



The CORTEVA AGRISCIENCE - MSU PBGB  
Plant Science Symposium Series



Harvesting the Past, Cultivating the Future:

# Insights in Plant Domestication



## Schedule

Time	Event
9:00 am - 10:00 am	<b>Breakfast</b> MPS atrium <b>Lightning Talks &amp; Poster Presentations</b> PSSB A271
10:00 am	<b>Opening remarks</b> MPS 1200
10:15 am - 11:10 am	<b>Speaker 1 - Esther van der Knaap (UGA)</b> MPS 1200
11:15 am - 12:10 pm	<b>Speaker 2 - Corteva Speaker Jen Jaqueth (Corteva)</b> MPS 1200
12:15 pm - 1:15 pm	<b>Lunch Roundtable Discussions with Speakers</b> Consequences of trait/ideotype selection during domestication (Dr. Gepts Dr. van der Knapp, and Dr. Van Tassel) PSSB A271
1:30 pm - 2:25 pm	<b>Speaker 3 - Paul Gepts (UC Davis)</b> MPS 1200
2:30pm - 3:25 pm	<b>Speaker 4- David Van Tassel (The Land Institute)</b> MPS 1200
3:30 pm	<b>Closing Remarks</b> MPS 1200
3:45 pm	<b>Coffee Break</b> MPS Atrium

# Invited Speakers

## Esther van der Knapp

University of Georgia, Athens, GA

### **Domestication and selection driving fruit quality traits in tomato**

**Abstract:** The process of domestication and selective breeding has played a crucial role in shaping tomato fruit quality traits, making it one of the most popular and widely cultivated crops today. Wild tomato feature fruits that are small, round, full of seeds, and produce an aroma that, collectively, has evolved to attract seed dispersers in native habitats. The evolutionary process from wild to contemporary fruit types was driven by human preferences for increased sizes, variable shapes, characteristic tastes, and other attributes, where selective breeding further refined these traits. This resulted in a phenotypically diverse germplasm that produces fruits varying in morphological and aromatic properties. The emergence of genomics and molecular biology has allowed for a much deeper understanding of the processes, including the genes, that regulate the transition from wild to cultivated types in the regulation of fruit quality. This knowledge enables breeding strategies that are targeted at specific market classes by enabling the selection of beneficial haplotypes. The research in our laboratory delves into the molecular genetic basis of these forces that have influenced the evolution of the tomato plant, with extensions to other fruit and vegetable crops. Examples include SUN, TRM, and OVATE that regulate fruit shape; CSR and SIKLUH that regulate fruit size; and various genes that regulate fruit aroma.



## Jean Jaqueth

Corteva Agriscience

### **Deploying Genome Editing for Native Disease Resistance: Maize Disease Super Locus**

**Abstract:** Corteva Agriscience uses innovative genome editing technology to package multiple disease-resistant genes into a single location in the genome to better address devastating corn diseases facing farmers today. By using genome editing to combine and reposition disease-resistant genes that already exist within the corn genome, Corteva is able to bolster disease tolerance and increase yield potential. The Disease Super Locus concept is intended to simplify disease management and improve sustainability by reducing the need for additional fungicide applications.



## Paul Gepts

University of California Davis

### **The Natural History of a Wild Crop Relative: Its Applications in Domestication Studies, Conservation, and Genetic Improvement**

**Abstract:** For most of its existence, the hominin evolutionary lineage leading up to Homo sapiens has procured food and other biological necessities as hunter-gatherers. In a major subsistence transition (which, as yet, is not fully understood), modern humans initiated the crop cultivation process (and animal rearing). One cannot exaggerate the importance of this transition as it affected, in the most significant way, crop properties through domestication, biodiversity, ecosystems, and habitats, and the activities, organization, and health of human societies. Within this broader context, I will focus on the natural history of a crop wild relative (CWR) - namely, wild common-bean (*Phaseolus vulgaris*) - and what this knowledge tells us about this crop's domestication process. I will discuss various aspects, like its vast geographic distribution in the Americas and how it came to be, the issue of gene flow between wild and domesticated types despite its predominant autogamy, and the molecular basis of its transformation into the most widely cultivated pulse in the world, through a remarkable diversification in pod and seed types and photoperiod insensitivity. In turn, this knowledge guides the process of genetic conservation, both in-situ and ex-situ, and the use of this CWR in breeding more resilient cultivars.



