National Association of Plant Breeders

NAPB

Improving Plants to Improve Lives

ANNUAL MEETING

AUGUST 8-11, 2022 AT IOWA STATE UNIVERSITY

2021-22 Leadership

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Awards
Chair- Jim McFerson, Washington State Univ (retired)

Annual Meeting Planning, 2022
Thomas Lübberstedt, Iowa State University
Paul Scott, USDA Corn Insect & Crop Genetics Research Unit

Schedule

MONDAY, AUGUST 8

Pre-conference activities (see also: https://www.regcytes.extension.iastate.edu/napb2022/pre-conference-tours/)

TUESDAY, AUGUST 9

TIME	WHAT
6:30-8:00	**Borlaug scholar and George Washington Carver scholar breakfast** *North Prairie, Gateway Hotel and Conference Center*
8:00-8:30	**Welcome addresses** *Benton Auditorium, Scheman Building* *Thomas Lübberstedt, Paul Scott (Meeting co-hosts)* *James M. Reecy (ISU Vice President for Research)* *Ksenija Gasic (NAPB president)* *William Duke Pauli (Incoming PBCC chair)*
8:30-9:00	**Borlaug and GW Carver Scholar Introductions** *Benton Auditorium, Scheman Building* *Allen van Deynze, Borlaug scholars* *Gurleen Kaur, GW Carver scholars*
Session 1: Lessons from 100 Years of Corn Breeding *Benton Auditorium, Scheman Building Chair: Jode Edwards*	
9:00-9:30	**Kendall Lamkey** 100 years of corn breeding
9:30-10:00	**Mario Carlone** Long-term maize germplasm development
10:00-10:30	**Break** *2nd Floof, Scheman Building*

TIME	WHAT
10:30-12:00	**Poster session I - Odd Numbered Posters** *2nd Floor Lobby, Scheman Building*
11:30-1:30	**NIFA project directors meeting** *Room 250, Scheman Building*
12:00-1:30	**Lunch** *Room 220-240, Scheman Building*
12:00-1:30	**NIFA/NAPB/PBCC leadership luncheon** *Room 208, Scheman Building*
Session 2: Awardee session *Benton Auditorium, Scheman Building Chair: Jim McFerson*	
1:30-1:50	**Patricio Munoz, Early Career Scientist** Breeding blueberries with a local focus but a global impact
1:50-2:10	**Don Blackburn, Lifetime Achievement** A Plant Breeders Tale
2:10-2:30	**Gina Brown-Guedira, Public Sector Plant Breeding Impact** A journey in genotyping for wheat improvement
2:30-2:50	**Andy Lavigne, Friends of Plant Breeding** Can They Hear Your Plant Breeding Voice?
3:00-3:30	**Break** *2nd Floor, Scheman Building*
3:30-5:00	**Poster session II - Even Numbered Posters** *2nd Floor Lobby, Scheman Building*
5:30-7:30	**NAPB Graduate Student Working Group** *Jethro's, Ames*
5:30-7:30	**NAPB Early Career Working Group** *Dublin Bay, Ames*
5:30-	**Dinner on your own / Shuttles provided**

Schedule

WEDNESDAY, AUGUST 10

TIME	WHAT
Session 3: Plant Genetic Resources: Challenges and Opportunities *Benton Auditorium, Scheman Building* *Chairs: Stephen Smith and Vivian Bernau*	
8:00-8:25	**Peter Bretting** Need Plant Germplasm and Data for Breeding and Research? There's an App for that: the National Plant Germplasm System!
8:25-8:45	**Patrick Byrne** GRIN-U.org: Online learning materials on plant genetic resources
8:45-9:05	**Shui-zhang Fei** Turfgrasses as perennial groundcover for maize production
9:05-9:25	**Rebecca Grumet** Cucurbit germplasm – genomic tools and disease resistance
9:25-9:45	**Addie Thompson** Seeding new research opportunities in tar spot genetics and plant phenomics through public germplasm
9:45-10:00	**Student presentation: M. Nelly Arguello-Blanco** Effects on the wheat (Triticum aestivum L.) genome from five rapid genomic selection (GS) cycles
10:00-10:30	**Break** *1st Floor, Scheman Building*
Session 4: Plant Breeding Innovation *Benton Auditorium, Scheman Building* *Chairs: Arti Singh and Shui-zhang Fei*	
10:30-10:50	**Irwin Goldman** Not your grandmother's beet: Breeding biennial vegetables for specialty market classes
10:50-11:10	**Yufeng Ge** Integrating limited field samples into radiative transfer simulated data enhances machine learning estimation of leaf chlorophyll and water contents
11:10-11:30	**Allison Miller** Harnessing multiple dimensions of perennial plant phenotypic variation for crop improvement and de novo domestication

11:30-11:45	**Student presentation: Matthew Carroll** Soil Mapping Improves Spatial Adjustments for Breeding Trials
11:45-12:00	**Student presentation: Brian Rice** Flywheel Genomics Leads to Efficient Trait Architecture Dissection and Rapid Local Adaptation
12:00-1:00	**Lunch** *Room 220-240, Scheman Building*
1:00-5:00	**ISU and USDA-ARS (PI Station) field tour**
5:30-8:00	**Diversity and Inclusion Dinner** *Hansen Agriculture Student Learning Center, Ames* *Chairs: Jamie O'Rourke and Michelle Graham* **Theresa Cooper** Communicating across culture **Roy Scott** Diversity and Inclusion: Teaching and Learning Moments **Diane Okamuro** From Coastal Farming Community to DC – Lessons Learned **Tabare Abadie** Mentoring as a Powerful Tool to Advance IDE

THURSDAY, AUGUST 11

Session 5: Breeding for a sustainable future *Benton Auditorium, Scheman Building* *Chair: Rick Harrison, NAPB Commercial Plant Breeding Committee*	
8:00-8:15	**VK Kishore** Breeding for Sustainable Innovations from Seed to Consumer
8:15-8:30	**Jose Rotundo** Innovative cropping systems: should we breed for novel traits and environments?
8:30-8:45	**Christine Diepenbrock** Effecting change, improving emergent properties, and evaluating preparedness
8:45-9:00	**Kevin Smith** Breeding for Continuous Cover Cropping Systems - Forever Green Initiative
9:00-9:30	**Panel discussion**
9:30-10:00	**Break** *1st Floor, Scheman Building*
Session 6: Predicting the Unknown *Benton Auditorium, Scheman Building* *Chairs: Jode Edwards and Addie Thompson*	
10:00-10:30	**Charlie Messina** Crop improvement for climate change

