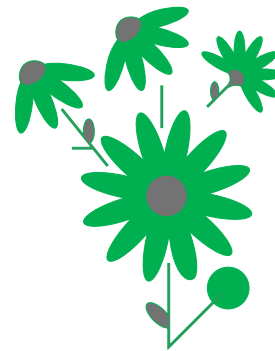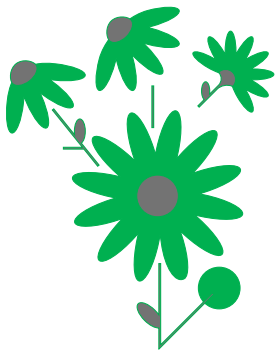The 21st Annual

PLANT SCIENCE GRADUATE STUDENT RESEARCH SYMPOSIUM

April 25th, 2024

Michigan State University

Schedule

	Time
Poster Set-up Molecular Plant Science Atrium	**8.30 – 10.00 AM**
Oral Presentations – Basic Research Plant Biology 168	**10.00 – 11.15 AM**
Poster Presentations Molecular Plant Science Atrium	
Basic and Applied Research	**11.30 – 1.00 PM**
Lunch Molecular Plant Science Atrium	**12.00 – 1.00 PM**
Oral Presentations – Applied Research Plant Biology 168	**1.15 – 2.30 PM**
Poster Take-down	**2.30 PM**
Announcement of Winners	**3.00 PM**

Contents – Poster Presentations

Contents – Oral Presentations

Location Plant Biology 168

Poster

Presentations

Herbicide Sensitivity Spectrum in Johnsongrass Populations Across the US

Connor Purvis

Department of Plant, Soil and Microbial Sciences

Johnsongrass (*Sorghum halepense*) is a troublesome perennial weed, inflicting environmental and economic damage. Winter temperatures in Michigan have increased, therefore rhizomes are overwintering making this weed problematic to control. Further exacerbating control are herbicide resistant populations. Over 30 cases of herbicide resistance have been reported. Given these factors, the objectives of this study were to establish baseline sensitivity in populations collected from across the United States and to determine resistance mechanisms. Dose response assays were conducted to determine baseline herbicide sensitivity to commonly used herbicides in corn and soybean. Assays consisted of seven nicosulfuron, glyphosate, clethodim, imazethapyr, or thiencarbazone-methyl rates with four replications. Treatment rates ranged from 0.125 to 64 times the field use rate of 0.09 kg ha^{-1} nicosulfuron and 0.125 to 8 times the field use rates of 1.61, 0.65, 0.26, and 1.4 kg ha^{-1} for glyphosate, clethodim, imazethapyr, and thiencarbazone-methyl, respectively. Three weeks after application, aboveground plant biomass was collected, dried, and weighed. Data were analyzed using the drc package in R to estimate the dose that causes 50% biomass reduction (ED$_{50}$). DNA was isolated from resistant populations and followed a CTAB protocol. All populations screened are susceptible to glyphosate and clethodim. Thirty-three percent are resistant to nicosulfuron and imazethapyr, while 20% are resistant to thiencarbazone-methyl. Isolated DNA from resistant individuals showed a SNP at Trp$_{574}$, which is known to give broad-spectrum resistance. Level of resistance varied depending on SNP presence in sub genomes. This work gives an overview of the trends in herbicide resistance evolution.

