



TEXAS TECH UNIVERSITY
 Davis College
Plant & Soil Science™

PSS Student Research Symposium

Date: April 19, 2023

Location: TTU Dairy Barn

Program Schedule

9:00 - 9:30 AM Coffee social				
Time	Presentation Title	Speaker	Student Level	Program Area
9:30 AM PSS Student Research Symposium: Opening Remarks & Introductions				
Session 1				
Oral Session				
9:35 AM	Novel genetic variation for reduced glanding identified in the cotton landrace Hopi	Avinash Shrestha	Ph.D.	Plant Breeding & Genetics
9:50 AM	Increasing vitamin C in arugula and broccoli microgreens	Shivani Kathi	Ph.D.	Horticulture
10:05 AM	Influence of legume inclusion on greenhouse gas emissions from pasture systems in the Southern High Plains of Texas	Raavi Arora	Ph.D.	Soil Science
10:20 AM	Axant™ Flex cotton response to Topramezone in the Texas High Plains	Megan Mills	M.S.	Weed Science
10:35 AM Break				
Session 2				
10:50 AM	Crop rotation and cover crop effects on soil moisture in a transitional organic system	Lauren Selph	Ph.D.	Soil Science
11:05 AM	An improved method for protoplast isolation and gene-editing from soybean root, callus and transgenic hairy-roots	Lois Nwoko	M.S.	IGCAST
11:20 AM	Evaluating community garden signage and elements	Jonah Trevino	Ph.D.	Horticulture
11:35 AM	Investigating adsorption capacities of WWTP products and their potential use as fertilizer	Katherine Coyle	M.S.	Soil Science
Lunch Break				
Session 3				
Poster Session				
1:00 - 3:00 PM	Investigating a putative immune receptor specific to grapevine fanleaf virus strain GHu infection and symptom development	Cary Hicks	B.S.	Crop Science
	Marker-assisted introgression of QTLs regulating number of grains and primary branching in rice towards yield improvement	Christian Stephens	B.S.	Plant Breeding & Genetics
	Temperature and flooding impacts on nutrient release from soils treated with swine waste	Koy Stanley, Victoria Winkler, Aliah Cardenas	B.S.	Crop Science/Soil Science
	Genetic variation of stomatal density in corn	Madeline Jordan	B.S.	Horticulture
	Soil physical quality indicators as affected by long-term pasture management practices	Mei Gill	B.S.	Soil Science
	Effects of seed technology and microbial inoculums on arbuscular mycorrhizal fungi colonization in cotton	Nick Wilson	B.S.	Crop Science
	Impact of cold stress on sphingolipid and glycerol lipid profile of upland cotton during seed germination (<i>Gossypium hirsutum</i> L.)	Bandana Osti	M.S.	Plant Breeding & Genetics
	Palmer amaranth control with Isoxaflutole applied preplant incorporated or preemergence in cotton	Megan Mills	M.S.	Weed Science
	Effect of planting dates and seeding densities on growth and yield of Industrial hemp in West Texas.	Preetaman Bajwa	M.S.	Crop Science
	Nutrient niches of orchid mycorrhizal fungi (OMF)	Sharandeep Chahal	M.S.	Plant Ecology & Conservation
	Transcriptome analysis of high-temperature stress in sorghum seed development	Adil Khan	Ph.D.	IGCAST
	Green microalgae as a source of biopesticides to improve agricultural practices	Alethia Brito-Bello	Ph.D.	IGCAST
	Efficacy of neonicotinoid seed treatment under water-stress in cotton seedlings	Aqeela Sehrish	Ph.D.	Horticulture
	Effect of deficit irrigation and biochar application on growth, physiology, yield, and water productivity of cucumber in West Texas	Arjun Kafle	Ph.D.	Horticulture
	Tissue-culture-free genetic transformation and gene-editing in plants	Arjun Ojha Kshetry	Ph.D.	IGCAST
	Deciphering the dynamics of sugarcane aphid resistance mechanism in sorghum	FNU Pallavi	Ph.D.	IGCAST
	Development of a chemical switch to improve phosphorus assimilation and usage efficiency in plants	Hector-Rogelio Najera-Gonzalez	Ph.D.	IGCAST
	Allelopathic cover crops for palmer amaranth control in a semi-arid organic system	Lauren Selph	Ph.D.	Soil Science
	Developing single nucleus transcriptome technology for the study of soybean root nodulation	Leonidas D'Agostino	Ph.D.	IGCAST
	Synthetic tetraploidization as a strategy to face abiotic stresses in crops	Mylea Lovell	Ph.D.	IGCAST
	Exogenous salicylic acid helps to mitigate saline stress in cotton	Sanjida Keya	Ph.D.	IGCAST
	Develop PACE markers for waxy-sorghum Marker-Assisted Selection	Zhiyuan Liu	Ph.D.	IGCAST
3:30 PM Awards Ceremony				



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Oral Session Abstracts

Student/Presenter: Avinash Shrestha, Ph.D student, Plant breeding and molecular genetics
Format: Oral presentation

Novel genetic variation for reduced glanding identified in the cotton landrace Hopi

Avinash Shrestha¹, Puneet Kaur Mangat¹, Junghyun Shim^{1,2}, Lakhvir Kaur Dhaliwal¹ and Rosalyn Shim¹