Schedule

THURSDAY, AUGUST 11

TIME	WHAT
10:30-10:48	**Diane Wang** Modeling historical rice yields in the U.S.
10:48-11:06	**Jacob Washburn** Predicting Plant Phenotypes with Deep Learning
11:06-11:24	**Lizhi Wang** Descriptive, Predictive, and Prescriptive Models for Plant Breeding
11:24-11:42	**Arti Singh** Rapid Advancements in Phenotyping Through Data Driven Deep Learning Models
11:42-12:00	**Milad Eskandari** Machine Learning and Optimization Algorithms in Plant Breeding: Modeling Soybean Yield using its Components
12:00-1:30	**Lunch** *Room 220-240, Scheman Building*
12:00-1:30	**PBCC session** (lunch provided) *Room 250, Scheman Building*
1:30-3:00	**NAPB business session** *Benton Auditorium, Scheman Building*
3:00-3:30	**Break** *1st Floor, Scheman Building*
Session 7: The Future of Plant Breeding *Benton Auditorium, Scheman Building* *Chairs: Carolyn Lawrence-Dill and Paul Scott*	
3:30-4:00	**Fiona McCarthy** Lessons learned and the way ahead: cross-disciplinary opportunities for applying genome-to-phenome
4:00-4:30	**Paul Zankowski** Using a roadmap to guide USDA future plant breeding endeavors
4:30-5:30	**Community Session** *220-230, Scheman Building*
6:00-10:00	**Banquet** *Gateway Hotel* **Presentation of 2022 Poster Award Winners** **Presentation of 2022 Professional award winners** **Presentation of 2023 NAPB meeting** **Introduction of new NAPB leadership**

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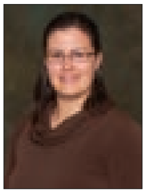
Speaker Bios & Abstracts

Addie Thompson



Addie Thompson received her BS in Genetics at Iowa State, completed her PhD at the University of Minnesota in Plant Breeding, and a postdoc at Purdue University. Since 2018 she has been an assistant professor at Michigan State in the department of Plant, Soil, and Microbial Sciences, where she conducts research in maize genetics and teaches plant breeding as well as computational plant sciences.

Seeding new research opportunities in tar spot genetics and plant phenomics through public germplasm

Public germplasm repositories are critical resources for the plant breeding community. The Thompson lab has utilized lines from the Wisconsin Diversity Panel to address multiple research questions, including screening for resistance to novel diseases, testing new phenotyping approaches, conducting studies of quantitative genetics of complex traits across environments, and optimizing breeding methodologies. This talk will focus on two projects in detail: screening and breeding for resistance to maize tar spot, and testing the applications of LiDAR data in modeling complex traits in maize. Tar spot is caused by the fungal pathogen Phyllachora maydis and has existed in Central and South America for over 100 years; however, the disease is new to the upper Midwest US as of 2015. After screening for temperate sources of resistance in the diversity panel, genetic mapping and genomic prediction was conducted across three states, and population development utilizing resistant sources is ongoing. In addition, the Germplasm Enhancement of Maize lines were screened for disease resistance as well. In a separate experiment, the diversity panel was used to test a proof-of-concept to model complex traits using LiDAR data. Modeling accuracy and heritability were very high for most traits examined, and comparable to that of the ground-measured traits. The accuracy of using LiDAR data to model phenotypes was in many cases higher than that of genome-wide markers.

Allison Miller

Allison Miller serves in a joint faculty position where she is a Member and Principal Investigator at the Danforth Plant Science Center and a Professor in the Department of Biology at Saint Louis University in St. Louis, Missouri. Allison's research program focuses on understanding evolution and plasticity in perennial crops and emerging perennial herbaceous crop candidate species. The long-term goals of her work are to improve existing perennial crops and to develop new ones to support sustainable agricultural systems.

Harnessing multiple dimensions of perennial plant phenotypic variation for crop improvement and de novo domestication

A new generation of crops are needed to diversify the economies of farmers and the biology of farm landscapes. Novel crop development could accelerate by adopting breeding value prediction models; indeed, genomic selection in a perennial cereal grain reduced breeding cycles to a single year. However, genome-wide genotyping requires considerable up-front and annual investment and may not be the best option for a diversity of early-stage candidates with complex genomes. This project explores the feasibility of phenomics to fundamentally accelerate new crop development through phenomic selection based on phenomics-estimated breeding values (PEBVs). Recent research suggests that with sufficient phenotypic dimensionality breeding values can be predicted in the same way as with genomic selection--using a kinship matrix. Phenomics could also enable accurate, early-stage selection for important later-stage traits. This project targets three emerging perennial crops: intermediate wheatgrass (*Thinopyrum intermedium*), sainfoin (*Onobrychis viciifolia*), and silphium (*Silphium integrifolium*). Work to date demonstrates that comprehensive early life-stage phenotypic data collected under controlled conditions is correlated with in-field phenotypes collected on mature plants. Further, preliminary data on these species indicate spectral signatures collected on seedlings may offer a promising source of multi-dimensional data with applications in phenomic selection models. This work aims to re-imagine innovations in plant traits, kinship matrices, genomic selection, phenotyping centers, and ultimately domestication, in order to expedite the development of an emerging generation of climate resilient, ecologically sustainable crops.