Integrated Strategies to Manage volunteer Potatoes and Colorado Potato Beetle

Hannah Johnson

Crop and Soil Science

Volunteer potatoes (Solanum tuberosum) are potatoes left in the field after harvest and are a very problematic weed in crops grown the following season. Historically harsh winter temperatures kill volunteers, however increasing winter temperatures has enhanced volunteer survivorship. Volunteer potatoes also enhance survival of two major pests that cause significant economic damage to potato production annually: late blight of potato (Phytophthora infestans) and Colorado potato beetle (Leptinotarsa decemlineata, CPB). Therefore, the main objective of this research is to evaluate integrated strategies to manage volunteer potatoes and CPB. To address this objective two field studies were conducted in Montcalm County, MI at the Michigan State University Potato Research Station. The first study evaluated the impacts of tillage intensity, herbicide, and insecticide treatments on volunteer potato management in corn (Zea mays). This study followed a split plot design with four replications. Potatoes were hand spread to simulate volunteers, then two tillage treatments were applied (moldboard plow-aggressive vs. disk-light intensity), followed by corn planting. Subplot factors included factorial combinations of tank- mixed herbicides and insecticides applied at two corn growth stages: V5 and V7. Herbicide treatments included mesotrione or topramezone plus atrazine. Insecticide treatments included spinetoram or chlorantraniliprole. Percent corn injury was evaluated 7, 14, and 21 days after application (DAA). Injury data was analyzed in R using linear mixed effects models and means were separated using Tukey's HSD. Treatments including mesotrione when applied at V5 resulted in greater corn injury than all other treatments at all evaluation timings ($p = 0.0018, <0.0001$, and <0.0001). Mean injury associated with this treatment was 5.4%, 5.4%, and 3.5%, 7,14, and 21 DAA, compared to 0.6% for all other treatments. Corn ears were evaluated at the end of the season and had no visible signs of injury. There was no difference in volunteer emergence amongst tillage intensities due to dry hot conditions at planting. The second study evaluated the use of late planted potato trap crops to manage second generation CPB populations. This study followed a randomized complete block design with four replications. Treatments included planting the potato trap crop 0, 2, and 4 weeks after the primary potato crop. Percent canopy loss and CPB density were assessed throughout the season. Yield data was collected at the end of the season. Canopy data was analyzed in R using the drc package. Beetle density and yield data were analyzed in R using linear mixed effects models and means were separated using Tukey's HSD. Canopy loss from CPB defoliation decreased when trap crop planting was delayed by 4 weeks ($p < 0.05$). There was no difference in CPB density between trap crop planting timings ($p > 0.05$). Yield was impacted by trap crop planting timing. At the field edge, yield increased by 41% in the 4-week delayed planting treatment compared to the 0-week delayed planting treatment ($p = 0.03$). Both field trials will be repeated in 2024. Overall, the integrated management techniques investigated in these studies can be combined to reduce yield loss from volunteer competition in corn rotations and reduce yield loss from CPB damage in potato rotations.

Management of Problematic Weeds in Truvera Sugarbeet

Ian Waldecker

Crop and Soil Science – Weed Science

Michigan sugarbeet growers struggle to control several weed species in glyphosate-resistant sugarbeet. Problematic weeds that commonly escape management strategies include glyphosate-resistant (GR) waterhemp (Amaranthus tuberculatus), GR horseweed (Conyza canadensis L.), and common lambsquarters (Chenopodium album L.). 'Truvera' is a new herbicide-resistant trait package in sugarbeet that confers resistance to glyphosate, glufosinate, and dicamba. Implementing these additional sites of action into current weed management strategies will help growers improve weed control. A field experiment was conducted in 2023 at three locations to examine various weed management strategies in 'Truvera' sugarbeets. Locations were chosen based on the presence of GR waterhemp, GR horseweed, and common lambsquarters. Each study consisted of 20 different treatments including a non-treated control. Treatments requiring the 'Truvera' trait were compared with three current strategies for waterhemp, horseweed, and common lambsquarters control, as well as three POST applications of glyphosate. Herbicide programs were separated into three different application timings: PRE followed by (fb.) 2- and 8- leaf sugarbeet (8 total treatments); 2- fb. 6- and 12-leaf sugarbeet (6 total treatments), and 2- fb. 8-leaf sugarbeet (5 total treatments). Herbicides used in the PRE treatments consisted of dicamba or a reduced rate of S-metolachlor (0.53 kg ha-1); dicamba, glyphosate, glufosinate, and various combinations of these products were applied alone and in combination with acetochlor as a residual at the 2-, 6-, and 8-leaf applications. The 12-leaf application only included glyphosate. Each herbicide treatment was kept within the maximum application amounts for each product. At the waterhemp location, eight of the 19 herbicide treatments examined provided greater than 90% waterhemp control at sugarbeet harvest. One or more applications of an effective POST of glufosinate or dicamba combined with POST acetochlor was needed to control waterhemp. These treatments provided significantly greater control than the current strategy of overlapping residual applications of acetochlor alone or S-metolachlor PRE followed by overlapping acetochlor. At the horseweed location, 16 of the 19 treatments provided 95% or greater horseweed control at harvest. At least two applications of an effective POST, glufosinate, dicamba, or clopyralid, were needed. There was no difference between treatments that contained either glufosinate and/or dicamba compared with the current strategy of multiple applications of clopyralid. At the common lambsquarters location, 10 of the 19 treatments provided 94% or greater common lambsquarters control. The best treatments included a 12-leaf application of glyphosate, or treatments with 8-leaf applications of glyphosate tank-mixed with acetochlor. Poorest control occurred in treatments with glufosinate only, which provided only 30% common lambsquarters control. Similar treatments of glufosinate only with dicamba PRE improved control to 86%. Sugarbeet yields at the horseweed and common lambsquarters locations were not different between the herbicide treatments. However, sugarbeet yield was 38 and 75% lower when weeds were not controlled at the horseweed and common lambsquarters locations, respectively. 'Truvera' sugarbeet will provide growers with additional effective herbicide options that can be combined with residual herbicides for improved control of problematic weeds, especially GR horseweed and waterhemp.

