist with the United States Department of Agriculture. As part of the Cover Crop Breeding Network, Lisa improves cover crops, including hairy vetch, winter pea, crimson clover, and cereal rye. She worked alongside farmers, bakers, and chefs to develop wheat varieties for organic and local food systems during her doctoral research at Cornell University. For two decades, Lisa has enjoyed collaborating with farmers and researchers across the Western Hemisphere to improve sustainability in agriculture.

Marceline Egnin

Dr. Marceline Egnin, Ph.D., is an 1890 Land sector Educator, Professor, Scientist, and serves as the program coordinator for the Plant Biotechnology & Genomics Research Lab in the College of Ag., Envi., and Nutri. Sciences, Tuskegee University. After earning her PhD at Penn State University, Prof. Egnin joined Tuskegee University as a Plant Breeder and Molecular Geneticist with an interest in Plant Biotech and Genomics research for crop improvement and environmental sustainability. Dr. Egnin's most prized and cherished achievement over the past 30 years at Tuskegee University has been the mentoring and training of countless minority students, faculty and international scholars in breeding & horticulture, biotechnology, Genomics, CRISPR gene editing, microbiome, bioenergy, and biosafety. She has established the Innovative Plant Breeding Experiential Education & Training Initiative for Minority Students (iBREED) to reshape minority students' view and love of plant breeding and change the outlook of students in the expanding and evolving field. Dr. Egnin is fluent in both French and English and in addition to her PhD, she also holds BS and graduate degrees (Maîtrise) in Genetics from her native country of Côte d'Ivoire, West Africa. Dr. Egnin is a Board Member of representatives in Council for Agricultural Science and Technology (CAST), a Member of the Plant Breeding Coordinating Committee executive, and a member of the ILSI Task Force.

She is the recipient of several awards including:

Outstanding Faculty Performance Award In Research & Service; Sigma-XI Russel Brown Outstanding Honor Research Award; The Honor Society of Agriculture; USDA/CSREES: Group Honor Award for Professional Excellence in Research & Outreach, & Invited Success Stories; Salzburg Fellow, Outstanding Faculty Trainer Awards by ASPB-CSIR-CRI Biotech-to-High-School-Ghana & ABSF-Kenya & SABRAD; Outstanding Chapter President Plaque, World Food Prize-Borlaug Youth Forum Invitee; Invited Speaker & Member Next Einstein Global Forum-Africa.

Michael Mazourek

Michael Mazourek is the Calvin Knoyes Keeney Associate Professor of Vegetable Breeding at Cornell University. Michael is a breeder of peas, beans, squash, cucumbers and peppers and has released numerous cultivars and breeding materials that are shared by small, regional seed companies and incorporated into breeding program of the world's largest seed companies. Michael's specialty is biochemical genetics in vegetables; he explores the diverse phytochemistry that plants use to repel pests and herbivores, reward and nourish pollinators and seed dispersers and cope with environmental stresses, with a goal of harnessing to maximize nutrition and sustainability.

Nicolas Enjalbert

Nicolas Enjalbert, PhD, is the CEO and Co-Founder of SeedLinked, an innovative company digitizing collaborative breeding. Originally from rural France, Nicolas studied Agronomy and Plant Breeding in Europe before pursuing a PhD in Plant Genetics from Colorado State University in the US. With a decade of experience working for international seed companies, Nicolas founded SeedLinked to make collaborative breeding more accessible and mainstream. SeedLinked brings together growers, breeders, chefs, universities, seed companies, and consumers in a groundbreaking crowdsourcing platform. It utilizes digitalization, crowdsourcing technology, and novel statistical models to revolutionize participatory plant breeding. By democratizing the breeding process, SeedLinked aims to create a decentralized and resilient seed system, which is crucial for a healthy and sustainable food system. The company not only innovates in data models for crowdsourcing but also explores business models that benefit society as a whole. Nicolas Enjalbert's expertise in data architecture, crop modeling, and participatory breeding strategies, combined with his background as a plant breeder, drives the continuous development of SeedLinked. His visionary leadership propels the company's mission to transform collaborative breeding into a widely adopted practice, leveraging the power of digital tools and collective efforts.

Peter A. Coclanis

Peter A. Coclanis is Albert R. Newsome Distinguished Professor of History and Director of the Global Research Institute at UNC-Chapel Hill. He took his Ph.D. at Columbia in 1984 and joined the faculty at UNC-Chapel Hill that same year. He is an economic historian, and over the course of his career he has published widely in global history and on themes relating to the economic history, agricultural history, and demographic history of both the U.S. South and Southeast Asia. In 1997-98 he was President of the Agricultural History Society (AHS), is an elected Fellow of this society. In 2019 the AHS awarded him its Gladys L. Baker Award for lifetime achievements in the field of agricultural history. He received a similar honor from the Chinese Agricultural Museum/Chinese Agricultural History Society in 2001 as well as an honorary concurrent professorship at the Museum. Among his works on agriculture in the U.S. South are *The Shadow of a Dream: Economic Life and Death in the South Carolina Low Country, 1670-1920* (Oxford University Press, 1989), which won the Allan Nevins Prize of the Society of American Historians, and a co-authored *Plantation Kingdom: The American South and Its Global Commodities* (Johns Hopkins University Press, 2016). More recently, he wrote the essay “Agribusiness” in the award-winning *Companion to American Agricultural History*, ed. R. Douglas Hurt (Wiley-Blackwell, 2022).

Rushawnda Olden

A native of South Carolina, Rushawnda lives with the belief that her purpose in life is to be a catalyst of change in every arena she is in. Inspired at a summer camp, she developed a strong sense of devotion to the nonprofit sector and underrepresented youth working as a student mentor nearly 12 years ago. Her passion for youth and focus on community collaboration has led her to numerous volunteer opportunities and community leadership roles here in the Upstate of South Carolina. Prior to working at Clemson Rushawnda spent three years serving as a Program Coordinator with Communities In Schools of Greenville; where she created intentional programming for youth in underserved communities. Rushawnda holds a Bachelor of Science in Marketing from South Carolina State University, and a Masters of Public Administration and Nonprofit Management from the University of Nebraska Omaha. As a former congressional page for the late Senator Pinckney, Rushawnda looks forward to continuing his legacy of empowering the next generation of leaders with the skills necessary to succeed. https://www.clemson.edu/cafls/faculty_staff/profiles/rolden

Sandra Branham

Dr. Sandra Branham is an assistant professor of vegetable breeding and genetics at Clemson University's Coastal Research and Education Center in Charleston, SC. Her research focus is genomics-enabled improvement of vegetable crops, particularly for resistance to diseases and heat stress. Prior to joining Clemson University, Dr. Branham completed a PhD at the University of Texas at Austin in Plant Genetics and was a postdoctoral research scientist at the US Vegetable Laboratory (USDA-ARS).

Solveig Hanson

Solveig Hanson joined Dr. Virginia Moore's Sustainable Cropping Systems Breeding group at Cornell University in January 2023. In her Research Support Specialist role, she coordinates research and outreach for the nationwide Cover Crop Breeding Network, including participatory on-farm trials of pre-commercial cover crop varieties. Solveig received her Ph.D. in Plant Breeding Plant Genetics from University of Wisconsin-Madison in 2020, where she conducted genetic, genomic, and participatory research focused on flavor in table beet. In a subsequent postdoctoral fellowship at the University of British Columbia, she coordinated a nationwide farmer variety trialing network and led a participatory carrot breeding project. When not in plant breeding mode, Solveig loves to be outside – hiking, swimming, paddling, biking, or amateur-style birding – or inside baking, writing, or providing a lap for her cat.

Clemson highlights 5: Peach bloom during the spring season at Musser Fruit Research Center.

Autumn Brown

Autumn Brown is originally from Mammoth Spring, Arkansas. She obtained her bachelor's degree from the University of Arkansas, majoring in Horticulture and double minoring in History and Crop Biotechnology. She is currently obtaining her master's degree at the University of Wisconsin studying Plant Breeding and Plant Genetics.

Clayton Carley

Clayton Carley recently graduated from Iowa State University with a Ph.D. in Plant Breeding and Genetics & Genomics with a specialization in predictive plant phenomics. While at Iowa State, Clayton worked with the Singh Soybean Breeding and Soynomics group, where he researched novel methods of improving and leveraging soybean root genetics. As a National Science Foundation Predictive Plant Phenomics Research Trainee, he engaged in numerous transdisciplinary collaborations with engineers and data scientists and worked to develop innovative methods of extracting data from roots by building the Soybean Nodule Acquisition Pipeline, or SNAP, a machine learning system to count and gain insights on soybean nodules and root system architecture. With this work, he found useful relationships between taproot nodules and seed protein and redefined nodulation for future improvements in soybean breeding. He evaluated numerous soybean lines to identify and propose some of theunderlying genes controlling root system architecture and nodulation traits. Clayton currently works with Corteva Agriscience, based in Johnston, Iowa, as the Field Experimentation Lead over the Central and Eastern United States. In this role, he oversees numerous small plot and on-farm trials to drive innovative science and create value for farmers through Corteva's Research and Development -Farming Solutions and Digital team

Clemson highlights 6: Greenhouses at Clemson accommodate several agriculture related research projects

Sarah Jones

Sarah Jones is a Ph.D. student in Plant Breeding in the Soynomics group at Iowa State University. Studying with Dr. Danny Singh, she researches phenotyping strategies to improve drought tolerance breeding in soybean. Sarah earned a BS in Horticulture Science with a minor in Spanish from Texas A&M University and her M.S. in Plant Breeding from Iowa State University. She interned at the Antique Rose Emporium, a rose breeding company in Texas, worked on a discovery team at Monsanto, and served as a staff member in two programs including the vegetable breeding program at Texas A&M University and the Singh soybean breeding program at Iowa State University. Sarah gained breeding experience in over 12 crops from high value horticultural crops and ornamentals to agronomic row crops. She has held multiple leadership positions at Iowa State University including co-chair for the Corteva sponsored R. F. Baker Plant Breeding Symposium and treasurer of Women in Agriculture and Artificial Intelligence (Women in Ag and AI).

Leonardo Volpato

"I have earned an M.S. and Ph.D. degree in Plant Breeding from the Federal University of Vicosa (UFV), Brazil. During my Ph.D., I had the opportunity to be a Visiting Student at the International Maize and Wheat Improvement Center (CIMMYT) and a Research Scholar at the University of Minnesota (UMN). In these roles, I worked on developing High Throughput Phenotyping (HTP) pipelines for wheat, corn, and soybeans using drone imagery. From 2021 to 2023, I worked as a Postdoc Research Associate at the Department of Plant Soil and Microbial Sciences at Michigan State University (MSU), where I led an applied phenotyping breeding program in dry beans. At MSU, I have been involved in developing artificial intelligence approaches and implementing several HTP pipelines to improve the dry bean program, specifically in traits such as plant height, stand count, maturity date, and others, as well as handling mixed models data analysis. Recently, I embarked on a new career journey in the industry at Corteva, where I am currently part of the Precision Phenotyping team, based in Johnston, IA."

Clemson highlights 7: Clemson Small Grains Field Day wheat official variety trial at the Pee Dee REC near Florence, SC

ORAL ABSTRACTS

Benjamin Dennis

“Seeds for Communities”

The history and future of yard and community gardens, particularly in the Lowcountry and sea islands. How seeds can play a big role in sustaining and feeding communities on a local level.

Christopher Saski

“Improvements in Somatic Regeneration and Plant Architecture in Upland Cotton”

Agrobacterium-mediated genetic transformation and somatic regeneration offer a promising approach to create stable, genetically modified plants with consistent traits. However, in many crop species, only a limited number of genotypes can efficiently regenerate whole plants from a single somatic cell. This is due to the suppression of totipotency, a crucial ability encoded in the genome but often inactive in most genotypes, making them resistant to regeneration. In this study, we describe our endeavors to enhance our understanding of the genetic mechanisms behind somatic regeneration and present a case study showcasing the rapid generation of new phenotypes in upland cotton using our improved transformation system.

Glenn Roberts

“40 Days to Green Pizza from Where?”

Flatbreads are endemic to Western staple culture dating back thousands of years. The core genetic diversity supporting that culture is now conserved in seed banks, not community culture. Landrace staple seed diversity in seed banks could be increased and used in hundreds of combinations in the field to accelerate production by very early green staple harvest to address increasing global climate field risk. The standard one or two crop growing season can become a four crop normal season dramatically reducing field risk and increasing tilth, bio density and biosecurity. Breeders can select combinations of successful green early harvest landrace genetics as breeding material for high production 40 day direct seed to harvest green staples in polyculture to improve tilth and human nutrition per acre. The staple breeding targets are landraces with maximum tolerance profile and the ability to harvest easily in green state: Avena Verde, Ceci Verde, Farro Verde, Ponk, Grano Saraceno Verde, and dozens of other symbiotic polycrop elements from the Old World are excellent trial targets. All produce exceptional aroma/flavor profile green staple flours for flatbreads, including delicious green pizza. A 40 day to harvest balanced green polyculture field system is the oldest biosecure staple farming system in the world: the African Sun Cycle.

Julie Dawson

“Connecting local food systems to regional plant breeding through flavor”

Diversification of our agricultural system in many regions is important to long term responses to climate change. Growing interest in local food systems also presents an opportunity for farmers to diversify their cropping systems. Yet we currently do not have enough formal public or private plant breeding programs to support the needs of many crops in many regions of the country. Because formal programs may be limited, engaging other actors in the food system in the creation of new varieties is important. In addition, for many emerging crops that are important to diversification, participation of culinary professionals or other end users may be critical to ensure that markets develop concurrently with production. Focusing on quality for local markets and involving farmers, gardeners and chefs in variety selection is one way of building more diverse regional seed systems. Independent breeders and small regional seed companies are also critical to producing varieties that are regionally adapted and suited to local markets. These breeding programs need access to more cost-effective variety trialing options, and increased visibility for variety releases. We are working to develop a model of connecting independent breeders to networks of farmers, gardeners and chefs interested in participating in variety development, and developing tools to facilitate the expansion of regional participatory plant breeding focused on local food systems.

Lane Selman

“Culinary Breeding Network: How working with chefs can impact your breeding program”

The Culinary Breeding Network (CBN) strives to bridge the gap between plant breeders and consumers by creating unique opportunities for stakeholders to taste in-development vegetable and grain cultivars, share opinions, and be an active participant in variety development. Since 2011, CBN convenes small stakeholder focus groups and executes large public outreach events where plant breeders gain valuable input they rarely have access to. Incorporating chefs, farmers and other end users into the breeding process gives plant breeders deeper insight into preferred traits while also increasing awareness and understanding of plant breeding to a broader audience.

CBN events have taken place in Oregon, Washington, Hawaii, New York City and Italy and focus on finding desirable traits and identifying consumer preferences, as well as celebrating local foods in general. The participatory CBN approach has resulted in new partnerships, collaborations and relationships among breeders, farmers, chefs and eaters to create improved varieties with superior flavor.

During this session, Selman will share how CBN evolved, lessons learned from working with chefs, and the importance of creating buzz in the marketplace.

Marceline Egnin

“Cultivating Diversity in Southern Hospitality through Educating and Training of the Next Generation of Plant Breeders under The Tuskegee University iBREED Program”

NAPB “Southern Hospitality Through Food and Agriculture” feeds into a critical prerequisite of food production, Plant Breeding, which is a dynamic and rapidly expanding field with applications in all aspect of life. However, there is a shortage of students pursuing careers in plant breeding, particularly among minority groups, to meet the demands of Big Data Agriculture 3.0 and food innovations. Bridging southern educational culture, the program, "Innovative Plant Molecular Breeding Research and Experiential Education" (iBREED), was developed in response to the “Dying Breed” concept of students avoiding plant breeding with the aims of reshaping minority students' perception of plant breeding, increasing their awareness of opportunities, and address the declining interest in plant sciences. Through the program, cohorts comprising 120 iBREED minority students from Tuskegee University, ranging from freshmen to graduates and a notable female-to-male ratio. A significant difference in the gender ratio (49-77 Female: 17-27 Males) were recruited over three years and engaged in a collaborative and creative hospitality environment (in Classroom, Lab, Greenhouse, and Field), working in teams of peers, conducting hands-on plant research and learning modern molecular breeding techniques under the guidance of distinguished experts in CRISPR technology, government agencies and agricultural corporations. The program also emphasized education outreach to K-12 schools, promoting agricultural disciplines among young learners to help pipeline the youth to Agriculture disciplines. Financial incentives played a crucial role in student recruitment and students were motivated by experiential internships and participation in National meetings fostering a new appreciation for the meaning and relevancy of plant breeding and related precision sciences. Near-peer mentors contributed to the program's success by helping students overcome initial disinterest and envision their future careers. The **iBREED** program achieved significant milestones, especially in gender ratios, reflecting the disproportionate trend in female/male participation exhibited in national colleges, especially HBCUs. Over the course of the project, the audience expanded to include K-12 youth (25), educators (10), small farmers (5), community leaders, and on-campus faculty through outreach activities and speaking invitations. **PROJECT IMPACT:** Students benefitted from visits and interactive engagement with experts in plant breeding, CRISPR technology, government agencies and agricultural corporations. Modest financial incentives and internship opportunities for professional development played an important role in recruiting students, sustaining their drive to master the **iBREED** training and molding professionals in precision breeding and invitro plant science. Research training opportunities at NC State University, Iowa State University, UC-Davis, Tuskegee University and at several private Institutions in molecular and plant breeding were provided. Project funding was utilized to provide travel for 10 undergraduates, five graduate and 3 faculty members to attend and present research findings at scientific meetings. The success of this project in near-peer mentors roles helped overcome students’ indifference and leverage research opportunity for their next generation career; thus, fostering a new appreciation for the meaning and relevancy of plant breeding and related precision sciences. About 50% were very satisfied with their own efforts while 37.5% were satisfied. The majority (87.5 %) said that they would recommend the course to others while 6.25% said they do not know whether they would recommend the program to others.

Michael Mazourek

“The Art of Vegetable Breeding”

The culinary aspects of the plant cultivars we consume has generally been in decline. Without distinctiveness or branding in commodity systems, its for consumers challenging to identify cultivars with superior flavor so there is little incentive to breed, grow or distribute cultivars with superior flavor. We can change this by creating a non-commodity system, with chefs that look for novel, exceptional ingredients for their diners as our natural allies. In this talk, I will share case studies of cultivars I have developed for culinary purposes and how we distinguish integrating insight versus feedback to guide this process.

Peter A. Coclanis

“The Ambiguities of Innovation: Agricultural Patterns and Processes in the Southeast, c1600-c1950”

Until fairly recently, the agricultural sector in the South was generally viewed as backward and slovenly, and southern farmers as hidebound and certainly non-entrepreneurial. Evidence for this depiction was typically drawn from the period commencing with the end of the Civil War and running through the 1930s, a period in which southern agriculture and the region’s farmers were both in very bad shape, to be sure. During that period of seventy-five years or so, the agricultural sector of the South was characterized by small, undercapitalized units, worked by owners, tenants, sharecroppers, and wage workers, many poor and deeply in debt. Generally speaking, these farmers specialized, however inefficiently, on a small number of cash crops, particularly cotton, which generally sold for low prices, leaving the sector and the region far behind other parts of the U.S. The most invidious comparison is made with the rapidly modernizing and developing agricultural sector of the Midwest, which is often seen as the key to the rise of the wealthy and justly famous “agro-industrial complex” of that region.

The above depiction of southern agriculture is not so much wrong as partial and insufficiently contextualized. In this brief presentation, I shall employ evidence from the South Atlantic region to argue that at earlier periods in the South’s history its agricultural sector was quite dynamic and its agriculturalists both innovative and entrepreneurial, generating considerable growth and wealth for the region. Their innovations and entrepreneurship were such, however, as to lead the region’s agricultural sector down a deeply rutted path that would later impede adjustments as conditions changed, as they did after Appomattox. Only with the total collapse of the sector in the 1930s and new economic opportunities opening up with the Second World War were the sector and the region able to begin anew.

Sandra Branham

“Genomics-enabled vegetable breeding for production in the Southeastern US”

The Southeastern region of the United States represents a critical component of vegetable production for our nation both in terms of diversity of cropping systems and total quantity. The warm, wet climate of the Southeast is not only a direct stress on crop production but leads to high disease pressure in the region. Breeding for locally adapted germplasm (particularly for heat tolerance and disease resistance) will be necessary to ensure a sustainable production system. The focus of my research is genomics-assisted breeding of vegetable crops (Brassica leafy greens, spinach, snapbeans, Cucurbits) through 1) development of genomic resources, 2) exploring the genetic and phenotypic diversity of the USDA germplasm repositories, 3) identifying QTL associated with resistance to heat and disease, 4) developing and testing molecular markers associated with phenotypes of interest, and 5) population development for marker validation, trait introgression and gene pyramiding. The presentation will provide an overview of my current progress in establishing a new vegetable breeding program at Clemson University.

Lisa Kissing Kucek, Solveig Hanson, and Nicolas Enjalbert

“The practice and potential of participatory plant breeding: Leveraging decentralization, stakeholder knowledge, and digital connectivity”

This session will focus on participatory plant breeding (PPB) and its potential to enhance both germplasm improvement and variety adoption. The session will feature three distinguished speakers: Dr. Lisa Kissing Kucek, Dr. Solveig Hanson, and Dr. Nicolas Enjalbert, who will collectively present core principles of PPB, case studies of its application, and their perspectives on its future potential.

The session will introduce PPB as a spectrum of decentralization and/or stakeholder participation in the breeding process. The speakers will explore how combining the toolkits of scientists (statistics, experimental design, genetics, and complex data analysis) with knowledge of farmers and food system stakeholders (local environments, agronomics, and markets) can amplify breeding success and variety adoption. Case studies will illustrate PPB approaches tailored to grain, forage, and vegetable contexts. The speakers will describe diverse approaches to PPB, ranging from controlled models with a limited number of growers to wider-reaching community science approaches.

Given the extensive variation among crop types, breeding stages, crops, regions, stakeholders, and cultures, managing PPB can be complex and requires keen attention to context. Successfully facilitating PPB often requires a change in the approach, assumptions, expectations, and time allocation of scientists. Speakers will discuss both successes and challenges of PPB facilitation, and they will highlight the potential of digitalization to mitigate obstacles around trial administration, data quality, and researcher-participant communication, such that PPB could become a normative practice in plant breeding.

The latter part of the session will center on the utilization of digital tools, with a particular focus on the Seedlinked platform. The speakers will discuss the next frontiers of PPB, showcasing use case scenarios from early-generation breeding to commercial cultivar trialing that demonstrate how context-appropriate use of digitalization can overcome logistical and communication challenges and facilitate broader variety adoption. By leveraging digital tools, PPB has the potential to enhance collaboration, streamline data collection and analysis, and foster innovation, ultimately transforming plant breeding practices.This collaboratively presented session on PPB and its integration with digital tools aims to inspire plant breeders, researchers, and industry professionals to explore this innovative approach. With strategic use of participatory plant breeding, supported by the power of digitalization, greater potential for advancements in crop improvement and agricultural sustainability can be unlocked.

Clemson highlights 8*: The Old Tillman Hall Bell at Clemson*

Autumn Brown

Phenotypic and Genotypic Characterization of Hemp (*Cannabis sativa L.*) Fiber Traits”

Hemp (*Cannabis sativa* L.) is a dioecious (XY), diploid (2n=2x=10), photoperiod sensitive crop cultivated worldwide for a variety of uses including food, feed, medicine, and fiber. It has been utilized by humans for nearly 12,000 years and is currently having a resurgence in America due to recent relegalization. Current interest from growers and consumers in new alternative and potentially more sustainable crops has caused a rapid increase in hemp production and need for hemp research. Existing knowledge of best agronomic practices, underlying genetic architecture of fiber traits, and combining ability between gene pools is still largely unknown. Results from a plant density trial on plant height, stem diameter, and branching will be discussed as well as the general and specific combining ability of fiber traits between progeny from 15 lines and 5 testers. Providing US farmers with information regarding best agronomic practices and superior cultivars will allow them to produce a high-yielding and high-quality hemp crop that is able to compete economically and environmentally with other fiber sources.

Clayton Carley

“Knowing Nodulation, Let's Dig In”

Soybeans [*Glycine max* L. (Merr.)] serve as a primary source of food, fuel, and commercial products around the world. As a legume they serve a critical role in crop production cycles where they are capable of fixing the majority of their required nitrogen endogenously. This nitrogen production occurs through the symbiotic relationship between soybeans and a soil born bacteria, most often *Bradyrhizobium japonicum*, in specialized root structures known as nodules. Within these nodules, diatomic atmospheric nitrogen (N^2) is fixed into a plant bioavailable form of ammonia (NH^3) which is used for vegetative growth, protein production, and seed fill. The roots these nodules grow on are also diverse and adaptive to their environments with variations in their physical structure known as root system architecture (RSA). The value of understanding the variation and adaptability of nodulation, RSA traits, and their interactions serves as a critical turning point to breeding and optimizing soybeans for specific environments and output traits. With recent developments in machine learning and computer vision this work presents the development of Soybean Nodule Acquisition Pipeline (SNAP), a novel tool, for evaluating nodulation which we re-define as the total nodule area on a root or root growth zone as a function of nodule count and individual nodule area. SNAP combines RetinaNet and Unet deep learning architectures to dramatically reduce the human labor needed to quantify nodule size and locations on roots. With the deployment of SNAP in early growth stages we show that nodule count does not statistically differ from V1 to V5 in the taproot growth zone, but nodulation continues to increase in every growth zone at each growth stage. We also found that in the panel assessed, the percent of nitrogen in end season seed has a moderate (r^2 = 0.5) and significant ($p = 0.04$) correlation specifically to tap root nodulation. We also deployed SNAP on a large diversity panel (n=300) of soybeans in three field environments to conduct genome-wide association studies. As a result, we report three quantitative trait loci (QTL) across four traits and explore a putative gene that may impact the Nodulation Carbon to Nitrogen Production Efficiency (NCNPE). Additionally, we explored the same diversity panel in controlled growth environments across the first 12 days of growth using the Advanced Root Image Analysis (ARIA) system for the underlying genetics of RSA and report 19 QTL across 21 traits in addition to finding five overlapping QTL with previously reported RSA traits.

Sarah Jones

“Multi-modal phenotyping for drought tolerance breeding in soybean”

Climate resilient crops that can withstand weather fluctuations and produce stable yield are important to sustainability and breeding. Because the Midwest region is the highest row-crop producer in the United States, it is important to develop soybean lines that can withstand periods of drought to maintain security and resource efficiency of United States agriculture production. Three replications of a 450-member mini-core collection representing the diversity of soybean germplasm from USDA GRIN was screened for drought tolerance in sandy soil in Muscatine, Iowa for 3 years. This project used novel drought phenotyping methods to collect a broader range of information compared to visual drought scores alone and utilized these deep phenotypes to explore genetic architecture of drought response in soybean. Drought symptoms were quantified by various methods including visual wilt score, RGB drone imagery, and hyperspectral reflectance. Drone imagery increases the speed of phenotyping to improve detection of drought stress across increased breeding population size or wide geographic areas opening routes of drought stress monitoring. Multispectral imaging and hyperspectral reflectance capture spectral reflectance from regions of the electromagnetic spectrum beyond human vision, and therefore have the potential to detect symptoms not yet visible to the human eye. These methods can be used to increase efficiency of drought phenotyping in large breeding trials.