Andy Lavigne

Arti Singh

Rapid Advancements in Phenotyping Through Data Driven Deep Learning Models

Machine Learning (ML) approaches are continually and rapidly advancing leading to their application at an exponential scale in agriculture to generate automated solutions with higher accuracy. Plant phenotyping is at the forefront of application of ML methods, including deep learning. To train a robust DL model, large quantities of data are needed. With recent improvements in high throughput phenotyping platforms as rovers and drones equipped with various sensors, we are now collecting large amounts of data minimizing data collection bottleneck in plant phenotyping. However, training a supervised DL model with large, annotated data remains a major bottleneck due to high costs and time-consuming process. Earlier methods utilized transfer learning where pre-training of models was done on independent samples, generally unrelated to the objective. More recently, to overcome this challenge of limited available annotations, DL methods namely weakly-supervised and self-supervised learning (SSL) have been used. These are proposed to overcome the need for huge amounts of labelled/annotated data. Transfer learning with SSL pretraining on even limited unlabeled in-domain data can significantly improve the classification accuracy. In our work, we investigated the performance of weakly- and self-supervised models using a large insect-pests dataset by testing various levels of annotated data, as well as pre-training of DL models using in-domain vs out-of-domain data. We report that weakly supervised pre-training on high-capacity models provide efficient insect-pests classification. Our results provide a strategy to overcome data annotation challenges when working with DL based plant phenotyping tasks including diseases, insect-pests, and other stress classification in the absence of large, annotated dataset.

Brian Rice

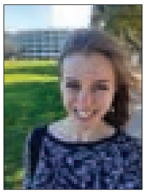
Brian received his PhD from University of Illinois in quantitative genetics and currently works as a post-doctoral research at Colorado State University in the lab of Geoff Morris. His research focuses on the challenges of predicting crop fitness by utilizing information concerning biological and evolutionary constraints. Immediately, his work assists the Universite Quisqueya breeding program in Haiti to understand the genetic basis of Sugarcane Aphid resistance and drought tolerance.

Flywheel Genomics Leads to Efficient Trait Architecture Dissection and Rapid Local Adaptation

Genetic trait dissection should directly impact a breeding program. Conversely, if a breeding program is used to test hypotheses on trait genetic architecture, then the results are directly relevant to the program's needs and lead to direct action. We refer to this framework of intensive collaboration where this is a smooth and efficient transfer of information between breeding and genetic research as Flywheel Genomics. The ideal breeding program for this framework has three key components: i) well defined and measured traits under selection; ii) lack of confounding structure due to long range LD; and iii) ability to generate mapping populations segregating for traits of interest. Using simulation, we show how a program implementing recurrent selection is better suited, compared to biparental population development, for this framework. Using Flywheel Genomics, we tested hypotheses on the genetic architecture of Sorghum Aphid (SA) resistance in the Université Quisqueya Sorghum Breeding Program. Heritability estimates indicate that trait architecture contains oligogenic and polygenic components. We show that there exists enough variation in the population to strengthen resistance through continued selection. Association studies and fixation scans confirmed that two a priori candidates, RMES1 and SbWRKY86, are contributing to resistance. Several new QTL were identified as potential candidates for selection. These results are being disseminated back into the breeding program where they will have immediate impact on Haitian farmers.

Charlie Messina

Christine Diepenbrock



Christine Diepenbrock is an Assistant Professor in the Department of Plant Sciences at UC Davis. She obtained her Ph.D. in Plant Breeding and Genetics from Cornell University and subsequently worked on the Predictive Agriculture team at Corteva AgriscienceTM before moving to UC Davis in 2019. Her research group is focused on improving crop nutritional quality and abiotic stress tolerance (namely to drought and high temperatures) in staple and specialty crops.

Effecting change, improving emergent properties, and evaluating preparedness

In this talk, case studies will be used to prime discussion on the following topics within breeding for a sustainable future: 1) We will explore what effecting change through plant breeding ultimately means, within and across breeding programs (including across crops, priority traits/product profiles, regions, and sectors). 2) We will discuss the logistics of breeding for (and in) cropping systems contexts, and the ever-important ties to agronomic and social scientific questions therein. 3) We will assess opportunities and limitations (in the near and longer terms) that are conferred by productivity and quality being emergent properties—arising from the main and interaction effects of Genotype, Environment, and Management. 4) We will consider factors influencing the adaptability (and preparedness) of breeding pipelines in the face of predictable and unpredictable change.

Diane Okamuro

Dr. Diane Jofuku Okamuro serves as a Program Director in the Plant Genome Research Program (PGRP) Cluster at the National Science Foundation, Directorate for Biological Sciences, Division of Integrative Organismal Systems. The PGRP supports basic discovery research on a genome-wide scale in and/or relevant to plants that are important to the U.S. economy as well as the development of tools, genetic resources and technology breakthroughs that further enable functional plant genomics. In addition, the Cluster manages the Plant Genome Postdoctoral Research Fellowships track of the Postdoctoral Research Fellowships in Biology (PRFB) program. Dr. Okamuro received her Ph.D. in Biology from UCLA and is a plant molecular geneticist by training. She has broad-based experience in cutting-edge genomics technologies and has held research and management positions in both academia and industry prior to joining NSF in 2005.

Diane Wang

Diane Wang is an Assistant Professor in the Department of Agronomy at Purdue University in Indiana. Her group focuses on understanding processes that give rise to genotype by environment interactions by leveraging genetic and physiological datasets and process-based modeling. The lab works on a variety of crop species, including rice, cotton and soybean and is particularly interested in plant responses to water deficit conditions.

Modeling historical rice yields in the U.S.

This talk will describe on-going efforts to model and predict rice yields by integrating molecular marker variation, varietal productivity, and weather variation at the landscape level. Rice production in the United States occurs primarily in two regions: California (where *temperate japonica* varieties are grown) and Southern U.S. (where *tropical japonica* varieties are grown). We focus our study on the Southern U.S. states as production spans a larger area, mainly in Arkansas, Louisiana, Texas, and Mississippi. By digitizing and combining four decades of county-level variety acreage information with genotyping-by-sequencing data, we estimate historical county-level allele frequencies that are then used in conjunction with county-level yield data from NASS to develop ensemble machine learning models for yield prediction with and without weather variables. Models are evaluated against observations from the Uniform Rice Regional Nursery trials and used with forecasted weather data from the Coupled Model Intercomparison Project (CMIP) in the rice-growing counties to predict variety performance and rice production in the coming decades.