## David Van Tassel

The Land Institute

### **Farmers need new tools. Wild plants have impressive adaptations. Domestication could bring them together. Everyone will have to help**

**Abstract:** Farmers face more erratic weather, fiercer competition for irrigation water, increased fertilizer cost, rising sea levels, and more social pressure to help conserve biodiversity. The plant kingdom is immensely species-rich and contains a wealth of evolutionary adaptations: deep roots, mutualisms with beneficial insects and fungi, perennial regrowth in the spring, heat and flooding tolerance, an array of defensive structures and chemistry. These adaptations could help farmers conserve soil, produce during droughts, and use applied nutrients more efficiently. However, bringing completely new species to the farm requires major investment in genetic improvement, horticultural and ag. engineering innovation, and social/economic/cultural capacity-building: a truly transdisciplinary challenge. Genetic innovations including gene editing and genomic selection could accelerate yield gains during de novo domestication, but do not overcome concerns that strong directional selection will lead to loss of the "wild adaptations" that attracted us to these plants in the first place. I will illustrate these general domestication challenges and opportunities using examples from The Land Institute's work to domesticate perennial cereal, legume, and oilseed grains, including my work domesticating *Silphium integrifolium* (Asteraceae)--a North American prairie perennial.





# Lightning Talks

## John Hawkins

### Lack of Genetic Gain in White Mold Resistance within Dry Bean National White Mold Trials

**Abstract:** White mold caused by *Sclerotinia sclerotiorum* (Lib.) de Bary is the critical yield-limiting disease of dry bean in the US, causing millions of dollars in damages annually. Many approaches to control of this disease have been explored, including crop rotation, fungicides, prediction, and various biocontrols. Genetic resistance shows great promise for averting white mold damage. However, white mold resistance is a highly complex quantitative trait controlled by a large number of QTL. Two major mechanisms of resistance are discussed in the literature, physiological resistance and avoidance. Many dry bean breeding programs have done some amount of selection for white mold resistance. In order to compare the white mold resistance of current dry bean lines across multiple locations, the National White Mold Trials have been carried out from 2008 until the present day. White mold resistant material from various breeding programs is grown out at multiple locations along with three control lines. White mold incidence and severity are measured at each location. Data from these trials between 2008 and 2022 (excluding 2020 when no trials could be conducted) was analyzed for genetic gain using a control population model. The trend identified by the model was a very slight but significant increase in white mold severity over time, suggesting that overall white mold resistance of the lines entered in the NWMT is not increasing, or is not keeping pace with pathogen evolution.

## Mohit Mahey

### Gene co-expression network analysis in *Poa annua*

**Abstract:** *Poa annua* is an annual weed in southern USA turf fields. It has been showing resistance to multiple herbicides with different modes of action and is a serious problem. Indaziflam, a cellulose biosynthesis inhibitor herbicide is a good option to control this weed, however recently resistant populations were reported. My project is to dissect the *Poa annua* mechanism of the resistance towards indaziflam. We performed an RNA-seq study comparing 3 susceptible and 3 resistant populations to find candidate genes able to metabolize the herbicide. The transcriptome data were analyzed through differential gene expression (DEG) and weighted correlation network analysis (WGCNA). We found the group of genes that are positively correlated with resistance phenotype. We have identified a cytochrome P450 that is very similar to CYP81A10 reported to confer resistance to five different herbicide modes of action in *Lolium rigidum*. The multiple herbicide resistance is currently being tested in *P. annua* populations in combination with a P450 enzymes inhibitor (malathion). We hypothesize that the cytochrome P450 up regulated is associated with indaziflam resistance, and potentially conferring resistance to other herbicides. The results will give insights to better understand herbicide metabolism resistance, its regulation, and the herbicide management strategies associated with herbicides modes of action rotation to delay the herbicide resistance evolution.

## Stephen Stresow

### Vegetables are a social construct: how definitions limit food security

**Abstract:** The idea that “vegetables are a social construct” is an introductory botany lesson that embodies the legacy that colonialism and imperialism have had on the global food system. Instead of having a botanical definition, vegetables are defined by human values ranging from beauty to masculinity. This narrow conceptualization of what a “proper” vegetable is has reduced the types of crops cultivated globally. In many instances, climate-resilient indigenous vegetables have been replaced with crops that meet Euro-centric demands. Vegetables being a social construct is critically analyzed through the lens of queer theory. As an academic discipline, queer theory challenges normativity and the process of normalization. It is used to expand one’s thinking, which is critical for addressing food security issues. This paper serves as an introduction to queer theory that horticulturists can use to approach their work. The social construction of vegetables extends across the food system and has historically been used to indicate that some diets and cultures—because of the food they ate—were superior to others. Negative social attitudes towards vegetables limit their consumption, especially because they challenge hegemonic masculinity. This paper aims to “queer,” i.e., challenge, the idea of vegetables and analyze 1) the plants we call vegetables, 2) how these crops are grown, and 3) how these crops are consumed. It is a call for horticulturists to engage more with social theories to make them better collaborators and be better able to apply their work to a broader audience.