Leonardo Volpato

"Digital phenotyping to measure agronomic traits in plant breeding"

The use of RGB images collected via drones has the potential to replace traditional measurements in field trials to measure traits such as relative maturity (RM), stand count (SC) and plant height (PH). Deep learning (DL) approaches have enabled the development of automated high-throughput phenotyping (HTP) systems that can quickly and accurately measure target traits using low-cost RGB drones. In this study, a time series of drone images was employed to estimate dry bean relative maturity (RM) using a hybrid DL model combining Convolutional Neural Networks (CNN) and Long Short-Term Memory (LSTM). The performance of the Faster-RCNN object detection DL algorithm was also examined for stand count (SC) assessment during the early growth stages. Moreover, plant architecture was analyzed to extract plant height (PH) using digital surface model (DSM) and point cloud (PC) data sources. The CNN-LSTM model demonstrated high performance in predicting the RM of plots across diverse environments and flight datasets, regardless of image size or flight frequency. The Faster R-CNN model accurately identified bean plants at early growth stages, with correlations between the predicted SC and ground-truth measurements in average of 0.8. Appropriate flights altitude, and growth stage should be carefully targeted for optimal SC results, as well as precise boundary box annotations. On average, the PC data source marginally outperformed the DSM data to estimating PH, with average correlation results of 0.55 for PC and 0.52 for DSM. Additionally, the results demonstrated that the CNN-LSTM and Faster R-CNN models outperforms other state-of-the-art techniques to quantify, respectively, RM and SC. The subtraction method proposed for estimating PH in the absence of accurate ground elevation data yielded results comparable to the difference-based method. In addition, open-source software developed to conduct the PH and RM, as well as vegetation indices analyses can contribute greatly to the plant phenotyping community.

Clemson highlights 9: Sikes Hall, Administrative Building, Clemson University

POSTER ABSTRACTS – PhD

P-001. Ambar Carvallo Lopez

University of Wisconsin-Madison

Evaluation of novel markers for Septoria leaf spot resistance in tomato

Open-field tomato production is still the most popular way of producing tomatoes in the Upper Midwest, but high disease pressure is making it harder for farmers to achieve the desired goals. Two of the most important diseases in open-field are Early blight (EB) (Alternaria solani) and Septoria leaf spot (SLS) (Septoria licopersici). Developing highly resistant tomato varieties is key to decrease losses, especially to organic farmers. In this project, one novel marker for Early blight, EB9, and two for Septoria leaf spot, SLS1 and SLS2, resistance is evaluated in a F2 segregating population. The F2 population was generated by crossing an inbred line that was homozygous for all 4 markers with a susceptible inbred line. The F2 population was grown in open-field organic conditions in the Summer of 2022. The plants were visually scored for each disease once a week from week 28 to week 35, where the score ranged from 0 to 100, where 0 was no disease symptoms, and 100 was a completely affected plant (dead plant). The weekly scores were then combined into a single score using the Area Under the Progress Curve (AUDPC) formula. Overall, there were significant differences between the different genotypes for both SLS markers evaluated. For SLS2, the best genotype is the homozygous dominant, followed by the heterozygous form, but with significant differences between both genotypes. For SLS1, the best genotypes were the homozygous dominant and heterozygous, with no significant differences between them. If both markers are to be stacked, the best results are obtained when using the homozygous dominant genotype for both markers. No significant results were obtained from the EB5 marker evaluation. These results show that using both SLS markers can significantly decrease the disease spread, and thus can reduce the yield losses that farmer suffer each year.

P-002. Andrew Herr

Washington State University

Capturing a More Complete Picture: Utilizing UAS imagery in Genomic Prediction of a Large Scale Wheat Breeding Program

Multispectral imaging with unmanned aircraft systems (UAS) is a promising high-throughput phenotyping technology that has been shown to help understand the mechanisms associated with crop productivity. Imaging technology can predict complex agronomic traits like grain yield within a given generation, creating the potential to fast-track selections in plant breeding and increase genetic gains. Spectral reflectance indices (SRI), including both vegetation and water indices like NDVI, NDRE, NWI, as well as secondary HTP traits like percent canopy cover were all used to evaluate Washington State University winter wheat breeding lines between 2019 and 2022. Data was collected using a DJI Inspire 2 drone, equipped with a Sentera Quad Multispectral Sensor, and collected at antheses. Lines were observed from single location, single replication preliminary yield trials to multi-location, replicated advanced yield trials. The calculated SRIs and canopy cover were used individually and in combination with genomic data in rrBLUP model prediction for grain yield. Prediction Accuracy was evaluated on an omitted year dataset. Established HTP research has shown success when making predictions within year but little research has been done when prediction with large populations across years. Preliminary results show that including SRI data in genomic prediction models improves overall performance in across year prediction, especially when dealing of years with extreme environmental variability. This research is vital for plant breeders to understand the utility of UAS imaging in variety improvement when dealing with abnormal growing seasons and an example of how to implement HTP technology while also improving genomic selections strategies.

P-003. Ashley Schoonmaker

North Carolina State University

iCottonQTL: A web-based application for downstream processing of CottonSNP arrays data

One of the cheapest, highest quality, and most common methods for identifying genetic regions associated with important traits is the use of high-throughput genotyping arrays. For cotton, the CottonSNP63K array has been developed as a standardized resource for genotyping, containing 38,822 functional polymorphic markers for research purposes. To aid in the pre-processing of raw marker data from the CottonSNP63K array and the future CottonSNP30K release, we have created iCottonQTL, a publicly accessible web-based tool. The iCottonQTL is a R/Shiny app which provides a simple method of filtering markers for biparental projects and providing some visual statistics on the raw data. The tool can automatically reformat the data into the input format for the commonly used linkage mapping program JoinMap. The app seeks to make biparental genetic mapping analysis more accessible to researchers with less experience in bioinformatic methods. Additionally, iCottonQTL provides one click conversion of the data from the genotyping arrays to the community database standard, with a built-in button for emailing the CottonGen formatted data to the relevant person. The tool is designed to facilitate the submission of genotyping data of raw array data with instructions of what to include when submitting genotyping data to CottonGen, as supported by scientific FAIR data standards. Sharing raw data to community databases is extremely useful for future array development and expands the impact of your published results.

P-004. Cassondra Newman

North Carolina State University, Raleigh

New Best Practice Method for Accessing Leaf Spot Severity in Peanut using Digital High Throughput Phenotyping

Peanut, Arachis hypogaea, is a widely cultivated crop which is used as a source of protein and oil. It is grown in sandy soils and is cheaper to produce when compared to alternative protein sources such as meat and tree nuts. Leaf Spot, caused by pathogens Passalora arachidicola and Nothopassalora personata, is the most damaging disease to cultivated peanut across all growing regions. If fungicide is not used to combat the disease, yield can be reduced by half. Leaf Spot resistance has been a target trait for peanut breeders for decades, however many intricacies in the disease and how the disease is rated, has slowed progress towards this goal. Leaf spot has been historically rated by visual score 1-9 which aims to describe both lesions and defoliation concurrently. This scale is not effective in that there is within and between rater subjectivity and the scale is rating two different symptoms. A high throughput phenotyping strategy must be employed to reduce subjectivity, reduce manual labor, increase accuracy and allow for archiving raw data. First, this work explores the relationship between UAV-captured multispectral bands, UAV-captured high-resolution RGB, leaf scans, and the breeder rating. Broad sense heritability is used to compare the best digital phenotyping strategies with traditional breeder ratings. Lastly, a new standard operating procedure is outlined for determining leaf spot severity.

P-005. Dionne Martin

University of Georgia

Comparative transcriptomics as a tool to investigate Asteraceae tuber development

Plants produce underground storage organs to withstand abiotic and biotic pressures such as overwintering and herbivory. Underground storage organs also serve as important food crops such as potato tubers, onion bulbs, and sweet potato storage roots. *Solanum tuberosum* L. (potato) produces tubers and has served as a model for understanding underground storage organ development. Studies in potato have shown that genes involved in the circadian clock and flower induction have evolved to regulate the development of tubers suggesting that neofunctionalization of ancestral pathway genes are key components in the initiation and development of underground storage organs. However, despite also producing edible tubers, little is known about the genetic regulators involved in the development of *Helianthus tuberosus* (Jerusalem Artichoke or sunchoke) and *Dahlia* spp. To address this knowledge gap, we generated transcriptome assemblies of Jerusalem artichoke and Dahlia. Furthermore, using gene co-expression analysis, we aim to uncover potential genetic regulators involved in tuber development of Asteraceae species. By doing so, our research aims to broaden our understanding of underground storage development across plant lineages and uncover potential genetic targets for plant breeding to ultimately enhance storage organ production.

P-006. Dylan Oates

Washington State University

Identification of Key Cold Response Determinants in Triticum aestivum: Elucidating the Interaction between Vernalization and Photoperiod for Low-Temperature Acclimation

Most temperate crops, including wheat, undergo cold acclimation when exposed to low, non-lethal temperatures. Chilling and freezing stress affects all aspects of the plant including growth, development, reproductive capabilities, metabolism, and overall plant yield. Cold and freezing stress are perceived by several cellular signaling molecules some of which are calcium, ROS, protein kinases, and lipids. When cold temperatures are sensed by membrane receptors, regulation of cold-responsive genes and transcription factors occurs, such as LEA, COR, and VRN. These genes are regulated by specific promoter elements that include CBF and phytohormone-responsive elements; thus, low-temperature stress is regulated by a complex gene regulatory network. The Norstar variety of winter wheat displays high freezing tolerance. However, if Norstar undergoes flowering induced by a shortened photoperiod without exposure to low temperatures, it becomes more susceptible to freezing damage in subsequent generations. Therefore, the goal of this project is to reveal the underlying vernalization and photoperiod determinants driving freezing tolerance in T. aestivum. To this end, we performed QTL analyses of three Norstar bi-parental mapping populations for low-temperature tolerance. While 2 QTL were identified in the winter Manitou and 5 QTL in the Manitou populations, no significant QTL were identified in the Cappelle Deprez population. Next, we performed RNAseq analysis of Norstar F1 progeny that was either vernalized or subjected to photoperiod-induced flowering in response to cold temperatures at 0, 1, 2, 4, 8 and 24 hours after freezing. Cumulatively, we found 806 genes were differently expressed across the data set. DEG are being validated by qRT-PCR. Taken together, these data will help to identify genetic markers and genes that can help breed cold and freezing tolerant wheat varieties to improve winter survival.

P-007. Gaurab Bhattarai

University of Georgia

Characterization of muscadine grape germplasm for aroma-related volatile compounds

Muscadine grapes (Vitis rotundifolia) are native to the southeastern U.S. where they are valued for their unique flavor and fruity aroma. Despite having a diverse aroma profile, muscadine germplasm is virtually unexplored for its aroma volatile content and composition, which is crucial in determining the value of its products. The aim of this research was to characterize 24 muscadine genotypes with distinct uses and origin for their aroma-related volatile profile using headspace solid-phase microextraction method coupled with gas-chromatography mass spectrometry. In total, 63 volatile compounds were detected and genotypes significantly differed for 43 volatile compounds. We also profiled the aroma volatile content and composition of the commercially cultivated muscadine cultivar Carlos at various stages of berry ripeness. Characteristic differences were observed in the composition of volatile compounds as ripening progressed. The results obtained from this study will help identify muscadine genotypes and better design crosses to produce fresh fruit and wine selections with desired aroma profiles. This knowledge will lead to the development of new muscadine cultivars and significantly contribute to the expansion of muscadine use in the future.

P-008. Gurleen Sidhu

University of Guelph

Genome-wide association mapping of spear quality and andromonoecy traits in asparagus

The mapping of quantitative trait loci can provide insights into genetic architecture and facilitate marker assisted selection in breeding programs. Genome wide association studies were conducted to map two traits in asparagus, andromonoecy and spear quality. The former is assessed as the number of berries on male plants (NOB), while the latter is measured as the ratio of plant height to height of the first branch off the ground (PH/BH). A total of 760 diverse asparagus genotypes were evaluated for variation in these two traits over two years (2014-2015) at the Simcoe Research Station, Ontario, Canada and genotyped using a genotyping-by-sequencing (GBS) approach. PH/BH varied (1.63 to 7.50) as well as the number of berries on male plants (0 to >30). Among the genotypes three subpopulations with the presence of admixtures were identified and LD decay for all chromosomes was approximately 6965 bp. Four and seven QTL were associated with PH/BH and NOB ($p<0.0003$), respectively and mapped near genes encoding uncharacterized proteins. This study demonstrates the application of GBS and association mapping in asparagus and can be useful to understanding the genetic complexity of traits, for the identification of candidate genes, and marker-assisted selection in the future.

P-009. Habib Akinmade

University of Florida

Enhancing Cowpea's [Vigna unguiculata (L.) Walp] Potential: Genetic Analysis of Key Traits and Protein Content in a Diverse Collection

Cowpea holds numerous potentials as a crop that can help achieve food security for the globe. It has multi-purpose use as food for humans, forage for livestock, as well as benefitting the rhizosphere. Exploring this potential requires examining genetic resources for important traits that can be introduced into elite varieties. Protein content is a key factor that determines the value of different varieties, to meet the evolving demands of consumers. Additionally, understanding the genetic components governing pod, seed morphology, and yield traits is essential for improving overall crop quality. We sought to achieve this by conducting genome-wide association studies on a set of 375 accessions that represent a mini-core collection, of which 56 were further assessed for protein content. A set of 41k single nucleotide polymorphisms (SNPs) were used for GWAS. Eight traits were measured: pod number, pod length, seed length, seed width, seed area, 100-seed weight, seed perimeter and grain yield were the focus of genome-wide analyses. Results revealed an average of 27% seed protein content among the accessions evaluated and protein range between 21.92% to 37.85% among accessions. Significant phenotypic and genotypic correlations were discovered among the traits. Heritability estimates ranged from 0.51 for yield to 0.93 for pod length. GWAS revealed 47 SNPs significantly associated with the traits, except yield. In the search for candidate genes, we identified 59 candidate genes within a 10kb genomic window around the SNPs, out of which 23 had gene ontology terms associated with important functional annotations. Six of the genes were also responsible for multiple biological functions. The valuable insights gained from this diverse collection showed their potential for selection to improve protein content, and trait manipulation. These accessions not only hold promise for cowpea improvement but also serves as a valuable medium for exploring the untapped genetics in cowpea.

P-010. Hannah Stoll

University of Minnesota

Perennial Progress: Genetic Gain for Domestication Traits in Intermediate Wheatgrass (Kernza®)

Intermediate Wheatgrass (Thinopyrum intermedium, IWG, Kernza®) is an emerging perennial grain crop that provides notable ecosystem services and numerous opportunities for profitability across the supply chain. Despite the obvious ecosystem and economic benefits of Kernza® as the first perennial grain crop, there are still several factors that limit the immediate, widespread commercialization of this crop. One main limitation, and the focus of this research, is needed improvements for grain-related domestication traits such as reduced shattering, free grain threshing, and seed size. Domestication efforts for IWG as a grain crop began a mere 30 years ago, and at the University of Minnesota, in the last decade.

Parents from Cycle 2 through 5 of the U of M's Intermediate Wheatgrass breeding program were cloned and planted in an Augmented Experimental Design at 2 locations: St. Paul, MN and Lamberton, MN and evaluated for the following traits in 2021 and 2022. Key domestication and agronomic traits include height, heading, anthesis, shattering, threshability, yield, seed characteristics (i.e. seed size, color), and other inflorescence traits. Each genet was genotyped using Genotyping by Sequencing (GBS). Specifically, this research showed meaningful gains to improvements in shattering, yield, and free-threshing, proving breeding efforts for IWG at the U of M are both fruitful and rapid. Using this information, genetic gain was calculated; a statistic which can be leveraged for more rapid improvements for various traits in future breeding cycles.

P-011. Harsimardeep Gill

South Dakota State University

Including small-scale and rapid phenotyping in multi-trait genomic prediction models improves prediction for baking traits in hard winter wheat

Improvement of end-use quality remains one of the most important goals in hard winter wheat (HWW) breeding. However, the evaluation of end-use quality traits is confined to later development generations owing to resource-intensive phenotyping. Genomic selection (GS) has shown promise in facilitating selection for end-use quality; however, lower prediction accuracy (PA) for complex traits remains a challenge in GS implementation. Multi-trait genomic prediction (MTGP) models can improve PA for complex traits by incorporating information on correlated secondary traits, but these models remain to be optimized in HWW. A set of advanced breeding lines from 2015 to 2021 were genotyped with 8725 single-nucleotide polymorphisms and was used to evaluate MTGP to predict various end-use quality traits. The MTGP model outperformed the ST model with up to a twofold increase in PA. The PA was improved from 0.38 to 0.75 for bake absorption and from 0.32 to 0.52 for loaf volume. Incorporation of simple traits, such as NIR based flour protein (FLRPRO) and a simple-assay based sedimentation weight value (FLRSDS), substantially improved the PA of MT models. Thus, the rapid low-cost measurement of traits like FLRPRO and FLRSDS can facilitate the use of GP to predict important baking traits in earlier generations and provide breeders an opportunity for selection on end-use quality traits by culling inferior lines to increase selection accuracy and genetic gains.

P-012. Julia Brose

Michigan State University

Evolutionary Origins of Tubers

Tubers are a modified underground stem that forms from a stolon and serves as a method of asexual reproduction in plants. Potatoes (Solanum tuberosum) are the most popular and economically important tuber forming plant. For these reasons, research efforts to understand tuberization centered around potato have revealed the importance of daylength and temperature as well as the role of flowering and circadian rhythm homologs in tuber formation. However, the evolutionary history of tuberization and the mechanism of tuberization across the angiosperms remains unknown. Comparative genomic and transcriptomic resources have been developed for four sets of tuberizing species and non-tuberizing species as well as seven tuberizing species from distinct angiosperm lineages. Candidate genes involved in tuberization are being identified using synteny, orthology, and robust gene co-expression networks. This will provide insights into the development of tubers and their evolution throughout angiosperms.

P-013. Juliana Cromie

University of Florida

Blueberries Beyond Bees: Exploring Molecular Breeding Strategies for Blueberry Parthenocarpy

Blueberry yield is heavily reliant on cross-pollination, which is primarily facilitated by bees. Despite significant investment in seasonal pollination services, achieving optimal pollination remains a challenge due to blueberry's partial self-incompatibility and pollen limitation resulting from low pollinator efficacy and adverse weather during the short bloom period. Therefore, parthenocarpy, which is the ability to set fruit without pollination, may help guarantee stable yield under diverse climactic and pollinator-limited conditions. However, developing parthenocarpic cultivars is challenging due to the difficulty of evaluating large breeding populations, which requires flower emasculations, application of pollinator exclusion netting, and tracking of fruit set. Thus, parthenocarpy is an ideal trait for developing molecular breeding tools. Here we compared the predictive abilities (PA) of three molecular breeding strategies: genomic prediction (GP), GS de novo GWAS, which incorporates significant markers derived from genome-wide association studies (GWAS) in a GP model, and marker-assisted selection (MAS) which employs only significant GWAS markers in a linear regression model. To compare these strategies, we evaluated parthenocarpic fruit set (# seedless fruits / 10 emasculated flowers) in two breeding populations (n=310; n=194). GWAS including 59,000 biallelic SNPs were performed for each population, and significant additive markers explaining the highest proportion of phenotypic variance were selected for inter-population cross-validation. GP using RR-BLUP achieved a moderate PA of 0.27, while GS de novo GWAS improved the PA to 0.33. Furthermore, a single marker linear regression demonstrated a PA of 0.19, suggesting that this individual marker could be useful in predicting parthenocarpy across populations. Together, these results indicate that molecular breeding techniques can effectively enhance blueberry parthenocarpy, with MAS using a single marker exhibiting more than half of the PA achieved by GP utilizing 59k markers. Therefore, the development of a diagnostic assay for MAS has strong potential for the genetic improvement of parthenocarpy in blueberries.

P-014. Kelly Goode

University of Georgia

Identification of the *Rmi-1* gene from cultivar Forrest for soybean resistance to *Meloidogyne incognita*

Soybean (Glycine max) is one of the most widely grown crops in the United States, with an estimated production value of $61 billion in 2022. Root-knot nematodes are the greatest pathogen threat to soybean production in the Southern US, accounting for 1.3% yield loss in 2022. The Southern root-knot nematode (SRKN), Meloidogyne incognita, is the most widespread species in the Southern US. A single, additive gene for resistance to SRKN, Resistance to M. incognita-1 (Rmi-1) was identified in a cross between the resistant cultivar Forrest and the susceptible cultivar Bossier, but never mapped to a specific genomic region and the causal gene(s) remain unknown. A KASP marker used for SRKN resistance breeding was developed using genetic mapping from unrelated soybean lines. To confirm the genomic location of Rmi-1, 474 F2:3 progeny derived from a Bossier x Forrest cross were screened for SRKN resistance and genotyped using existing SRKN breeding markers. SRKN resistance is significantly associated with the marker on chromosome 10 ($P < 0.001$; $R2 = 0.5$). Further confirmation of this association was found by genotyping and phenotyping 18 F2:3 families found to be segregating at the chromosome 10 marker ($P < 0.001$; $R2 = 0.6$). These results indicate that Rmi-1 is in the chromosome 10 region most commonly associated with SRKN resistance, regardless of the genotypes used. For fine mapping of the Rmi-1 region, 883 F5 Bossier x Forrest lines were genotyped using markers throughout the candidate region. Twenty lines were identified as possibly recombinant in the candidate region and will be evaluated for SRKN resistance to prioritize candidate genes for confirmation through CRISPR gene knockouts and further functional analysis.

P-015. Kyle Parker

Texas A&M AgriLife Research

Is Chinese Spring Enough? A Comparison of Alignment of Whole Genome Sequencing of Elite Great Plains Wheat Germplasm to Alternative Reference Genomes

In this era of genomics, the question comes to arise, is my reference genome ideal for my material? In this study 32 publicly available elite Great Plains hexaploid wheat (Triticum aestivum L.) germplasm lines with whole genome sequencing ranging from 5-20x's coverage were aligned to three reference genomes, Chinese Spring V2.1 (CS), Jagger (JG), and a custom Synthetic reference (DT). The Synthetic reference is an 'in silico' hybridization of SvevoV1 (Triticum turgidum subsp. durum) reference, and AL 7/8 V5 Aegilops tauschii reference. The collinearity of each reference was compared, resulting in percentage of colinear genes ranging from 66.88% to 75.42% for the JG/DT and CS/DT, respectively. Alignments were compared utilizing alignment, coverage, and discovered variant Ustatistics. There were significant differences between supplementary aligned reads, properly paired reads, reads with mapping quality (MQ) of 0, alignment error rate, percentage of reference alleles, percentage of heterozygous calls, and percentage of missing alleles. For most metrics, CS and JG performed significantly better than the DT reference. However, for percentage of reads with MQ of 0, error rate, percentage of reference alleles, and percentage of missing alleles, JG performed significantly better than the other references. Initially the DT reference called the most variants, followed by CS and JG, however after filtering, JG retained the most variants, followed by CS and DT. The result of this study reveals reference bias that can affect downstream analysis by the position and the type of variants identified.

P-016. Lucas M. Roberts

University of Minnesota

Breeding Soybean for Intercropping with Pennycress: Genetic Variation of Target Traits

Pennycress, (Thlaspi arvense) is a newly domesticated winter oilseed adapted to the Upper Midwest US. Due to its life history, pennycress can be planted in the fall between current summer rotations of maize and soybeans. In this novel intercropping system, pennycress provides the benefits of a cover crop while still producing a valuable oilseed. Through providing a continuous living cover over winter, pennycress can reduce nitrate leaching and soil erosion. The shorter growing season in Minnesota necessities that the following summer row crop overlap in time and space with pennycress 4 – 8 weeks. Soybean (Glycine max) fits into this cropping system due to its high plasticity and ability to rebound from early season stress. Competition for resources during this overlap period is high and there is a need to develop adapted soybean varieties to ensure the adoption of pennycress into the cropping landscape. Our objectives include quantifying genotype-by-cropping system interactions and characterizing soybean traits potentially relevant to winter oilseed intercropping systems. Towards identifying the natural genetic variation in soybean responses to intercropping, 40 soybean genotypes were planted into the pennycress variety MN-106 in 2020, 2021, and 2022. Field experiments in western and southern Minnesota utilized a split block design with two cropping treatments – soybeans intercropped into pennycress and monocropped soybeans. Intercropping with pennycress only reduced soybean yield in 2 of the 5 environments. Additionally, there were significant genotype-by-treatment interactions where a few varieties outperformed the rest. Interestingly, some soybean architectural changes under pennycress were unexpected and may be the reason greater yield reductions were not observed. These results indicate the potential need for a separate breeding pipeline with intercropping objectives. This characterization of soybean traits under pennycress facilitates a trait-informed approach for the selection of new soybean varieties adapted to a winter oilseed intercropping system.

P-017. Luis Salazar

University of California

Genetic Analysis of Lettuce Root System Architectural (RSA) Changes in Salinity

Differential RSA traits were identified in the lettuce landrace PI 251246 (Lactuca sativa) and wild accession Armenian 999 (Lactuca serriola) when grown on ½ MS media with 0 and 100 mM NaCl, including primary root length and lateral root development. One-hundred twenty lines from an F7 recombinant inbred line population of Armenian 999 x PI 251246 was evaluated for linkage analysis of RSA traits using composite interval mapping and multi-QTL mapping. Major (>15%) and minor (15%<) QTLs related to the maintenance of root length in salinity and lateral root development were identified on chromosomes 4, 5, and 9. Potential candidate genes were identified using the v11 lettuce genome assembly.

P-018. Lushan Ghimire

University of Florida

Genome-wide association analysis reveals genetic factors underlying resistance of Southern Highbush Blueberry to postharvest fruit decay caused by Botrytis cinerea

Botrytis fruit rot, caused by Botrytis cinerea, is a prevalent post-harvest disease in blueberries worldwide. Despite its significant impact, the genetic basis of botrytis fruit rot resistance in blueberries remains poorly understood. In light of growing concerns surrounding the use of botryticides, the imperative for the development of botrytis-resistant cultivars has escalated. Therefore, in this study, we aimed to develop genomic tools for fruit rot resistance by screening advanced selections of Southern Highbush Blueberries at the University of Florida Blueberry Breeding Program and identifying underlying candidate genes. Fully ripe berries from 219 genotypes out of a representative breeding population were collected in 2022, and three replicates were spray inoculated with a B. cinerea suspension at a concentration of 1*10^6 conidia/mL. The berries were incubated at room temperature for 3 days, followed by incubation in a growth chamber at 10°C and 90% relative humidity for 5 days to create optimal disease conditions. Subsequently, the berries were returned to room temperature until the final assessment of disease severity. The population was also genotyped with Capture-Seq approach for SNP detection. Best Linear Unbiased Estimates for the decay percentage was estimated using mixed models. The narrow-sense heritability of the fruit-rot resistance trait was estimated to be 0.46. Through a genome-wide association study, two significant loci were identified on chromosomes 20 and 22, each explaining about 13.5% of the variance. Candidate genes associated with defense responses, including TIR-NBS6, PHOX1, NAC04, and pathogenesis-related thaumatin superfamily protein, were identified within the significant genomic region. Further validation of these loci will enhance our understanding of their role in disease resistance. Ultimately, these findings can inform strategic breeding decisions and expedite the development of disease-resistant cultivars through marker-assisted selection.

P-19. Madhav Subedi

University of Georgia

Genetic Analysis of Major Agronomic Traits in Soft Red Winter Wheat using Genome-Wide Association Study

Wheat is a crucial crop for global food security, and its production must increase by at least 50% by 2050 to meet the growing demand. Grain yield is a complex quantitative trait, heavily influenced by environmental factors, making it challenging to improve through conventional breeding. However, breeding for correlated secondary traits, such as plant height and kernel characters, has shown success in indirect selection for improved yield. The objective of this research is to identify novel genes that govern agronomic traits in SRWW and to develop markers for marker-assisted breeding. We evaluated 236 genotypes of SRWW for eight major agronomic traits across two locations over two years and genotyped them using GBS libraries, resulting in 27,466 SNPs after marker filtration. GWAS was performed using the FarmCPU model in R, reporting markers above -log10 p-values of 5.74 based on Bonferroni correction. Population structure and linkage disequilibrium were also estimated. Seven MTAs were identified for yield and 29 more for rest of the seven agronomic traits. A stable QTL for yield, QYld-2A, explained approximately 12-20% PV in two tested environments and is potentially associated with the gene producing disease resistance protein RGA3. Additionally, another major QTL for yield, QYld-5A, was also identified that overlapped the gene producing MYB transcription factor during heat and drought stress. Two major QTLs were identified for heading date, QHd-5B and QHd-7D, explaining 14 and 10% PV, respectively. Further research is needed to identify the novelty of these identified QTLs. The QTLs/genes identified in this study can be considered as targets for improving the SRWW cultivars for southeast.