Don Blackburn

A Plant Breeders Tale

In this talk, I'll reflect on key experiences that shaped my career. I will offer my views on key career path decisions made by every plant breeder, private or public plant breeding and scientific or management career tracks. I will also share insights from a lifetime of skill development in leading strategy, teams. and people, including the importance of core people management processes, mentors and mentorship opportunities, and core career trainings. I will also reflect on what it means personally to receive the NAPB Lifetime Achievement Award.

Fiona McCarthy

Fiona McCarthy is a Professor at University of Arizona's School of Animal Comparative & Biomedical Sciences, serves as a Bioinformatics Co-coordinator for the USDA National Animal Genome Research Program and is a founding member of the AgBase Databases. She develops resources that integrate genetic information, tools, training and support for researchers, and has works closely with public databases and resources providers to improve genetic information for agricultural species. Fiona has 19 years experience in supporting the application of genomics to agricultural systems, and during this time has worked with a diverse range of livestock, aquaculture, crops and agricultural pest species.

The Future of Plant Breeding

Fiona McCarthy, University of Arizona

Title: Lessons learned and the way ahead: cross-disciplinary opportunities for applying genome-to-phenome.

Yufeng Ge

Yufeng Ge is Associate Professor in the Department of Biological Systems Engineering at University of Nebraska-Lincoln. He got his PhD from Texas A&M University. His research focuses on advanced sensing and automation systems for agriculture.

Integrating limited field samples into radiative transfer simulated data enhances machine learning estimation of leaf chlorophyll and water contents

Water and nitrogen are two major factors in terms of crop production and improvement. Water and nitrogen status of plant shoots can be rapidly estimated through optical and spectroscopic means, which have led to tools used by breeders and growers to improve their utilization and management efficiency. In this talk I will introduce a hybrid method of combining machine learning and radiative transfer modeling (RTM) to improve the estimation of plant leaf water and nitrogen. The key idea is to use RTM to simulate leaf hyperspectral data, which are augmented by the real measurements, to form a model calibration set and train machine learning models. A new strategy to replicate the real data to increase its weight in the calibration set is investigated. The results show that the new "RTM + machine learning" approach outperformed the traditional RTM model inversion method, or pure machine learning applied on either simulated or real measurement data. The new approach also showed greater robustness as it maintained higher accuracy of estimation for both plant species tested, corn and sorghum. We anticipate this research would lead to next generation tools to benefit plant breeders and growers for high throughput, non-destructive analysis of plant water and nitrogen status.

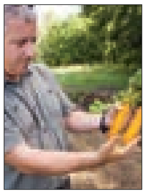
Gina Brown-Guedira

Dr. Brown-Guedira is a Research Geneticist with the USDA-Agricultural Research Service and USDA Professor in the Department of Crop and Soil Sciences at North Carolina State University. Her research group at the Eastern Regional Small Grains Genotyping Lab facilitates use of genomic resources by the breeding community. The lab collaborates with wheat breeders to map traits, develop cost-effective genotyping technologies, and implement genomic selection. Her research has also focused on characterizing genes underlying heading date in winter wheat.

A Journey in Genotyping for Wheat Improvement

Public and private wheat breeding efforts in the U.S. are complimented by research done at USDA Agricultural Research Service (ARS) programs on resistance to disease and insect pests, germplasm conservation and evaluation, germplasm enhancement, quality testing and multi-location yield testing through regional performance nurseries. In keeping with this model, Regional Small Grains Genotyping Labs were established in the early 2000s to ensure that advances in genomic technology, which has been slower for wheat due to the large polyploid genome, are accessible to breeding programs funded primarily by state grower's associations. Since 2004, the eastern regional genotyping lab at Raleigh, NC has conducted collaborative research with programs in the eastern winter wheat region. The lab has facilitated use of marker technologies for trait mapping, marker assisted selection and, more recently, genomic selection. Technological changes require that the lab continuously adjust and seek out the best approaches to provide useful data efficiently and cheaply. Breeding programs have also had to adjust their pipelines to incorporate genomics assisted methods. In the eastern region, our genotyping lab has been central to new a model revolving around consortia of smaller breeding programs that exchange and test genotyped lines at earlier stages.

Irwin Goldman



Irwin Goldman is professor of horticulture at University of Wisconsin-Madison, where he has worked for 30 years. His lab focuses on breeding and genetics of table beet, carrot, and onion. He and his students have released inbred lines, improved populations, and cultivars of these three crops, and they investigate horticulturally relevant traits with both classical and molecular approaches.

Not your grandmother's beet: Breeding biennial vegetables for specialty market classes

Many root and bulb vegetables are viewed as traditional foods that possess unique flavors and textures. Some of these crops form important connections to culture and cuisine. Table beet is considered by some to be a polarizing vegetable; appreciated by those who like earthy flavors and despised by those who don't. The puzzling presence of earthy flavors in beet, as well as in some other members of the *Amaranthaceae* family, led us to question their origin. Prevailing wisdom suggested that earthiness was a byproduct of the plant's close association with soil-based actinomycetes. These bacteria produce volatiles that humans detect as earthy, like the smell of soil. However, research over a period of years revealed that earthy plant-based terpenoid-derived compounds such as geosmin are produced endogenously by beet, for reasons that remain obscure. Armed with this information, and the awareness of consumer complaints about earthy flavors, we sought to breed for low levels of earthiness in order to make a new type of beet that could be consumed raw. One of the challenges to this type of breeding program is that plants in the *Amaranthaceae* also possess relatively high levels of oxalic acid, which functions as a defense against pests. Consumption of raw beet, Swiss chard, and in some cases spinach, can result in an abrasive mouth feel due to oxalate crystals in the leaf and root tissue. Therefore, selection took place for lower levels of earthiness and oxalic acid over a period of 15 years. Finally, we sought to modify the shape and color of the beet in order to produce an elongated root that contained alternating layers of betacyanin and betaxanthin, or red and yellow color, respectively, in the supernumerary cambial rings. These efforts were largely focused on producing a vegetable that would be attractive when consumed raw, rather than the traditional beet that was typically cooked or processed. Cultivars of this new ideotype are now being grown in a number of locations worldwide, and the products are sold in grocery stores and used on restaurant menus. This presentation will trace the process of breeding a new vegetable ideotype that departs from the traditional form in shape, color, flavor, and astringency, and share what we have learned about breeding for specialty markets along the way.