## MacKenzie Jacobs

### Anthracnose fruit rot

**Abstract:** Anthracnose fruit rot, caused by the fungal pathogen *Colletotrichum fioriniae*, is among the most destructive and widespread fruit disease of blueberry, impacting both yield and overall fruit quality. Blueberry cultivars have highly variable resistance against anthracnose fruit rot. To date, this pathogen is largely controlled by applying various fungicides; thus, a more cost-effective and environmentally conscious solution for anthracnose fruit rot is needed. Here we report three quantitative trait loci associated with anthracnose fruit rot resistance in northern highbush blueberry (*Vaccinium corymbosum*). Candidate genes within these genomic regions are associated with the biosynthesis of flavonoids (e.g., anthocyanins) and resistance against pathogens. Furthermore, we examined gene expression changes in fruits following inoculation with *Colletotrichum* in a resistant cultivar, which revealed an enrichment of significantly differentially expressed genes associated with certain specialized metabolic pathways (e.g., flavonol biosynthesis) and pathogen resistance. Using non-targeted metabolite profiling, we identified a flavonol glycoside with properties consistent with a quercetin rhamnoside as a compound exhibiting significant abundance differences among the most resistant and susceptible individuals from the genetic mapping population. Further analysis revealed that this compound exhibits significant abundance differences among the most resistant and susceptible individuals when analyzed as two groups. However, individuals within each group displayed considerable overlapping variation in this compound, suggesting that its abundance may only be partially associated with resistance against *C. fioriniae*. These findings should serve as a powerful resource that will enable breeding programs to more easily develop new cultivars with superior resistance to anthracnose fruit rot and as the basis of future research studies.

# Lightning Talks

## Huijia Gong

### Growth-defense tradeoff in plants: a perspective from Cyclin-dependent kinase 8 (CDK8)

**Abstract:** Growth-defense transition is an essential process for plants because they live in diverse and complicated environments with various abiotic and biotic stresses. The regular growth and development of plants are affected by different stresses, resulting in reduced growth, development, and reproduction. Hence, plants have developed a sophisticated system of growth-defense balance. Though details of such a system have not been fully understood, literature has shown that phytohormone crosstalk and transcriptional regulation are likely involved. Understanding the growth-defense transition in plants will benefit fundamental plant biology studies, plant breeding, and agriculture. Plant cyclin-dependent kinase 8 (CDK8) has been studied as a critical component in transcription, regulating genes and transcription factors responsible for growth, reproduction, and defense responses against biotic and abiotic stresses. Despite the critical role of CDK8 in plant growth and defense, details on CDK8's regulatory and catalytic mechanisms remain unclear due to the lack of an in-depth understanding of the kinase domain and overall protein structure of plant CDK8s, hindering our in-depth understanding of the structure-function relationship of plant CDK8s. In Aim 1, I will investigate the structure-function relationship of *Arabidopsis thaliana* CDK8. The hypothesis is that the kinase active site and specific post-translational modification sites are critical to the regulatory roles of AtCDK8 in growth-defense tradeoff. To investigate the role of CDK8 in a wider array of agricultural plants, it will be informative to apply the knowledge we learned from *A. thaliana* to an agricultural model organism like *Solanum lycopersicum*, also known as the garden tomato. In Aim 2, I will characterize the role of CDK8 in regulating growth and defense in *S. lycopersicum* by generating CRISPR-Cas9 knockout lines and identifying potential *S. lycopersicum* CDK8 (SlCDK8) interactors using yeast two-hybrid assays. The hypothesis is that CDK8 is necessary for the growth-defense transition in *S. lycopersicum* and functions by phosphorylating the target protein.