¹Plant and Soil Science Department, Texas Tech University, Lubbock, Texas, 79409

²Olam International Limited, Rukubi, Doma, Nassarawa 962, Nigeria

The presence of the toxic chemical gossypol in cotton glands limits the use of seed byproducts for edible oil and meal production. The landrace Hopi has sparse glands which can be exploited to potentially reduce gossypol levels in cotton seeds. In this study, we performed quantitative trait loci (QTL) analyses on an F₂ population generated from crosses between Hopi and TM-1 to identify genetic variation for reduced glanding. A high-density genetic map spanning 2253.11 and 1932.21 cM for A and D sub-genome, respectively, with an average marker interval of 1.14 cM was generated using CottonSNP63K array. The linkage map showed a strong co-linearity with the physical map of cotton in terms of marker order. A total of five QTLs regulating the target trait were identified, three of which have not been previously reported. The new QTLs *qGC_A11.1* and *qGC_A11.2* in chromosome A11 spanned 380 and 570 kb, respectively, whereas *qGC_D11* from chromosome D11 covered a 2010 kb region. *In silico* analysis of the novel QTLs regulating gland formation in cotton identified a total of 13 candidate genes. Tissue-specific, comparative expression analysis of the candidate genes showed significant downregulation of the transcription factors *bHLH1*, *MYB2* and *ZF1* in Hopi but not in TM-1. Sequence analysis identified early stop codons in the coding region of the transcription factors in Hopi, which likely caused the downregulation in the expression of the genes. This, consequently, translated to reduced gland formation in the landrace. The results of the study provide basis for the cloning and functional validation of genes regulating glanding in cotton towards applications in breeding for this target trait in cotton. The successful reduction of gland formation in cotton has important implications in our ability to reduce gossypol content in cottonseeds that will allow its widespread utilization for meal and oil production.

Increasing vitamin C in arugula and broccoli microgreens

Shivani Kathi^{*1}, Haydee Laza¹, Sukhbir Singh¹, Leslie Thompson², Wei Li³, and Catherine Simpson¹

¹Department of Plant and Soil Science, Texas Tech University, Lubbock, Tx, 79409,

²Department of Animal and Food Sciences, Texas Tech University, Lubbock, Tx, 79409,

³Department of Chemical Engineering, Texas Tech University, Lubbock, Tx, 79409

Vitamin C is an essential antioxidant which aids in strengthening the immune system and preventing anemia. However, humans do not have the ability to biosynthesize vitamin C and must acquire it through diet. The supply of vitamin C through food is often inconsistent because plants vary widely in concentrations. Limited research is available on agronomic vitamin C biofortification, especially microgreens. Biofortification of microgreens for increased vitamin C offers a solution to address vitamin C deficiencies. In this study, arugula and broccoli microgreens were grown in enhanced nutrient solutions with five different concentrations of ascorbic acid (AA) (i.e., 0% control, 0.05%, 0.1%, 0.25% and 0.5%). Microgreens were harvested with the appearance of the tip of first true leaves, and analyzed for biomass, AA, and chlorophylls in arugula and broccoli. Additionally, broccoli microgreens were analyzed for essential minerals concentration. Results showed that increased application of AA improved vitamin C concentration in both arugula and broccoli microgreens. However, the biomass was reduced with application of highest concentration of AA (i.e., 0.5%) in arugula microgreens. Alternatively, AA supplementation in broccoli microgreens improved chlorophylls, biomass, and K concentration. In conclusion, vitamin C can be biofortified in microgreens with application of AA. Furthermore, the effect of AA supplementation is species-specific and resulted in improved yield parameters in broccoli microgreens.

Presenter: Raavi Arora, Graduate Research Assistant (Ph.D.), Soil Microbial Ecology

Format: Oral presentation

Influence of legume inclusion on greenhouse gas emissions from pasture systems in the Southern High Plains of Texas

Raavi Arora¹, Lindsey C. Slaughter¹, Charles P. West¹, Sanjit K. Deb¹, Veronica Acosta-Martinez², Krishna Jagadish¹, and Caitlyn Cooper-Norris¹

¹Texas Tech University Department of Plant and Soil Science, Lubbock, TX, USA

²USDA-ARS Cropping Systems Research Laboratory, Wind Erosion and Water Conservation Unit, Lubbock, TX, USA

Semi-arid ecosystems, such as the Southern High Plains (SHP) of Texas, hold enormous potential for providing a variety of ecosystem services such as agricultural production, nutrient and water cycling, and extreme weather mitigation. Although these systems cover over thirty percent of the arable land area in North America, agricultural productivity is severely limited by water scarcity and degraded soils. The Ogallala Aquifer, which is the main source of irrigation in the SHP, is at a risk of extinction due to over-extraction and pollution, forcing the growers to switch from row crops to less soil disturbing and more water efficient perennial forages and livestock. Some studies have shown that incorporation of legume plants to these perennial grasses can potentially reduce methane emissions from the soil and nurture healthier livestock in addition to minimizing the need for external inputs. The information regarding the influence of these soil improving practices on soil greenhouse gas (GHG) emissions is currently lacking. Our objective is to quantify and comprehend the role of legume (alfalfa, *Medicago sativa* L.) presence and density on soil GHG flux in established long-term pastures (WW-B.Dhal Old World bluestem) as compared to N-fertilized monoculture pastures. Soil GHG samples (CO₂, CH₄, N₂O) were collected using static chamber method on a monthly basis (fall to spring), and on a bi-weekly basis (late spring to early fall) to see the greenhouse gas flux throughout the year. Microbial community structure, nitrate and ammonia in the soil will also be analysed. The results of our study will help producers make management decisions to increase profitability and reduce climate impacts with more efficient use of resources, as well as allow us to prepare a model that builds healthy and productive soils in regions facing water and nutrient scarcity.