Jacob Washburn

My lab works on understanding the genetic and physiological basis of plant phenotypes and adaptations to both environmental (drought, heat, etc.) and human imposed conditions (fertilizer, density, monoculture, etc.). We use traditional phenotyping, drones, rovers, physiology, and other methods to evaluate plants in the field, greenhouse, and growth chamber. We apply quantitative genetics, physiological models, and machine/deep learning to biological, evolutionary, and agricultural systems.

Predicting Plant Phenotypes With Deep Learning

Predicting plant phenotypes from complex genetic and environmental factors is an ongoing challenge with significant implications for increasing crop productivity and sustainability. Even small increases in predictive accuracy can have significant economic impacts. We developed, tested, and improved upon a Deep Neural Network model predictive framework using a large maize dataset developed by the Genomes to Fields (G2F) Initiative. Specifically, we developed a novel method for the separation of training, validation, and testing sets which, along with imputation, allows us to maintain larger training sets (for better model development) while still controlling for overfitting. We created a standard framework for optimizing these models efficiently and we systematically tested different model architecture strategies with more or less training time focused on genetic and environmental factors individually versus interactions between the factors. Our results show that deep learning models can – but do not always – perform better than other common predictive methods. We also find that, at least in our models, greater emphasis on genetic and environmental factors individually resulted in higher accuracy.

Jose Rotundo

Innovative cropping systems: should we breed for novel traits and environments?

Most crop production fields are used with a single crop species per year, but the intensification of most cropping systems is changing this rapidly. Newer scenarios have intensified temporal rotations (more cash crops per year), intensified spatial rotations (more than one cash crop grown simultaneously), or rotations that include companion crops providing specific ecosystem services (i.e., carbon sequestration, weed control, N fixation, ground cover). Plant breeding has commonly released genotypes targeting the traditional management of a single crop per growing season, and mostly all intensification strategies assume that the best genotype in the sole cropping system is also the best genotype in other intensified cropping situation. The presentation will discuss to what extent crop varieties react differently to the effect of growing more than one species in the same field, and the potential plant breeding role to improve ecosystem services.

Kendall Lamkey

100 Years of Corn Breeding

The Cooperative Federal-State Maize Breeding Program located on the Iowa State University campus is celebrating its 100th anniversary in 2022. The program began just as Shull's (1909) breeders were starting to investigate ways to inbreed maize and the consequences of inbreeding on phenotype. Enough was becoming known about inbreeding and inbreeding depression that Jones (1917) proposed double-cross hybrids to overcome the low yields of inbred lines. Merle Jenkins was the first breeder that F.D. Richey, who was head of corn investigations at the USDA, hired to start the program. Jenkins developed a corn breeding program that has proved to be one of the most productive in the history of corn breeding. Jenkins first nursery in 1922 produced several important inbred lines that went on to be parents of some of the most widely grown double-crosses of their time. This talk is a brief tour of some of the people, questions, and germplasm that made the program so successful.

Kevin Smith

Breeding for Continuous Cover Cropping Systems - Forever Green Initiative

The Forever Green Initiative (FGI) is a research platform to deliver continuous cover agriculture to the Upper Midwest. FGI is developing and improving winter-hardy annual and perennial crops and cropping systems that protect soil and water while driving new economic opportunities and for growers, industry, and Minnesota communities across the state. The FGI portfolio includes sixteen crops, each supported by a multidisciplinary team that may include expertise in the areas of genomics, breeding, agronomics, natural resource sciences, food science, sociology, economics, and commercialization.

Lizhi Wang

Lizhi Wang is a Professor and Director of Research in the Department of Industrial and Manufacturing Systems Engineering at Iowa State University. He is also a faculty scholar in the Plant Sciences Institute at Iowa State University. His research interest includes improving the effectiveness and efficiency of plant breeding using engineering principles and techniques, such as mathematical modeling, computational optimization, data analytics, and artificial intelligence.

Descriptive, Predictive, and Prescriptive Models for Plant Breeding

This talk will present three data analytic models for data-driven plant breeding. First, a data-driven crop model will be introduced to address genotype-by-environment interactions, which helps breeders to extract genetic traits of new genotypes that are invariant across environments. Second, an opaque breeding simulator will be introduced, which attempts to overcome the flaws and limitations of the commonly used transparent simulators. Third, the look-ahead selection approach will be introduced, which can be used to make optimal breeding decisions in trait introgression and genomic selection.

Matthew Carroll

Matthew Carroll is a PhD candidate in Plant breeding with a minor in statistics, and a specialization in predictive plant phenomics at Iowa State University. He has a bachelor's degree in Agronomy, and Genetics from Iowa State. Matt's work focuses on improving efficiency in soybean breeding programs utilizing remote sensing, and machine learning techniques.

Soil Mapping Improves Spatial Adjustments for Breeding Trials

Spatial adjustments are commonly used within plant breeding programs to reduce the effects of field heterogeneity. Adjusting for field effects reduces the standard error of the estimate of genotypic values and increases the accuracy of selection, which ultimately results in improved genetic gain. Current methods of spatial adjustment consider the performance of neighboring plots to adjust for non-random spatial trends within the field. These trends are typically thought of as fertility gradients, but soil fertility effects are never directly quantified while applying these methods. With advances in remote sensing and digital soil mapping, accurate high-resolution soil maps can now be used to estimate plot level soil fertility values. We propose a method that utilizes high resolution soil fertility maps in combination with the XGBoost algorithm to predict the quality of the growing conditions for every plot within a breeding program. This method effectively removes spatial-autocorrelation, reduces the similarity of selected lines, and increases the relative efficiency compared to other methods of spatial adjustment. This method can also be used to meet specialized breeding objectives, for example, breeding for nutrient use efficiency. With continual advancement of remote sensing techniques and machine learning models, we envision that breeders can include modelled dynamics of the entire ecosystem of breeding trial fields to better understand pathways of distinct varieties to reach their yield potential.