Exploring winter wheat canopy architecture for variety-specific management strategies

Paulo Arias

Department of Plant, Soil and Microbial Sciences

Winter wheat varieties differ in canopy architecture, and this trait can influence their solar radiation interception, radiation use efficiency (RUE), and yield potential. Management strategies can be modified to maximize yield by pairing varietal canopy type with other factors. However, research is lacking in evaluating wheat varieties for their canopy architecture and under management factors such as planting date and seeding rate. Field trials were conducted from 2021-2023 in Mason, MI using a split plot design with four replications. The main plots consisted of two planting dates (PD, early: late September and late: late October), while the sub plots had a combination of two seeding rates (SR, 1.98 and 3.95 million seeds ha-1) and eight wheat varieties. Four wheat varieties (AgriMAXX 513, Hilliard, DF 121R and Dyna-Gro 9070) were planophile, while the other four (MCIA Wharf, Branson, ISF 12203 and KWS405) had erectophile canopy architecture. Tiller angle was used to measure varietal canopy type and was significantly higher for planophile compared to erectophile varieties. Erectophile varieties were slower in reaching canopy closure but showed an increase in RUE as radiation interception increased, resulting in similar yields to planophile varieties. Early PD had higher yield (Mg ha-1) compared to late PD (Mg ha-1) across all canopy types and SR. Optimum SR for erectophile or planophile varieties was similar under both early and late PD. Although varieties yielded similarly across PD and SR, planophile architecture had higher radiation interception indicating potential benefits under lower yield potential environments (e.g., late PD, wider rows). Erectophile varieties showed increase in RUE with increasing radiation interception, an important trait for higher yield environments (e.g., early PD, narrow rows). Overall, we showed that winter wheat varieties have differences in canopy architecture and growers can implement variety specific management based on their yield environments.

Genetic Analysis of Colombian Coca Plants to Strengthen their Control

Alejandra Saavedra Rojas

Department of Plant, Soil and Microbial Sciences

Colombia reported a record 230,000 hectares under coca cultivation (Erythroxylum sp.) in 2022, according to the United Nations. Over the past three decades, glyphosate has been the primary herbicide employed for eradicating illicitly grown plants, raising questions about its potential resistance. Therefore, the objective of this study was to investigate the molecular-level variability in coca responses to glyphosate. A dose-response experiment was conducted by applying glyphosate doses from 0 to 3560 g ha-1 to two E. coca varieties: Boliviana Roja and Gigante, under greenhouse conditions. Visual injuries were documented three weeks after treatment. DNA samples were sequenced for Thr102, Ala103, and Pro106 mutation in the 5-enol pyruvyl-shikimate-3-phosphate synthetase (EPSPS) gene. Additionally, EPSPS copy number variation was examined in DNA from both mentioned varieties and 14 others. Glyphosate dose-response showed Gigante's ED50 at 491.2 g ha-1, whereas Boliviana Roja's ED50 was 2369.7 g ha-1, indicating a 4.82-fold resistance factor. The sequencing analysis revealed the absence of target site mutations in these varieties. Furthermore, none of the 16 tested varieties showed differential EPSPS copy number variation, indicating that resistance is not linked to the target site. Future research will include differential gene expression to elucidate distinct coca responses to glyphosate. Additionally, the study aims to explore the genome of coca for a deeper understanding of the mechanisms underlying the glyphosate-resistant biotype, offering insights for formulating strategies to enhance herbicide use in the agronomic management of illegal coca plantations.