P-020. Matthew Brooke

Washington State University

Novel Stem Rust Resistance Identified from the Wild Barley Core Collection Utilizing GWAS

Stem rust (Puccinia graminis f. sp. tritici) is an important foliar disease of barley and wheat worldwide. The Pacific Northwest (PNW) region of the United States serves as a center of stem rust diversity due to the completion of the sexual cycle in primary hosts, barley, wheat, and Elymus, and secondary hosts, Mahonia and common barberry. We generated an extensive collection of Pgt isolates (n = 200) from Eastern Washington and Northern Idaho from the primary cereal hosts barley and wheat and secondary sexual hosts Mahonia and common barberry in 2019 and 2020. Seedling assays on barley resistance gene (R-gene) differentials showed that 99% of the isolates (n= 100) collected from barley were virulent on the barley stem rust R-gene Rpg1, 16% were virulent on the rpg4/Rpg5-mediated resistance locus (RMRL), and 10% were virulent on both genes when combined in the barley line Q21861. This virulence on the two broad and effective stem rust R-genes is unprecedented Pgt virulence on barley that had never been reported worldwide. To identify novel sources of stem rust resistance effective against this virulent PNW population, a set of 318 lines from the Wild Barley Diversity Collection representing the genetic diversity from the Fertile Crescent was screened for seedling resistance using the PNW Pgt isolate Lsp21, which is virulent on line Q21861. Of the 318 lines in the collection, only eighteen were resistant to Lsp21. The two most resistant lines (WBDC-94 & WBDC-238) were found to have the stem rust resistance gene Rpg7. After screening for resistance, a genome-wide association study was conducted to map stem rust resistance using 37,338 single-nucleotide polymorphic markers generated by next-generation sequencing. Three novel loci associated with resistance to isolate Lsp21 were identified on chromosomes 3H and 5H. These novel QTL will help breeders enhance lines for resistance to stem rust in cultivated barley.

P-021. Merritt Khaipho-Burch

Cornell University

The perils and promise of single-gene solutions to crop yield: extraordinary claims require extraordinary evidence

Agriculture relies on plant breeding and genetics to deliver the best crop varieties and agronomic practices to deploy results across nearly a billion hectares of cropland. We regularly see industry delivering on this objective, although optimized for their goals and limited geographies. However, many public sector efforts that feed most of the planet are not meeting these objectives or working effectively across disciplines. A key example is repeated publications on single genes, multiple gene constructs, or similar edits that claim to confer incredible yield increases. Many of these publications are flawed in how they measure and report yield. Often, they lack replication across environments, have low sample sizes, compare yield estimates in non-commercially competitive germplasm, and report on experiment-specific yields that massively underperform as compared to local or global yields. Here, we detail how the plant breeding community can explain common issues in yield testing experiments so that the greater scientific community and the peer review process can catch misleading results early on.

The common issues that need to be explained differently to unfamiliar communities when evaluating the impact of single genes on crop yield include the following:

- Robustly measure crop-relevant yield, not plant-level yield.
- Create field designs that pay attention to plant competition and genotype-by-environment interactions.
- Use elite germplasm.
- Prioritize genes that evolution may have missed or whose variation has been exhausted within elite germplasm.
- Develop collaborations and use public sector frameworks such as the Genome to Fields Initiative to test changes at scale.

Accurate measurement and reporting of crop productivity have drastic consequences for feeding the planet. With the onset of climate change and the degradation of Land and water supplies, there is no more important time to collaborate as a community to accurately measure, improve, and deliver on crop resilience and yield.

P-022. Mohamed El-Walid

Cornell University

Mapping Freezing Tolerance in Tripsacum by Bulk Segregant Analysis

Increased variability in weather patterns is one of many consequences of climate change. Shifting planting zones or early planting can help, but also increases the risk of freezing events. For these reasons, it is imperative to improve freezing and chilling tolerance in maize to maintain and improve plant productivity. Tripsacum dactyloides is a cold-tolerant close relative of maize that diverged about 650 thousand years ago, and can be found across the Americas. As a perennial, this species must withstand elongated freezing temperatures in northern latitudes. By studying the genetic similarity between Tripsacum and maize, we can potentially transfer freezing tolerance traits. To identify causal freezing tolerance genes, we used a bulk segregant analysis (BSA) to find QTL for freezing tolerance within a diverse Tripsacum population. An initial founder population of 304 geographically distinct clones was collected from across the US and used to generate an F1 population from crosses between northern and southern clones. F2 seed was then generated for use in freezing screens where seedlings were subjected to -7°C overnight temperatures. Illumina short-read sequencing was performed on the founders, F1 population and F2 freezing tolerant and susceptible bulks. The diversity and structure of this population allows the contributions of founders to be observed at the chromosome scale as well as site-by-site resolution, by testing alleles for significant segregation between bulks. To identify founder contributions to each bulk, chromosome level genome assemblies have been generated for two founders to be used as reference genomes. Preliminary results have shown founders contribute at varying rates across the genome between bulks and have highlighted candidate loci associated with freezing tolerance.

P-023. Nathan Fumia

University of Hawai'i at Manoa

Leveraging genomics and phenomics to speed improvement in mung bean

Mung bean is one of the most important warm season grain legume crops in Asia and rapidly spreading across the globe. The crop is grown on 7 million ha and provides significant amounts of protein, carbohydrates, and a range of micronutrients. Under the forecasted increases to climate extremes, mung bean could serve to fill an ever-widening gap for warm season leguminous crops. However, selection of accessions becomes difficult where phenotypic and genotypic variation is great alongside a varied preference of seed traits across consumer markets.

We set out to perform selection of elite genebank accessions, held as the mini-core collection at the World Vegetable Center, for yield and yield component traits via an index. Our selection uses refined accuracy by leveraging genomics, phenomics, and genotype-by-environment interaction. BLUP is used to predict genotypic effect of the 292 mini-core accessions towards seed yield, based on genomic relationships formed from 200k SNPs. We expand BLUP analysis to predict phenotypic effect based on the phenomic relationships formed from 75K measurements from 3D multispectral systematic data. Although these methods are restricted to a single environment, our multi-environment trials across 8 countries and 4 years serve to quantify the genotype-by-environment effect. K-fold cross validation finds predictive ability to vary by method but to relate by narrow-sense heritability of the yield component trait. Our weighted rank sum selection index linearly combines yield component traits to proxy yield within our single environment phenomics trial by first ranking genomic and/or phenomic BLUPs, then weighting by predictive accuracy from the cross validated model, and then summing the component weighted ranks for each accession. Selections were made from the predicted random effects in each location finding 3 unique accessions overlapping across all methodologies: PI 369787 (VI001339A-G) from the Philippines, EG-MD-6D (VI000380A-G) from the Philippines, and PI 363534 (VI003220A-G) from India.

P-024. Prabhjot Kaur

Michigan State University

Identification of differentially expressed and co-expressed genes between Petunia RILs exhibiting contrasting development rates

The rate at which plants produce new nodes (development rate) is one of the primary factors controlling crop production time. Petunia (Petunia × hybrida) is an annual bedding plant grown in greenhouses during winter and spring in the northern U.S. which requires considerable heating to provide optimal growing temperatures (18-24℃). Understanding the genetic factors controlling development rate would facilitate accelerating crop timing at cooler temperatures, thus, reducing the production time and input costs due to greenhouse heating. F7 recombinant inbred lines (RILs) developed between the wild progenitor species of petunia, P. integrifolia x P. axillaris (the IA population), were previously utilized to identify 209 differentially expressed genes (DEGs) between lines exhibiting slow and fast development rate. The current study was designed to employ a second RIL population derived from P. axillaris and P. exserta (the AE population) to identify common DEGs between fast- and slow-developing IA and AE RILs, and to utilize the narrower AE cross to identify novel DEGs involved in development rate control. In this study, five AE RILs each exhibiting fast or slow development rates were selected for RNAseq. Based on the principal component and clustering analysis, three samples each of fast and slow development rates were selected for differential gene expression. A total of 183 genes were commonly downregulated in all the low lines versus all the high lines and 29 genes were commonly upregulated in the low lines versus the two high lines (p-value ≤ 0.05 and a log2fold change ≥ |1.5|). Seven DEGs from this study were common with the IA DEGs. Additionally, WGCNA analysis revealed that four modules are correlated with the development rate. The genes in these four modules and the robustly differentially expressed genes are being further evaluated to understand their role in regulating development rate.

P-025. Richard Tegtmeier

Cornell University

Identification and development of markers for a moderate-effect fire blight resistance QTL in M. sieversii, the primary progenitor of domesticated apples

Fire blight, a bacterial disease caused by Erwinia amylovora, is a major and most devastating threat to apple production. Most commercial apple cultivars are susceptible to fire blight driving the need to develop fire blight resistant cultivars. Although several major fire blight resistance QTLs have been identified from wild species of Malus, the challenges of breeding apples due to long juvenile phase and heterozygosity greatly limit their use. M. sieversii, the primary progenitor of domesticated apples, is one of the wild Malus species that is sexually compatible with M. domestica and has some favorable fruit quality traits. In this study, we performed QTL analysis on two F1 apple populations of M. domestica cv. 'Royal Gala' × M. sieversii (GMAL4591 and GMAL4592) to identify fire blight resistance QTL. Parental linkage maps were constructed for each family using marker sets of approximately 20K GBS-SNPs. Phenotype data was collected from parents and progeny through controlled fire blight inoculations in the greenhouse for two subsequent years. A significant ($P < 0.0001$) moderate-effect fire blight resistance QTL on linkage group 7 of GMAL4591 was identified from the paternal parent M. sieversii 'KAZ 95 17-14' (Msv_FB7). Msv_FB7 explains about 48-53% of the phenotyping variance. Additionally, a significant ($P < 0.001$) minor effect QTL explaining 18% of the phenotypic variance was identified in population GMAL4592 on LG10 from 'Royal Gala'. We developed diagnostic SSR markers flank-ing the Msv_FB7 QTL to use in apple breeding. These findings have the potential to accelerate the development of fire blight-resistant cultivars.

P-026. Savanah Dale

Cornell University

A practical approach to utilizing a maize Practical Haplotype Graph: Genomic imputation of sweetcorn biparental populations for speed breeding

In plant breeding, the rate of genetic gain is often constrained by the time it takes to advance generations. Many breeding approaches and tools have been developed with the goal of reducing the amount of time a breeding cycle takes. One such approach is speed breeding, in which abiotic factors such as light and temperature are manipulated to encourage reproductive growth earlier in plants. Through this, seed-to-seed time can be reduced. However, it is necessary to incorporate a method through which selection can be efficiently employed on shorter-time generations for advancement of desirable germplasm in a breeding program. In particular, if a phenotype is expensive or measured later in plant development, this can be challenging; genomic prediction can be used to mitigate this challenge. The Practical Haplotype Graph (PHG) is a useful tool for imputation of genotypes that have low-coverage sequence data, thus enabling genomic prediction and selection of target phenotypes. The potential applications of the PHG are broad, but have yet to be explored in depth. In particular, more information is needed to determine the practicality of using an existing PHG to impute genotypes in populations whose founders are not included in the PHG itself. To test this, a collection of four sweetcorn breeding populations with high-coverage whole-genome sequencing data for the founders and low-coverage whole-genome sequencing data for F2 progeny was used. Methods for determining the practicality of using an existing maize PHG without the sweetcorn founders to impute genotypes in their F2 progeny were tested. Results provide insight into methods to efficiently assess if an existing PHG needs to be updated with information from relevant founders before imputation in populations is conducted. This approach will allow breeders to avoid spending unnecessary time updating or creating a new PHG for imputation in breeding populations with different founders.

P-027. Seren Villwock

Cornell University

Examining the regulation of carotenoid content and its interaction with carbohydrate metabolism in cassava roots to inform biofortification breeding pipelines

Cassava (Manihot esculenta) is a food security crop that is a vital source of calories for millions of smallholder farmers in tropical regions, where there are high rates of vitamin A deficiency. Recent efforts have focused on breeding yellow cassava varieties as a sustainable source of provitamin A carotenoids to help address this issue. However, an undesirable trade-off between carotenoids and dry matter content, a measure of starch yield and a key driver of consumer acceptance, has been a persistent obstacle in African breeding pipelines. Determining the biological basis of the negative correlation between these traits, which may be driven by genetic linkage or pleiotropy, is needed to guide future breeding strategies. This project integrates genomic, transcriptomic, and metabolite data to provide insight into the regulation of carotenoid and carbohydrate metabolism across genetic diversity, developmental time, and spatial variation. Carotenoids, starch, and soluble sugar contents were measured from two storage root tissue layers in a population of 47 Colombian x African cassava accessions and their ten parents. 3’RNAseq is in progress to profile gene expression in these samples, which will be used to identify genes involved in regulating quantitative variation in carotenoid content both within root samples and between genotypes. A gene-metabolite association network will be constructed to integrate these data and characterize interactions between carotenoids and carbohydrate metabolism. Preliminary results will be presented from the first two years of greenhouse trials, which show different relationships between carotenoids and dry matter content among root tissue layers.

P-028. Ali Said Yusuf

University of California

Tackling Aluminum Toxicity in Chickpea: From Digital Genomes to the Agricultural Field

Roughly 40 per cent of the earth’s arable lands are classified as acidic (Uexküll and Mutert, 1995). The global phenomenon of declining pH on arable lands is primarily attributable to agricultural intensification and in particular to the use of nitrogenous fertilizers, which when subject to microbial metabolism release protons into the soil. The risk of low soil pH is largely the consequence of aluminum toxicity. Under acidic conditions, aluminium is released into the soil solution and is directly toxic to plant cells, inhibiting cell division and root elongation. Soluble aluminium also reduces soil nutrition by forming insoluble complexes with phosphate and other ions, creating a situation in which low pH soils are both toxic and nutritionally poor. Pulse legumes including chickpea are notoriously sensitive to aluminium in acid soils, causing significant economic loss worldwide. To address this problem in chickpea, we screened a genetic resource of advanced recombinant inbred lines for sources of aluminum tolerance using a quantitative assay to evaluate plant growth and root architecture responses to aluminum. We identify aluminum tolerance in a subset of lineages and using molecular genetic tools we delineate a 2Mb causal haplotype containing a single major effect QTL derived from wild Cicer reticulatum. Agricultural relevance of the trait was established by evaluating penetrance under field conditions, sowing genotypes in low pH aluminum-toxic soils and corresponding limed controls. Root growth tolerance to toxic aluminum was observed only in lines containing an ~2 Mb introgression from the wild species and not in segregants lacking this haplotype. To facilitate gene identification and trait introgression we developed new genomic resources, including chromosomal-level genome assemblies that have greatly improved assembly statistics and gene annotations. We will describe strategies and initial steps towards gene identification and varietal improvement through introgression into the cultivated species.

P-029. Amaka M. Ifeduba

Texas A&M University

Developing Potato Cultivars for Future Climate Scenarios: Understanding the Mechanisms of Heat Tolerance in Vanguard Russet

Global warming is raising concerns about food availability, and potato production is no exception. The detrimental effects of heat stress on potato production have intensified in recent years, resulting in economic losses and challenges for farmers. Cultivating heat-tolerant potato varieties capable of producing high yields of marketable tubers under challenging conditions has emerged as an effective strategy to overcome high-temperature stress. To develop such varieties, breeders must identify parental plants and select offspring based on specific phenotypic traits or molecular markers associated with heat tolerance. We compared the heat-tolerant fresh market russet variety Vanguard Russet from Texas A&M Breeding Program and the heat-sensitive processing variety Russet Burbank under growth chamber conditions (normal versus high-temperature). Differences in tuber initiation time, bulking, tuber number, plant height, and biomass were sequentially documented at 30, 45, 75, and 100 days after planting (DAP). Our findings revealed distinct characteristics between Vanguard Russet and Russet Burbank in response to heat stress. Vanguard Russet exhibited slower above-ground plant growth and appeared later in maturity than Russet Burbank. However, Vanguard Russet initiated tuber formation earlier (<30 DAP) and produced more tubers than Russet Burbank at all time points evaluated. Under heat stress, both clones experienced a significant increase in above-ground biomass, although this increase was more pronounced in Russet Burbank. Heat stress significantly reduced tuber formation in Russet Burbank. These results suggest that Vanguard Russet employs several mechanisms to cope with heat stress. It initiates tuberization early and efficiently directs photoassimilates towards tubers, utilizing early tuberization, timely allocation, and preferential partitioning of photoassimilates to mitigate the impact of heat stress. After applying the heat treatment, Vanguard Russet maintained a significantly higher tuber number and weight than Russet Burbank under heat stress at 45, 60, 75, and 100 DAP; whereas Russet Burbank had significantly taller plants with more biomass.

P-030. Anne Frances Jarrell

University of Georgia

Mining the wild species Solanum microdontum for improvement of cultivated potato

Solanum microdontum is a wild Andean relative of potato that has shaped the domestication and adaptation of modern cultivated potato to diverse environments. S. microdontum is a diploid species that crosses readily with cultivated potato and has the potential to provide a wealth of untapped genetic material for use in modern potato breeding. Advances in potato breeding are becoming especially critical as climate change brings about new challenges including elevated temperature, increased frequency of extreme weather events, and evolving disease pressure. This project addresses these needs by providing breeders with genetic, molecular, and germplasm resources to be used within the context of newly developed diploid potato breeding programs. This project has two objectives, the first of which is to identify accessions of wild S. microdontum with characteristics that make them favorable for crossing with cultivated potato (S. tuberosum). Traits of interest include resistance to the late blight pathogen (Phytophthora infestans) and tolerance to heat stress. The second objective is to is to generate a high-quality reference genome sequence for S. microdontum and to characterize genetic diversity with publicly available accessions of S. microdontum. This project will contribute to much-needed publicly available potato genome resources and permit robust data mining of S. microdontum trait loci. Access to these phenotyped and genotyped accessions will allow breeders to cross key S. microdontum lines with cultivated breeding lines to create more resilient varieties. These efforts are underway and will ultimately become a rich resource that can be used to help address major challenges in potato production.

P-031. Audrey (Kruse) Morrison

University of Wisconsin- Madison

Identifying QTL associated with resistance to bacterial leaf spot in table beet and Swiss chard

Bacterial leaf spot (BLS), caused by the bacterial pathogen Pseodomonas syringae pv. aptata, is an emerging foliar disease affecting table beet and Swiss chard crops. This disease favors cool, humid environments, which are conditions that occur at the beginning of the growing season. These conditions are also often produced by overhead irrigation and densely planted rows for the baby leaf and salad mix production. BLS is a seedborne disease, so the seed production industry is exploring many different management practices. Defoliation of the above ground leafy material harms commercial root production of these crops, too. BLS presents itself as tan, circular lesions on the leaves, and if the crop has red petioles, often betacyanin “splotches” are seen on the leaves as part of the disease response cascade. My research objective is to identify quantitative trait loci (QTL) associated with BLS resistance. A diversity panel spanning the Beta vulgaris crop complex, including 220 accessions, was subjected to genotype-by-sequencing (GBS) and aligned to the W357B table beet reference genome. These accessions were grown in a controlled environment that favored disease development, and in a randomized complete block design with three replications per accession. Inoculations were followed by disease ratings based on an ordinal rating scale, representing the percentage of diseased leaf area. A GWAS was performed, identifying regions of the beet and chard genome that are statistically associated with resistance to BLS. An application of these identified QTL includes introgressing them into breeding material; when paired with informative management practices, this may alleviate crop devastation and the need for foliar spray application. A candidate gene search was completed. Further applications and next steps, such as linkage mapping, will be discussed.

P-032. Boris M.E. Alladassi

Iowa State University

Using UAV Imagery to Investigate the Dynamics of Sorghum Plant Height Genetics

Plant height is a critical agronomic trait controlled by multiple interacting genetic and environmental factors throughout development. Genetics studies based solely on the final measurement of plant height provide only a snapshot of the complex and dynamic process. Uncovering the genetic basis underlying the temporal dynamics of plant height will enhance our understanding of the genotype-to-phenotype connection. Here, we used time-series plant height data extracted from UAV-based RGB imagery and functional mapping to investigate the temporal dynamics of plant height genetics in two sorghum populations. First, we compared the UAV-extracted measurements with manual measurements, and there were significant correlations of up to 0.94, indicating the 3D reconstruction of the field successfully captured the differences in the genotypes’ height. Next, we used the logistic function to model each genotype’s growth trajectory. Treating the model parameters (asymptote and maximum growth rate) of the genotypes as derived traits, we detected strong signals of QTLs, co-localizing with the loci of Dw1, Dw3, and qHT7.1, controlling the overall growth trajectories of the genotypes. We also used the logistic function to estimate each genotype’s height and growth rate at a five-day interval from 20 to 100 days after planting (DAP). Genome scans of the model-estimated heights detected QTLs with dynamic effects. Four QTLs detected on chromosomes 4, 5, 6, and 7 were transient and only expressed at an early stage (20-35 DAP), while those co-localizing with the loci of Dw1, Dw3, and qHT7.1 expressed at a later stage (40-100 DAP) and were persistent. These results demonstrate that we can leverage the high spatial and temporal resolutions of UAV imagery combined with modern genomic technologies to decipher the genetic basis underlying the temporal dynamics observed in plant height during the developmental process.

P-033. Brayden Blanchard

Louisiana State University Agricultural Center

Optimizing Sugarcane Breeding with R and Python: An Interactive and Improved Database for Daily Crossing Decisions

The success of any variety development program heavily relies on the availability of heritable variation that is exploited through selection to deliver new and improved cultivars. Crossing is the foremost means through which heritable variation is achieved in variety development. However, the breeder must consider a wide range of information to plan the crosses that will provide the desired levels of variation for traits of interest. The LSU AgCenter sugarcane variety development crossing program currently uses SAS 9.4 and a relational Microsoft Access Database for data management and viewing, but improved, open-source tools now exist. This paper describes the construction of an improved database for the crossing program using R and Python and all specified packages. With simple drag and drop features, one can easily store and retrieve necessary data in a way that reduces error and combines previously separate reports and tables into user-friendly data viewing options. Automation features allow for the efficient elimination of undesirable crosses from potential cross combinations using reliable and objective data. The new database provides improved capacity to discern relatedness among individuals using both pedigree and genetic marker data. As further discoveries are made in areas such as molecular genetics and quantitative genetics, this database can be used to continually integrate useful metrics to further guide decision making during crossing. The new database provides a user-friendly, interactive interface that can automate certain decisions, include new information, and provide a simpler, more informed, and more holistic approach to making crossing decisions.

P-034. Bukhtaawer Talat

University of Georgia

Evaluation of root architecture for improvement of cultivated Upland cotton.

Future climatic variations and unpredictable weather patterns likely will exacerbate challenging growing conditions faced by farmers such as extreme heat and drought. An avenue for breeding crops with better tolerance to drought stress is by breeding varieties with a substantial root system such as having a long taproot and a large number of lateral roots to take advantage of water and nutrients available in the soil. In this study, our objective is to assess the phenotypic diversity of cotton (Gossypium hirsutum L.) germplasm for taproot length and lateral root numbers at the seedling stage. We evaluated a panel of 183 cotton lines, consisting of mostly wild accessions of G. hirsutum as well as from three related species (G. hirsutum, G. barbadense, and G. mustelinum). Our results suggest that plant height is not a good predictor for root system development. While root length and lateral root number were significantly correlated, the improved germplasm generally was inferior in both traits compared to the wild germplasm. Finally, a number of wild genotypes possessing exceptional taproot length and lateral root number were identified, and they potentially could be useful for the introgression of root architecture traits to improve cultivated upland cotton.

P-035. Chelang'at Sitonik

University of Wisconsin-Madison

Secondary traits from remote sensing for genomic prediction of potato yield

Genomic prediction and phenomics have the potential to revolutionize potato breeding. High-throughput phenotyping (HTP), based on proximal or remote sensing, enables the rapid acquisition of secondary traits, such as canopy cover, plant height and vegetation indices, at early stages of a breeding program. The objective of this study is to evaluate the potential use of secondary traits for yield prediction in potato. To assess the prospects of using reflectance data from Uncrewed Aerial Vehicles (UAV), breeding populations comprising of different market categories were evaluated during the 2021—2023 growing seasons in Hancock, WI. Plot-level characteristics were extracted from orthomosaics using the FIELDimageR software. The multi-year data were analyzed in a two step-approach using the StageWise R package. Best linear unbiased predictions (BLUPs) were compared based on three models: (1) using marker data, (2) using secondary traits, and (3) using both markers and secondary traits. Prediction accuracies were estimated by cross-validation both within and across environments. For the 2022 season, broad sense heritabilities for canopy cover and plant height ranged from 0.55 to 0.82 and 0.71 to 0.99, respectively, across multiple time points. The heritability estimates of normalized difference vegetation index (NDVI) ranged from 0.76 to 0.77 at 96 and 105 days after planting (DAP), respectively. We anticipate the results will show promise for the use of UAV-based remote sensing to improve selection at the early stages of potato breeding.

P-036. Erin Farmer

Cornell University

Integration of multi-modal proximal remote sensing data for improved prediction of agronomically important crop traits

High-throughput phenotyping has allowed for the collection of agronomic data at higher temporal and spatial resolutions, which has important implications for crop improvement and precision agriculture. With these advancements, there is a need to analyze large amounts of new, complex, and high-dimensional data. However, methods are often crop and trait-specific, and sensors are largely used separately for characterizing phenotypes. Here, we focus on multispectral images (MSIs) collected by unoccupied aerial vehicles (UAVs) and lidar scans collected by unoccupied ground vehicles (UGVs). MSIs and lidar scans were collected on maize hybrids as part of the Genomes to Fields project, from 2018 to 2022, in Aurora, NY. The MSIs capture canopy-level spectral information, including the red, green, blue, red edge, and near infrared bands. The lidar scans are converted to point clouds, which allow for three-dimensional constructions of entire plots and capture subcanopy architectural information. As each modality contains unique structural and spatial features, our goal is to integrate these data streams for improved predictions of agronomically important crop traits, such as grain yield. We plan to use machine learning methods to extract latent space phenotypes (LSPs) from both the MSIs and lidar point clouds. An autoencoder model, which is an unsupervised deep learning method, has been developed and trained for the MSIs, encoding the original images of size 5 x 396 x 94 to vectors of length 256. The reduced representations of each image therefore contain both necessary and sufficient information to generate reconstructions, capturing the important features and complexity of the MSIs. Ultimately, LSPs will also be extracted from the lidar point clouds, which will be used together with the MSI LSPs to characterize manually measured traits, and prediction accuracies of models using each data stream separately and jointly will be compared.

P-037. Estefania Tavares Flores

University of Florida

Dissecting anthocyanin variation in a southern highbush blueberry

Blueberry fruits (Vaccinium spp.) are recognized worldwide as superfoods due to being one of the richest natural sources of antioxidants among fruits and vegetables for human consumption. The demand for high-nutrient blueberries is increasing as the food industry trends toward healthier produce. Total anthocyanin content and composition in blueberries are highly variable traits. Genetic, environmental, and fruit development stages play a critical role in the regulation and composition of these bioactive compounds. While recent studies have described total anthocyanin content in blueberries, there is still an essential gap about this trait's genetic basis and its variation under different environments and post-harvest conditions. To develop new breeding resources for targeting anthocyanin content, we carried out a metabolite analysis of a large southern highbush blueberry breeding population evaluated over three different post-harvest time points and in four different locations. Principal component analyses included 13 anthocyanin types and traditional fruit quality traits (e.g., firm, brix, TTA, berry size, weight) to characterize current variation in advanced blueberry breeding genotypes. Results from this analysis showed no significant correlations between fruit quality traits and anthocyanin composition. An analysis of variance was performed to uncover environmental effects, including 5 SHB varieties across four environments. This analysis showed significant GxE effects on total anthocyanin content and acylation and differences across varieties. In addition, gathered genotypic and phenotypic data were used to calculate genetic parameters and breeding values. Medium-to-large broad-sense heritability values were estimated for different anthocyanin types. Future steps will include using this information to carry out a genome-wide association study that will help pinpoint potential genetic loci in a SHB genomic framework. These findings will serve as a basis for developing breeding resources to target this trait in SHB.