Mario Carlone

Dr. Mario Carlone received his BS in 1983 from University of Connecticut in Environmental Horticulture and his MS (1985) and PHD (1987) from Iowa State University in Plant Breeding. He started his corn breeding career in 1987 for the Garst seed company breeding for Southern Iowa and coordinating hybrid development for Southern Europe. In 1995 he accepted a position with Pioneer. During his 25 years at Corteva/Pioneer Mario has worked in numerous Corn Breeding R & D roles including China Corn R&D, Research Coordinator, Evaluation Zone Lead, Germplasm Discovery Lead and Global Breeding Zone Lead. He currently runs a breeding program in Northcentral IL and has been an inventor on over 100 issued patents and is a Distinguished Corteva Agrisciences Laureate, the company's highest level science position.

Long-term Maize Germplasm Development

Mario Carlone, Edwin Grote, Eli Rodgers-Melnick and Dave Bubeck—Corteva Agriscience

The foundation of Pioneer's maize germplasm began with Henry Wallace and Raymond Baker, Pioneer's first maize breeder, obtaining a few publicly available inbreds and numerous open pollinated (OP) varieties. These initial sources of germplasm were used directly in double cross hybrids and in germplasm development via pedigree selection. The transition from double cross to single crosses within Pioneer during the 60's and 70's also brought about a concerted development of heterotic pools, which ultimately resulted in a largely female pool and a male pool. Within these heterotic pools are distinct genetic groups (sub-heterotic pools) and one key group within Pioneer is known as Iodent. The development of the Iodent pool for commercial use can be initially attributed to Baker's dedication to adding ear length to this genetic pool which allowed it to flourish for over 70 years, remaining as impactful commercial genetics to this day. From the 80's to the present time our germplasm base has continued to grow, develop and change to meet the needs of the environments and farmers. However, the rate of genetic gain has varied among key genetic backgrounds, resulting in a range of realized breeding values from key inbreds, but continued to show steady progress when evaluated in commercially sold products (Duvick Era studies). In conclusion, genetic pools continue to evolve over time to meet the changing needs of the farmers, end-users, consumers, and environments.

Milad Eskandari

Dr. Eskandari is an associate professor in the Department of Plant Agriculture at the University of Guelph, Canada. His breeding and research program focuses on developing food-grade soybean cultivars and germplasm with improved agronomic and seed quality traits as well as resistance to important diseases of soybean that address the specific needs of Canadian's soybean growers and end-users. The program is also focused on advancing knowledge in the areas of high throughput phenotyping and genotyping in soybean with a goal of developing more efficient breeding methods that facilitate the development of new cultivars. Dr. Eskandari has participated in the release of 13 soybean cultivars and several germplasm. He has authored and co-authored over 35 peer reviewed research papers, cultivar descriptions, and book chapters.

Machine Learning and Optimization Algorithms in Plant Breeding: Modeling Soybean Yield using its Components

Plant breeders have always been interested in increasing genetic gain of complex traits such as yield. The current advances in high-throughput phenotyping and genotyping technologies, along with efficient computational methods, have provided breeders with unique opportunities for designing more promising crosses and better evaluation of progenies. In this presentation, the results of our study on using soybean yield components for estimating the yield and modeling "ideotype" high-yielding cultivars will be conveyed. The phenotypic and genotypic data were collected from a panel of 250 soybeans evaluated across four environments in Ontario, Canada. Multilayer Perceptron, Radial Basis Function, and Random Forest machine learning (ML) algorithms, individually and collectively using a bagging ensemble method, were used to estimate the final yield using its components. To model the optimum values of yield components in a maximized yield "ideotype", the best ML algorithm was allied with the genetic algorithm, as a well-known single objective optimization method. The results may provide a better understanding of the combination effect of yield componets on final yield production, which in turn can help soybean breeders to design better crosses for improving yield genetic gain in new cultivars.

M. Nelly Arguello-Blanco

Nelly is originally from a small village in Colombia, she is passionate about ways to improve farmers' life with Ag Science. She is supervised by Dr. Clay Sneller at The Ohio State University. Her Ph.D. dissertation focused on measuring the rate of changes in allele frequency, population structure, and linkage disequilibrium in populations of wheat subjected to genomic selection. Nelly graduated yesterday with her PhD in Plant Breeding and Genetics.

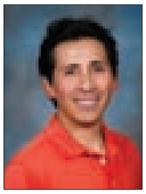
Effects on the wheat (Triticum aestivum L.) genome from five rapid genomic selection (GS) cycles

Breeders can use genomic selection (GS) to shorten the breeding cycle compared to phenotypic selection. Genome changes resulting from rapid cycling have not been characterized. The OSU winter wheat breeding program has completed five cycles of GS in five years initiated from a training population (TP) that was phenotyped for yield. Our objective was to assess the effect of this selection on the wheat genome. We genotype the TP and individuals from the five cycles with 3927 single nucleotide polymorphism markers to assess the dynamics of allele frequencies, genetic diversity (simple matching coefficient, SMC), population structure (Fst), and linkage disequilibrium (LD). Over the cycles we quantified a reduction in genetic diversity, an increase of the genetic differentiation of cycles from the TP, and changes in the LD patterns. About 27% of the markers had a significant change in allele frequency relative to the TP, with 18% of these attributed to selection: the others could be due to drift or selection. Of all markers, 18.5% were fixed by cycle 5. The SMC increased 0.02 units per cycle, revealing a reduction of genetic diversity. The TP and cycles significantly differentiated from one another at 0.046 Fst units per cycle. The correlation between the LD matrices of each cycle decreased -0.057 units per cycle indicating that the LD pattern in the TP was changing through the cycles. The accuracy of GS depends on similarity of the genome of the TP and the genome of the prediction population. Our findings suggest that rapid cycling causes significant genome changes that could quickly decrease the accuracy of GS in the subsequent cycles. Although the change in the genome is desired for breeding purposes, they can also reduce GS accuracy that could hamper genetic gain and the benefits of GS rapid cycling.