Student/Presenter: Megan Mills, M.S. Student, Weed Science

Format: Oral Presentation

Axant™ Flex cotton response to topramezone in the Texas High Plains

Megan Mills¹, Peter A. Dotray^{1 2}, Gregory. B. Baldwin³, Scott Asher⁴, Adam C. Hixson⁴, and Bobby Rodriguez²

¹Texas Tech University, Lubbock, TX; ²Texas A&M AgriLife Research and Extension Service, Lubbock, TX; ³BASF, Research Triangle Park, NC; ⁴BASF, Lubbock, TX

Abstract: The surge of herbicide-resistant weeds such as Palmer amaranth (*Amaranthus palmeri* S. Watson) is an issue across the Cotton Belt. Axant™ Flex technology developed by BASF Corporation is the first four-way herbicide tolerant trait in cotton that can tolerant glyphosate, glufosinate, dicamba, and specific *p*-hydroxyphenylpyruvate dioxygenase (HPPD)-inhibiting herbicides including isoxaflutole. The ability to use HPPD-inhibiting herbicides would give cotton producers in the Texas High Plains an additional unique mode of action to control Palmer amaranth and other problematic weeds. A field study was conducted in 2022 at the Texas Tech University New Deal Research Farm in New Deal, Texas to evaluate Axant™ Flex cotton response to topramezone, another HPPD-inhibiting herbicide, applied alone or in tank-mix combinations when applied postemergence at a 2- to 4-leaf growth stage. Applications consisted of isoxaflutole or prometryn applied preemergence (PRE) followed by (fb) topramezone applied alone, or tank mixed with isoxaflutole, glufosinate, glyphosate, or dicamba applied early postemergence (EPOST). No EPOST treatment made to 3-leaf cotton caused greater than 3% crop response at 7 days after application. Visual crop response was $\leq 6\%$ at 14 days after EPOST applications. At 28 days after EPOST applications, crop response did not exceed 1% across all treatments. Treatments containing isoxaflutole or prometryn PRE fb topramezone POST did not vary in crop response at 7, 14, and 28 DAA. No differences in lint yield were observed. These results support the potential use of topramezone EPOST at a 2- to 4-leaf growth stage in Axant™ Flex cotton to help manage herbicide resistant weeds.

Crop rotation and cover crop effects on soil moisture in a transitional organic system

Lauren E. Selph¹, Katie L. Lewis^{1,2}, and Paul B. DeLaune³

¹Texas Tech University

²Texas A&M AgriLife Research – Lubbock, Texas

³Texas A&M AgriLife Research – Vernon, Texas

Format: Oral Presentation

Water conservation is a top priority for organic producers in the southern high plains region of Texas. Crop rotation and cover crops have potential to influence soil moisture storage. This study seeks to investigate the influence of crop rotations (continuous cotton, cotton/peanut, cotton/sesame, and cotton/wheat/forage) and cover crops (fallow, rye at 17 and 34 kg/ha) on stored soil moisture in 2022 and 2023. In 2022, no differences were observed between cover crop treatments. Continuous cotton resulted in lower profile seasonal stored moisture than all crop rotations and significantly lower moisture than cotton/sesame and cotton/forage rotations. Stored soil moisture increased through cover crop termination and declined following crop planting. Significant differences in profile moisture between crop rotations were only observed on three of the five dates of measurement. Results in 2023 are expected to be comparable to 2022. Cover crops did not remove excess moisture compared to fallow and crop rotation resulted in conservation of water compared to continuous cotton. Intense weed pressure, tillage for cover crop termination, and crop failure had potential to influence moisture dynamics during the year of testing.

Student/Presenter: Nwoko Chidinma Lois, Msc. Student, Crop Molecular Improvement Research

Format: Oral Presentation

An improved method for protoplast isolation and gene-editing from soybean root, callus and transgenic hairy-roots.

Chidinma Lois Nwoko, Arjun Ojha Kshetry, Vikas Devkar and Gunvant B. Patil

Institute of Genomics for Crop Abiotic Stress Tolerance, Department of Plant and Soil Sciences,
Texas Tech University, Lubbock, TX, 79409, USA

Abstract: Protoplasts are a useful system in plant biology because they provide a platform for the rapid evaluation of a variety of signaling pathways, the investigation of gene function, as well as a high-throughput instrument for the study of functional genomics. This makes protoplasts an important component of the study of plant biology. This technique is less explored in various crops, the most notable of which is soybean, because it is difficult to isolate high-quality protoplast from a varied variety of plant tissues. While isolating protoplasts from leaf mesophyll is the most common method, isolating them from other tissues can provide researchers with other alternatives and provide a wider range of cells for tissue-specific experiments like single-cell transcriptomics. In addition to this, it helps to ensure that the cells that have been gathered are a representation of the plant as a whole and not just of a certain tissue. In conclusion, the isolation of protoplast from transgenic tissues, such as hairy roots and transgenic callus, is a quick method that may be used to assess gene activity. To facilitate future regeneration, we created a streamlined method of isolating, transfecting, and editing genes in both transgenic (hairy-roots and callus) and non-transgenic (roots) protoplasts.

Student/Presenter: Jonah E. Trevino, Ph.D. student, Horticulture

Format: Oral Presentation

Evaluating community garden signage and elements

Jonah E. Trevino¹, Laura Fischer¹, Leslie Thompson¹, Vikram Baliga¹, and Catherine Simpson¹

¹Texas Tech University, Lubbock, TX

Abstract:

The ever-growing urbanization of rural land has led to urban agriculture gaining popularity. From the many urban production systems being utilized for the issues that arise with urbanization, community gardens can be a holistic approach for many of the ailments that urbanization causes. Community gardens not only produce locally grown, nutrient dense foods, they also provide green spaces, stimulate exercise, and assist in facilitating a social area for a community. However, just like any production system, community gardens have challenges. An overlooked aspect in community garden challenges is education and guidance for volunteers that may not be familiar with garden settings, and practices are not consistent between gardens. Signage can aid by educating garden volunteers and providing information on how to manage plants in the garden without the need for a supervisor. In the literature, the role of signage in a community garden is under-discussed. If community gardens plan to thrive as a sustainable production system for urban communities, then self-learning volunteers will be needed to increase productivity. To assess the current state of community gardens, our objectives were to determine what signage elements are common across community gardens, what role the signs perform in community gardens, and what elements may improve or hinder productivity in the garden. A survey was deployed through the American Community Garden Association email list to community garden leaders to collect different elements and signage in gardens across the United States. Respondents (N=51) submitted pictures, detailed text, and geographical data which was coded and analyzed for common themes. Preliminary data suggests that signs welcome, identify, instruct, educate, assist with contact details, and organize the garden for volunteers. However, there are wide variations in signage styles, few consistencies between gardens, and there has been little feedback on what is the best approach for designing signage.