P-038. Flavia Furlan

Louisiana State University

Uncovering the genetic basis of crown rust resistance in a Northern-by-southern oat biparental population

Crown rust, caused by the pathogen Puccinia coronata, poses a significant threat to oat cultivation globally, resulting in substantial crop losses. Breeding programs have historically focused on race-specific resistance, but there is growing research on partial or quantitative resistance to the devastating disease. Southern US oat breeding programs have made progress in developing oat lines with varying levels of resistance, yet the specific resistance type and underlying genes remain unknown. This study aims to identify sources of resistance that continue to control crown rust in the southern US region and investigate the inheritance and patterns of resistance sources using genomic prediction. A recombinant inbred line derived from the cross LA07065_SBSBSB_32-2/CDC Dancer was genotyped using the Illumina 6k SNP chip. Crown rust severity and disease reactions were evaluated across multiple locations and years, including Baton Rouge (LA), Winnsboro (LA), and Citra (FL). The severity of crown rust was observed to be higher in 2022 compared to 2021 and 2020, potentially due to weather patterns. While various levels of resistance were identified among segregating genotypes, evidence suggests that the disease can overcome resistance under highly favorable environmental conditions. By performing a Genome-Wide Association study, a significant Quantitative Trait Locus was identified on chromosome 7D. Furthermore, through genomic prediction analysis, it was observed that the trait in the population may be controlled by a major gene, providing insights into the genetic basis of crown rust resistance. This research highlights the importance of integrating advanced genomic tools into oat breeding programs to accelerate the discovery of resistance genes. The identification of sources that retain effective disease control in the southern US region, coupled with an understanding of the inheritance patterns, will aid in the development of improved varieties with enhanced resistance and ensure sustainable oat production.

P-039. Foster Kangben

Clemson University

Phylogenetic and Functional Analysis of Tiller Angle Control (TAC1) Homeologs in Allotetraploid Cotton

Plants have a remarkable ability to adjust their growth to optimize light capture in competitive environments. Branch angle is a critical aspect of plant architecture that influences plant phenotype and physiology. In cereal crops, increased branch angles have been shown to enable improved productivity in high-density plantings. The Tiller Angle Control (TAC1) gene, initially discovered as a regulator of tiller inclination in rice and corn, has been found to control branch angle in eudicots. Consequently, manipulation of TAC1 in field crops such as cotton offers the potential to improve crop productivity. While most plant species possess a single copy of TAC1, we identified gene duplication events of TAC1 specific to the Gossypium lineage, with 3 copies present in the diploid progenitor species and up to 6 copies in allotetraploid cotton. Sequence analysis of the 6 TAC1 homeologs in Gossypium hirsutum (Coker 312) revealed that these gene copies have diverged from the single copy found in peach, suggesting possible neo- or sub-functionalization. Consistent with this, TAC1 homeologs displayed distinct gene expression patterns in various tissues over developmental time. Significantly elevated expression levels of GhCoker.A11G109300 and GhCoker.D11G112200 were specifically observed in the flower and stem, respectively. The loss of the A11/D11 TAC1 homeologous gene pair created via CRISPR led to a 3-fold reduction in branch angle with altered petiole angles, confirming a role in predominantly controlling branch and petiole angle. These findings present a promising strategy for improving commercial cotton varieties by genetically engineering branches and petiole angles, potentially leading to increased productivity.

P-040. Gonzalo Casorzo

University of Florida

Understanding the Genetic Basis of Postharvest Softening in Blueberries

Blueberries are a commonly consumed soft fruit known for their health benefits. However, they are perishable and prone to spoilage due to fruit softening during postharvest storage. Modern breeding programs are focusing on improving fruit quality and extending the shelf life of fresh blueberries. However, it is uncertain how genetically controlled postharvest softening is in blueberries. The goal of this research was to examine how the genetic makeup of blueberries influences their firmness during postharvest storage, intending to establish effective breeding strategies for developing cultivars with longer shelf life. To achieve this goal, we measured the firmness of 391 southern highbush blueberry genotypes after they had been stored for up to 7 weeks at a temperature of 1°C. Using best linear unbiased prediction (BLUP) and restricted maximum likelihood (REML), we fitted longitudinal mixed models and estimated genetic parameters. Fruit softening exhibited substantial genotypic variation in all postharvest time points, with some surprising individuals that consistently maintained or increased their firmness even after seven weeks of cold storage. Heritability values for fruit softening ranged from 0.32 to 0.48, reaching its maximum value at the 7-week postharvest period. Our results suggest that we can effectively delay blueberry postharvest softening through breeding. If successful, the outcomes can increase the value of blueberries by providing opportunities for selling in far markets or storing the fruit for a longer duration until the market prices increase.

P-041. Gopika Gopinathan

University of Wisconsin-Madison

Speed breeding with early harvest in naked barley to accelerate genetic gain

Speed breeding strategies have been developed for crops such as wheat, oats, barley, and others, where light and nutrient management is used to decrease the total time to complete a full breeding cycle. It is especially successful for line development using single-seed descent strategies. Some studies have shown success at shortening the cycle even further by harvesting the grain before full maturity. The goal of our study was to evaluate the use of speed breeding in combination with early harvest to decrease the cycle time in naked (hull-less) barley. Eleven spring genotypes were exposed to two environmental systems: speed (22 hrs. in light (22.2 °C) and 2 hrs. in dark (16.1°C)) and normal (16 hrs. in light (22.2°C) and 8 hrs. in dark (12.2°C)) in a greenhouse. Plant growth stages and plant height were recorded from the date of emergence to the date of physiological maturity. Seeds were harvested at 14, 21, and 28 days after flowering and at maturity to evaluate grain germination associated with early harvest. A significant genotype by system interaction was observed for all the traits. Therefore, BLUEs were estimated for all the genotypes within each system. Plants were initially taller and reached tillering sooner under speed breeding condition than under normal condition for all genotypes, although the difference was genotype dependent. However, plants were taller in normal conditions at heading for 9 out of 11 genotypes. For all genotypes, the time from the sowing to the flowering stage was reduced by 14 days on average in the speed breeding condition compared to the normal condition. Incorporation of speed breeding and early harvest can help plant breeders enhance genetic gain by increasing the number of breeding cycles per year.

P-042. Grant Billings

North Carolina State University

Genetic and phenotypic changes in cotton over time

How has cotton changed over the past century of breeding? Humans have cultivated the allotetraploid cottons (Gossypium hirsutum and G. barbadense) for over seven thousand years, but only in the past few decades have we had the means to measure traits of high value to cotton consumers. Furthermore, cotton breeding in the United States, at least anecdotally, arose from a small number of introductions of new germplasm, resulting in a narrow genetic base. To understand how cotton has changed over time, a set of 164 cotton cultivars, germplasm releases, and genetic stocks were re-sequenced to ~30X coverage with short reads. In addition, a series of field trials were conducted at three diverse locations in 2020, where data for traits of economic importance including fiber quality, yield, and seed composition traits were collected. Population structure analysis was conducted, with an emphasis on understanding how measures of genetic diversity have changed over time, followed by a genome wide association study. Overall, our study contributes to our understanding of genetic diversity in cotton and reveals some impacts of breeding on the cultivated cotton gene pool.

P-043. Harmeet Singh

University of Missouri

Screening diverse soybean germplasm for early-season flooding tolerance

Soybean is a major oilseed crop grown worldwide. Its production is often threatened by various environmental stresses, such as flooding, resulting in significant yield losses. Heavy rainfall driven flooding conditions worsened by climate change including submergence and waterlogging can cause slow growth, spindly plants and up to 40% yield loss in soybean producing regions of the US. The project aims to identify the genetic basis of early-season flooding tolerance (V2 stage) in soybean. A diverse soybean germplasm (maturity group 2-6) consisting of 324 accessions was screened for tolerance to the early season flooding stress in greenhouse conditions. A wide range of tolerance response was observed in the germplasm screened. The heritability for the early season flooding stress tolerance in this germplasm set was found to be relatively low (30%). Thus, the substantial proportion of variation seems to be attributed to the function of other factors including genotype X environment interactions. Based on flooding injury score (FIS), fifty lines with extreme phenotypes were selected and rescreened with replications. Complete submergence treatment was given for 8 days (severe stress) at V2 stage followed by observation of their injury scoring (FIS). Three lines showed substantial levels of tolerance to the severe stress belonging to different MGs. Subsequent genome-wide association studies (GWAS) in diverse set will be conducted to reveal the genetic architecture of the early season flood tolerance in soybean and to identify the significant Marker-trait associations (MTAs) underlying the tolerance mechanism. This will lead to the development of molecular markers for trait selection. Superior breeding lines will be incorporated into breeding pipelines to transfer the flooding tolerance trait into elite soybean backgrounds using identified markers. The study will ultimately lead to the development of soybean varieties with improved early-season flooding tolerance for target climatic regions of the US especially Midwest.

P-044. Jaideep Kaur Deol

University of Florida

Understanding the defence mechanism in a HLB Tolerant Finger lime hybrid seedling population

Huonglongbing (HLB), a bacterial disease caused by Candidatus Liberibacter asiaticus (CaLas), has resulted in a major loss of citrus production in Florida. The finger lime (Citrus australasica) is an Australian native citrus species which is tolerant to HLB. To understand the tolerance mechanism in the finger lime, a F1 hybrid population derived from the HLB susceptible “Lee” mandarin and a HLB tolerant finger lime tree was produced. Four-year-old F1 hybrids growing under endemic HLB field conditions were evaluated. The CaLas titer in phloem tissues was measured using CQUL primers and calculated based on a standard curve. F1 hybrids from this population having no (undetermined) to low (<33) Ct values were selected for further investigation. We subsequently evaluated the transcript expressing of several defense related genes that have been determined to exhibit differential expression based on a previous study. We also selected twenty-five genes which encode for leucine rich repeats and threonine specific protein kinases for our study. Additionally, we also analyzed the expression of phloem protein associated gene (PP2-15) along with several callose synthase genes. Our results revealed that the defense related transcripts identified in HLB tolerant finger limes are also expressing differentially in `several F1 progenies. Moreover, the transcripts associated with Phloem protein and callose synthase genes were also expressed differentially between these hybrids and HLB susceptible controls. These findings provide an insight on some the factors responsible for the tolerance mechanism in the finger lime and can be used for the development of HLB tolerant citrus.

P-045. Jaspal Singh

University of Florida

Environmental Characterization of Miscanthus Trials

Miscanthus is a perennial grass with high biomass productivity ideal for bioenergy production and carbon sequestration helping climate change mitigation. Growing miscanthus in different locations can result in Genotype by environment G×E interaction complicating the breeder's labor of develop superior cultivars. Proper understanding of G×E requires the study of response changes to different environmental patterns during the growing season. The aim of this study was to consider the environmental characterization of survival spring and biomass yield dry weight based on weather covariates. Phenotypic data derived from 569 Miscanthus Sinensis (MSI) and 9 Miscanthus sacchariflorus (MSA) was considered. These were observed in 6 locations (HU-Hokkaido, Japan; NEF-Leamington, Canada; CSU-Fort-Collins, Colorado; CHA-Urbana, Illinois; KSU-Chuncheon, Korea; and ZJU-Zhuji, China) during three growing periods (July-2012:November-2013; December-2013:November-2014, and December-2014:November-2015). In addition, information on 9 weather covariates were collected from NASA using the EnvRtype R-package. The environmental characterization based on the principal component analysis of all the weather covariates shows groups of environments with similar weather patterns: CHA, KNU and NEF locations cluster together, ZNU is different, and CSU and HU depicted intermediate similarities. The linear regression analysis was implemented to model the phenotypic environmental means as function of the cumulative weather information for different periods of time. The objective was to find specific windows of time when the weather covariates have a significant impact on the response. For example, or both traits, temperature highly impacted the mean responses at different periods of time. Also, total precipitation during December to March significantly impacted spring survival. Hence, the information derived from the optimum periods of time provides insights of the response of the plants to different environmental stimuli during the growing season highlighting the importance of incorporating weather data prediction analysis. Further studies will consider non-linear models to study the relationship between trait responses and weather covariates.

P-046. Jennifer A. Myers

North Carolina State University

Evolution of native blueberry Vaccinium species and ploidy levels in North America

Blueberries are an important fruit crop in North America with extensive breeding efforts to improve blueberries for production and consumption. Some major difficulties in this endeavor include the slow breeding process of blueberries as a woody crop, the multiple species of blueberries, and varying ploidy levels within blueberry species. Differing ploidy levels and species can specifically limit crossing ability and create a high level of heterozygosity in crosses. As trends in plant breeding shift due to climate change and a higher demand for genetic diversity, there is an ever-increasing need to incorporate both elite and native traits in cultivated varieties and a high demand for faster molecular breeding methods for longer cycled plants, such as blueberries. Fortunately, blueberry species in the genus Vaccinium exist natively in North America, however, not a lot is known about the relationship between many of these species, the evolution of blueberry species, and how these native species contribute to cultivated species grown today. The addition of different ploidy levels within Vaccinium and blueberry species adds another level of complexity in understanding blueberry evolution. Without this background knowledge of blueberry evolution, it can make it difficult to identify the best sources of improvement traits that have the easiest and fastest ability to be incorporated. This project focuses on identifying native Vaccinium species and their relation to each other through phylogenetic and sequence analysis as well as ploidy analysis. Native species can be compared both within the different ploidy levels as well as a whole set to better understand how these species relate to each other and how these varying ploidy levels developed within blueberry species. Wild species can also be compared via sequencing to cultivars and breeding lines to identify the best source of native traits for incorporation into blueberry breeding programs both across North America.

P-047. Jonathan S. Concepcion

Michigan State University

Infrared Thermal Imaging-Based Selection and Genome Wide Association for Fusarium Head Blight Resistance in Soft Winter Wheat

Fusarium Head Blight (FHB) is one of the most economically important diseases in wheat. Therefore, continuous development of high yielding FHB-resistant wheat varieties is a top priority for wheat breeding programs. Since selection for FHB-resistance under field conditions remains a challenge due to the scale of manual phenotyping required and potential subjectivity in selection criteria, an on-ground plot-level infrared thermal imaging was carried out during the on-set of FHB-infection in 2022 and 2023. Plot Level infrared thermal readings showed moderate significant correlation with FHB-Severity, FHB-Incidence and FHB-Index. K-Means clustering grouped a larger portion of the evaluated genotypes with susceptible genotype Ambassador. Resistant breeding lines selected based on K-Means clustering using thermal readings in 2022 were validated in 2023. Since Infrared Thermal Imaging was able to delineate FHB-resistance among breeding lines, we conducted genome wide association for FHB-related traits and infrared thermal readings. Significant SNPs associated with FHB Severity were mapped in chromosomes 2A, 3A, 3B, 4A, 5A, 7A, 7B, and 7D, while significant SNPs in chromosomes 2A, 5A, 6A, and 7A were mapped for FHB Index. We found a significant SNP coming from chromosome 2B associated with field level infrared thermal reading co-localized with a previously reported QTL for FHB resistance. Based on the results, infrared thermal imaging showed higher capacity to identify susceptible genotypes over FHB-Index. Further, incorporating infrared thermal imaging with FHB-Index increases efficiency and intensity in selecting putative FHB-resistant wheat genotypes. Lastly, the study showed the integration of infrared thermal imaging with genome wide association studies in identifying putative SNPs associated with FHB Resistance.

P-048. Jordan McBreen

University of Florida

Leveraging UAV-Derived Spectral Imaging Data to Enhance Genomic Selection for High-Performing Wheat Varieties in Heat-Stressed Environments

Creating high-performing wheat varieties that are well-suited to diverse environments in a timely manner is crucial for successful wheat breeding, particularly in regions where post-anthesis heat stress often hampers crop yields. To enhance and optimize the selection of superior breeding lines capable of thriving in various conditions, genomic selection techniques can be augmented by incorporating data obtained from spectral imaging captured by unmanned aerial vehicles (UAVs). In this study, our objective was to investigate the impact of integrating multiple types of sensor data into a genomic selection scheme and its influence on the predictive ability of the selection model. We specifically focused on enhancing genomic selection accuracy for wheat yield data in a single-location, heat-stressed environment by fusing spectral sensor data derived from thermal, multispectral, and hyperspectral sensors mounted on UAVs. We compared the predictive accuracy of single-location, multi-trait genomic selection with sensor fusion on wheat lines grown in small seed increase plots to that of large yield trial plots. The aim was to assess the potential of utilizing spectral data collected through UAV-based imaging to improve grain yield selections in wheat during the early generation and seed-limited stages of the breeding program. Results suggest correlations between the prediction accuracies and selections made by genomic selection models trained on small seed increase plots that included various combinations of UAV-derived thermal, multispectral, and hyperspectral data, and those made by models trained on larger yield trial plots. Integrating genomic selection techniques with UAV-derived spectral imaging data can effectively enhance the selection of high-performing wheat varieties suited for diverse environments. The study highlights the potential of utilizing UAV-based imaging and spectral data to improve grain yield selections in the early stages of wheat breeding programs, providing valuable insights for the optimization of genomic selection strategies in wheat improvement.

P-049. Kabita Poudel

University of Minnesota

Gene Edited Alfalfa (Medicago sativa L.) for Hyper Phosphorus Accumulation

Low Phosphorus (P) concentration affects crop yield and extra P runoff from the soil into waterways results in eutrophication. This research utilizes a gene edited alfalfa line (Photm65-2) generated by targeted mutagenesis of PHOSPHATE2 (PHO2) using CRISPR/Cas9 reagents. The mutant accumulates 5- to 6-fold more phosphate ion (Pi) in herbage than the wildtype control in greenhouse experiments. The objectives of this research are to: (1) determine P acquisition and utilization efficiency of gene-edited alfalfa in the field, (2) characterize the hyperaccumulating alfalfa responses under various phosphorus fertilizer rates, (3) Integrate hyper P accumulating traits into elite and high biomass lines of alfalfa. Hyperaccumulating alfalfa with improved Pi uptake will reduce the cost of alfalfa production. Similarly, it will have practical applications in reclaiming Pi from contaminated or enriched soil, thus decreasing eutrophication and protecting the environment.

P-050. Khushwinder Kaur

Clemson University

Breeding bacterial leaf blight resistant turnip greens

Bacterial leaf blight is a major disease of Brassica species caused by the bacterial pathogen, Pseudomonas cannabina pv. alisalensis (Pca). Pca can infect all brassica crops including B. juncea, B. napus, B. rapa and B. oleracea. Pca lesions can cover over 90% of the older leaves causing significant yield losses in the Southeastern US. There are no effective chemical management options. Currently, there are no bacterial leaf blight resistant B. rapa cultivars and the commercial cultivars are highly susceptible. No acceptable resistance was identified in the USDA core collection of B. rapa. Hence, 250 additional accessions were artificially inoculated with Pca in the greenhouse and four were found to be significantly resistant. An inbred line, CHAS-Top with desirable horticultural characteristics was crossed to r1000 (a resistant breeding line) to develop a horticulturally desirable, Pca resistant B. rapa cultivar. In the past few years, we collected three pathogenic Pseudomonas isolates from commercial fields during seasonal bacterial leaf blight outbreaks. Molecular tests concluded that none were Pca. The genomes of these three isolates were sequenced and analyzed to identify the causal Pseudomonas species. Our preliminary data indicates that these isolates can infect B. rapa, B. juncea and spinach. Our strategy now is to develop a horticulturally desirable B. rapa cultivar that is highly resistant to both Pca and these emerging isolates.

P-051. Liam Dixon

University of Wisconsin-Madison

Cultivar reaction to Cercospora leaf spot in organic and conventional table beet production

Cercospora leaf spot (CLS), caused by the fungal pathogen Cercospora beticola, is the most destructive foliar disease of table beet [Beta vulgaris (L.) subsp. vulgaris] in Wisconsin, USA and globally. Under conducive conditions, symptomatic lesions on the leaf expand and coalesce forming large necrotic areas that can ultimately lead to complete defoliation. This damage detracts from the visual appeal of fresh market bunched beets to such an extent that growers risk buyer rejection if disease severity is observed to be greater than 5%. The application of host-resistance to disease management is constrained by limited knowledge of cultivar reaction to CLS in table beet. This study aimed to address this knowledge gap by conducting replicated field trials in multiple table beet growing environments across Wisconsin. Broad variation for resistance to CLS was observed among the 10 included cultivars. The mean area under disease progress curve (AUDPC) across environments for the most susceptible cultivar, Rhonda, was 267% greater than the most resistant cultivar, Bull's Blood. A multi-environment analysis of cultivar AUDPC values demonstrated no evidence for cultivar x environment interaction, revealing consistent CLS reactions across organic and conventional production systems. While susceptible cultivars surpassed 5% severity in all environments, the resistant cultivars remained below this threshold in six of the 10 evaluated environments. By comparison to resistant sugar beet [Beta vulgaris (L.) subsp. vulgaris] cultivars, however, all tested table beets appeared susceptible to CLS, highlighting the potential for a CLS breeding effort in table beet. These findings may provide helpful guidance to table beet growers affected by CLS in Wisconsin and beyond.

P-052. Maliheh Shaltouki Rizi

Purdue University

Machine Vision enables detecting small differences and their timing in wheat under limited watering scenario

Machine vision techniques, including RGB imaging, are valuable in measuring plant growth by capturing changes in size and shape over time. By employing non-destructive and continuous monitoring, these techniques are particularly useful in assessing canopy growth under varying experimental conditions such as drought. However, there are limitations to canopy monitoring, such as the inability to observe kernel growth hidden within spikes. To address these challenges, we conducted a study focusing on the growth of a recurrent parent Yecora-rojo (referred to as Yecora) and its 2nd backcrossed progenies under pre-heading water limitation. The objective was to evaluate the capability of RGB imaging in quantifying differences in their tolerance to limited watering conditions. The plants were grown in a controlled environment. RGB sensors were used to capture images three times a week until 20 days after heading. The side projected area (SPA) was utilized as an indicator of growth. We demonstrated the difference in recovery after stress by using the numerical approximation of the area under the curve, for two of the progenies that performed better than Yecora under a limited watering scenario. Furthermore, the continuous measurements allowed us to identify the specific time points that contributed to these differences. The grains from individual plants were phenotyped using a laser-based size determination system, evaluating length, width, and area per kernel. This method avails a complete picture of the total kernels produced by a single plant and facilitates studying varietal differences. This study identified two BC2 progenies Yecora147 and Yecora190 as targets of further field studies and breeding to develop the next breeding population.

P-053. Inés Rebollo

University of Minnesota

Heterogeneous genetic covariances in genomewide prediction in maize

Models commonly used for genomewide prediction assume a single genetic variance for all individuals, even when the individuals belong to different populations that may vary in their genetic covariances. Our objective was to determine if predictive ability in structured populations is higher with heterogeneous genetic covariances than with a homogenous genetic covariance. We analyzed data from four biparental maize populations, each with 134 to 242 individuals testcrossed to one or two testers, that were phenotyped in 18 environments and genotyped with 1260 single nucleotide polymorphism markers. By genomic best linear unbiased prediction, we assessed predictive ability for grain yield in each biparental population with all of the remaining biparental populations serving as the training population. We calculated genomewide marker effects in each biparental population by ridge regression-best linear unbiased prediction, then estimated the genetic covariance between each pair of populations from the correlation between their genomewide marker effects. We found that predictive ability was higher with a heterogeneous covariance structure. Compared with the homogeneous-variance model, the predictive ability with a heterogeneous covariance structure across eight population x tester combinations was higher by a mean of 0.12 (range of 0.00 to 0.28). In the future, we will investigate ways of estimating the heterogeneous covariances prior to phenotyping any of the individuals in the test population.

P-054. Maria Roberta De Oliveira

North Dakota State University

Using Canopy Measurements to Predict Dry Bean and Soybean Seed Yield

Increasing the yield is the primary goal of most plant breeding programs for major crops, such as dry beans (Phaseolus vulgaris) and soybeans [Glycine max (L.) Merr.]. Therefore, adopting breeding strategies that focus on secondary traits strongly associated with the primary trait allows plant breeders to effectively identify promising lines during the early stages of growth. The incorporation of new technologies, such as unmanned aerial systems (UAS), into plant breeding, can help to improve efficiencies by allowing the implementation of high-throughput phenotyping (HTP) approaches, which in turn can accelerate crop improvement. Therefore, the overall goal of this study was to assess the association between canopy coverage and dry bean and soybean grain yield using RGB cameras mounted on a UAS platform. The study was carried out on field trials belonging to the dry bean and soybean breeding program at North Dakota State University, located at Prosper and Casselton, North Dakota during the 2022 growing season. Images were collected using an Autel Evo II 6K aircraft, which is outfitted with a 20-megapixel (MP) camera. Flights were conducted once a week at an altitude of 50 meters above ground level (AGL), starting from early vegetative growth stages until the last plots matured. After each flight, images were processed using Pix4DMapper software from Pix4D (v4.7.5; Pix4D SA, Switzerland). The resulting orthomosaic was brought into ArcGIS Pro (ESRI, United States) for further analysis, where vegetation indices were calculated, and statistics (mean, median, max, min, and range) were generated for each individual plot. These metrics will be used to develop a regression model to establish the relationship between the ground cover data obtained using image analysis and grain yield.

P-055. Marjorie Hanneman

Cornell University

Genetic Analysis of Vitamin B3 Levels in Maize Grain

Malnutrition is a prevalent human health concern in regions relying on a limited selection of staple crops that do not provide sufficient micronutrient levels. Biofortification, the genetic improvement of nutrient content in crops, has become a major focus of plant breeding. Vitamin B3 (commonly known as niacin) is an essential compound that is largely unavailable in maize-based diets, potentially leading to niacin deficiencies in human populations primarily subsisting on maize grain processed without nixtamalization, a treatment to make niacin bioavailable. This is because trigonelline, a methyl derivative of niacin, is inactive and unavailable to humans. Trigonelline accounts for a major portion of the total, potential vitamin B3 compounds in unprocessed maize grain. Identifying the genes involved in the accumulation of total bioactive vitamin B3 and conversion of niacin to trigonelline would help in optimizing the bioavailability of vitamin B3 in maize grain intended for human consumption. Through an analysis of vitamin B3 levels in grain samples from ~3,000 lines of a maize inbred line association panel, three inbred lines were identified to have an ~80% lower level of trigonelline (near-zero) and a ~55% higher level of niacin. A biparental population of more than 250 F2 individuals was constructed with a phenotypically extreme line and an average trigonelline line, for genetic mapping of vitamin B3 levels in maize grain. This analysis detected a major quantitative trait locus (QTL) on maize chromosome four that explained nearly two-thirds of the phenotypic variation for trigonelline concentration. Of the 51 genes included in this QTL interval, two potential causal genes are involved in the vitamin B3 pathway. Additional studies are being conducted to further reveal the genetic regulation of vitamin B3 accumulation and guide future maize breeding efforts to decrease niacin deficiencies globally.

P-056. Mark Dempsey

Clemson University

Adapting and Optimizing Lentil for Organic Production in the Southeastern U.S.

Lentil is a nutrient-rich cool-season pulse crop typically grown in dryland farming systems in north-central North America. Organic lentil production represents only a small fraction of total lentil production in North America (ca. 1%), but sells for approximately two-fold conventional lentils. Still, it has yet to be adapted to the warmer and more humid climate of the Southeastern U.S., owing to its limited disease resistance and ability to compete with weeds. Thus, it would be advantageous for organic grain producers in the Southeast to access lentil cultivars that resist disease pressure and compete well with weeds. To identify candidate genotypes for adaptation to organic production in the Southeast, we established a diverse lentil population (298 accessions) in February 2022 and February 2023 at two certified organic farms in South Carolina with contrasting soils: one with lighter soil (2022 and 2023) and one with heavier soil (2023 only). Key traits quantified include days to maturity, canopy cover, and disease incidence. Accessions exhibited significant variation among traits, suggesting there is adequate diversity to select breeding parents for organic production in the region. While most accessions performed well in lighter soil, disease pressure was problematic in heavier soil, and root rot diseases (Fusarium, Verticillium, and an oomycete) were the primary production constraint. However, in heavier soil, several accessions exhibited moderate resistance to root rot diseases, and early- and mid-maturing accessions were more likely to reach maturity before disease led to their death. Additionally, accessions with high canopy cover are more likely to out compete weeds, but the earliest maturing accessions had very low canopy cover. From this, accessions possessing the right combination of disease resistance, maturity timing, and high canopy cover can be used as parents in a breeding pipeline to optimize lentil traits for organic production in the Southeastern U.S.