Pat Byrne

Dr. Pat Byrne is semi-retired from the Department of Soil and Crop Sciences at Colorado State University, USA, where he taught and conducted research in plant breeding and genetics of wheat, maize, and dry beans. He has done extensive outreach on the benefits and risks of genetically engineered crops. He currently leads a project to develop learning materials on the conservation and use of plant genetic resources. Before coming to CSU in 1997, Dr. Byrne worked for USDA-ARS in Columbia, Missouri, and in agricultural development in Mexico, West Africa, and Nepal.

Patricio Munoz



Patricio Munoz is an associate professor in blueberry breeding at the University of Florida. He has responsibilities in teaching, curriculum development, research, and breeding. He focuses on developing cultivars with a local focus but a global impact. His research is related to improve the breeding process of outcrossing tetraploid species. He co-led the development of a PhD degree program in plant breeding at the University of Florida of which he is the program director.

Blueberry Breeding with a Local Focus but a Global Impact

Blueberries were domesticated at the beginning of the last century. The main species *Vaccinium corymbosum* (Northern Highbush) could not be grown in the South due to the lack of chilling hours. Hybridization with native Vaccinium species started in 1950 at the University of Florida, with the first cultivar released in 1976. Breeders at that time did not realize the impact of their work, as the newly developed varietal type commonly known as "Southern Highbush Blueberry" (SHB) expanded the cultivation of blueberries to subtropical and tropical areas around the world. Currently, the University of Florida Blueberry Breeding Program has released more than 100 cultivars directly and indirectly. Our principle still is "local focus but global impact" as we license our cultivars in every country where SHB grow. During the talk I will briefly cover my early career goals, expectations, successes, and challenges, as well as the strategy, methods and techniques, traits, and management of the University of Florida Blueberry Breeding Program.

Peter Bretting

Peter Bretting, Ph. D., has served as USDA/ARS National Program Leader, Plant Germplasm and Genomes since 1998, and became a Senior National Program Leader in 2004. Previous to this position, he served as Research Leader and Coordinator, USDA/ARS, North Central Regional Plant Introduction Station (NCRPIS), and USDA/ARS Collaborator-Associate Professor of Agronomy and Botany, Iowa State University. Prior to joining USDA/ARS, he served as Research Program Director, Indiana Crop Improvement Association, and Adjunct Assistant Professor of Botany and Plant Pathology, Purdue University.

Need Plant Germplasm and Data for Breeding and Research? There's an App for that: the National Plant Germplasm System!

Thanks to application software, access to information, data, and to numerous different products often involves just a few keystrokes or finger taps. Although it does not function yet as seamlessly as an "app," the USDA Agricultural Research Service's National Plant Germplasm System (NPGS) does resemble an app by successfully delivering through an online website an annual average of 200,000+ different samples (accessions) of valuable plant genetic resources (PGR) and associated information to thousands of plant breeders and researchers. The NPGS, one of the largest national PGR systems, conserves 600,000+ accessions of 16,000+ plant species, encompassing field, horticultural, and specialty crops. The NPGS comprises 20 different geographically dispersed genebanks, most of which located on the campuses of, or closely associated with, leading US land-grant universities. Conserving and providing ready access to PGR and associated information require that the NPGS genebanks conduct complicated, coordinated, multi-phase operations over extended periods. How does the NPGS conserve and distribute PGR and associated information successfully? Dedicated and diverse PGR managers (curators) are crucial, as are continual and persistent financial support for PGR genebanks, and 44 different Crop Germplasm Committees that supply technical input for priority PGR to conserve, key traits to evaluate, and other needs for specific crops or groups of crops. The NPGS's common information management system, Germplasm Resources Information Network (GRIN)-Global, serves as an international standard and a crucial element for NPGS operational integration. How might the NPGS "app" evolve in the future? If crucial research goals can be attained, and NPGS infrastructure and operational capacities can be expanded, a greater spectrum of PGR will be safeguarded true-to-type and pathogen-tested in state-of-the art genebank facilities or in situ reserves; characterized genotypically; and evaluated through high through-put phenomics. Vastly greater volumes of accumulated descriptive information would enable requestors to identify, perhaps even to the level of haplotypes or alleles, optimal PGR for their research and breeding needs. Many PGR management operations might be conducted more frequently and more adequately by expanded multi-locational networks enabled by advances in information technology and artificial intelligence.

Rebecca Grumet

Rebecca Grumet is a Professor in the Department of Horticulture and the Graduate Program in Plant Breeding, Genetics and Biotechnology. She is a W.J. Beal Outstanding Faculty at Michigan State University and a Fellow of the American Society for Horticultural Science. Her research deals with vegetable genetics and genomics, with a primary emphasis on cucurbit flower and fruit development and disease resistance. She is currently the lead PI, along with 20 co-PIs, for the USDA-SCRI CucCAP project: CucCAP: Leveraging applied genomics to increase disease resistance in cucurbit crops.

Cucurbit germplasm – genomic tools and disease resistance

The USDA-SCRI funded project, CucCAP, seeks to advance understanding of the genomics of the Cucurbitaceae family and apply genomic tools to practical breeding challenges. CucCAP is a collaborative effort by the U.S. cucurbit community with research groups from twelve institutions. Outcomes of the project include development of the cucurbit genomics database and associated analysis and visualization tools; GBS-based genetic characterization of the USDA National Plant Germplasm System collections for watermelon, melon, cucumber, and squash; elucidation of phylogenetic relationships of accessions within the collections and establishment of molecularly informed core populations representing >95% of the genetic diversity present for each crop. Current efforts are directed toward deep resequencing the core populations, development of pan-genomes, and development of linked genetic-phenotypic databases. The genomic tools are being used to identify, map, and develop markers for resistances to priority diseases identified by the cucurbit industries. Breeders are working in collaboration with pathologists to introduce and combine resistances in advanced breeding lines, perform multi-location, multi-isolate trials of resistances, and improve integrated disease management strategies.