Identification, Mapping, and Haplotype Analysis of Novel Seed Protein Stability QTL in Soybean

Mitchell Drew

Department of Plant, Soil and Microbial Sciences

Soybean seed protein content is a complex physiological trait regulated by many small-effect genes that show significant environmental interaction. Seed protein content stability across diverse growth environments is therefore often low even in elite soybean cultivars. In this study, the potential for mapping genetic loci significantly associated with static protein content stability across diverse growth environments was investigated using QTL and SNP-based haplotype analysis. One large effect QTL for seed protein was detected on Chromosome 20 across all environments, while two moderate effect QTL for protein stability were detected on chromosomes 18 and 10, respectively. The stacking of favorable alleles at these three loci showed significant improvement for protein stability without associated protein content reduction. Following mapping validation efforts and marker development, these QTL may therefore be useful for the improvement of protein content stability within the context of the MSU high-protein soybean breeding program.

Expression of Arabidopsis coumarin response genes varies under combined stress conditions

Megan A S DeLoose

Department of Plant, Soil and Microbial Sciences

Under iron deficiency (-Fe), Arabidopsis thaliana releases coumarins into the rhizosphere in a response believed to aid iron uptake. This response requires sufficient phosphorous, yet the regulatory network under varied iron/phosphorous conditions remains unexplored. Through a genome-wide association study, the coumarin transporter gene PDR9 was identified as key in coumarin response under the specific iron/phosphorous joint deficiency condition (-Fe-P). Genetic variation in the promoter region of PDR9 is implicated in natural variation in coumarin response to -Fe-P amongst Arabidopsis accessions. Through use of the TRANSPLANTA inducible transcription factor collection of Arabidopsis lines, the transcription factor MYB63 is also implicated in -Fe-P response. MYB63 was found to regulate expression of PDR9, as well as the coumarin biosynthesis genes COUMARIN SYNTHASE (COSY) and FERULOYL-CoA 6'-HYDROXYLASE 1 (F6'H1), in response to -Fe-P. This study establishes the presence of and key players in regulatory interplay of coumarin response to -Fe-P. Further exploration into the reasons behind the mechanism is warranted and could include detailed soil chemistry analysis and effects of coumarin on the rhizosphere microbiome.

Unraveling Leaf Phenotypic Diversity: Epigenetic Insights into the Role of *XTH19* in *Arabidopsis thaliana* Growth and Adaptation

Hannah Cushman

Department of Plant Biology

Leaf is the source of energy for most high plants, and leafy vegetables provide critical nutritional values for human health, yet the underlying mechanism controlling leaf size has not been fully understood. Understanding the intricate relationship between epigenetic modifications and genotype-specific responses is crucial for unraveling the underlying mechanisms of leaf phenotypic diversity. Here, we conducted a chemical epimutagenesis screen to explore the ecotype-specific responses to Zebularine, a DNA demethylating agent, and uncovered intriguing variations in Arabidopsis thaliana phenotypes. Transcriptomic analysis revealed XTH19, a cell wall modifying enzyme, as the key player exhibiting a genotype-specific response to demethylation, which directly correlated with rosette diameter. To elucidate the causal relationship between XTH19 and rosette diameter, CRISPR-Cas9 technologies were utilized to generate knock out mutants in XTH19, demonstrating that disruption of XTH19 expression directly influences rosette diameter in a genotype-dependent manner. Our study highlights the pivotal role of XTH19 expression in driving ecotype differences in rosette diameter and underscores the utility of epimutagenesis as a powerful tool for elucidating genomic variation underlying complex phenotypic traits. These findings contribute to a deeper understanding of the molecular mechanisms governing plant growth and adaptation. Further exploration of the interactions and pathways involving the XTH19 gene promises to deepen our comprehension of plant growth processes and may pave the way for innovative strategies in crop management and yield optimization.