P-057. Nick Stelling

Kansas State University

The Potential Effects of GW7 on Grain Dimensions and Plant Height in Wheat Domestication

In addition to loss of shattering and glume tenacity, wheat domestication was accompanied by changes in grain dimensions and increase in grain size. Selection for grain dimension traits is likely associated with their correlation with yield, treatability, and the grain milling properties. Our results indicate that the knock-out of TaGW7 results in shorter and wider grains, increased grain weight, and shorter plants. GW7 is a potential target of domestication as TaGW7-A1 falls into a domestication selective sweep region on chromosome 2A. The GW7-A1 alleles in hexaploid wheat and domesticated emmer wheat have a 1.9 kb insertion in the promoter region, which is present only in part of the wild emmer wheat accessions. The decreased expression of TtGW7-A1 in wild emmer is associated with the 1.9 kb insertion, and the expression of GW7-A1 in domesticated emmer is lower than in wild emmer. To investigate the phenotypic effects of the 1.9 kb insertion, the TaGW7-A1 allele from wheat cultivar Bobwhite was introgressed into wild emmer, and the allele from wild emmer was also introgressed into the Bobwhite cultivar. The introgression from Bobwhite into wild emmer did not result in shorter plants, or shorter and wider grains as expected, which suggests that wild emmer has other allelic variants of genes in the pathways that effect these phenotypes. Bobwhite plants with the TtGW7 allele without insertion had longer grains than the Bobwhite plants. These results suggest that GW7 is one of the domestication genes that contributed to plant height and grain dimension traits of cultivated forms of wheat.

P-058. Nicolas A. H. Lara

North Carolina State University

Identifying height controlling QTL in southeastern soft red winter wheat

Bread wheat (Triticum aestivum, hereafter wheat) is one of the world’s principal food crops, accounting for one fifth of all calories and protein consumed by humans1. Dwarfing genes such as Rht-B1 and Rht-D1 confer gibberellin-insensitivity in wheat, resulting in dwarfism. Semi-dwarf wheat varieties were crucial for improving wheat yield during the Green Revolution by reducing lodging and increasing the amount of resources devoted to seed production in a plant, increasing net yield2. However, a growing body of literature indicates that gibberellin-insensitivity can have unintended side effects such as reduced nitrogen-uptake efficiency3, prompting the search for alternative genes controlling height.

In this study we aim to identify qualitative trait loci (QTL) controlling height in eastern US soft red winter wheat germplasm. We used a set of recombinant inbred line (RIL) populations representing crosses between many representative wheat lines from breeding programs across the southeast to carry out this experiment. Fourteen parent lines having Rht-D1b were crossed to make 17 RIL populations, and approximately 150 individuals were grown from each population at three location years. We measured height at senescence at each location and employed genotyping-by-sequencing (GBS) to obtain high-density genotypic data from each RIL. We created linkage maps for each population, then did composite interval mapping (CIM) to identify significant QTL regions in order to identify the most significant height QTLs. We also used a mixed linear model approach to identify significant markers via association mapping. Markers on chromosome 6A were consistently associated with plant height. Our results suggest the widespread presence of gene(s) on this chromosome in eastern wheat germplasm that influence plant height in the presence of major dwarfing allele Rht-D1b.

P-059. Pablo Sipowicz

University of Florida

Effect of marker density in the predictive ability of multivariate models for yield and quality traits in alfalfa (Medicago sativa L.)

Alfalfa is a forage crop highly appreciated for its nutritive value and biomass production. Genetic gain for complex traits in alfalfa has been stagnant for recent years and genomic selection has been proposed as a mean to accelerate genetic gain. Several genotyping platforms have been developed for alfalfa in recent years, ranging from few thousands of DNA markers up to the order of hundreds of thousands. In the era of multi-omics there is an increased need to reduce dimensionality of datasets as it allows to lower the complexity of models and computational resources required. The objectives of this study were to optimize marker density for genomic prediction in a multi-trait genomic prediction framework for dry matter yield (DMY), crude protein (CP), neutral detergent fiber (NDF) and in vitro organic matter digestibility (IVOMD). Predictive ability (PA) of models with varying number of DNA markers genotyped by Sequence capture (SC) was estimated. The genomic best linear unbiased predictor G-BLUP model was implemented. The predictive ability with 70000 markers was of 0.27, 0.17, 0.25 and 0.27 for DMY, CP, NDF, and IVOMD respectively. Similar results were found with as low as 100, 50, 50, and 100 markers for DMY, CP, NDF and IVOMD respectively. Based on our results, reduction of genotypic data to hundreds of markers will not penalize genomic prediction across traits.

P-060. Pablo Sandro

University of Wisconsin

Stability prediction using random regression gBLUP

Cultivar stability is key to assure the viability of agricultural production systems. Stability can be measured using different indicators and is difficult to measure on highly quantitative traits such as grain yield. One of the limitations is the representation of the possible environments where the cultivar would grow, this requires a big data set. Breeding programs have access to historical information from phenotypic information from Multi environment trials (METs). METs are highly unbalanced due to the cycling of genotypes as the breeding cycles advance. The availability of genomic information allows us to leverage the historical METs and use genomic prediction models to improve the accuracy of the selection using information from relatives tested in other environments. This work aims to use a historical data set to train a genomic prediction model for grain yield stability to help select stable genotypes in the early stages of the breeding program. We used a historical database for oats (Avena sativa L.) comprising 139 environments considered as combinations of year and locations in Wisconsin, in combination with a set of 3000 SNP markers, both retrieved from T3/Oat (https://oat.triticeaetoolbox.org). We estimated the genetic relationship matrix, trained a random regression GBLUP model, and evaluated it under a new environment (CV0), new genotype (CV1), and new genotype by environment datapoint (CV2) cross-validation schemes using asreml-r in R statistical program. The predictive ability for stability (regression slope) was 0.97 (0.90-0.99) for CV0, 0.19 (-0.07-0.34) for CV1, and 0.96 (0.95-0.97) for CV2. Our results suggest that information from better-tested genotypes can be borrowed to predict the stability of genotypes in early testing stages. This would help to perform an early selection for the stability type in the early stages of testing, saving resources doing selection over genotypes tested in a small sample of environments.

P-061. Paul Adunola

University of Florida

berrycv-worfklow: A python-based computer vision tool for quantifying waxy bloom in blueberries

The outermost surface of blueberry fruits is covered by a whitish bloom-like wax that serves as a virtual index of freshness and consumer appeal. Phenotyping for bloom in blueberry fruits is traditionally through visual scoring. This approach is subjective and could lead to inconsistency in ratings. To address this challenge, we developed a computer vision and machine learning workflow for automated bloom phenotyping from blueberry fruit images. berrycv-workflow is a python-based data extraction workflow designed to provide simple, fast, and accurate method for phenotyping multiple blueberry traits simultaneously. We phenotyped fruit samples from 197 Southern Highbush Blueberry individuals in the University of Florida Blueberry Breeding program using visual scoring and image-based approach from berrycv-workflow. All individuals were phenotyped for bloom at 1 day, 1 week, 3 weeks, and 7 weeks storage time points (STP). High correlation coefficient (r = 0.74) between both approaches across STP indicated that similar physiological information for the trait was captured. Furthermore, we carried out effectiveness comparison using different genetic metrics to validate the superiority of image-based phenotyping using the berrycv-workflow software. The results revealed higher broad-sense and narrow-sense heritability for image-based approach compared to visual scoring across- and at each STP. Results from genome-wide association study identified 5 and 12 significant SNP-bloom associations using visual scoring and image-based phenotyping, respectively. However, 6 stable SNP-bloom associations were found for image-based phenotyping at 3 weeks and 7 weeks STP and across time points. Finally, we developed a phenotyping workflow that provides superior relationship between phenotypic trait and genetic merits, allowing breeders to select superior genotypes accurately for wax bloom in blueberry. The repository for the project can be found in https://github.com/tj-schultz/berrycv-workflow.

P-062. Shalini P. Etukuri

Clemson University

Revolutionizing Cotton Fiber Quality Assessment: A Case Study Empowering an Advanced Fiber Phenotyping Method

Cotton (Gossypium spp.) is a pre-eminent natural textile fiber that generates annual revenue exceeding $120 billion in the United States. Cotton fiber maturity and fineness are essential characteristics to evaluate cotton fiber quality. However, despite the significance of these fiber parameters, no measurement methods have proven satisfactory, quick, and reliable. Cross sections of cotton fibers provide direct measurements of fiber fineness and maturity, which provides reference data for calibrating or validating other indirect measurements. Despite this importance, existing sample preparation methods and image analysis procedures are tedious and error-prone, limiting their broad application in measuring cotton fiber quality. In this context, we have improved a method for measuring individual cotton fibers, introducing a high-throughput fiber phenotyping strategy that minimizes or eliminates experimental errors and provides error-free quantitative data on fiber properties. To demonstrate the effectiveness of this method, we conducted a case study involving two parental Gossypium hirsutum, Upland lines: Siokra-250, known for its superior fiber quality, and U-1, characterized by poor fiber quality. A minimum of 400 cross-individual measurements were taken from each parent using a light microscope (Olympus LEXT Optical Profiler). Average values for various parameters, including area, perimeter, the circularity of lumen and outer area, true fiber area, theta, fineness, and maturity ratio, were obtained. Our results indicate that U-1 exhibits higher maturity than Siokra-250. U-1 has slightly lower fineness when compared to Siokra-250.

These findings provide evidence of significantly different fiber properties between the two parents. Based on these results, we plan to utilize our improved phenotyping method to construct a genetic map controlling fiber quality traits. This will involve using F7 Recombinant Inbred Lines (RILs) from these two parents. By leveraging our enhanced phenotyping approach, we aim to gain a deeper understanding of the genetic factors influencing cotton fiber quality.

P-063. Shatabdi Proma

University of Florida

Miscanthus hybrid prediction using general and specific combining ability (GCA, SCA) in interaction with environment

Miscanthus is a C4 grass with great potential for biofuel production. Current Miscanthus breeding programs are focusing on increasing the adaptation of new Miscanthus×giganteus (M×g) clones, derived from Miscanthus sinensis (Msi) and Miscanthus sacchariflorus (Msa). The evaluation of the adaptation of these clones requires the establishment of multi-environmental trials. The utilization of genomic prediction (GP) models accounting for the genotype-by-environment (G×E) interaction could help optimize breeding efficiency by reducing the phenotyping costs. The aim of this study was to develop elaborated GP-G×E models (M1:E+P1+P2; M2:E+P1+P2+P1×P2; M3: E+P1+P2+P1×P2+P1×E+P2×E+P1×P2×E; E: environment, P1: parent 1, P2: parent 2, P1×P2: Interaction between parents, and P1×E, P2×E, P1×P2×E resembling interactions with environments) that can exploit the genetic diversity of parental genotypes to identify potential unobserved hybrids derived from the crosses between 569Msi and 9Msa (n = 5,121). The performance of these models was assessed using four cross-validation schemes. CV2: sparse testing design; CV1: prediction of novel genotypes; CV0: prediction in novel environments; CV00: prediction of novel genotypes in novel environments. All genotypes were observed in 5 locations for three years and scored for 15 yield components. Predicting parental genotypes, the results showed limited improvements of G×E model with respect to the conventional GP model; however, the mean square error was significantly reduced to about 20%. These results highlight the importance of adding weather data in the GS models. Additionally, the prediction of within-environments hybrid performance returned many specific crosses with increased yield biomass compared to the parental genotypes. This offers the opportunity to consider potential crosses between parental lines to develop superior hybrids showing stability in diverse environments. In conclusion, this study suggests that the identification of parents with general combining ability (GCA) and specific combing ability (SCA) could be crucial for the development of hybrids with enhanced yields showing stability across different environmental conditions.

P-064. Sonia Salaria

Clemson University

Genome Wide Association Studies (GWAS) to explore fatty acid composition of a chickpea (*Cicer arietinum* L.) diversity panel for biofortification

Chickpea is a highly nutritious crop rich in proteins, carbohydrates, micronutrients, fibers, and low levels of fats. Chickpea fats reduce the risk of cardiovascular diseases (CVDs), blood cholesterol, and obesity in humans. The study was conducted in a chickpea diversity panel with 256 accessions (Kabuli and desi types) to explore the genetic diversity for four primary chickpea fatty acids, palmitic acid (PA), linoleic acid (LA), alpha-linolenic acid (ALA), and oleic acid (OA), which are crucial for human health as well as contribute to plant stress responses also. The wide phenotypic genetic variation for fatty acid concentrations, PA (45and 0.7–912.6 mg/100 g), LA (1605.7–3459.9 mg/100 g), ALA (416.4–864.5 mg/100 g), and OA (1035.5–1907.2 mg/100 g), was found. Likewise, the percent recommended daily allowances (% RDA) was also variable for PA (3.3–6.8%), LA (21.4–46.1%), ALA (34.7–72%), and OA (4.3–7.9%). However, the fatty acids demonstrated weak correlations among each other. Genome-wide association studies (GWAS) were conducted to explore genotypic variation using genomic tools. A total of 38 significant single nucleotide polymorphisms (SNPs) were identified for PA. A gene, cicar.*CDCFrontier.Ca_07489* and associated with significant SNPs, SCM001768.1_39576741 was found on chromosome 5. Two genes, *cicar.CDCFrontier.Ca_15893* and *cicar.CDCFrontier.Ca_11085* associated with SNPs SCM001769.1_38680762 and SCM001769.1_23676626, respectively were found on chromosome 6. One gene, *cicar.CDCFrontier.Ca_26609* was associated with a significant SNP, SCM001770.1_28220559 (chromosome 7). Admixture population structure analysis revealed seven subpopulations in this panel based on ancestral diversity. To our knowledge, this is the first study to characterize the fatty acid profiles in a chickpea diversity panel and, consequently, the first GWAS of chickpea fatty acids. These findings demonstrate the possibility to biofortify the chickpeas for fatty acids using conventional and genomic breeding techniques and aim to breed superior cultivars with better fatty acid profiles for improved human health and plant stress responses.

P-065. Uzezi Okinedo

University of Massachusetts Boston

Discovering the Genetic Basis of Rice Grain Shape

Breeding for high-quality rice can be accelerated by high-throughput phenotyping, leading to the identification and assessment of the genetic basis of rice grain structure. In this study, we used a recently described phenotyping pipeline to analyze rice grain size and shape, which are essential components of rice quality, in the diverse USDA rice mini-core collection. We measured nine grain phenotypes and identified significant differences among the five sub-populations represented in the mini core only for solidity, with aus sub-populations exhibiting substantially lower solidity values.

Solidity measures the ratio of grain area to the area of a convex hull surrounding the grain. These ratios vary from 0–1, where values closer to one indicate rounder seeds and smaller values signify curved or abnormal shapes. We identified genome-wide associations for variation in solidity on chromosomes 3, 7, 8, and 9, with 913 candidate genes within 1 MB upstream and downstream of these associated loci. Seven of these candidate genes have known function in seed-related traits and 38 genes have no known function. These candidate genes for solidity may provide novel insight into the genetic control of rice grain shape and assist future breeding efforts. Our ongoing work focuses on characterizing haplotype diversity at these loci across rice varieties.

P-066. Venkata Rao Ganaparthi

Clemson University

Mapping and validation of Fusarium wilt race 2 resistance QTLs from Citrullus amarus line USVL246-FR2

Fusarium oxysporum f. sp. niveum (Fon) race 2 causes Fusarium wilt in watermelon and threatens watermelon production around the world. Grafting to resistant root stocks can reduce economic losses but increases the cost of cultivation. While management practices can lessen disease severity, these measures do not prevent financial losses. The development of resistant cultivars is an effective and important component of disease management. Implementation of marker-assisted selection to develop resistant cultivars requires the identification of resistance quantitive trait loci (QTL), development of molecular markers and validation of marker-phenotype association with an independent population. An intra-specific Citrullus amarus recombinant inbred line (RIL) population was generated from a cross of resistant USVL246-FR2 and susceptible line USVL114 and used for mapping Fon race 2 resistance QTLs. KASP markers were developed (N=51) for the major QTL on chromosome 9 and for minor QTLs on chromosomes 1, 6 and 8. An inter-specific F2:3 population was developed from resistance donor USVL246-FR2 (C. amarus) and a susceptible cultivar 'Sugarbaby' (Citrullus lanatus) to validate the utility of the markers for introgression of resistance from the crop wild relative into cultivated watermelon. While 45 KASP markers were polymorphic in the intraspecific C. amarus population, only 27 segregated in the interspecific validation population. Four of the polymorphic markers (two on chromosome 9 and one each on chromosomes 1 and 8) showed significant difference in separation of genotypes based on mean disease severity, but together explained only 16% of the phenotypic variance. Haplotype analysis was more effective at predicting mean disease severity of families than single markers. Families that inherited resistant parental alleles at three KASP marker loci on chromosomes 9 and 8 had 42% lower disease severity than families with susceptible parental alleles. The haplotype markers identified in this study will be valuable for development of Fon race 2 resistant watermelon cultivars.

Clemson Highlights 10: Clemson University Graduation Ceremony (Little John Coliseum)

POSTER ABSTRACTS – MS

P-067. Alexandra Smith

University of Guelph

Investigating genomic prediction accuracies within and across breeding cycles and generations in a Canadian barley breeding program

Major advantages of genomic selection, such as reducing breeding cycle time and increasing selection intensity, require predictions to be made across breeding cycles or generations. However, predictions across breeding cycles or generations can result in a trade-off with prediction accuracy, due to factors including genotype x environment interactions, relationships between the training and validation sets, and non-additive gene action. The objectives of this project are to explore these factors by comparing prediction accuracies within and across breeding cycles, and by determining how the addition of genomic relatedness impacts phenotype-based predictions of future performance. The project uses three breeding cycles of the Agriculture and Agri-Food Canada barley breeding program. In each breeding cycle, approximately 150 lines from 30 crosses were evaluated in preliminary yield trials and genotyped at approximately 6,700 SNPs. 30 lines were selected using phenotype alone for an advanced yield trial the following year. Preliminary results of predictions within the same generation of the same breeding cycle (within preliminary trials), across different breeding cycles at the same generation (across preliminary trials), and across generations of the same breeding cycle (across preliminary and advanced trials) will be presented. As new parents are introduced in different breeding cycles, it is hypothesized that lower prediction accuracies will be observed across cycles in comparison to within cycles. Predictions across generations are expected to benefit from the addition of genomic information, relative to phenotypic selection alone. This project aims to contribute to the practical application of genomic selection in breeding programs.

P-068. Ansari Shaik

University of Florida

Enhancing Genomic Prediction Models in Miscanthus by Incorporating the Genotype-by-Environment Interaction

Miscanthus is a genus of perennial grass used for biofuel production. Breeding efforts for increasing biofuel production have been focused on Miscanthus sinensis (MSI) due to its high biomass production and Miscanthus sacchariflorus (MSA) for its cold tolerance. A significant expansion of the cultivation of these species grown at multiple locations is crucial for the development of efficient and alternative energy sources to replace fossil fuels. Genomic prediction(GP) models can exploit the MSA and MSI multi-location information to obtain genomic estimated breeding values(GEBVs) of untested genotype-in-environment combinations for biomass dry yield. The aim of this study was to utilize different genomic prediction models to account for the interaction between genotypes and environments of miscanthus populations at multiple locations. Four elaborated GP models (E+G+G×E-[M2]; E+G+T+T×E-[M3]; E+G+T+G×T-[M4]; E+G+T+G×E+G×T+T×E+GTE-[M5];[E: environment; G: SNPs; T: harvesting year; G×E SNP-by-environment interaction; T×E harvest-by-environment interaction; G×T SNPs-by-harvest interaction; G×T×E SNPs-by-harvest-by-environment interaction]). These models were contrasted with the conventional prediction model E+G-[M1]. Four prediction scenarios (CV2, CV1, CV0, and CV00) and 10 replicates of a five-fold cross-validation were considered to evaluate the model's performance (CV2, predicting tested genotypes in observed environments; CV1, untested genotypes in observed environments; CV0, tested genotypes in unobserved environments; and CV00 untested genotypes in unobserved environments). Results showed that for MSA the interaction models consistently outperformed the conventional model in all the cross-validation scenarios, exhibiting high within-environment correlations(0.72-0.83). On the other hand, MSI in CV2 and CV0 M1 returned the best results(0.32-0.42). While for CV1, M2 showed the best performance(0.55). Finally, for CV00, M3 (0.268) demonstrated a slight improvement compared to the M1 model. These results highlight the importance of incorporating genotype-by-environment interactions in models for accurate miscanthus yield prediction in multi-environment trials. A follow-up study will focus on integrating weather data in the GP models to improve within environments biomass predictive ability.

P-069. Audrey Mahon

University of Florida

Leveraging High-Throughput Phenotyping and Bioinformatics to Improve Selection of Phytoglycogen in Sweet Corn Breeding

Phytoglycogen (PG), a polymer of glucose found in sweet corn, has received increased interest for its unique properties. Stemming from a highly dendritic form, PG has notably high absorbance, retention, solubility, and stability in water with a low viscosity. In addition to being valued in fresh corn for imparting creamy texture, it has potential application as a natural nanoparticle in pharmacology, food science, cosmetology, and biotechnology. Phytoglycogen is largely sourced from the endosperm of sweet corn kernels mutant for the sugary1 (su1) gene, known as sugary lines. These are known to accumulate PG due to mutations in the starch debranching enzyme isoamylase1. Multiple su1 alleles have been characterized, each producing differing levels of PG content. In addition to this variability, the same allele in different backgrounds will vary in PG content, indicating that PG accumulation is a quantitative trait. Breeding for high PG lines will thus be a complex task, particularly considering the difficulties of selection for the trait due to destructive and time-consuming phenotyping. Therefore, the aim of this research is to streamline breeding by leveraging high-throughput phenotyping and genomics to improve selection methods for PG content. A diverse population of ~700 inbred lines was phenotyped for PG. A genome wide association study was performed using these to find significant single-nucleotide polymorphisms, finding 28, with one found in an exon of the gene glk20, a transcription factor expressed during endosperm development. A method to improve phenotypic selection was developed using single-kernel Near-Infrared Spectroscopy (skNIR), a high-throughput and nondestructive method of observing kernel composition. Spectral readings of six kernels from 130 of these lines were compared to PG content quantified with wet chemistry. This data was used to build a model to predict PG content, with a prediction accuracy R2=0.67, allowing for high-throughput intrafamily selection of PG content.

P-070. Brianna Cheek

University of Georgia-IPBGG

In vitro Inoculation and Field Evaluation of Peanut Lines in Search of Resistance to Aflatoxin Contamination

Aflatoxins are a toxic, carcinogenic secondary metabolite that is produced by the fungi Aspergillus flavus and Aspergillus parasiticus. Aflatoxin resistance in peanut has been sought after for many years but has remained elusive in cultivars because of large amounts of variance due to genotype-by-environment interactions, making it difficult to capture. Previously, four Quantitative Trait Loci (QTLs) have been identified on chromosomes A01, A02, B03, and B10 of the peanut genome. We evaluated several lines from a population (ICB population) derived from a cross between the resistant genotype ICG1471 and the resistant line Carolina Black, and one line from a population made from a cross between ICG1471 and the susceptible Florida-07. We also evaluated the parents of our 18-parent and 8-parent MAGIC (Multi-parent Advanced Generation Intercross) populations, since it would be beneficial for us to see the resistance levels of the parents as we test the progeny for aflatoxin resistance. Seeds from these lines were inoculated with Aspergillus flavus. The aflatoxin was then extracted using methanol and quantified using Aflatest affinity columns and a fluorometer. We compared the Fisher's Least Significant Difference groupings to the genotypes of each line to see how they differed with the log-transformed aflatoxin production levels. Through this in vitro inoculation of lines, we were able to see how the groupings corresponded with the QTLs for resistance in the ICB population, but more testing needs to be done to confirm the QTLs. There was also good differentiation between many of the MAGIC parents. From the ICG1471 x Carolina Black population, line ICB_11_02 shows promise as a germplasm with resistance to aflatoxin production.

P-071. Carolina E. Weldt

North Carolina State University

Using high throughput phenotyping methods to identify QTL associated with drought tolerance in S. secundatum

Unmanned Aircraft systems (UAS)-assisted high-throughput phenotyping holds significant potential for enhancing the efficiency of data collection, reducing variability in visual ratings, promoting standardization across trials, and ultimately improving phenotyping accuracy. By utilizing multispectral an RGB imagery, valuable drought-related data such as normalized difference vegetation index (NDVI) and percent green cover (PGC) can be obtained. Extensive research has demonstrated a strong correlation between aerial and ground-based NDVI measurements, establishing it as the preferred vegetation index for drought monitoring. St. Augustinegrass [Stenotaphrum secundatum (Walt.) Kuntze] is a warm-season turfgrass widely utilized in residential lawns and landscapes throughout the southeastern and south-central regions of the United States. Its exceptional shade tolerance and dense stoloniferous growth habit have contributed to its popularity. However, the species experiences adverse effects drought conditions, significantly impacting its performance. To address this issue, a mapping population derived from a cross between 'XSA10098' and 'XSA10127', two breeding lines selected due to their divergent responses to drought in both greenhouse and field environments was planted at the Sanhills Research Station (Jackson Springs, NC) in randomized complete block design with three replicates. Both NDVI and PGC were collected before irrigation was withheld and, subsequent measurements were taken every three days during the drought period. The study will continue with a third year of data collection and analysis in 2023, with the gathered traits serving as a basis for mapping quantitative trait loci. Ultimately, this information will guide marker-assisted selection to enhance drought resistance in St. Augustinegrass.

P-072. Dalton West

University of Georgia

Linkage Drag Associated with Introgression of Meloidogyne incognita Resistant Genes from Wild Relatives into Upland Cotton

Meloidogyne incognita (southern root-knot nematode - RKN), is the most economically detrimental endoparasitic pathogen to cotton. Cotton germplasm resistant to RKN has been available since the 1970s and genetic markers linked to major resistant QTLs have been developed, yet a majority of the modern cotton cultivars are susceptible to RKN. The objective of the present study was to determine the potential yield and fiber quality linkage drag associated with the incorporation of the resistance QTLs. We developed eight resistant experimental lines possessing either both resistance QTLs qMi-C11 and qMi-C14 or only a single QTL. Field evaluation conducted in multiple Georgia environments showed that a number of the resistance lines had higher lint yield than both the donor parent and commercial resistant check cultivars. In addition, the experimental lines performed exceptionally well for fiber quality traits such as length and strength. Hence, the data suggests that while linkage drag due to incorporation of the resistance QTLs may affect yield and quality components, such negative associations could be overcome by breeding with elite germplasm and rigorous selection to produce high yielding lines with excellent fiber quality.