## Prabhjot Kaur

### Understanding the genetic mechanisms underlying development rate in *Petunia* and *Stevia*

**Abstract:** The rate at which plants produce new nodes (development rate) is one of the primary factors controlling crop production time or time to first yield of agricultural crops. Crop timing is a function of temperature with production time generally increasing as temperature decreases. It is desirable to understand the genetic factors controlling vegetative development rate to accelerate crop timing at non-optimal temperatures and for increasing the biomass/yield of crop plants. We study development rate in two different crops, *petunia*, and *stevia*. *Petunia* is an annual bedding plant grown in greenhouses during winters in northern states of the United States and is highly demanded for its flower color variation and bedding nature. The study of elucidating genetic factors underlying development rate in *petunia* will facilitate breeding of cultivars that develop faster under relatively cooler conditions. This will reduce the production times and input costs due to greenhouse heating and other resources used by the floriculture industry. Additionally, vegetative development rate is an important trait to be studied in crops such as *stevia* which are desirable when harvested at vegetative stage. The leaf extract of *Stevia* contains a special kind of low-calorie sweetener compounds which could be used as sugar alternatives. Breeding cultivars that develop faster will facilitate multiple harvests of *stevia* during its annual production season and increase the biomass. The results of this study could be more rapidly applied for the improvement of several important fresh market vegetable crops that are grown in limited seasons. This will fulfill the desire of the general public for locally grown produce which has increased dramatically in recent years.

# Poster Abstracts

## Robert Shrote

**Abstract:** Choosing a suitable breeding strategy is essential to the success of a plant breeding program. Simulations are an important tool that allow plant breeders to propose and assess the merits of alternative breeding strategies. The Python package PyBrOpS provides a highly flexible and modular framework to make optimized breeding selection decisions and perform stochastic simulations of plant breeding programs. PyBrOpS utilizes a customizable scripting-based approach to constructing breeding simulations and optimizations. Through the use of software interfaces that allow for extensibility, the user may implement custom PyBrOpS modules that provide additional functionality. PyBrOpS offers pre-built subroutines for selection strategies such as conventional genomic selection, weighted genomic selection, optimal contribution selection, optimal population value selection, and optimal haploid value selection. Additionally, PyBrOpS is capable of both single- and multi-trait selection. For multi-trait selection scenarios, PyBrOpS offers the novel capability of mapping trade-off frontiers through the use of multi-objective evolutionary algorithms. Here, we describe the main features of PyBrOpS and provide example use cases for breeding program simulation and optimization.

## Stephen Stresow

**Abstract:** Effective weed management strategies that do not rely on tillage or herbicides are crucial for small-acreage organic vegetable farming. Applying black polyethylene tarps to the soil surface before plantings has become an increasingly popular tactic to manage weeds and prepare the seedbed. The impact of tarps on the weed seedbank, however, has not been thoroughly explored. This study assessed the weed seedbank following a 7-year organic vegetable cropping systems experiment. Four tillage systems (conventional tillage, no-till, tillage with tarp, no-till with tarp) and three different mulches (rye, compost, no mulch) were examined to determine their effects on weed density and species composition. Conventional tillage systems exhibited the highest weed density (672 weed seeds/m<sup>2</sup>), followed by conventional tillage with a tarp (439), no-till (278), and no-till with a tarp (179). Rye and deep compost mulches had one-third the weeds as unmulched treatments. In addition to having the fewest weeds, no-till and no-till, tarped systems had the greatest species evenness and Shannon-Diversity Index. Mulches were most effective at reducing summer annuals like hairy galinsoga, while tarping reduced winter annuals like common chickweed. Integrating tarps or mulch can help organic growers, regardless of tillage system, reduce weeds.

## Claudia Miranda Cekalovic

**Abstract:** The United States is the top producer of strawberries in the world, accounting for nearly a third of total strawberry yield production. The loss of production due to abiotic stressors, namely increasing soil salinity levels, results in the loss of millions of US dollars annually to growers. The primary goal of this project is to develop a cost-effective solution to address crop loss in strawberry associated with high levels of salt present in the soil or irrigation water. The proposed research will provide valuable insight into the underlying genetics of strawberry salinity tolerance, as well as develop molecular markers that will enable breeding programs to release superior cultivars. The objectives of this research are to identify candidate gene(s) associated with improved salinity tolerance in strawberry, to functionally characterize candidate genes, and the development of diagnostic molecular markers for high salinity resistance. This research project has at its disposal genomic resources, as the genetic source of high salinity tolerant strawberry and a commercial sensitive variety, also a genetic mapping population is available for this research project. The development of molecular markers for high salinity resistance will be expedited by using high-resolution mapping of the candidate genes merged with the information of the reference genomes of the highly tolerant parent and the salinity-sensitive one plus the information of the existing genetic mapping populations. In addition, ion content measurement in different structures of the plant is being carried out to characterize the distribution and ratio of Na<sup>+</sup>, Cl<sup>+</sup>, and K<sup>+</sup> knowing which are the main organs involved in salinity stress. This enables to perform of transcriptome analyses. The development of molecular markers for high salinity tolerance in strawberry will contribute to increase yields and facilitate the introgression of this gene/genes of interest improving the crop's adaptability to climate change.