Fibrillin 1A uses separated binding faces for binding mono- and bi-layer membranes

Duncan Boren

Department of Biochemistry and Molecular Biology

Plastoglobules are specialized lipid droplets of plant chloroplasts derived from the thylakoid membranes of photosynthetic organisms. Plastoglobules are appear to be intimately connected with photosynthetic capacity and stress tolerance but the mechanisms which specific proteins associate with plastoglobules to dictate their proteome are unknown. It is believed that amphipathic helices are required for the association of the most abundant protein family of the plastoglobule, the Fibrillins. In A. thaliana, the protein Fibrillin 1a is suspected to bind to plastoglobule membranes to facilitate plastoglobule formation. To investigate binding mechanics, we perform protein-lipid binding simulations consisting of the Fibrillin 1A protein above simulated thylakoid and plastoglobule membranes to find favorable binding poses and investigate specific amino acid residues involved in membrane binding. We find that fibrillin 1a binds to thylakoid and plastoglobule membranes with distinct and spatially segregated binding faces, indicating that fibrillin proteins may play a role at the membrane interface.

Planting Date and Hybrid Selection Decisions for Optimizing Corn Yield and Kernel Dry Down

Benjamin K Agyei

Department of Plant, Soil and Microbial Sciences

The past few growing seasons have brought many weather-related challenges to corn (Zea mays L.) growers in the northern Corn Belt. Spring precipitation has been highly variable while fall has stayed mostly wet. Wet or dry spring delays planting or emergence while damp fall impacts kernel drydown. It is important to reassess how to match hybrid maturity and planting date to optimize yield and kernel drydown. Field trials were conducted in Lansing, MI during 2021–2022 to evaluate the impact of planting date (late April to early June) and hybrid relative maturity (RM, 89–109) on yield and kernel drydown rate. Corn phenology and growing degree unit (GDU) requirement to physiological maturity were also examined. Interaction between hybrid maturity and planting date for yield was examined using response surface models. Corn required less GDU to mature with delayed planting, averaging 5.6 and 7.2 per day delay for 2021 and 2022, respectively. Yield response to hybrid maturity was minimal under typical planting (mid-May), with all hybrids averaging □13,500 kg ha -1. Under early planting (late April), late- maturity hybrids (104–109 RM) provided a significant yield (□15,500 kg ha -1) gain compared to other hybrids (□14,500 kg ha -1). Under late planting conditions (late May), late-maturity hybrids showed some yield advantage over the early-maturity hybrids. No yield response to hybrid selection was observed with early June planting (average yield of 12000 kg ha -1). Kernel dry down rate under typical planting averaged 0.66 and 0.77% day -1 across hybrids in 2021 and 2022, respectively. As planting was delayed into late May, drydown rate stayed high averaging 0.75 day and 0.70% day -1 across hybrids in 2021 and 2022, respectively. Overall, results showed that late-maturity hybrid increases benefits from early-season planting. This research can help growers in northern Corn Belt choose hybrid maturities that maximize yield and profits.

Oral

Presentations

UAV-Guided Genetic Dissection and Genomic Prediction for Grain Yield in Soft Winter Wheat

Jonathan Concepcion

Department of Plant, Soil and Microbial Sciences

The rapid advancement of high throughput phenotyping platforms warrants integration of phenomics with genomics to enhance genomic prediction accuracy and understand the genetics of complex traits, such as grain yield. In 2022, 369 soft winter wheat genotypes were evaluated for grain yield. From UAV-based RGB and multispectral imaging of the yield trial, 30 vegetation indices were computed, with 27 showing significant correlations with grain yield. A total of 16 significant marker trait associations (MTAs) were identified from 12 UAV-derived vegetation indices across various chromosomes. Notably, a grain yield MTA on chromosome 1A coincided with GBNDVI. Additionally, an MTA on chromosome 2D was found to be in linkage disequilibrium with MTAs identified using several other indices. Single-trait genomic prediction accuracy ranged from 0.35 to 0.44, with Bayesian Ridge Regression yielding the highest accuracy. Integrating UAV-based RGB and multispectral imaging indices in multi-trait genomic prediction notably enhanced grain yield prediction accuracy. Using the first 3 principal components of significant grain yield-correlated VIs in a Factor Analytics model achieved a cross-validation accuracy of 0.65, and 0.63 using Random Effects with Unstructured Covariance Matrix. This study demonstrates the potential of UAV-based RGB and Multispectral for genetic dissection and improving genomic prediction accuracy in soft winter wheat grain yield.