P-073. Dwight Davidson

Kansas State University

UAS-based Evaluation of Wild Relative Introgression into Winter Wheat

Wild relatives of wheat such as wild emmer and Aegilops tauschii are a valuable source of genetic diversity for improving wheat and developing of high-yielding varieties. To identify lines with traits improving wheat performance in Kansas environments, we developed and characterized a population of 3000 wild emmer introgression lines (ILs) in winter wheat. Specifically, we have focused on biomass, which acts as a source of assimilates for developing grains and has potential to improve wheat yield potential. ILs planted at four locations in Kansas (Colby, Hays, Hutchinson, Ashland) were analyzed in 2022 and 2023 seasons. RGB, red edge, and near inferred (NIR) data were collected using UAS and used to create a digital elevation model (DEM) and calculate Normalized Difference Vegetative Index (NDVI), uniformity, and canopy height. Biomass data was collected for subsets of samples immediately or the day after each flight. A positive correlation between canopy height (CH), canopy volume (CV), NDVI and biomass was observed, indicating that UAS-based data could be useful for developing models to predict biomass in ILs. A model incorporating reflectance data, canopy height, volume and temperature is currently being trained to predict biomass accumulation throughout the growing season and identify high-biomass ILs with optimal harvest index and improved yield. In addition, we have observed broad range of variation in CH, CV, and NDVI in ILs compared to checks, suggesting that the developed population could be also valuable source novel phenomic diversity for improving winter wheat in the Great Plains breeding programs.

P-074. Jared Weaver

Clemson University

Metabolic profile of Armillaria Root Rot fungi affecting the United States Stone Fruit Industry

Armillaria Root Rot (ARR) is an economically significant replant disease causing stone fruit growers an estimated $3-4 million annual loss. Understanding how fungi cause ARR function, interact with stone fruit crops or with the environment, and act as plant pathogens are lacking. Therefore, we used untargeted metabolomic techniques on the three prevalent U.S. ARR causing fungi, Armillaria mellea, Armillaria ostoyae, and Desarmillaria tabescens, to establish a baseline fungal metabolite profile. Fungal cultures were grown in two different media, malt extract liquid media and malt extract liquid media appended with the ground-up root of the ARR susceptible peach rootstock Guardian®. Liquid Chromatography in combination with Mass Spectrometry, revealed a metabolic profile of 1,546 unique metabolites in the three fungi with a total of 551 significantly expressed metabolites across all fungi samples. Of these 551 metabolites, 162 were upregulated with a fold change ≥ 2 in the malt extract media appended with Guardian® ground root and 12 were potentially phytotoxic. The results of this study provide a metabolic baseline for future plant-pathogen interactions and could identify biologically significant metabolites involved in ARR.

P-075. John Oscar S. Enriquez

University of Wisconsin-Madison

Genomic Prediction with Environmental Covariates in Potato

Prediction and modelling of complex traits is heavily influenced by genotype-by-environment interactions (GEI). For the past decade, quantitative characterization of environmental factors has been shown to improve model performance and prediction accuracy. In the present study, mixed models with main marker effects, as well as interactions between markers and environmental covariates (ECs), were used to predict yield in potato. The models were evaluated using data from the 2011-2022 U.S. National Chip Processing Trials (NCPT), which spanned 10 states and included 627 genotypes. Additive and dominance genetic effects were estimated using 12K genome-wide markers from SNP array genotyping. ECs were based on environmental information acquired through remote-sensing technologies: 17 weather parameters from the NASA POWER Project and 40 soil characteristics from the USGS Polaris Soil Series Map. Bayesian regression models were fitted by Markov Chain Monte Carlo using the BGLR R-package. Three prediction scenarios were considered: predicting untested genotypes in previous locations, predicting existing genotypes in new locations, and predicting untested genotypes in new locations. The proportion of variance for the different effects and cross-validation prediction accuracies will be presented.

P-076. Julio Sellani

Louisiana State University

Characterizing the Genetic Architecture of Metribuzin Tolerance in a Soft Red Winter Diversity Panel

Wheat is one of the world's most important food crops and provides nearly 20% of the calories consumed. Wheat is the third most important crop after corn and rice on a global production scale. Wheat production is negatively affected by several biotic and abiotic factors including weather, diseases, and weeds. Metribuzin is a broad-spectrum herbicide commonly used in wheat because it is inexpensive and controls most of the common weeds in wheat fields. Identification of markers closely linked to metribuzin tolerance is an important way to make selections for this important trait in wheat breeding. Marker assisted selection (MAS) could speed and improve the efficiency of breeding for metribuzin tolerance. Through field screening in two locations in Louisiana, some lines have shown significant levels for the grower controlling weeds that might cause yield loss in varieties or lines that are tolerant to its application. Reactions of wheat varieties to metribuzin vary from tolerant to sensitive, injury damage is influenced by the environmental conditions. The interaction of environmental conditions and wheat varieties makes metribuzin reaction rating more difficult and time-consuming, which makes growers decide not to use this inexpensive and effective chemical to control weeds. Understanding the genetic architecture of metribuzin reaction and breeding for resistance are desirable goals. Metribuzin tolerance is quantitative and is controlled by a level of resistance to metribuzin with minimal foliar damage. The present project focuses on the identification of the genetic architecture of metribuzin tolerant in soft red winter wheat using the progeny of AGS2035 and AGS2060 and a diversity panel named "Gulf Atlantic Wheat Nursery" (GAWN). Following the results obtained in this study, 8 SNP markers were selected in the GAWN. An analysis of markers in the two populations revealed that information in six chromosomes is common in the two populations.

P-077. Glenn S. Cole

University of California

FIVE HIGH-YIELDING, FUSARIUM WILT-RESISTANT CULTIVARS FOR SHORT-DAY, DAY-NEUTRAL, AND SUMMER-PLANT MARKETS

There is a rising concern about strawberry diseases affecting productivity considerably; one of them is Fusarium oxysporum f. sp. fragariae, commonly known as Fusarium wilt. The University of California, Davis breeding program is developing cultivars with improved disease resistance, competitive yields, and fruit quality for the strawberry industry. Here we present five new strawberry cultivars for commercial release, three day-neutral varieties: UC ECLIPSE (17C242P023), UC KEYSTONE (17C138P062), UC GOLDEN GATE (17C139P045), and two short-day varieties: UC SURFLINE (16C555P053), UC MONARCH (17C138P021). In-field experimental trials were established in multiple growing locations in the coastal area of California during three years (2020-2022). These five cultivars are all high yielding (up to 38% above commercial checks), resistant to Fusarium, moderately resistant to Verticillium dahliae and Phytophthora cactorum, and improved for fruit quality and aroma. Other important traits we can highlight are yield earliness for short-day environments (UC SURFLINE), later yield production for day-neutral environments (UC KEYSTONE), suitability to machine harvest (UC MONARCH, UC GOLDEN GATE), and excellent performance in fall- and summer-planted fields (UC ECLIPSE).

P-078. Katherine J. Fortune

University of Guelph

Phenotypic Assessment of Genetic Variation in a Canadian-Elite x Wild-Derived Soybean NAM Population: Yield and Seed Composition Traits

Continuous releases of high-yielding cultivars are crucial to meet the growing demand for conventional food-grade soybean. However, the average annual genetic gain for yield in soybean is relatively low (~0.8%) due mainly to a limited genetic base comprised of approximately 35 ancestral lines forming the North American germplasm. To address this limitation, the utilization of wild-derived exotic germplasm holds great potential for introducing new genes and alleles associated with yield and agronomic traits into the University of Guelph soybean germplasm. The research utilizes a nested association mapping (NAM) population to identify novel genetic diversity and exotic-based high-yielding alleles. This population consists of four recombinant inbred line (RIL) families resulting from crosses between the Canadian elite cultivar OAC Bruton and four wild-derived lines. Yield, agronomic and seed composition are complex quantitative traits controlled by multiple genes and influenced by environment. As such multi-environmental testing was carried out in three locations in Southern Ontario to capture environmental influence.

The primary objectives of this study are as follows: 1) To perform a comprehensive phenotypic analysis to investigate genotype and genotype x environment interaction factors affecting yield and seed composition traits. 2) To assess the genetic variance and breeding value of parental lines, with a specific focus on wild-derived lines. 3) To identify exotic-based genomic regions underlying yield, agronomic and seed composition traits within the NAM population using both QTL linkage mapping and genome-wide association studies.

The findings will contribute to genomics-based toolkits for facilitating the introgression of favourable exotic-derived gene variants into cultivar development programs and ultimately the development of high-yielding food-grade soybean cultivars.

P-079. Kyle Fahey

North Carolina State University

Trait Marker Association for Non-Race 1 Verticillium dahliae Resistance using a Targeted Genotyping-by-Sequencing Approach

Verticillium dahliae is a soil-borne vascular wilt that greatly impacts worldwide tomato production in temperate areas. Race 1 is defined as strains showing avirulence on tomatoes containing the qualitative resistance gene Ve1. The rootstock 'Aibou' reportedly has qualitative resistance to a subset of the non-race 1 V. dahliae population, from which races 2 and 3 are separated, with race 3 being virulent on 'Aibou'. Previous studies have shown that race 3 is the most dominant race in the tomato-growing regions of NC and lacks commercialized or known host resistance sources. Additionally, outside of methyl bromide, which has been phased out due to severe environmental impacts, control measures have been ineffective on Verticillium wilt caused by race 3 strains of V. dahliae in tomatoes. In this project, Single Primer Enrichment Technology (SPET) was used to identify genetic variants highly associated with non-race 1 resistance within an F5 mapping population derived from a cross between two genetically distant parental lines. The mapping population with 215 recombinant inbred lines (RILs) was generated using single seed descent. A collection of twenty most resistant and susceptible RILs were genotyped by the targeted genotyping approach and assessed for verticillium wilt across two replicated on-farm trials in western North Carolina. Each trial was phenotyped for Verticillium wilt symptoms and degree of infection during 2022 using a categorical rating scale ranging from 0-12. Trait-marker association analyses through generalized linear model revealed that genetic variants on chromosomes 4 and 10 are highly associated with the Verticillium race 3 resistance in the mapping population. Further, potential test markers have been developed and will be tested in 2023. By developing germplasm and DNA markers that cosegregate with the resistance of interest, current and future breeding efforts for verticillium wilt can be accelerated, delivering critical varieties to the tomato industry.

P-080. Luke Dojack

University of Guelph

QTL-Sequencing of Seed Quality Traits in Soybean: The Effect of Bulk Selection on Trait Correlation

Quantitative Trait Loci-Sequencing (QTL-Seq) has emerged as a powerful technique for the detection of QTL of major effect in several species. By separately bulk sequencing the most and least promising lines for the trait of interest, we can swiftly identify QTLs within a population. QTL that are over-represented in the bulk of promising lines and under-represented in the bulk of undesirable lines can be investigated as likely major QTL. Despite the efficiency and reliability of QTL-sequencing in uncovering genetic regions of major effect, we cannot expect all identified QTL to be of use in commercial breeding programs. As a result of either pleiotropy or close linkage to alleles with an undesirable effect on either seed quality or agronomic traits, QTL of major effect may be unusable as markers for selection. Limiting such inutile outcomes is therefore a major concern for breeding programs that wish to make use of QTL-sequencing. Through close examination of the relationships between the fatty acid profile and other important agronomic and seed quality traits in both the whole population and the selected QTL-sequencing bulks, we can identify concerning characteristics of major QTL present in a population before sequencing has even taken place.

The objective of this study is to identify differences in the correlations between fatty acid profile, seed quality, and agronomic traits in QTL-sequencing bulks and their respective populations. This study consisted of three populations of recombinant inbred lines that have been developed to identify QTL associated with high-oleic acid content and reduced polyunsaturated fatty acid content in conventional soybean [Glycine max (L.) Merr.]. These populations were grown in two locations in southern Ontario in 2022. Relationships between seed quality and agronomic traits were assessed in each population as a whole, a selected low-oleic QTL-seq bulk, and a high-oleic QTL-seq bulk.

P-081. Manoj Kumar Reddy Sangireddy

Fort Valley State University

Association Mapping of Aphid Resistance in Sorghum using different phenotyping approaches

The Sorghum aphid (SA) Melanaphis sorghi (Theobald) constitutes a persistent and detrimental insect pest, profoundly encumbering sorghum production across the United States. This research utilized a subset of Sorghum Association Panel (SAP) to explore the genomic regions underpinning aphid resistance, which currently have been limited to RMES1 locus on the chromosome SBI-06. A combination of traditional visual examination and novel high-throughput phenotyping (HTP), facilitated by drone-based imaging and automated robot, was deployed for assessing plant phenotype for aphid resistance loci and other traits. The genome-wide association mapping was performed using recently available new genomic resource set, consisting of nearly 7 million variants included 5,420,745 single nucleotide polymorphisms (SNPs), 1,349,015 insertions/deletions (indels), and 171,907 copy number variants (CNVs). These whole-genome sequencing resources enabled us with the identification of numerous marker-trait associations (MTAs) that linked to aphid resistance loci and related morphological traits. Adding new genomic resources bolstered our ability to detect more regions for aphid resistance and other physiological traits. Our results captured all previously known four genomic loci associated with plant height, Dw1-Dw4 including some new locations. We found several locations where manual, drone and robot assessed plant height was found co-located or at unique single loci. GWAS for plant stem thickness was identified using ground robot. These results support high throughput phenotyping as a tool for future breeding. The markers identified have potential applications in genomics-assisted breeding.

P-082. Mary-Frances Behnke

Clemson University

Meta-GWAS of anthracnose-resistance in global sorghum lines

Anthracnose of sorghum (causal agent: Colletotrichum sublineola) is the most detrimental disease of sorghum (Sorghum bicolor) worldwide, significantly reducing grain yield. This meta-analysis of genome-wide association studies (GWAS) of anthracnose-resistance in sorghum seeks to elucidate genetic sources of the trait by increasing sample size, thus improving statistical power of the GWAS. The meta-analysis includes genotypic and phenotypic data from 5 unique studies and 1,349 sorghum lines. Original genotype-by-sequencing data from were obtained primarily from National Center for Biotechnology Information’s Sequence Read Archive (NCBI-SRA) and prepared and processed using the Tassel 5 GBS v2. pipeline. Phenotypic data were standardized across studies by reconciling different disease-rating scales and generating BLUPs based on standardized disease ratings. GWAS models were produced using the GAPIT3 R package. Two SNPs, Chr5:65194648 and Chr9:1173266, were statistically significant across multiple models. The site on chromosome 5 may be associated with the previously identified Cg1 locus for anthracnose resistance, and the position lies on the transcript for an F-box domain which is a protein structure linked to disease resistance in many crops. Similarly, the site on chromosome 9 was identified as a candidate SNP in one of the composite studies, and it lies within the transcript for a leucine-rich P-loop, also associated with plant defense.

P-083. Morgan Stone

Clemson University

A Genome Wide Association Study of Heat Tolerance in Snap Bean (Phaseolus vulgaris)

Snap bean production is valued at over $300 million dollars in the United States annually. Most of the snap bean producing states are in the colder, northern areas due to the reduction of pod set under heat stress. As temperatures steadily increase it is crucial to breed for increased heat tolerance to improve yield and maintain quality lines throughout the growing season for growers. A snap bean diversity panel (N=268 accessions) was evaluated for flowering time and pod production in replicated field trials in the Southeast at two planting dates to compare production under optimal and heat stress conditions. Through this two-year study we observed a 48.75% average decrease in pods produced from each plot under heat stress. The diversity panel was genotyped with GBS and 28,927 SNPs were used for a genome-wide association study (GWAS). Several significant associations were identified and will be used to design markers for future breeding efforts.

P-084. Namrata Acharya

North Dakota State University

Marker-Assisted Introgression Of A Race-Nonspecific QTL Conferring Resistance To Tan Spot Into The NDSU Durum Wheat Cultivars

Tan spot is a fungal disease of wheat caused by necrotrophic fungal pathogen Pyrenophora-tritici-ripentis. It affects the leaves of wheat, causing a reduction in the total photosynthetic area and a subsequent decrease in production. To control the disease in an environmentally friendly and sustainable manner much current research focuses on developing wheat varieties with resistance to tan spot. From previous genetic mapping studies, a race-nonspecific QTL was discovered on chromosome 3B. In this study, we integrated the favorable allele of the 3B-QTL into the NDSU durum wheat cultivars “Grano” and “Riveland” via marker-assisted backcross selection. The efficiency of the 3B-QTL were tested using 21-days old seedlings of BC4F2, BC4F2:3, and BC5F2:3 progenies for multiple isolates including 331-9, DW5, and ND1 in greenhouse and found that the introgression lines with the favorable allele had significantly lower disease severity than the recurrent parents “Grano” and “Riveland”. These results suggest that the 3B-QTL has been successfully introgressed into the durum wheat cultivars and improved tan spot resistance. Further research will be conducted to test efficiency of the 3B-QTL on disease severity in field conditions, as well as the effects on grain yield and quality related traits.

P-085. Navdeep Kaur

New Mexico State University

Genome-wide association study and genomic selection for Phytophthora root rot resistance in chile peppers (Capsicum spp.)

Phytophthora root rot caused by the soil-borne oomycete Phytophthora capsici, is a major constraint in chile pepper production worldwide. The main objectives of this study were to implement a multi-locus genome-wide association study (GWAS) to identify significant genomic regions associated with Phytophthora root rot resistance and perform genomic predictions. A diversity panel consisting of 157 Capsicum spp. genotypes were screened for resistance against three P. capsici isolates, ‘PWB-185’, ‘PWB-186’, and ‘6347’ . Most of the genotypes displayed root rot symptoms upon P. capsici infection, where only five accessions were completely resistant to all the isolates. Multi-locus GWAS using 55,117 genotyping-by-sequencing (GBS)-derived single nucleotide polymorphism (SNP) markers identified 330 significant SNP markers associated with disease resistance. Further, 56 SNP markers were common across the isolates and distributed on all the chromosomes. Candidate genes including nucleotide-binding site leucine-rich repeat (NBS-LRR), receptor-like kinase (RLKs), and systemic acquired resistance (SAR8.2), were identified within 0.5Mb of the associated markers, demonstrating the complex nature of genetic resistance to P. capsici root rot. Genomic best linear unbiased prediction (gBLUP), Bayesian Generalized Linear Regression (BGLR), and Genome Association and Prediction Integrated Tool-Genomic best linear unbiased prediction (GAPIT-gBLUP) were used to perform genomic selection. The average prediction accuracies using N-fold cross-validations for isolates ‘PWB-185’, ‘PWB-186’, ‘6347’, and the combined dataset were 0.36, 0.17, 0.57, and 0.50 respectively using 55,117 SNP markers. The mean prediction accuracies using 12,569 SNP markers obtained by linkage disequilibrium-based pruning for ‘PWB-185’, ‘PWB-186’, ‘6347’, and the combined dataset were 0.34, 0.18, 0.56, and 0.48 respectively. The GAPIT-gBLUP (0.43) prediction model performed better than gBLUP (0.40) and BGLR (0.38) models . Results from this study will be used to develop Kompetitive allele-specific markers (KASP®) for marker validation and marker-assisted breeding to improve P. capsici resistance in chile peppers.

P-086. Rafaela P. Graciano

University of Florida

Phenomic selection using single kernel NIRS for predicting complex field traits in sweet corn

Genomic selection (GS) is an efficient approach that has been shown to improve genetic gain in breeding. However, the cost and labor associated with this technique can limit its application. As a cost-effective and efficient alternative, phenomic selection (PS) has been proposed for predicting complex traits. This technique maintains the same statistical procedure used in GS-based prediction models but replaces the molecular marker data with near-infrared spectroscopy (NIRS) or other multi-trait phenotype to estimate the relationship between samples. To our knowledge, PS has not yet been evaluated in the context of sweet corn breeding. The goal of the study is to explore the use of this technology for predicting 22 field-based traits of economic importance in sweet corn inbred lines over two years, including ear and vegetative traits. We aim to provide new insights into the use of single kernel NIRS, which involves collecting data from a single seed and may enable the scanning and selection of individuals before planting. To achieve this, three models were employed: G-BLUP and NIRS-BLUP models, which utilized relationship matrices based on SNP and NIRS data respectively, and a third model using both matrices as independent terms. We evaluate the predictive ability of these models by estimating the correlation between observed and predicted values using a replicated fivefold cross-validation process. The results showed that the three models had a similar predictive ability for most traits. However, the NIRS and NIRS plus markers models outperformed GS for important traits such as germination, plant height, and days to pollination. For instance, the mean accuracy across traits was 6% (PS) and 9% (using both matrices) higher with the use of the NIRS compared with GS. Our findings highlight the potential of PS as a low-cost and high-throughput breeding tool that could be implemented in sweet corn breeding programs.

P-087. Samantha Jo Wan

University of Georgia

QTL validation and identification of candidate genes in qFL-Chr.25, a G. barbadense-sourced QTL conditioning for increased fiber lengths in four diverse G. hirsutum backgrounds

Stagnation in fiber quality improvement created by the narrow genetic base of elite cotton germplasm has hindered long term improvement of Upland cotton (Gossypium hirsutum L.). A closely related species, G. barbadense, has been used with some success to transfer favorable alleles for fiber quality into Upland cotton. An obsolete Upland line with introgressions from G. barbadense, Sealand 883, was shown to carry a quantitative trait locus (QTL) for fiber length (qFL-Chr.25). This QTL was later transferred into four diverse genetic backgrounds (Acala SJ-4, Deltapine 50, GA 2004089, and Paymaster HS-26) that represented four major cotton-growing regions of the United States Cotton Belt. To more precisely determine the effect of the QTL, it necessitated the development of near-isogenic lines (NILs). A three year, multilocational study was conducted to test the deployment of qFL-Chr.25 into the four different backgrounds. The fiber analysis results showed a significant positive effect with the introgression of the qFL-Chr.25 locus on the length of fibers in all four backgrounds. In tandem with the field evaluation study, a transcriptome profiling study via RNA sequencing (RNASeq analysis) was conducted to identify putative candidate genes for the causal fiber length gene. The RNASeq analysis revealed three potential candidate genes (Ghir_D06G000180, Ghir_D06G000680 and Ghir_D06G000880) that showed significant down-regulation during early fiber elongation stages in lines carrying the G. barbadense alleles. The three candidate genes in the qFL-Chr.25 region provide targets for functional validation using reverse genetics approaches.

P-088. Stephanie Botton

University of Georgia

Characterization of an Arachis cardenasii introgressed region in cultivated peanut, Arachis hypogaea, that provides peanut root knot nematode, Meloidogyne arenaria, resistance

Cultivated peanut, Arachis hypogaea, is an important row crop in the United States. Peanut root knot nematode (PRKN), Meloidogyne arenaria, are roundworms that infect peanut and can cause devastating damage to a grower's crop. While nematicides and crop rotation are used in combating infestations, having cultivars with genetic resistance is a more ideal tool for growers. However, cultivated peanuts do not have strong resistance to PRKN. To alleviate this, peanut breeders performed an interspecific cross with cultivated peanut using a wild peanut relative, A. cardenasii, that has strong resistance to PRKN. This led to the development of peanut cultivars that have PRKN resistance. It was discovered that the introgression was located on the 9th chromosome of the A genome, taking up 92% of the chromosome. Further studies with two recombinants of this introgressed region pinpointed to the upper portion of yielding a strong resistance to PRKN infection while the lower region was noted to have a moderate resistance. To further characterize the introgressed region, this study identified additional recombinants through genetic studies and tested the lines through phenotyping studies. While the phenotypic data corroborated strong resistance in the upper portion of the introgression, additional experiments will be needed to quantify the resistance response conferred by the lower portion of the introgression.

P-089. Subash Thapa

South Dakota State University

Close-range hyperspectral imaging coupled with machine and deep learning approaches to predict DON content in wheat flour

Fusarium head blight (FHB), caused by a necrotrophic pathogen Fusarium graminearum Schwabe is one of the most destructive fungal diseases of wheat which is known to produce a harmful mycotoxin called deoxynivalenol (DON). DON contamination of wheat grains and/or flours is a serious problem for food safety globally. Currently, DON levels in grain or flour samples can be measured using a variety of methods, including enzyme-linked immunosorbent assay (ELISA) and gas chromatography-mass spectrometry (GC-MS) but these methods are time-consuming, costly, and destructive. Therefore, a limited number of samples were analyzed for DON content in the elite and advanced breeding nurseries and the majority of the selections in early and preliminary trials were made based on visual score for FHB or Fusarium Damaged Kernels (FDK). Development of rapid and non-destructive and economical methods to estimate DON content can help to better facilitate breeding for lower DON. In the present study, GC-MS was used to estimate the DON content in 250 advanced breeding lines from SDSU wheat breeding program that were evaluated in the 2020-21 FHB nursery. The DON content of the 250 selected lines ranged from 0 to 77.6 ppm. The flour samples (3 grams) were analyzed for moisture and protein content on NIR and subjected to close-range hyperspectral imaging (400–1000 nm). Four different machine learning models (PLS regression, Xgboost, RF, and SVM) and one deep learning model (1D CNN) were evaluated on the training (70%) and test (30%) sets to ascertain the most efficient model based on accuracy with the coefficient of determination in prediction (R2) and root mean squared error (RMSE). Overall, advanced hyperspectral imaging coupled with machine and deep learning approaches shows great potential in high-throughput estimation of DON content and will enable breeding for lower DON content.

P-090. Ufuk Caglar

Clemson University

Enabling Breeding for Fruitlet Freeze Tolerance in Peach Germplasm

The adverse effects of climate change on the cultivation of temperate fruit crops are becoming increasingly apparent, specifically in relation to the crucial role of cold temperatures as a limiting factor for plant growth and overall productivity. The occurrence of frost damage, particularly during the spring season, has led to substantial economic losses in the peach industry in the southeastern United States region. The primary emphasis of research in peach and Prunus species has centered on the analysis of dormancy-related characteristics that are connected to the bloom time, such as the requirements for chilling and heat accumulation. In contrast, a relative lack of equal attention has been given to exploring fruitlet freeze tolerance. The development of climate-resilient peach varieties necessitates a combination of these traits, encompassing targeted chilling requirements and elevated heat requirements to enable late blooming, along with fruitlet tolerance towards late spring frosts. A total of seventy-five peach accessions sourced from the peach collection at Clemson University were assessed for their capacity to withstand six freezing temperatures (-10, -8, -6, -4, -2, and 0 ºC) throughout two consecutive seasons (2022/23), using the electrolyte leakage method. Our preliminary results indicated that the inflection point (LT50), determined using an asymmetric sigmoid curve, provided a comprehensive representation of fruitlet freeze tolerance, with similar LT50 values showing consistent patterns of freeze damage. Distinct patterns of the graphical representation of the LT50 and broad-sense heritability (H2) estimates of 0.52 and 0.80, for LT50 and the area under the curve, respectively, suggest genetic control of this trait with a potential for improvement via breeding. The outcomes of this study establish the basis for understanding the genetic regulation of fruitlet freeze tolerance in peach germplasm and the development of climate-resilient varieties through breeding efforts.

P-091. Varun Kumar Reddy Cheruku

Fort Valley State University

Influence of intercropping in manipulating the rhizobiome

Soil can accommodate several thousands of individual microbial taxa, a key component of ecosystems. Microbial composition in the rhizosphere is variable due to heterogeneous environmental conditions; type of soil, host plant-growth stage, and species. Root exudates play a major role in the assemblage of microbes, creating complex interactions between plants and microbe. Individual microorganisms such as endophytes, symbionts, etc. have been well studied but the gains of several other microbial species remain unexploited, which might have more far-reaching effects. It is postulated that diseases of crops can be alleviated by manipulating the rhizosphere microbiome through intercropping. The objective of the study was to survey the changes in dynamics of the rhizobiome of sorghum and lespedeza when intercropped. The experiment was carried out in both field and controlled conditions. The ITS1 and 16S rRNA amplicon sequencing results revealed that sorghum and lespedeza had slightly varied rhizobiomes when intercropped compared with monocropping. It increased the microbial diversity and richness of rhizobiomes at different operational taxonomic units (OTUs). Depending on these results, we have conducted a similar experiment with sorghum and peanut, to see the effect of peanut in manipulating the rhizobiome of sorghum and vice versa. Soil analyses indicated increased levels of nitrogen in the pots with peanut plants. In conclusion, intercropping with specific species may help manipulate the rhizobiome, therefore garnering many hidden beneficial associations. Future research directions may include the selection of genotypes for breeding, based on the analyses of microbial taxa and investigations into the importance of horizontal gene transfer in shaping the rhizobiome. Furthermore, manipulating rhizobiome can help increase soil fertility, improve crop production, and improve our understanding to harness the power of the ecosystem.