Student: Katherine Coyle, M.S. student, Environmental Soil Chemistry

Format: Oral presentation

Investigating adsorption capacities of WWTP products and their potential use as fertilizer

Katherine Coyle¹, Lindsey Slaughter¹, Christian Alvarez-Pugliese², Gerardine Botte², Matthew Siebecker¹

¹Texas Tech University, Department of Plant & Soil Science and ²Texas Tech University, Department of Chemical Engineering

Abstract: As the global population rapidly grows, food producers of the world are faced with the task of feeding as many as ten billion people by 2050. The current state of fertilizer use cannot support this growth, and the overuse and poor management of synthetic/organic fertilizers has degraded soil, water, and air quality over time. Several studies have shown that the recovery efficiency of N by crops is only 55% due to the fast dispersion/loss of applied fertilizers to the environment. This leaching of fertilizer components often leads to eutrophication and hypoxia of surrounding water bodies, creating further pollution. A potential solution to this issue is the use of biosolids and recycled nutrients from wastewater treatment plants (WWTP) as a fertilizer. Biosolids are insoluble biological solid residue resulting from varying sewage treatment processes and have been shown to increase organic matter and nutrient content when applied to soils. This research will examine nutrient adsorption from two types of WWTP products onto soils. The first product is an ion exchange nitrogen/phosphorous based fertilizer produced via municipal wastewater being pumped through a synthetic zeolite mineral (ZeoNPBF). Zeolites are open 3D frameworks comprised of SiO_4^{4-} and AlO_4^{5-} tetrahedral sheets with open channels that can be filled by extra-framework cations, such as NH_4^+ . These minerals possess a high cation exchange capacity that allows them to adsorb nutrient cations that are essential to plant growth, thereby making wastewater-treated zeolites a potential fertilizer resource. The second product that will be investigated is waste activated sludge, a byproduct of municipal wastewater treatment, that has been electrochemically treated to remove pathogens (EWAS). These solid materials will be used in a batch adsorption study and reacted with local and potting soils, and analyzed to determine the adsorption capacities of N, C, and OC from the ZeoNPBF and EWAS to the soil.



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Poster Session Abstracts

Investigating a putative immune receptor specific to grapevine fanleaf virus strain GHu infection and symptom development

Cary Hicks^{1,2}, Brandon G. Roy², Marc Fuchs²

¹Department of Plant and Soil Science, Texas Tech University, Lubbock TX 79409

²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva NY 14456

Grapevine fanleaf virus (GFLV) infects *Vitis spp.*, causing reduced foliage, lower grape yields, poor crop quality, and decreased longevity of grapevines. Mechanically inoculating the experimental host *Nicotiana benthamiana* with GFLV strain GHu causes foliar symptoms, while no other GFLV strains display symptoms. Vein clearing symptoms in the apical leaves of GHu-inoculated plants are exhibited 6-10 days post inoculation (dpi). A recent study analyzed transcription profiles of GFLV strains GHu and F13, and their mutants in the GFLV-encoded protein 1E^{Pol}, in infected *N. benthamiana* plants. Treatment contrasts identified a putative plant receptor, termed *gflv-r1*, as potentially important for symptom development. In this project, reverse transcription quantitative PCR analysis confirmed differential expression levels of *gflv-r1* transcripts in plants infected with GFLV strain GHu. A 300-base pair region of *gflv-r1* was amplified by PCR with specific primers, cloned into a GFLV-based expression vector and subsequently transformed into *Agrobacterium tumefaciens*. We hypothesized that the successful silencing of *gflv-r1* in plant can prevent GFLV symptom production in the model host. Validation of the GFLV-based vector by delivering a short fragment of the *N. benthamiana* phytoene desaturase gene was shown to result in virus-induced gene silencing and photobleaching. Further research is needed to determine how the recombinant GFLV-*gflv-r1* vector will inform the mechanism of vein clearing symptom development.

Student/Presenter: Christian J. Stephens

Format: Poster Presentation

Marker-assisted introgression of QTLs regulating number of grains and primary branching in rice towards yield improvement

Christian J. Stephens, Avinash Shrestha, and Rosalyn A. Shim

Department of Plant and Soil Science, Davis College of Agricultural Sciences and Natural Resources, Texas Tech University

Abstract: Rice (*Oryza sativa*) is the main dietary staple for more than half the world's population. The estimated rise in human population by the year 2030 requires a 40% increase in rice production to meet the high demand for the crop. Plant breeding is an excellent strategy to meet this demand. The goal of this research is to introgress the genes *Wealthy Farmer's Panicle* (WFP) and *Grain Number 1a* (Gn1a) from the landrace ST-12 into the background of Presidio, a Texas inbred rice cultivar, using marker-assisted backcrossing (MABC). *WFP* and *Gn1a* are known yield determinants in rice and have been validated to improve the yield of various rice genotypes. Within an 8-month duration, Presidio and ST-12 were grown and maintained until maturity in a controlled setting. Direct and reciprocal crosses between the two genotypes were carried out by manual emasculation and pollination. From approximately 150- 200 rice flowers that were pollinated, 15 F₁ seeds were produced. Whole genomic DNAs isolated from leaf tissues of the F₁ plants were genotyped using SSR markers (RM3323, RM 3360, RM10329, and RM5493) that were determined by PCR to differentiate between the Presidio and ST-12 genomes. Genotyping of the F₁s identified six true hybrids out of the 15 that were produced. The F₁s are currently being maintained in the greenhouse and will be backcrossed to Presidio upon flowering. Backcrossing is expected to recover 75% of the Presidio genetic background in the breeding line carrying both *WFP* and *Gn1a*. This research will bring us closer to our target of significantly increasing the yield of the inbred rice cultivar Presidio.