Oral Presentation

Understanding cyp-mediated metabolic resistance in *Poa annua*

Mohit Mahey

Department of Plant, Soil and Microbial Sciences

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. We performed an RNA-seq study comparing 3 susceptible and 3 resistant populations to find candidate genes that might be able to metabolize the herbicide. The transcriptome data were analyzed through differential gene expression (DGE) 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 rigidium. The multiple herbicides were screened for resistance in P. annua populations in combination with malathion (CYP-450 enzyme inhibitor). We hypothesize that the cytochrome P450 up regulation is associated with indaziflam resistance, and potentially conferring resistance to other herbicides. The results will give insights to better understand herbicide metabolization resistance, its regulation, and the herbicide management strategies associated with herbicides modes of action rotation to delay the herbicide resistance evolution.

Lessons about photosynthesis from hot-spring algae: Investigating the Cyanidioschyzon merolae carbon-concentrating mechanism

Anne Steensma

Department of Plant Biology

Extreme conditions impede photosynthetic organisms from efficiently acquiring and using carbon dioxide in photosynthesis. To learn more about how photosynthetic organisms overcome environmental challenges, we study Cyanidioschyzon merolae, an organism which relies on photosynthesis in a challenging environment. This extremophilic single-celled red alga was first isolated from volcanic geothermal waters and grows optimally at pH ~2 and temperature ~42 °C. We report that C. merolae achieves its environmental resilience in part by increasing its photosynthetic efficiency. Specifically, C. merolae's physiological traits are consistent with a photosynthesis-boosting process called a carbon-concentrating mechanism (CCM). CCMs raise the efficiency of photosynthesis by increasing the carbon dioxide concentration around the carbon-dioxide-fixing enzyme rubisco. The presence of a CCM in C. merolae suggests an unusual mechanism for carbon concentration, as C. merolae appears to lack mechanisms and structures typically associated with a CCM (namely, the ability to take up carbon as bicarbonate; and a chloroplast structure called a pyrenoid which creates a favorable environment for CO_2 fixation). To explore how C. merolae's CCM could function, we used mathematical modelling. This modelling pointed to cell anatomy and proteins that are likely important for the CCM in this species, and we are now characterizing those experimentally. This work will further reveal the diversity of mechanisms that help organisms resist environmental stress. Understanding these mechanisms through basic research may inspire biotechnological efforts such as increasing crop productivity or developing extremophilic algae as bioproduction platforms.

Maximizing protein expression through codon optimization: Can Poaceae have too much GC?

Isaiah Kaufman

Department of Biochemistry and Molecular Biology and Molecular Plant Sciences

Codon optimization is required for efficient protein expression. But what is an "optimal" codon? We systematically investigated how codon preference regulates translation efficiency in two monocots (maize and rice) and two eudicots (Arabidopsis and tomato) with Ribo-seq and RNA-seq. Interestingly, highly translated genes in maize and rice show strong bias favoring high GC codons, but this GC bias is absent in Arabidopsis and tomato. Moreover, stronger bias was observed at the 3 rd position of each codon in highly translated genes, i.e., 85% GC in maize and 75% GC in rice. To study the connection between GC content and translation efficiency, we analyzed the coding sequences from 74 diverse photosynthetic species. We found that GC content distribution can vary considerably within lineages, but eudicots and monocots both seem to diverge from a moderate GC ancestor. Further analysis found that GC-rich codons are also associated with higher translation efficiency in some non-Poaceae species based on orthology with Arabidopsis high translation efficiency genes. While the mechanism linking GC content and translation efficiency remains an open question, our results suggest that increasing codon GC content could maximize protein expression in economically important Poaceae crops.

Genetic and Metabolite Markers of Anthracnose Fruit Rot Resistance

MacKenzie Jacobs

Department of Biochemistry and Molecular Biology and Molecular Plant Sciences

Anthracnose fruit rot, caused by the fungal pathogen Colletotrichum fioriniae, is among the mostdestructive 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.