P-092. William Walker Spivey

Clemson University

Heat-Proofing Crops: Leaf Lipid Remodeling as a Key Strategy for Developing Heat-Tolerant Peanuts

Given the persistent upward trend in global temperatures, the imperative to develop heat-tolerant varieties has never been more realized. In peanut (Arachis hypogaea), progress in developing heat-tolerant varieties has been hindered because of a limited understanding of the physiological and genetic factors contributing to heat tolerance and a shortage of efficient screening tools capable of reliably evaluating large germplasm collections for heat tolerance. At the cellular level, a fundamental cause that leads to yield loss under heat stress (HT) is membrane damage. This work reports our investigations of a subset of a peanut (Arachis hypogaea) recombinant inbred line population demonstrating lipid remodeling which serves as a mechanism of homeoviscous adaptation used to maintain membrane fluidity when exposed to high temperatures. The major alterations we see in the peanut leaf lipidome under HT is a reduction in the unsaturation levels of plastidic and extra-plastidic membrane diacyl lipids. This is achieved predominantly through a reduction in the 18:3 acyl chains. Our findings show that levels of 18:3 containing triacylglycerols (TG) increased under HT, consistent with their role in sequestering fatty acids during membrane lipid remodeling. The polyunsaturated acyl chains removed from membrane diacyl lipids were also found to be sequestered into phytosterols, forming sterol esters (SEs). This work indicates these reactions as novel roles of SEs in HT adaptation. The sequestration of 18:3 acyl chains from the membrane is a beneficial physiological modification under HT that decreases the availability and susceptibility of molecules that can be oxidized. Overall, this is beneficial for maintaining membrane integrity through a reduction of oxidative damage within membranes. Taken together, our results suggest that the interplay among the 18:3 acyl-containing membrane diacyl lipids (downregulation under HT), 18:3-acyl-containing TGs (upregulation), and polyunsaturated acyl-containing SEs (upregulation) is at the core of the lipid remodeling for HT adaptation in peanut.

Clemson Highlights 11: Peach pollination at the Musser Fruit Research Center

POSTER ABSTRACTS – OTHER

P-093. Anju Biswas

USDA Vegetable Laboratory, Charleston

Genomic prediction approach to improve Fon race 2-resistance in watermelon cultivars (Citrullus lanatus)

Complex traits are governed by numerous loci with small effects. Marker-assisted selection (MAS) approach is not sufficient in incorporating complex traits into elite cultivar background. On the other hand, the application of genomic prediction has been proved to be a promising plant breeding approach for achieving higher genetic gains in incorporating complex traits. This might be particularly relevant in our breeding efforts targeting the complex trait of Fon race 2-resistance in watermelon, as this trait is controlled by multiple genes with moderate heritability. The primary objective of this study was to assess the effectiveness of genomic prediction models in predicting genotypes with respect to Fon race 2-resistance. To investigate the possibility of employing a genomic selection approach to incorporate Fon race 2-resistance into watermelon cultivars, we conducted an experiment using an F2:F3 population derived from a cross between USVL252-FR2 (Fon race 2 resistant) and PI 244019-PRSV-R (Fon race 2susceptible), using it as a training population. The phenotyping experiment was arranged in a randomized complete block design. Genotyping was carried out using 356 F2 parent plants, the F1 hybrid, and the parental lines, employing a genotyping-by-sequencing (GBS) technique. Disease response evaluation of each F2:3 family was conducted at 28 days, measuring the percentage of F3 plants exhibiting complete health (without chlorosis or wilting). We employed two different genomic prediction models: RR-BLUP and G-BLUP. Model performance was evaluated using ten-fold cross-validation. Results indicated that G-BLUP outperformed RR-BLUP, as it successfully predicted 48% of the marker effects associated with unaffected plants, whereas RR-BLUP only achieved 39% accuracy based on the marker data. These findings demonstrate that genomic prediction can be a highly effective technique for selecting superior progenies at early stages of breeding, thereby increasing the genetic gain, and enhancing disease resistance in watermelon cultivars.

P-094. Brandon Monier

Cornell University

Breeder Genomics Hub: cloudifying reproducible breeding pipelines by leveraging genomic tools

Analyzing, translating, and applying genomic and genetic data is crucial for advancing crop improvement to achieve the goals of the Global Food Security Strategy through USAID. Despite its significance towards global agriculture, the widescale integration of this type of data can be limited for end-users across African, Caribbean, and Latin American countries. One bottleneck many research institutions face is data processing capacities, which we can overcome using server-based infrastructure, applications, and new methodologies that reduce dimensionality for genomic predictors. Here, we present the "Breeder Genomics Hub," a server-based platform utilizing JupyterHub for deploying, running, and sharing computational notebooks amongst research groups using server-based computational resources. This Hub has been customized with an extension that provides authentication and retrieval of data from breeding data management systems, such as BMS and Gigwa. The Breeder Genomics Hub is also preloaded with open-source tools curated for efficient data handling and analyses for genomic breeding. Included in this collection of curated tools are the packages rTASSEL and rPHG: R interfaces to Trait Analysis by aSSociation, Evolution, and Linkage version 6 (TASSEL 6) and the Practical Haplotype Graph (PHG), respectively. These packages are user-friendly tools in the R language, giving users access to powerful command-line-driven software to run analyses on large phenotype and genotype datasets. Recent updates to rTASSEL and rPHG allow users to query haplotype data and perform genic allele activity analyses. By coercing rTASSEL and rPHG objects into native R objects, users can build interoperable analytic pipelines to exploit the best tools to suit researchers' needs.

By placing computational power, tools, data, and documentation together on one platform, the Breeder Genomics Hub provides breeding and genetics groups with a shared platform for better reproducibility of informatics pipelines, enhanced computation, and a foundation for training, empowering, and teaching early-career scientists.

P-095. Carlos Cardon

University of Georgia

Variation in gene expression associated with peanut reproductive phenology

The cultivated peanut (Arachis hypogaea L.) ssp. hypogaea never produces flowers on the main stem whereas ssp. fastigiata does produce flowers on the main stem. Despite the economic importance of peanuts, there are few studies directed toward investigating the molecular regulation of flowering in peanuts. The present study aims to find key genes that control peanut flowering regulation and how they coordinate the flowering pattern between ssp. hypogaea and ssp. fastigiata. We used a transcriptional approach from 132 RNAseq libraries to compare samples of Tifrunner (ssp. hypogaea) and GT-C20 (ssp. fastigiata) at six-time points and four tissue types. Our results showed the gibberellin (GA) pathway gene GID1 was differently expressed between Tifrunner and GT-C20 at the time of first bloom (T3). The flower repressor TFL1, was expressed only in Tifrunner main stem (M) samples, and AGL42 showed differences in expression when M and lateral stem (L) samples were compared between Tifrunner and GT-C20, with high expression at all time points in Tifrunner L. DEGs between the beginning of the vegetative phases (T1), transition to flowering (T2), and first bloom (T3) showed more up-regulated genes (JAZ, MYC4, AOS3, AOC4) associated with the JA pathway for Tifrunner. Associated with ABA, PYR1 was down-regulated in Tifrunner and NCED5 up-regulated in GT-C20. SOC1, AGL24, GIGANTEA, and, DELLA were DE between Tifrunner and GT-C20 at the vegetative stage (T1 and T2), and beginning of flowering. Gene co-expression showed as hub genes, FRIGIDA, and two JAZs in the modules S02 and S03 respectively. The L14 module showed many genes associated with the JA pathway, which was more highly expressed in Tifrunner than GT-C20. Our findings show that JA, ET, and ABA could be important to peanut flower regulation, and TFL1 and AGL42 can be responsible for the absence of flowers in the ssp. hypogaea main stem.

P-096. Carolina Ballén-Taborda

Clemson University

Prediction and evaluation of parental combinations using winter wheat historical data

In plant breeding selecting cross-combinations that are more likely to result in superior lines for cultivar development is critical, yet this step remains largely subjective with decisions based on supporting data about potential parents. Genomic selection (GS) provides new opportunities to accelerate genetic gain within modern crop breeding programs. The application of GS has also been expanded to identify superior crosses by simulating variation in progeny performance for a target trait. In this context, the R package PopVar is available to predict genetic variance (VG) and progeny means (µ, µip and µsp) for all possible combinations from a set of phenotyped and genotyped parental lines. This study reports a retroactive PopVar analysis aimed at investigating whether the crosses that produced superior wheat breeding lines would have been made if progeny simulations had guided winter wheat SunGrains breeders' crossing decisions. Here, 217 parents representing two-way pedigrees of 670 historical wheat breeding lines were used to predict genetic variance and progeny means of 23,436 parental combinations for grain yield. Predicted and observed data for the 670 lines (including four released cultivars: GA09436-16LE12, AR09137UC-17-2, LA06146E-P4 and ARLA06146E-1-4) were compared to assess the accuracy of PopVar predictions. A prediction accuracy of 0.3 was observed for yield. Furthermore, the most advanced nursery each line entered was recorded to examine the overall usefulness of simulated VG and µ — and, by extension, µsp — to identify the most valuable crosses. Of the pedigrees that were predicted to give rise to progenies with above-average grain yield, 76% were selected and advanced (or released) by breeders in the SunGrains breeding cooperative. Simulation of progeny performance to select the most promising biparental crosses could accelerate and increase efficiency of the breeding process, especially within the framework of a rapid-cycling recurrent breeding scheme.

P-097. Claudio Fernandes Filho

University of Florida

Enhancing Predictive Ability for Dry Matter Yield in Alfalfa Using a Multilayer Model-based Approach

Alfalfa (Medicago sativa L.) is the most important perennial forage legume in the world because of its relatively high yield and nutritional value. In the United States, alfalfa is the fourth most valued crop behind corn, soybeans, and wheat, with an estimated value of $8.4 billion. Non-dormant alfalfa cultivars have been released and are grown in the southeastern United States. In Florida, nondormant cultivars have been developed for improved adaptation to the state's subtropical agroecosystem; however, these cultivars are not commercially available. Alfalfa breeding for complex traits requires frequent and multiple phenotyping efforts, which is labor intensive and costly. The implementation of multi-omics approaches in breeding can result in greater genetic gain for complex traits in alfalfa. Genomic prediction has been applied in alfalfa for yield, and previous studies used only genomic data in prediction models, resulting in predictive abilities between 0.2-0.4 for yield. The inclusion of enviromics data in prediction models resulted in greater predictive ability for complex traits. The objectives of this study were to: i) perform genomic prediction of dry matter yield (DMY) for alfalfa in a population of half-sib families, ii) perform phenomic prediction of DMY using spectral data from near infrared reflectance spectroscopy (NIRS), iii) compare the predictive ability of genomic and phenomic prediction models in alfalfa, and iv) explore strategies to improve predictive ability of prediction models in alfalfa breeding.

P-098. Andrew Horgan

Texas A&M University

Generating Improved Texture Phenotypes in Advanced Tomato Breeding Lines and Heirloom Cultivars

Heirloom and specialty market tomatoes are cherished for their exceptional flavor profile, high nutritional value, and unique phenotypes. Despite these end-use qualities, large-scale commercial production of heirloom-type tomatoes remains limited for several reasons including severe disease susceptibility, poor yield, rapid fruit softening, and postharvest deterioration. Our study aims to assess the potential and efficacy of CRISPR/Cas9 gene editing technologies for improvement of fruit texture traits in advanced tomato breeding lines and heirloom-type tomatoes, with particular emphasis on extended shelf-life. For this study, advanced tomato breeding lines with exceptional flavor, but insufficient shelf-life, were selected from two tomato breeding programs at Texas A&M University, along with the heirloom cultivar 'Brandywine Sudduth Strain'. CRISPR/Cas9 constructs were designed to generate mutations in three genes: PECTATE LYASE (PL), RIPENING INHIBITOR (RIN) and LATERAL ORGAN BOUNDARIES-1 (LOB1). All three genes influence fruit texture either directly as a cell wall metabolism enzyme (PL), as a transcriptional regulator of multiple cell wall genes (LOB1) or as a global ripening regulator (RIN). We hypothesize that generating novel variation in these genes could delay postharvest senescence without negatively impacting flavor or nutritional value. The potential impacts from this study will 1) address the efficacy of CRISPR/Cas9 technologies to improve shelf-life while maintaining the characteristically high end-use-quality of heirloom-type tomatoes, 2) provide novel alleles for the introgression of improved texture phenotypes in tomato breeding germplasm, and 3) further expand our understanding of the genetic variation for texture phenotypes in unique tomato genetic backgrounds.

P-099. Dominique D.A. Pincot

University of California

Linkage mapping as a classical approach to validate and correct genomic metadata

We constructed 138 genetic linkage maps consisting of wild accessions, heirlooms, and modern cultivars of strawberry (Fragaria spp.). Collectively, the 138 linkage maps that we constructed (A) were highly collinear with the 'Royal Royce' (FaRR1) genome, (B) contained 96.6% (47,821) of the markers present on the Affymetrix Axiom FanaSNP 50K array, and (C) are predicted to cover 95.5% of the FaRR1 genome with sub-100 kb resolution. We found that ~94% of the in silico physical assignments in FaRR1 were accurate, while 5% of the probe DNA sequences were assigned to an incorrect homeolog. We used the information generated by the genetic maps to correct in silico physical positions; these corrected positions can clarify results from analyses dependent on physical positions, such as genome-wide association analysis (GWAS), or aid in protocols reliant on correct physical positions, such as marker design.

P-100. Elad Oren

Cornell University

How does a maize relative withstand deep freezing temperatures?

By extending the growing season of annual crops, net primary productivity and yield can be improved, and the mismatch between soil nitrate availability and crop nitrate demand can be addressed. Early maize planting requires cold tolerance in temperate regions, which is not present in current elite maize. Tripsacum dactyloides, the closest perennial and cold-tolerant relative of maize, can be used to identify genes related to cold adaptation. To this end, we crossed Tripsacum accessions collected from high- and low latitude habitats and screened the hybrids in a field trial in Ithaca, NY over two years, where the winter reaches deep freezing temperatures. Rhizome samples were collected during both the winter dormant stage and the summer active stage in 2019 and 2022. Our analysis revealed 2,404 high-quality proteins that appeared consistently across both years (Spearman $\rho = 0.57$). Among these proteins, 146 showed differential expression between summer and winter. Notably, we identified a set of 30 proteins that were at least $\log_2 FC>2$ more abundant in winter compared to summer. This subset includes lipid transfer proteins, heat shock proteins, late embryogenesis abundant (LEA) proteins, and other drought-related proteins, some of which are known to play crucial roles in cold adaptation. We are leveraging genomic data available from ~40 related Andropogoneae grass species to further study candidate gene families and the regulatory evolution of these candidate proteins and expect to nominate candidate genes for improving cold tolerance in modern maize.

P-101. Emily Delorean

USDA-ARS Genomics and Bioinformatics Research Unit, Raleigh, NC

Representing true plant genomes: Assembly of highly contiguous haplotype-resolved hybrid chili pepper genomes

In many crop species, obtaining the genome assembly of a hybrid or heterozygous individual is necessary for systems that do not tolerate inbreeding or for investigating important biological questions, such as hybrid vigor. However, most genome assembly methods that have been used to date in plants result in a single sequence representation that is not biologically true of either haplotype within a diploid individual. The resulting genome assembly is often fragmented and exhibits a mosaic or chimera of the two haplotypes, referred to as haplotype-switching. Important haplotype level information, such as causal mutations and structural variation is therefore lost and results in difficulties in downstream analysis. To overcome this challenge, we have applied a method developed for animal genome assembly called trio-binning to an intraspecific hybrid of chili pepper (Capsicum annuum) and another hybrid between chili pepper and its wild ancestor (Capsicum annuum var. glabriusculum) The resulting 4 genome assemblies were highly contiguous with N50 values greater than 250 Mb and > 99% of the genome captured in chromosomes.

P-102. Francia Ravelombola

University of Missouri

Use of Mixed Model for Evaluation and Selection of Soybean Seed Yield: BLUP approach

Mixed linear models offer several advantages over ordinary linear models. One notable advantage is the flexibility to treat certain variables as random while treating others as fixed. This capability allows for a more comprehensive consideration of various factors within the model. Given that the analysis objective is to identify superior genotypes, and the genotypes themselves are a random sample, the genotypic effects are considered random, justifying the use of BLUP (best linear unbiased predictor). This study aims at evaluating the performance of 36 advanced soybean breeding lines developed by the University of Missouri regarding seed yield in six environments across different states in the United States, using a Mixed Linear Model approach. The tests were carried out in a randomized complete block design, with three replications and 4 different commercial checks. Statistical analysis was performed in R using Mixed Linear Models. Based on the models, the average predicted values of the hybrids were obtained in the average of the environments and within each environment, making it possible to select the most adapted soybean breeding lines for each environment. It was possible to identify superior genotypes adapted to certain regions of the study, as well as widely adapted. This statistical analysis methodology allowed a better estimate of the genotypic values, making the selection and decision-making process more efficient on the part of the breeders.

P-103. Jinesh Patel

Auburn University

Unveiling Genetic Determinants for Enhanced Resistance Against Cercospora Leaf Blight (CLB) in Soybean (Glycine max L.) Using GWAS Analysis

Cercospora leaf blight (CLB) is a severe disease of soybean [Glycine max (L.) Merr.] grown in regions with hot and humid conditions that have caused 56.12 million bushels to yield loss in the United States and Canada. However, limited efforts have been made to identify the genomic regions underlying resistance to CLB disease in soybean. To address this issue, ra Genome-Wide Association Study using a diverse panel of 460 soybean accessions from maturity groups III to VII. These accessions were evaluated for CLB disease in different regions of the southeastern United States over three years. The study identified 99 SNPs associated with the disease category and 85 SNPs associated with disease incidence. Additionally, 47 SNPs were associated with disease category and 23 SNPs with disease incidence across multiple environments. Candidate genes located within 10kb of these SNPs were found to be involved in biotic and abiotic stress pathways. This information will help develop soybean resistance germplasm. Further research is warranted to study the effect of pyramiding desirable genomic regions and investigate identified genes' role in soybean CLB resistance.

P-104. Jose Orlando Suazo

University of Florida

Increasing ploidy in Frogfruit (Phyla nodiflora L. Greene) seedlings using colchicine

There is increasing interest in Florida for ground cover alternatives to traditional turfgrass lawns. Frogfruit (Phyla nodiflora L. Greene) has garnered significant attention as a potential ground cover due to prostrate growth habit, resilience, and its status as a Florida native. Frogfruit is a perennial herbaceous dicotyledonous plant with distinctive white and pink flowers that are visited by a wide range of pollinators. Additionally, it produces an attractive ornamental groundcover that is also tolerant of mowing. Frogfruit has also been noted to withstand many environmental challenges, such as drought, high salinity, and high traffic. Due to its many benefits and overall hardiness, it merits consideration for use in landscapes and breeding for improvement. Chromosome doubling has been used to increase plant morphological characteristics, including flower size, to increase attractiveness to consumers. The objective of this experiment was to induce polyploidy in frogfruit, which is naturally diploid. Germinating frogfruit seeds were treated for two hours with either a 1% or 5% colchicine solution, grown in petri dishes, and subsequently transplanted into pots. To confirm a successful increase in ploidy, several plants with larger morphological features were selectively compared to their wild-type parents to evaluate the number and size of stomata, and flow cytometry was performed to estimate ploidy of the mutant progeny. Results indicated that an increase in ploidy was successfully achieved as several mutant phenotypes were produced in colchicine treated seedlings. Mutant phenotypes included larger, wider, and thicker leaves, as well as thicker stems and larger flowers. The stomatal size of the mutants varied with some having stomates twice the size of wild-type parents. Mutant plants also had higher picogram/nuclei values providing strong evidence that these methods were successful for induction of polyploidy in frogfruit.

P-105. Joshua Hegarty

University of California

PARTNERSHIP: Triticale research and breeding for grain quality and yield

In an era of rapid population growth, increasing fertilizer prices and limited water for agriculture, it is essential to maximize the efficiency of food production per unit input or acre. Triticale yields are on average 11% higher than wheat (20% under nitrogen stress) and is currently grown on over 2 million acres in the US and over 10 million acres globally. However, insufficient breadmaking quality has limited triticale use to forage and feed applications. Here we propose to improve triticale breadmaking quality with the ultimate goal of unlocking the use of this highly productive crop for direct human food consumption. We have already developed lines carrying different combinations of five genes from wheat known to have favorable effects on breadmaking quality, which are currently being tested by artisan millers and bakers. Our first objective is to evaluate the effect of these introgressed loci on breadmaking quality and grain yield. Our second and third objectives are to identify chromosome region responsible for the exceptional loaf volume produced by two Ukrainian triticale lines, validate them, and deploy them in existing breeding populations across the US. Finally, we propose to combine the new breadmaking QTL with the previous five wheat quality loci into highly productive triticales, and evaluate their effect on quality and yield. This work will be conducted by a collaborative triticale network including California, Washington, Colorado, Nebraska, Maryland (fusarium tolerant germplasm) and CIMMYT (global access). This network will accelerate the development of triticale germplasm that can be commercialize in multiple regions.

P-106. Leonardo Volpato

Michigan State University

Digital Phenotyping in Plant Breeding: Evaluating Relative Maturity, Stand Count, and Plant Height in Dry Beans (Phaseolus vulgaris L.) via RGB Drone-Based Imagery and Deep Learning Approaches

The use of RGB images collected via drones has the potential to replace traditional measurements in field trials to measure traits such as relative maturity (RM), stand count (SC) and plant height (PH). Deep learning (DL) approaches have enabled the development of automated high-throughput phenotyping (HTP) systems that can quickly and accurately measure target traits using low-cost RGB drones. In this study, a time series of drone images was employed to estimate dry bean relative maturity (RM) using a hybrid DL model combining Convolutional Neural Networks (CNN) and Long Short-Term Memory (LSTM). The performance of the Faster-RCNN object detection DL algorithm was also examined for stand count (SC) assessment during the early growth stages. Moreover, plant architecture was analyzed to extract plant height (PH) using digital surface model (DSM) and point cloud (PC) data sources. The CNN-LSTM model demonstrated high performance in predicting the RM of plots across diverse environments and flight datasets, regardless of image size or flight frequency. The Faster R-CNN model accurately identified bean plants at early growth stages, with correlations between the predicted SC and ground-truth measurements in average of 0.8. Appropriate flights altitude, and growth stage should be carefully targeted for optimal SC results, as well as precise boundary box annotations. On average, the PC data source marginally outperformed the DSM data to estimating PH, with average correlation results of 0.55 for PC and 0.52 for DSM. Additionally, the results demonstrated that the CNN-LSTM and Faster R-CNN models outperforms other state-of-the-art techniques to quantify, respectively, RM and SC. The subtraction method proposed for estimating PH in the absence of accurate ground elevation data yielded results comparable to the difference-based method. In addition, open-source software developed to conduct the PH and RM, as well as vegetation indices analyses can contribute greatly to the plant phenotyping community.

P-107. Lichun Cai

Clemson University

Transcriptomic analysis and genome assembly of an Armillaria root rot resistant rootstock

Armillaria root rot (ARR) poses a significant threat to the long-term productivity of stone-fruit and nut crops in the predominant production areas of the United States. To mitigate this issue, the development of ARR-resistant and horticulturally acceptable rootstocks is a crucial step towards the maintenance of production sustainability. To date, genetic resistance to ARR has been found in plum germplasm and a peach/plum hybrid rootstock, 'MP-29'. To understand the molecular mechanisms involved in ARR resistance in 'MP-29', transcriptomic analysis was performed using two casual agents of ARR, including Armillaria mellea and Desarmillaria tabescens. Differential gene expression analysis over time indicated an enrichment of defense related ontologies, including glucosyltransferase activity, monooxygenase activity, glutathione S-transferase (GST) activity, and peroxidase activity. Co-expression network analysis highlighted key hub genes involved in the sensing and enzymatic degradation of chitin, GSTs, oxidoreductases, transcription factors, and biochemical pathways likely involved in ARR resistance. In addition, we combined PacBio HiFi reads and Dovetail Omni-C data to achieve a chromosome-level, haplotype-resolved assembly for 'MP-29'. Two assembled haplotype genomes are 262 and 260 Mbp, with contig N50 values of 27.8 and 23.8 Mbp, respectively. Overall, 34,010 and 33,169 protein-coding genes were annotated from each haplotype genome. In the plum-derived haplotype genome, 1,647 and 1,645 gene families were identified with significant expansion and contraction, respectively. Gene ontology enrichment analysis of expanded genes revealed that they were mainly related to catalytic activity, transferase activity, kinase activity, hydrolase activity and nuclease activity, all of which could play a role in ARR resistance in 'MP-29'. These data provide valuable resources for the improvement of ARR resistance in Prunus rootstocks through breeding.

P-108. Luis Rivera-Burgos

North Carolina State University

Fine mapping of stem rust resistance derived from soft red winter wheat cultivar AGS2000 to an NBS-LRR gene cluster on chromosome 6D

Stem rust, caused by Puccinia graminis f. sp. tritici (Pgt), is an important pathogen causing economic losses in wheat (Triticum aestivum L.). Identification of markers that allow tracking of resistance genes is needed for deployment strategies to combat highly virulent pathogen races. Field evaluation of a DH population in Kenya located a QTL for stem rust resistance derived from the soft winter wheat cultivar AGS2000 to the distal region of chromosome arm 6DS where stem rust resistance genes (Sr42, SrCad, SrTmp) have been identified. Seedling evaluation with multiple isolates suggests that this stem rust resistance gene present in soft winter wheat may be the same as the SrTmp gene reported in the US hard winter wheat germplasm. We exploited exome capture data to discover new polymorphisms for marker development in a 10 Mbp region flanking the resistance locus. Our fine-mapping of seedling resistance in a RIL population and heterozygous inbred families derived from the cross AGS2000 x LA95135 identified three markers co-segregating with resistance and delimited the candidate region to an interval of 1.7 cM and corresponding to 0.3 Mbp region in the Chinese spring reference sequence (RefSeq v2.1). We have further exploited information from other genome assemblies, including a preliminary assembly of AGS2000, to identify a complex region having two F-box genes and five NBS-LRR genes in AGS2000. Evaluation of KASP assays corresponding to our co-segregating SNP suggests that they can be used to track this stem rust resistance in breeding programs.

P109. Paul P. Grabowski

HudsonAlpha Institute for Biotechnology, Huntsville, AL

The highly contiguous assembly of a drought tolerant genotype of peanut

Peanut (Arachis hypogaea L.) is an important food and oil crop grown across the world. Peanut is often grown in arid regions, and water limitation can significantly adversely affect yields. The peanut genotype Line 8 was generated from a cross of two drought-tolerant varieties and shows promising yields when grown under mid-season water stress. Here, we present a highly contiguous genome assembly of the peanut Line 8 genotype generated from PacBio HiFi reads and HiC chromatin conformation capture sequencing. The Line 8 assembly is generated using fewer contigs, has a higher contig N50, and has a higher percentage of sequence in chromosomes as compared to available peanut genome assemblies. The high contiguity allows us to identify high-confidence inversions and translocations, including several greater than 100kb in length. Surprisingly, the assembly includes a haplotype originating from an A. cardenasii introgression, and we investigate the origin and content of that introgression. The high contiguity and completeness of the Line 8 genome assembly make it a valuable resource for peanut breeders and researchers.