Student/Presenter(s): Koy Stanley, Victoria Winkler, Aliah Cardenas

Format: Poster presentation

Title: Temperature and flooding impacts on nutrient release from soils treated with swine waste

Authors: Koy Stanley^a, Victoria Winkler^a, Aliah Cardenas^a, Jessica Colvin^a, Emma Schmidt^b, Matthew G. Siebecker^b

Emails: jcolvin@wtc.edu, emma.schmidt@ttu.edu, matthew.siebecker@ttu.edu

Affiliations:

^a Agriculture Department, Western Texas College, Snyder, TX

^b Department of Plant and Soil Science, Texas Tech University, Lubbock, TX

Abstract:

Swine waste is rich in macronutrients plants need to thrive, which is why it is commonly land-applied to supplement soil nutrients and improve crop yield. However, in large quantities the swine waste can become more of a pollutant due to potential release of excess nutrients, such as nitrogen and phosphorus. Therefore, it is vital to understand how soil chemical reactions affect nutrient retention and what factors impact those processes. Our research objectives were to examine the impacts of temperature, flooding, and oxygen availability on nutrient release in soils treated with swine waste. Soils from three different sites located at Western Texas College farm were used for the experiments. One site was chosen as a control soil where no swine waste was applied. The Turf site, which was primarily turf grass, was treated with nursery pen swine waste for four consecutive months. The Farrow site was treated with piglet and sow swine waste. Winter wheat is the main crop planted in the Farrow and control fields. Once samples were collected, dried, and sieved, each site received treatments of heating to 35 °C, flooding or non-flooding, and capped or uncapped bottles (to create an oxygen-deprived environment). The treatments were replicated three times and conducted for 12 weeks, 6 weeks, and 3 days. Following the reaction periods, the soils were dried and 20 mL of Mehlich III solution was reacted with 2 g of soil from each treatment. The liquid extracted from the samples was subsequently filtered and analyzed using inductively-coupled plasma optical emission spectra (ICP-OES) and portable X-ray fluorescence (pXRF). Results are pending. Currently, it is hypothesized that the Turf and Farrow sites will have more available nutrients comparable to the control, that flooded samples will see higher release of select nutrients, and that heated samples will have the highest levels of nutrient release.

Presenter: Madeline Jordan, Undergraduate student, PSS Horticulture major

Format: Poster presentation

Genetic variation of stomatal density in corn

Madeline Jordan^{1,2}, Morgan Molsbee², Suhas Vyavhare², Wenwei Xu^{1,2}

¹Department of Plant and Soil Science, Texas Tech University, Lubbock, TX; ²Texas A&M AgriLife Research, Lubbock, TX

Stomata control the movement of gasses and water between the plant and atmosphere by opening and closing via guard cells. As the temperature and humidity of the environment change, the stomata will react to ensure the proper water pressure is kept inside and outside the plant, and to take in CO₂ and release O₂ during photosynthesis. Stomata play an important role in plant's response to temperature and water stress. Modifying the stomatal density may improve the drought and heat tolerance. The objective of this study was to determine the extent of the variation in the stomatal density among corn hybrids. Two temperate commercial and six experimental hybrids that are made with the parent lines derived from crossing corn with wild relatives -teosinte and *Tripsacum* were grown at Texas Tech Quaker Farm in 2022 and a RCBD design with two replications was used. Samples of a mature ear leaf were taken from three plants per plot. A leaf epidermal peel of the top and bottom surfaces per leaf was made with the nail polish and tape method, then mounted to a microscope slide. Four color microscopic images were taken from each peel, examined for stomata per row, stomata arrangement, and relative density of trichomes. Stomatal density was significantly different among the hybrids and between the top and bottom leaf surfaces, and greater in the bottom leaf surface than the top surface. The hybrids made with the lines from *Tripsacum* had higher numbers of stomata than the temperate hybrids. These findings suggest that *Tripsacum*-derived hybrids may have the advantage against temperate hybrids when it comes to control of water loss, water retention, and gas exchange. This could prove to be a valuable phenotypic trait that can be incorporated into other genetic backgrounds to improve photosynthetic ability and drought/heat tolerance.

Student/Presenter: Mei Gill, undergraduate student, Department of Plant and Soil Science
Format: Poster presentation

Soil physical quality indicators as affected by long-term pasture management practices