Roy Scott

Dr. Scott's initial Agricultural training and early career was in general agriculture. He earned his B.S. and M.S. degrees in Agronomy at Oklahoma State University and his Ph.D. in Agronomy at Kansas State University, with emphasis in agronomy, plant genetics and breeding. He worked in plant breeding in both the public and private sectors in several different crops, including sorghum, alfalfa, wheat, and soybeans. Dr. Scott is currently the National Program Leader with USDA-ARS Office of National Programs based in Beltsville, MD. He is responsible for research in Oilseed crops, Pulse Crops, and cotton. He co-leads the ARS National Program in Plant Genetic Resources, Genomics, and Genetic Improvement. Prior to joining the Office of National Programs in 2008, Dr. Scott served in the Plant Science Department at South Dakota State University for 18 years, where he was soybean breeder, Coordinator of oilseed crops research, and Director of the Drought Tolerance Center of Excellence in the College of Agriculture and Biological Science. He also taught courses in plant breeding and scientific writing.

Shuizhang Fei

Dr. Fei is a professor of grass genetics and breeding in the Department of Horticulture and an affiliate member of the Plant Breeding Program at Iowa State University. Dr. Fei's research include identifying and developing cool-season grasses for dedicated perennial groundcover in crop production, and studying molecular mechanisms underlying important agronomy traits in perennial grasses and model plants. Dr. Fei obtained his BS in agronomy and MS in horticulture from China Agricultural University and his PhD from the University of Nebraska-Lincoln.

Turfgrasses as perennial groundcover for maize production

Allen Chen, Shui-zhang Fei, Ken Moore and Andy Lenssen

Perennial groundcovers (PGC) provide a means for restoring ecological services while allowing the sustainable intensification of maize production, by providing groundcover for many years without replanting. Cool-season turfgrasses, with their C3 photosynthesis system, preference for cool-moist weather, good shade tolerance and winter hardiness are excellent candidates for PGC. We evaluated the compatibility of three cool-season turfgrass species, Kentucky bluegrass (Poa pratensis), Sandberg bluegrass (Poa secunda), and red fescue (Festuca rubra) with maize. Maize was interplanted into twenty unimproved USDA GRIN accessions of the three species in a field experiment with a randomized complete block design in Boone, IA. Data on maize grain yield, maize grain quality, and ground coverage of PGC were collected. There were no differences in maize grain yield across species in 2017. In 2018, maize grain yield under red fescue was 1.0 Mg ha-1, 1.8Mg ha-1, and 2.1 Mg ha-1 less than Kentucky bluegrass, Sandberg bluegrass, or the no-grass control. These results indicate that maize under Kentucky bluegrass and Sandberg bluegrass can perform similarly to conventional maize. Our most recent study with the summer-dormant bulbous bluegrass (Poa bulbosa) also showed that maize interplanted with P. bulbosa results in similar or even greater maize grain yield. Unimproved accessions maintained by USDA GRIN can be a valuable resource for intercropping breeding.

Key words: Perennial groundcover; Zea mays; Poa pratensis; Poa secunda; Poa bulbosa; Festuca rubra

Tabare Abadie

Dr. Tabare Abadie has held a number of prestigious plant breeding positions including as a wheat and barley breeder at La Estanzuela (Uruguay) a Professor in Plant Breeding at the Universidad de la Republica (Uruguay), and a consultant for EMBRAPA CENARGEM (Brazil) all prior to joining Pioneer (now Corteva). At Corteva, he is a senior research manager, probably best known for conceiving and developing the Corteva Agriscience Plant Symposia Series, a series of student organized and driven scientific symposia system hosted at leading academic and research institutions. These symposia are held at over 60 institutions in 16 countries on 6 continents. This program provides leadership and networking opportunities for the next generation of scientists.

Theresa Cooper

Dr. Theressa Cooper is the assistant dean for diversity in the College of Agriculture and Life Sciences at Iowa State University. In this position, which she has held since February 2013, she coordinates, manages and implements the college's diversity and inclusion programs, including directing the George Washington Carver Summer Internship Program. In her role as assistant dean she serves as a liaison connecting Iowa State with Minority Serving Institutions nationwide, building collaborations through teaching, research, and outreach activities. Theressa has specialized training in intercultural competency, organizational development, leadership development, youth development, coaching, intercultural conflict, and action learning. Her research focuses on increasing the representation of Black, Indigenous, People of Color (BIPOC) in agriculture and the food system, and cultural responsive planning and programming, that assists community members, educators and institutions build and strengthen intercultural competence. Dr. Cooper is a qualified administer of the Intercultural Developmental Inventory (IDI) and the Meyers Briggs Type Inventory (MBTI). In addition, Theressa holds an adjunct assistant professor position in the CALS department of agricultural education and studies. She has taught undergraduate and graduate courses in agricultural education, youth development, diversity, and cultural competence. Dr. Cooper earned her doctorate in cultural studies from the University of Tennessee. She earned her bachelor's degree in agricultural development and master's degree in agricultural education at Texas A&M University.

VK Kishore

Dr. VK Kishore has 20 yrs. of experience in research and development across Field crops and Vegetables in Americas, Asia, Europe, Middle East and Africa. Dr. Kishore has a Ph.D. in Crop Science from Oregon State University with a specialization in Plant Molecular Breeding and he also has an MBA from Illinois State University. Dr. Kishore is currently the Global Head of Smallholders and Sustainability for the Veg seeds organization in Bayer Crop Science and is based at St. Louis, USA. He also currently serves as a board member on the boards of two non-profit organizations: Hunger Free America and iDE (International Development Enterprises). Dr. Kishore has been named as an inventor on six granted patents and published 16 articles in scientific journals

Breeding for Sustainable Innovations from Seed to Consumer

Plant breeding innovation is essential to contribute to a sustainable agriculture production that fosters food security and healthy nutrition. It all starts with a seed and hence improved varieties are a starting point for a sustainable food system. At Bayer Vegetable seeds we are focused on providing climate resilient, innovative, and customized solutions to sustainably supply the world with nutritious and delicious fruits and vegetables. In this talk the author will share the sustianbility commitments of Bayer Crop science and examples of our innovations that our breeding teams have developed to help address these commitments.

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