Evaluation of Cercospora leaf spot and postharvest rot pathogen impacts on sugar beet storage

Carly Hendershot

Department of Plant, Soil and Microbial Sciences

In Michigan, sugar beets (Beta vulgaris) are stored for up to 200 days post-harvest. During storage, sugar content is reduced due to rot and regular energy use from respiration. Cercospora leaf spot (CLS) is further hypothesized to be a predisposing factor for storage losses. However, previous studies have presented conflicting evidence of this interaction and the effects of CLS remain unclear for specific storage pathogens. To investigate the impact of CLS on storage rot, post-harvest symptom development was evaluated in beets with relatively high or low in-season CLS severity. Roots of each CLS level were inoculated with Fusarium graminearum, Botrytis cinerea, or Penicillium vulpinum and symptoms assessed after 7 days. In the 2020 and 2021 storage periods, there were no significant differences between storage rot susceptibility to any of the tested pathogens in hand-harvested beets, regardless of CLS level, at any timepoint in any year ($P > 0.05$). To further investigate the effect of CLS on storability, a study comparing root rot susceptibility of bruised and non-bruised roots with high and low in-season CLS is currently being evaluated in 2022. This study will help increase the understanding of factors contributing to potential storage losses and will improve yield and profit for sugar growers.

Oral Presentation

How beans handle the heat: Using RNA-seq to understand gene expression patterns and changes in cooking time in beans stored in temperate and tropical environments

Hannah Jeffery

Department of Plant, Soil and Microbial Sciences

Dry bean (Phaseolus vulgaris L.) cooking time is under genetic (i.e. phytate, condensed tannin, and protein concentration) and environmental (i.e. temperature, relative humidity) control. The development of hard-to-cook (HTC) in dry beans greatly prolongs cooking times, thereby increasing the energy and time needed for cooking. Understanding how different dry bean germplasm responds to high temperature and high humidity storage could facilitate the development of varieties more resilient to developing HTC. This study investigated the effect different environments have on gene expression and cooking time in four dry bean varieties. RNA was extracted from pairs of brown and yellow beans (one fast cooking and one slow cooking variety) harvested from Entrican, MI (2020) that spent 0, 6, and 12 weeks either in temperate (25C/75% RH) or tropical (35C/75% RH) storage conditions. The beans were either raw or had been soaked for 6 hours. RNA-seq was performed and reads were subjected to DESeq2, WGCNA, and topGO analysis. Differential gene expression was compared in fresh and aged beans, as well as within and between varieties.

Are Vegetables a Social Construct?

Stephen Stresow

Department of Horticulture

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. 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.

Genetic Analysis of Colombian Coca Plants to Strengthen their Control

Alejandra Saavedra Rojas

Department of Plant, Soil and Microbial Sciences

Colombia reported a record 230,000 hectares under coca cultivation (Erythroxylum sp.) in 2022, according to the United Nations. Over the past three decades, glyphosate has been the primary herbicide employed for eradicating illicitly grown plants, raising questions about its potential resistance. Therefore, the objective of this study was to investigate the molecular-level variability in coca responses to glyphosate. A dose-response experiment was conducted by applying glyphosate doses from 0 to 3560 g ha-1 to two E. coca varieties: Boliviana Roja and Gigante, under greenhouse conditions. Visual injuries were documented three weeks after treatment. DNA samples were sequenced for Thr102, Ala103, and Pro106 mutation in the 5-enol pyruvyl-shikimate-3-phosphate synthetase (EPSPS) gene. Additionally, EPSPS copy number variation was examined in DNA from both mentioned varieties and 14 others. Glyphosate dose-response showed Gigante's ED50 at 491.2 g ha-1, whereas Boliviana Roja's ED50 was 2369.7 g ha-1, indicating a 4.82-fold resistance factor. The sequencing analysis revealed the absence of target site mutations in these varieties. Furthermore, none of the 16 tested varieties showed differential EPSPS copy number variation, indicating that resistance is not linked to the target site. Future research will include differential gene expression to elucidate distinct coca responses to glyphosate. Additionally, the study aims to explore the genome of coca for a deeper understanding of the mechanisms underlying the glyphosate-resistant biotype, offering insights for formulating strategies to enhance herbicide use in the agronomic management of illegal coca plantations.

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Erin Hill
Erin Burns
Rebecka Duecker
Michelle Hulin
Rachael Naegele
Ning Jiang (two sessions!)
Lihua Ning
Addie Thompson
Danielle Hoffman
Jessica Norling
Donghee Hoh

To our Sponsors and Organizers!