Mei Gill¹, Harrison Maples², and Sanjit Deb¹

¹Texas Tech University, Department of Plant and Soil Science

²Texas Tech University, STEM MBA Program, Rawls College of Business

Abstract: Understanding the effects of various pasture management practices on soil structural characteristics and aggregate stability is essential to develop effective soil and water conservation practices, especially in semi-arid pasture systems that support large acreages of forage and animal production. Our objective was to evaluate the effect of long-term perennial and annual pasture systems on soil physical quality using two indicators (i) the *S index* determined using the measured and modeled water retention curves and (ii) the aggregate stability determined using the wet aggregate stability (*WAS*) index. Measurements of soil physical and hydraulic properties, and aggregate stability (using automated wet sieving method) to determine *S index* and *WAS* data were made on soil samples collected in a previous study (2016-2017) from various long-term (>10 years) pasture systems. These pasture systems consisted of mixtures of Old World bluestem cv. WW-B.Dahl (OWB)+legume or alfalfa+yellow sweet clover, native grass-mix (native), alfalfa+tall wheatgrass (TW), and annual grass-mix (annual) pasture treatments on a clay loam area; and native, teff, OWB-grazed, and OWB-ungrazed treatments on an adjacent sandy clay loam area. The results suggested that perennial OWB-legume and native pasture systems, which supported enhanced soil organic matter, saturated hydraulic conductivity, and reduced bulk density, had significantly improved *S index* and *WAS* values compared to annual teff and alfalfa-TW systems, underscoring the benefits of permanent, perennial cover on semi-arid pasture productivity and soil physical quality. The grazed pasture system significantly decreased the *S index* and *WAS* compared to other pastures, likely due to its higher soil bulk density. The lower *S index* and *WAS* values in annual and teff pastures further suggested that annual tillage-based agriculture may adversely affect soil structural characteristics and aggregate stability, especially in semi-arid environments.

Student/Presenter: Nick Wilson, undergraduate student, Plant and Soil Science (Horticulture).

Format: Poster presentation

Effects of seed technology and microbial inoculums on arbuscular mycorrhizal fungi colonization in cotton

Nicholas Wilson¹, Nathan Feuquay¹, Glen Ritchie¹, Katie Lewis^{1,2}, Lindsey C. Slaughter¹

¹Texas Tech University, Department of Plant and Soil Science and ²Texas A&M AgriLife Research

Abstract: Commercial products containing beneficial microorganisms are frequently marketed to help increase soil health by alleviating drought stress and improving soil structure and nutrient availability, as well as cotton productivity in the Texas High Plains. However, the efficacy of such products is inconsistent between lab and field conditions, in addition to a lack of understanding about how added microbial inoculums as seed treatments may interact with defensive chemical technologies already coating commercial seed varieties. We tested two commercial inoculums containing either arbuscular mycorrhizal fungi (AMF) or plant-growth promoting bacteria in outdoor mesocosms containing field soil, applied to cotton seeds that were either untreated or already coated with fungicidal, nematocidal and insecticidal technology before microbial inoculation. We found that applied microbial inoculants significantly inhibited cotton germination rates compared to fertilized or unfertilized controls, with more pronounced differences in “black” cotton seeds without commercial seed technologies added to inhibit soil-borne pests and pathogens. Microbial inoculant treatments also supported significantly lower cotton boll counts at harvest, except for the arbuscular mycorrhizal fungi treatment applied to “black” cotton seeds. Root colonization by arbuscular mycorrhizal fungi was examined via root staining and microscopy in midseason tissues samples collected from each microbial treatment and seed type combination. These results will validate whether AMF applied in microbial inoculum treatments increased root colonization by AMF in cotton plants compared to those receiving bacterial inoculums or unamended controls, as well as reveal whether defensive seed technologies such as fungicides can negatively impact applied AMF.

Impact of cold stress on sphingolipid and glycerol lipid profile of upland cotton during seed germination (*Gossypium hirsutum* L.)

Bandana Osti, Lakhvir Kaur Dhaliwal and Rosalyn Shim
Department of Plant and Soil Science, Texas Tech university, Lubbock, Texas, 79409

Abstract

Cotton, a major fiber crop, is severely affected by biotic and abiotic stresses as consequences of climate change. One of the major factors leading to severe loss in cotton production is cold stress. Several studies have indicated lipid composition as a factor in cold stress tolerance mechanism. This study profiled the changes in sphingolipids and glycerol lipids of cotton cultivar Acala during phase I and II of seed germination at normal temperature (30°C) and cold temperature (12°C). Lipid content and composition were profiled by liquid chromatography–mass spectrometry. Changes in lipid subclasses namely, sphingolipids (Ceramide, hexosylceramide, sphingosine, sphingomyelin) and glycerolipids (triacylglycerol, diacylglycerol and monoacylglycerol) were studied. Imbibition of seeds for 3 hours and 6 hours of at normal and cold temperature resulted in corresponding increase or decrease in the average content of lipid subclasses. Analysis of unsaturation content measured in terms of double bond indices showed that imbibition for 3 hours at normal temperature increases the unsaturation of hexosylceramide, sphingomyelin and triacylglycerol while reducing the unsaturation of ceramide. With extended cold imbibition, the unsaturation of sphingomyelin and triacylglycerol decreased. Increase in sphingolipid activity during cold germination suggests its involvement in stress related signaling. Moreover, decrease in the unsaturation of triacylglycerol and sphingomyelin suggests membrane fluidity and permeability decrease. Increase in the ceramide activity with decrease in sphingomyelin during cold stress suggests biosynthesis of ceramide from sphingomyelin in presence of sphingomyelinase enzyme.