P-110. Marco Peixoto

University of Florida

Assessing long term trends in multi-trait selection using mate allocation and genomic selection: a case in maize breeding

Genomic selection is a well-established tool in plant breeding programs. However, the selection solely on genomic estimated breeding values can lead to a reduction in genetic variation in the breeding population. Here, the objective was to evaluate via stochastic simulations the long-term impacts of cross prediction and optimization accounting for genetic gain, variance, and coancestry in a maize breeding program. Four scenarios were implemented: i) conventional scenario (CS) with BLUP truncation selection; ii) genomic selection scenario (GS), with EBV truncation selection; iii) a pedigree-based parental selection program (PedS), with the crosses being selected aiming to minimize the inbreeding and maximize genetic gain; iv), and a scenario that uses EBV truncation selection with the crosses being selected aiming to minimize the coancestry and maximize usefulness, a measure of that combines both, genetic gain and variance (GSOpt). The usefulness calculation and the mate optimization were implemented in an R-package that we created, named SimpleMating. We compared them terms of genetic mean, genic variance, conversion efficiency, rate of inbreeding, and accuracy of selection. In general, our results show that GSOpt can ensure long-term success in the simulated maize breeding program. They confirmed that GS has immediate benefits compared to CS in almost all metrics, but genetic variance. The PedS also was superior in comparison with CS for the above-mentioned parameters, but lower compared with the GS. However, the best results came from the GSOpt scenario. It achieves the higher gain (6% higher than GS) with similar amount in loss of genetic variance. In addition, it had better conversion efficiency (25 vs 23), inbreeding rates (0.15 vs 0.33), and accuracy (0.32 vs 0.36), compared to GS. In summary, the incorporation of cross prediction based on restriction of coancestry rates and maximization of usefulness ensure positive long-term results and may enhance maize breeding programs.

P-111. Priscilla Glenn

University of California

Identification of bZIPC1 as a protein interactor of FT2 that affects spikelet number per spike in wheat

Loss-of-function mutations and natural variation in the wheat gene FLOWERING LOCUS T2 (FT2) have previously been shown to affect spikelet number per spike (SNS). However, while other FT-like wheat proteins genes interact with bZIP-containing transcription factors from the A-group, FT2 does not interact with any of them. In this study, we used a yeast-two-hybrid (Y2H) screen with FT2 as bait and identified a grass-specific bZIP-containing transcription factor from the C-group, designated here as bZIPC1. Within the C-group, we identified four clades including wheat proteins that show Y2H interactions with different sets of FT- and CEN-like encoded proteins. Combined loss-of-function mutations in bZIPC-A1 and bZIPC-B1 (bzipc1) in tetraploid wheat resulted in a drastic reduction in SNS with a limited effect on heading date. Transcript levels of genes previously shown to affect SNS showed no significant differences between bzipc1 and wildtype, suggesting that bZIPC1 may affect SNS through a different pathway. Analysis of natural variation in the bZIPC-B1 region revealed three major haplotypes (H1-H3), with the H1 haplotype showing significantly higher SNS, grain number per spike and grain weight per spike than both the H2 and H3 haplotypes. The favorable effect of the H1 haplotype was also supported by its increased frequency from the ancestral tetraploids to the modern durum and common wheat varieties. We developed markers for the two non-synonymous SNPs that result in N151K and V166M amino acid changes that differentiate the bZIPC-B1b allele in the H1 haplotype (KM) from the ancestral bZIPC-B1a allele present in all other haplotypes (VN). These diagnostic markers will be useful to accelerate the deployment of the favorable bZIPC-B1b allele in pasta and bread wheat breeding programs.

P-112. Priyanka Joshi

Clemson University

Genome-wide association mapping for seed protein concentration in chickpea (Cicer arietinum L.)

Chickpea (Cicer arietinum L) has been a major component of human diets for several thousand years. Nearly 15.9 million tonnes of chickpea were produced globally in 2021, making it the second most important pulse crop in terms of global production. Understanding the genetic basis of seed protein concentration is essential for developing improved chickpea varieties with improved nutritional quality. The objective of this research was to conduct a genome-wide association study (GWAS) to detect marker-trait associations for seed protein concentration in a diversity panel (256 accessions) that included 198 accessions from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) mini-core, and 54 advanced breeding lines or cultivars adapted to the USA Pacific Northwest. The panel included 165 desi accessions and 91 kabuli accessions. Accessions were evaluated in the field at Pullman, WA. Protein concentration ranged from 17.9–26.7% across accessions with a mean of 21.4. Accessions were genotyped using genotyping-by-sequencing (GBS) and after filtering and pruning 3984 single nucleotide polymorphisms (SNPs) were used for GWAS. The accessions were initially grouped into two major subpopulations, and then each of these major subpopulations was further divided into six subpopulations in the population structure analysis. FarmCPU model for GWAS and prediction integrated tool (GAPIT) package of R software was used to detect eight SNPs significantly associated with seed protein concentration. Candidate genes included a “serine/threonine-protein kinase CTR1-like isoform X1 [Cicer arietinum]” and “G2/mitotic-specific cyclin-2 [Cicer arietinum]” present on chromosomes 4 (Ca4) and 7 (Ca7).

Genetic markers and accessions with high protein concentrations identified in this study are useful for developing new varieties with enhanced nutritional qualities.

P-113. Renan Uhdre

Washington State University

Genetic study of seed protein concentration in a pea diversity panel

Pea (Pisum sativum L) is a significant rotational crop with increasing importance in the USA and other global production regions. In addition, pea has been highlighted market as a crop with high protein for the food processing industry. Over the past decade, the acreage dedicated to pea cultivation in the USA has seen a notable 26% increase compared to the previous decade. However, seed protein concentration varies widely among pea cultivars, and enhancing seed protein levels in commercial lines is crucial to meet the growing demand for plant protein. This study aims to investigate the natural variation of protein concentration in a diverse set of pea accessions and characterize the genes involved in regulating seed protein concentration. Here, we phenotyped a total of 487 accessions from USDA pea plant genetic resource collection based on yellow cotyledon and round seed surface using a randomized complete block design (RCBD) with three replicates over three years. Seed protein concentrations on plot sub-samples were determined using a near-infrared (NIR) spectrometer. The calibration curve was calculated based on protein concentration from nitrogen data and conversion factor 6.75 from a protein analyzer (FP-528, LECO Corporation) following AACCI Approved Method 46-30.01. A genome-wide association study (GWAS) using 74,000 high-quality single nucleotide polymorphism (SNP) markers was performed to identify associated variants and neighboring candidate genes with seed protein concentration. Further studies in multiple field locations are necessary to validate these associations. The findings from these surveys, along with recent research, provide valuable insights into the potential for further enhancing pea protein content reinforcing the potential for molecular-assisted breeding for protein concentration in peas to support the market demand within the food processing industry, cereal rotations, and human health.

P-114. Sarah A. Kostick

University of Minnesota

Genomewide selection in an apple breeding program: insights from postdiction analyses

Breeding apple (Malus domestica Borkh.) is a long, resource intensive process. Many important fruit quality traits in apple are highly quantitative (i.e., controlled by many small effect loci). Genomewide selection has been reported to be an effective breeding approach when targeting highly quantitative traits. The aim of this study was to determine the utility of genomewide selection for fruit quality traits within the context of the University of Minnesota apple scion breeding program. Representative breeding germplasm (n = 955 individuals), high-quality single nucleotide polymorphism (SNP) data (n = 977 SNPs), and breeding program fruit quality trait data were leveraged in this study. Breeding parent and important cultivar ‘Honeycrisp’ was highly represented. Moderate to high predictive abilities were observed for most fruit quality traits at harvest examined in this study. Postdiction (retrospective) analyses were used to determine if advanced selections identified via traditional selection procedures would have been kept or culled via genomewide selection. Depending on the selection threshold, selection decisions (i.e., keep, cull) for 55 to 85% of advanced selections would have been the same regardless of selection method (i.e., phenotypic versus genomewide selection). Results of this study indicate that genomewide selection is an effective breeding approach for certain fruit quality traits in apple.

P-115. Scott H. Brainard

University of Wisconsin-Madison

The first two chromosome-scale genome assemblies of American hazelnut enable comparative genomic analysis of the genus Corylus

The native shrub Corylus americana is currently utilized in breeding programs developing commercially viable hazelnut varieties for the Upper Midwestern U.S. Modern breeding methods (e.g, marker-assisted selection and genomic prediction) are greatly aided by a high-quality reference genome assembly, however this is currently lacking for C. americana. We have therefore developed the first chromosome-scale reference assemblies for C. americana, using the accessions 'Rush' and 'Winkler'.

Genomes were assembled using HiFi PacBio reads and Arima Hi-C data, and Oxford Nanopore reads and a high-density genetic map were used to perform error correction. N50 scores are 31.9 Mb and 35.3 Mb, with 90.2% and 97.1% of the total genome assembled into the 11 pseudomolecules, for 'Rush' and 'Winkler', respectively. Gene prediction was performed using custom RNAseq libraries and protein homology data. 'Rush' has a BUSCO score of 99.0 for its assembly and 99.0 for its annotation, while 'Winkler' had corresponding scores of 96.9 and 96.5, indicating high-quality assemblies. These two independent assemblies enable unbiased assessment of structural variation within C. americana, as well as patterns of syntenic relationships across the Corylus genus. Furthermore, we identified high-density SNP marker sets from genotyping-by-sequencing data using 1,343 C. americana, C. avellana, and C. americana x C. avellana hybrids, in order to assess population structure in natural and breeding populations. Finally, the transcriptomes of these assemblies, as well as several other recently published Corylus genomes, were utilized to perform phylogenetic analysis of sporophytic self-incompatibility (SSI) in hazelnut, providing evidence of unique molecular pathways governing self-incompatibility in Corylus.

These assemblies are an important first step in providing a resource for using next-generation sequencing data in the improvement of C. americana, while also enabling comparisons of structural variation across Corylus species. We hope these assemblies will aide in the application of modern breeding methods to the development of commercially viable hazelnut varieties for the Upper Midwest.

P-116. Shu Yu

University of California

Genetic dissection of the roles of β-hydroxylases in tetraploid wheat (*Triticum turgidum* L.)

Wheat is a globally important crop, and understanding the genetic basis of its nutritional and agronomic traits is critical for improving crop performance and enhancing nutritional value. Carotenoids are beneficial for human health and play critical roles in photosynthesis, photoprotection, and growth regulation in plants. β-hydroxylase (HYD) catalyzes the hydroxylation of β-carotene. Two HYDs (HYD1 and HYD2) have been identified in wheat while their functions have not been characterized in planta. To investigate the role of HYD genes in carotenoid metabolism and plant growth, we isolated loss-of-function mutants of each HYD homoeolog from the tetraploid wheat Targeting Induced Local Lesions in Genomes (TILLING) mutant population and generated different levels of mutant combinations to dissect the contribution of HYDs in a homoeolog resolution. Our findings revealed the functional redundancy and subfunctionalization of HYD genes and homoeologs in different tissues of tetraploid wheat. Our results on the molecular, biochemical, and physiological characterization of the HYD mutant combinations will be presented.

P-117. Shu Yu

University of California

Cloning and functional characterization of shikimate dehydrogenase genes from pomegranate (*Punica granatum* L.)

Shikimate dehydrogenases (SDH) play a vital role in plants due to their involvement in the shikimate pathway, a metabolic pathway that is essential for the synthesis of aromatic amino acids and numerous secondary metabolites including phenolic compounds, flavonoids, and lignin. Pomegranate (Punica granatum L.) outer peels contain two distinct groups of polyphenols anthocyanins (ATs) and hydrolysable tannins (HTs) which have valuable health properties. The primary function of SDH in the shikimate pathway is the catalysis of the reversible dehydrogenation reaction, converting 3-dehydroshikimate to shikimate. The non-conventional role of SDH to produce gallic acid was also reported in grapevine. However, SDHs have not been functionally characterized in pomegranate. To study the function of SDHs in pomegranate, SDH genes were cloned from pomegranate and heterologously expressed in E.coli. The purified SDHs were incubated with both shikimate and 3-dehydroshikimate to study the conventional and non-conventional activities of SDHs, respectively. The cloned pomegranate SDHs were also overexpressed in pomegranate hairy root culture and Arabidopsis. The content of aromatic amino acids and phenolic compounds derived from the shikimate pathway was quantified. Our results on the in vitro and in vivo characterization of SDH genes from pomegranate will be presented.

P-118. Vincent Njung’e Michael

University of Florida

Who’s your daddy? Using genetic tools to determine mango parentage and pollinator behavior

Hand pollination and/or caging mango cultivars to develop improved hybrids is inefficient and labor intensive. In this research, we demonstrate the application of single nucleotide polymorphism (SNP) markers to identify paternal parents of 575 open pollinated seedlings from 140 mango cultivars in a mango collection. The Dixon test of Gower's genetic dissimilarity (GD) values among identified triads revealed 161 significant triads ($P \leq 0.05$), indicating high confidence for paternal identification. The remaining triads had GD values less than 0.15 ($n = 323$), between 0.15 and 0.2 ($n = 10$), or between 0.2 and 0.3 ($n = 5$). In total, 70% of the hybrids were paired to a single paternal parent. Pollination is critical for high yields in mango and the pattern of self-pollination and cross pollination among cultivars across the groove was also determined. Analysis of selfing rates, indicated ‘Tommy Atkins’ had the highest selfing rate (40.4%) and ‘Glenn’ had the lowest (1.1%). The data enabled identification of cultivars capable of self-fertilization (successful pollination) and those requiring cross-fertilization to set fruit. In addition, the data was used to visualize the movement of pollen throughout the grove demonstrating the ability of some insects to successfully move pollen at least 121 meters. These results will increase mango breeding efficiency by eliminating need for manual/cage pollination while enabling mango producers to select superior hybrids and generate productive cultivars in a reduced time-line.

P-119. Yi-Wen Wang

University of Georgia

Genome-enabled breeding across Phaseolus species

Phaseolus vulgaris, common or dry bean, is the most widely cultivated dry seed legume and the most important source of plant protein for human consumption. Its sister species, tepary bean (Phaseolus acutifolius), which is native to the Sonoran Desert, is closely related to common bean and is also cultivated. Common bean is susceptible to several diseases and abiotic stresses for which resistance is present in tepary bean. While tepary bean is an alternative climate-resilient food legume, its growth habit, seed size, disease resistance, and mechanization potential are suboptimal for adoption by growers and for application to modern agricultural production practices. Currently, tepary and common bean can be interbred using recently developed bridging genotypes. In this project, we will transform common and tepary bean breeding by exploiting their close relationship with the development of a database that permits rapid trait discovery and subsequent breeding between the two species. To augment the knowledge of loci encoding agronomic traits in tepary bean, we have identified six tepary accessions with key traits of interest and sequenced their genomes. After genome assembly and annotation of protein-coding genes, the genomes will be useful for identifying genes and QTL for traits of interest.

P-120. Heather K Manching

North Carolina State University

Breeding Insight OnRamp - a New Initiative Helping to Advance USDA Breeding Programs

Predictive breeding leverages both phenotypic and genotypic data through advanced breeding methods. Breeding Insight OnRamp (BI OnRamp) is a new USDA-ARS initiative to collaboratively enable implementation of advanced breeding tools and predictive breeding methods across USDA-ARS commodity and specialty crops. BI OnRamp focuses on establishing collaborative partnerships aimed at promoting effective transdisciplinary predictive breeding programs. This effort involves leveraging historical data, data integration, and targeted tool and software development geared specifically for each commodity need identified through true collaborative communication and action. BI OnRamp efforts have been supported and initiated by stakeholders in citrus, sugarcane, soybean, and cotton with potential to expand to additional species.

P-121. Salvador A. Gezan

VSN International, UK

ASRgwas: An R package to perform complex Genome-Wide Association Studies (GWAS)

ASRgwas is a comprehensive R package designed to perform Genome-Wide Association Studies (GWAS) using the modelling flexibility available in ASReml-R in an efficient and reliable way. This library assists with preparing data and matrices, and verifies that they are adequate to perform GWAS. In addition, it has a set of complementary functions to be used for post-GWAS analyses to help with interpretation, use of the output information, and obtaining graphical outputs.
The main tasks considered within ASRgwas are:

- Preparing and auditing phenotypic and genomic data.
- Fitting GWAS models and identifying significant markers.
- Evaluating results and generating tables and graphical output.

The intent of this tool is to facilitate the execution of GWAS in a straightforward and efficient manner, along with providing full reproducibility of these analyses. We have used state-of-the-art approaches and algorithms to obtain reliable and fast estimation of marker effects. In addition, we have made use of parallelization, whenever possible, and fast matrix operation routines (e.g. C++) available within the software R.

ASRgwas is designed to allow for any number of fixed and/or random structures, and heterogenoeus error variances. It also accepts raw and replicated data. All of this allows for better use of the available phenotypic information and full use of the linear mixed model (LMM) methodology as available in ASReml-R (Butler et al. 2009). In addition, this package accepts missing values in the marker information avoiding the need to implement marker imputation. As part of ASRgwas we have extended the analytical options within GWAS by allowing the evaluation of phenotypic responses that follow a Binomial distribution.

ASRtriala is a free to use R library which can be downloaded from this web page: https://asreml.kb.vsni.co.uk/download-asrgwas/

P-122. Salvador A. Gezan

VSN International, UK

ASRtriala: An R package with complementary functions for single and multi-environment trial analyses

Performing statistical analysis in plant breeding is usually an overwhelming task. We developed ASRtriala (ASR-trial-analysis) with the above questions in mind. ASRtriala is a companion package for ASReml-R to help audit and prepare the data, and select a best model for the analysis of field trials.

The main goal of this package is to assist with semi-automatic pipelines to perform spatial and/or non-spatial analyses of field trials and to use this output in the fitting of MET models with complex variance-covariance structures to model GxE as nested effects.

You can set up of spatial and non-spatial models with a pre-defined set of hundreds of models to be fitted automatically, and then the best single-trial model selected can be used as final analysis, or as the first part of a two-stage multi-environment trial (MET) analysis (with their respective weights reported). For the second step, ASRtriala has functions available to fit a range of MET model structures, including unstructured, general correlation and factor analytic.

The main capabilities of the package include:

- Auditing/preparing single-trial data and multi-environment trial data.
- Fitting/selecting a single-trial model (spatial and non-spatial) using ASReml-R.
- Fitting/selecting a multi-environment trial model using ASReml-R.
- Enhancing output from multi-environment trial models.

We also have included some routines to assist with the post-analysis of MET models. These include additional output for factor analytic (FA) structures with the generation of genotype-specific plots that enhance the understanding of GxE (loadings, biplots, stability indexes) and facilitate the final ranking and selection of genotypes across environments.

ASRtriala is a free to use R library which can be downloaded from this web page: https://asreml.kb.vsni.co.uk/download-asrtriala/

P-123. Didier Murillo-Florez

North Dakota State University

Empowering Plant Breeders with FielD·Hub - a User-Friendly Design of Experiments App

FielD·Hub is an interactive open-source application that is revolutionizing the way users approach experimental design in plant breeding, forestry, agronomy, and life science. With a friendly graphical-user interface built in R Shiny, FielD·Hub caters to both non-coding users and R-savvy experts, making it their go-to tool.

Our comprehensive app offers a wide range of designs, from traditional experiments (CRD, RCBD, Split Plot, Split Block, Alpha Lattice, etc.) to advanced Unreplicated, Augmented, and Partially Replicated (p-reps) designs.

FielD·Hub' s reactive interface enables instant data input and generates interactive report tables and field layouts for the user. Furthermore, it provides precise control and seamless data ingestion features, allowing users to import entry lists and modify field dimensions on the go. This facilitates the printing of field books; data organization and it provides coordinates row/column that can be used subsequently for doing spatial analyses. This dynamic visualization capability empowers users to gain deep insights into their experiments, transforming the way they are randomizing and creating experiments.

With over 11K downloads worldwide, FielD·Hub has become a valuable educational resource for teaching experimental design, as it offers an integrated platform for demonstrating critical statistical concepts, including randomization, blocking, replication, simulations, and spatial designs. Such interactive features were not available in open-source tools until now, and FielD·Hub introduces a captivating visual component which is enhancing the learning and research experience.

P-124. Guo-Liang Jiang

Virginia State University

Comparison of Seed Compositions between Vegetable Soybeans Dried by Freeze and Thermal Drying as well as Mature Seeds

Seed composition is an important determinant of edamame quality and market acceptability or suitability. Rapid large-scale analysis of seed nutritional profiles is a great challenge for edamame breeding and related research. In this study, fresh edamame samples of 20 genotypes were dried using freeze and low-heat drying methods. The dried edamame seeds and mature beans were analyzed for seed composition for three years using NIR. Protein, oil, sucrose and fiber contents exhibited significant differences among genotypes. On average and dry weight basis, seed composition contents in freeze dried, low-heat dried and mature seeds were 43.9, 44.3 and 43.2% for protein, 19.7, 19.9 and 19.2% for oil, 4.9, 4.3 and 5.3% for fiber, and 6.0,6.2 and 5.1% for sucrose, respectively. Correlation coefficients between drying methods were significant for all traits. Under either drying method, there were significant differences between edamame and mature soybeans in most cases. The correlations between edamame and mature seeds were significant for protein, oil, sucrose and fiber contents, but the coefficients of correlation varied considerably with traits. In addition, analysis of 216 genotypes or entries in 2019 indicated that the contents of seed composition in low-heat dried edamame and mature soybeans averaged 45.0 (38.4-51.2) and 42.3 (37.4-46.9) % for protein, 23.2 (18.1-27.5) and 20.6 (18.3-24.7) % for oil, 5.7 (4.3-6.6) and 5.5 (4.6-6.3) % for fiber, and 5.4 (0.7-11.5) and 5.2 (3.9-6.7) % for sucrose, respectively. The correlation coefficients between edamame and mature seeds were significant for these traits, varying from 0.183

to 0.693. This study suggests that low-heat could be used for drying and analysis of large numbers of edamame samples. Composition contents in mature seeds can be indirectly used in improvement of some nutritional profiles but the evaluation of fresh edamame seeds is also needed.

P-125. Per McCord

Washington State University

Improving fruit size in sweet cherry via association mapping and genomic prediction

Large fruit size is one of the most important breeding objectives for sweet cherry. In the Washington State University (WSU) breeding program, large-fruited germplasm exists, and heritability is reasonably high. An important locus for cherry fruit size has been identified, but appears to primarily distinguish between wild and improved phenotypes, and has limited utility in the breeding program. We employed association mapping and genomic prediction approaches to identify markers and models that are predictive for fruit size in the WSU breeding germplasm.

The germplasm consisted of 246 individuals from two sub-populations. The “parent” group, 106 individuals representing a diverse group of parents, was genotyped with the cherry 6K Illumina SNP array. The “program” group, 140 first-selection-phase seedlings from 56 crosses, was genotyped with the cherry 6 + 9K SNP array. Each sub-population was phenotyped for fruit diameter for two seasons. Groups were analyzed individually as well as combined. SNPs for the combined dataset included those common to both arrays.

Significantly associated SNP markers for fruit diameter were identified on chromosomes 1, 2, 4, 5, and 7. Individual markers accounted for up to 33% of phenotypic variance. In all cases, the minor allele was associated with smaller fruit, suggesting selection pressure for increased fruit size. However, minor allele frequencies were greater than 40% for two significant SNPs, indicating the opportunity for continued selection. These markers are being converted to locus-specific assays for validation and potential use in marker-assisted selection. Genomic prediction accuracy ranged from 0.37 to 0.48 depending on the population and year. These results suggest that either approach may be used to select for greater fruit diameter in sweet cherry, although genomic prediction might be more efficient if a cost-effective genotyping solution is available.

P-126. Seth C. Murray

Texas A&M University

Facilitating community unoccupied aerial systems (UAS, drone) knowledge, communication, and data processing across agriculture

Unoccupied / Unmanned / Uncrewed Aerial Systems (UAS, also known as drones) are novel tools that can provide field based phenotyping and phenomics derived insights into plant breeding, biology, genetics and agronomy. There are many important, yet disparate agricultural UAS activities, occurring in silos which with better communication across research, education, and extension, could create transformative change for all stakeholders, regardless of species. The overall goal of this USDA-NIFA and AG2PI supported project is to advance phenotyping and phenomic knowledge and activities through advancing UAS data collection, processing, analysis, and community discussions. The objectives of this project are to: 1) Enhance networks and communication of best practices between groups and individuals currently successfully developing and using UAS tools as well as those that seek to use UAS tools. 2) As a case study and nucleating force, to process most existing Genomes to Fields (G2F) datasets (2017 to 2023, and up to eight locations) into consistent usable end products for the community to directly use, making them publicly available. And 3) Develop a user-friendly webpage that acts as a centralized platform to find necessary resources and information related to UAS based HTP. The overall activities of this project following the objectives are to: Support a UAS Activities Coordinator that can connect with existing UAS in agriculture user groups, to try to involve and organize livestock and rangeland users, listen to needs, and provide support for their communication, answer questions, summarize their knowledge and connections across discipline, institutions, and species; then ultimately distribute this wisdom. This project will lower the barrier of entry to new users of UAS tools in plant breeding and genetics as well as help to advance cutting edge users creating the next phases of novel use and discoveries.

P-127. Lucia Gutierrez

University of Wisconsin – Madison

Resource allocation optimization for multi-environment trials and genomic selection in barley

Optimizing field testing resources is a key component of agricultural evaluations, especially for large experiments such as multi-environment trials (METs). Testing efficiency can be improved by controlling micro- (spatial) and macro-environmental (genotype by environment, GEI) variability. Both, spatial variation, and GEI are common in agricultural field experiments and can largely influence the accuracy and efficiency of large plant breeding experiments. How to allocate resources within and among environments accounting for both spatial variability and GEI is still not entirely clear. Furthermore, because mixed models can be used to borrow information from relatives or across environments, sparse experimental designs could be superior to balanced designs. The goal of this study was to compare strategies for micro and macro-environmental variability control that include spatial and GEI modeling in a sparse-testing approach to optimize resource allocation in METs. optimizing the mega-environmental sparse testing designs (MEDs) in terms of replication within and across environments and the robustness of MEDs to different covariance structures among environment.

P-128. Antonio Brazelton

Washington University

Digital quantification and characterization of root architectural diversity across collard landrace varieties

Urban agriculture has been broadly acknowledged for its potential to reduce carbon emissions, increase food security, and improve economic growth in some of the most vulnerable communities in the United States. Collard (B.oleracea var. viridis) is a diploid leafy green, grown on urban farms and community gardens across the country, including the St. Louis Metro region. Beyond their nutritional importance, collards provide urban and commercial agronomic systems with a plethora of important ecosystem services. They scavenge nitrogen and available resources, suppress weeds, and act as a biofumigant to control soil-borne pests and pathogens. Recently, The Heirloom Collard Project characterized the above-ground growth habits of 18 landrace collard varieties across 250 organic gardens and farms. Little work has been published to investigate collard root system architecture, which influences both quality traits and ecosystem services that contribute to sustainable crop production. The objectives of this research are to 1) quantify root spatial and temporal diversity across 18 landrace collard varieties, and 2) evaluate the relationship between root phenotype and urban farmer crowd-sourced data for key traits such as germination rate, disease resistance, vigor, yield, flavor, and winter hardiness. This work will lead to the development of a participatory framework for urban farmers and chefs to select varieties with improved root architecture based on regional needs.

P-129. Vincent Njung’e Michael

University of Florida

Comparative transcriptomics in vanilla identifies key genes involved in vanillin biosynthesis

Vanilla is the most popular flavor in the world and the second spice with highest revenue. The natural vanilla industry is expected to reach 4.3 billion dollars by 2025 and the biggest importer of natural vanilla is the USA. Only 3 species and one hybrid of vanilloid orchids are used to produce natural vanilla: Vanilla planifolia, Vanila odorata, Vanilla pompona and Vanilla x tahitensis. From a market perspective vanillin is the most important metabolite of the natural vanilla extract. One of the principal breeding objectives around vanilla plants is to increase the vanillin concentration in the vanilla cured pods. The vanillin biosynthesis pathway has not been completely understood and at least three possible alternatives are considered. This study uses a comparative transcriptomic approach to propose candidate genes affecting vanilla (Vanilla planifolia Jacks. ex Andrews) pod vanillin accumulation. We compared RNA counts for two accessions (with contrasting vanillin content), as well as three time points (months 6, 7 and 8 after pollination) and two tissue types (outer epicarp and inner placental and seed tissue). The gene calls found in this project may also shed light on the proposed vanillin pathways as part of a redundant metabolic process. Negative regulation genes are also proposed that may be decreasing vanillin accumulation through precursor sequestration or enzymatic competition in the vanillin synthesis machinery of the vanilla pods.

Clemson highlights 12: Celebrating Clemson football at Death Valley (Memorial stadium)

National Association of Plant Breeders

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