Student/Presenter: Megan Mills, M.S. Student, Weed Science

Format: Poster Presentation

Palmer amaranth control with Isoxaflutole applied preplant incorporated or preemergence in cotton

Megan Mills¹, Peter A. Dotray^{1 2}, Scott Asher³, Adam C. Hixson³, Gregory. B. Baldwin⁴, and Bobby Rodriguez²

¹Texas Tech University, Lubbock, TX; ²Texas A&M AgriLife Research and Extension Service, Lubbock, TX; ³BASF, Lubbock, TX; ⁴BASF, Research Triangle Park, NC

Palmer amaranth (*Amaranthus palmeri* S. Wats) is a summer annual weed native to the southwestern United States. If not properly managed early-season, Palmer amaranth will compete with establishing cotton, which may result in stand loss, yield, and quality reductions. The use of soil residual herbicides is crucial for cotton establishment and to achieve early season control of Palmer amaranth and other problematic weeds. A bare-ground field study was conducted in 2022 at the Texas A&M AgriLife Research Center in Halfway, Texas to evaluate weed management following Alite 27TM (isoxaflutole) applied preplant incorporated (PPI) or preemergence (PRE). Herbicide treatments consisted of pendimethalin applied alone or in a tank mix with isoxaflutole applied PPI followed by (fb) PRE applications of prometryn, fluometuron, diuron, fluridone, fomesafen, acetochlor, or *S*-metolachlor applied alone or tank mixed with isoxaflutole at rates appropriate for the soil type. Palmer amaranth control 28 days after PRE applications (DAA) was $\geq 89\%$ in treatments containing isoxaflutole applied PPI, and $\geq 96\%$ in treatments containing isoxaflutole applied PRE. At 50 DAA, $\geq 90\%$ Palmer amaranth control was achieved with treatments containing isoxaflutole PRE fb diuron, fluridone, acetochlor, or *S*-metolachlor PRE, and pendimethalin PPI fb isoxaflutole tank mixed with fluometuron, diuron, fomesafen, acetochlor, and *S*-metolachlor. These results suggest that residual activity of isoxaflutole-based treatments applied either PPI or PRE can effectively manage Palmer amaranth up to 50 DAA.

Student/Presenter: Preetaman Bajwa, MS student, Agronomy and Crop science
Format: Poster

Effect of planting dates and seeding densities on growth and yield of industrial hemp in West Texas.

Preetaman Bajwa¹, Sukhbir Singh¹, Arjun Kafle¹, Manpreet Singh¹

¹Department of Plant and Soil Science, Texas Tech University,

Emphasis is growing on exploring alternative, water-efficient crops to enhance the efficiency of water withdrawn from the Ogallala aquifer and for increasing crop diversification in the West-Texas region. Industrial hemp (*Cannabis sativa* L.) is a summer annual multi-purpose crop that has a potential to grow well in the region, thanks to its deep root system and drought tolerance. However, there is a lack of fundamental knowledge about its agronomic practices under highly variable weather conditions in this area. Therefore, the objective of this study was to assess the effect of planting dates and seeding densities on biomass, fiber content, irrigation water use efficiency (IWUE) of industrial hemp in West-Texas conditions. A field experiment was conducted at Quaker Research Farm of Texas Tech University during summer of 2022 using a fiber-hemp cultivar, Eletta campana. All the experimental units were randomized four times in a blocked split-plot design involving planting dates (P1- April 19th, P2- May 10th and P3- June 6th) as main plot factor and planting densities (SD1- 25kg/ha, SD2- 40kg/ha, and SD3- 60kg/ha) as subplot factor. P1 was damaged by rabbits after seedling emergence, and we could not collect any data. Results showed that P2 accumulated 1.5 times higher biomass and produced on an average 35 cm taller plants than P3. IWUE was 19% greater in SD3 than SD1 and was comparable with SD2. On the other hand, a higher stem diameter was observed in SD1 followed by SD2 and SD3. Fiber (bast and hurd) content in P2 was 2.5 times greater than P3. SD3 observed 34% and 21% higher fiber content than SD2 and SD1, respectively. SD3 under P2 recorded the highest fiber content among all combinations. Based on the results, early planting (P2) at higher seeding density (SD3) is more productive in the West-Texas conditions.

Student/Presenter: Sharandeep Singh Chahal, M.S. student, Plant Ecology and Conservation Research

Format: Poster presentation

Nutrient niches of orchid mycorrhizal fungi (OMF)

Sharandeep Singh Chahal¹, Jaspreet Kaur², Shan Wong¹, & Jyotsna Sharma¹
¹Texas Tech University, Lubbock, USA, ²University of Wisconsin, La Crosse, USA
schahal@ttu.edu, jkaur@uwlax.edu, shan.wong@ttu.edu, jyotsna.sharma@ttu.edu

Distribution of orchid populations and their fitness is shown to be correlated to the identity, distribution, and abundance of the associated orchid mycorrhizal fungi (OMF), which in turn may be influenced by soil physicochemical characteristics. Roots of plants from larger populations of *Platanthera cooperi* were dominated by fungi belonging to the Tulasnellaceae (LT) and hosted Ceratobasidiaceae (LC) in low abundances. The soil in these populations had higher concentrations of soil phosphorus (P) and lower concentrations of soil zinc (Zn) in comparison to the smaller populations. We hypothesized that the dominant fungus (LT) in large populations has a competitive advantage at the natural levels of P (295 mg/l) supporting its mycorrhizal association with the orchid. Conversely, we expected suppressed growth of LT under high Zn (41 mg /l) conditions. We cultured isolates representing LT and LC, either individually or in co-culture, on media supplemented with P and/or Zn. Surface area comparisons after nine days showed that any media in which Zn was manipulated suppresses both fungi yielding smallest surface areas (LT=1.5 cm²; LC=0.1 cm²) whether cultured individually or together. Highest surface area was recorded for both fungi on media supplemented only with P (LC=81.5 cm²; LT=9.4 cm²) when they were cultured individually. The two fungi only physically encountered each other when co-cultured on P supplemented media, where LC was dominant over LT even though its growth was reduced. These results confirm the ability of both LT and LC to occupy similar P niches while suggesting that LC may outcompete LT if they co-occur in the same space. Contrary to our expectation, high Zn treatment led to the dominance of LT over LC. Altogether, our data suggest that while fungal interactions are important, the host orchid is likely the more direct determinant of which fungi get recruited into the roots.

Keywords: mycorrhizae, mycelium, population size, *Platanthera cooperi*, soil nutrients

Student name: Adil Khan, 3rd year PhD student at IGCAS in Jiao lab, majoring in Crop Science.

Format: Poster

Presentation title: Transcriptome analysis of high-temperature stress in sorghum seed development

Presentation authors: Adil Khan¹, Junping Chen², Yinping Jiao¹

Author affiliations:

¹Department of Plant and Soil Science, Institute of Genomics for Crop Abiotic Stress Tolerance (IGCAST), Texas Tech University, Lubbock, TX, 79409 USA

²Plant Stress and Germplasm Development Unit, Crop Systems Research Laboratory, USDA-ARS, 3810, 4th Street, Lubbock, TX, 79424, USA

ABSTRACT

As an important cereal crop, optimal seed development is a key trait determining quality and yield for sorghum, while heat stress (HS) is one of the major limiting factors for crops growth and productivity. To characterize the impact of high temperature to the seed development and grain quality on the transcriptomic level, we performed a series of heat treatment to the different development stages of seeds. Our objective was to investigate the global transcriptional dynamics of sorghum seed development through RNA sequencing under normal (28°C) and heat stress (35°C and 40°C) at eight distinct stages. The analysis of time series transcriptome of 18 time points of sorghum developing seeds (from 2 to 25 dpa) identified 21,014 genes expressed during seed development. Comparative analysis of time series data provides insight into the fundamental transcriptomic reprogramming, the phases of development, and phase specific expression pattern of seed development stage specific genes. It was observed that HS during early phase of seed development significantly decrease panicle width, seed size and number compared to middle and later phases. We found that HS negatively impacts keys genes in starch and protein biosynthetic pathways more during early phase of seed development. The observed reduced seed size from the HS is a result of the down-regulation of starch-related metabolism, kafirins, fatty acid, and lipid biosynthesis. The results of this study provide essential knowledge in the sorghum seed development under normal and HS conditions.

Student: Alethia Alejandra Brito Bello, Ph.D. student, Research on biocompounds produced by green microalgae, IGCASST.

Format: Poster

Green microalgae as a source of biopesticides to improve agricultural practices

Alethia A. Brito-Bello¹, Ricardo A. Chavez-Montes¹, Cristian D. Gutiérrez Reyes², Rogelio Najera-Gonzalez¹, and Damar L. López-Arredondo¹

¹ Institute of Genomics for Crop Abiotic Stress Tolerance, Department of Plant and Soil Science, Texas Tech University

² Department of Chemistry and Biochemistry, Texas Tech University

Abstract: The immoderate use of synthetic pesticides has caused environmental problems, human health risks, and increased weed resistance. Using allelochemicals, secondary metabolites produced as part of the defense mechanisms in plants and microorganisms, is an alternative to remedy this problem. Green microalgae, photosynthetic and unicellular microorganisms, are natural producers of a wide range of allelochemicals that have been reported to inhibit the growth of various organisms, especially photosynthetic organisms. Therefore, the use of allelopathy provides a new opportunity to discover secondary metabolites with pesticide effect and an alternative approach to discover new modes of action to reduce the problem of weed resistance. We screened a series of green microalgae for their capacity to produce biocompounds with algicidal, herbicidal and/or nematocidal effect. Some promising strains were identified and are now under characterization. Our approach considers differential gene expression analysis using RNA sequencing (RNA-seq) and metabolite profiling using HPLC-MS to get insights on the metabolic pathways and genes involved in the production of the bioactive compounds. In this poster, results from one of the strains with algicidal, herbicidal and nematocidal effect will be presented. Our findings suggest that green microalgae represent an untapped potential as a natural alternative sources of pesticides. Moreover, they offer the advantage of obtaining biopesticides in a cost-effective manner, and with less environmental risk and less toxicity to mammals.

Student/Presenter: Aqeela Sehrish, Ph.D. student, Urban Horticulture and Sustainability Group

Format: Poster presentation

Efficacy of neonicotinoid seed treatment under water-stress in cotton seedlings

Sehrish, A.¹, S. Vyawahare², M. Parajulee², C. Coldren¹, L. Haydee¹, and C. Simpson¹

¹Texas Tech University, Department of Plant & Soil Science, ²Texas A&M AgriLife

Abstract: Neonicotinoid pesticides suppress crop pests by acting as antagonists at the insect nicotinic acetylcholine receptor. Independent of their insecticidal action, these substances have occasionally been found to increase plant vigor and resistance to abiotic and biotic stressors. However, this mode of action has not been studied very well with regards to different neonicotinoids. It is also crucial to understand how drought conditions impact the efficacy of seed treatments in cotton seedlings given the deteriorating drought conditions in Southwestern Texas. In order to understand the influences of neonicotinoids as seed treatments, we evaluated cotton (*Gossypium hirsutum*) seedlings treated with thiamethoxam, imidacloprid, and clothianidin under three different water stress levels: 100%, 60%, and 30% of the recommended irrigation. From 15 days after germination (DAG), cotton plants were harvested thrice with intervals of 15 days each. The physiological characteristics of the plants were examined, including plant height, shoot fresh weight, leaf area, root length, and root biomass of harvested cotton seedlings, and cotton leaves were examined with GC/MS for residual neonicotinoid concentrations at every harvest. The outcomes of the experiments demonstrated that irrigation and seed treatments had a substantial influence on plant growth. In comparison to the control, the 30 and 60% of the recommended irrigation levels grew plants that were noticeably taller and had more biomass and leaf area. Thiamethoxam was closely followed by seeds treated with imidacloprid in terms of biomass, leaf area, and root biomass. In comparison to the controls, the concentrations of thiamethoxam and clothianidin were significantly greater in the 30% and 60% of suggested irrigation treatments. Overall, 60% of the recommended irrigation led to higher long-term residual neonicotinoid concentrations. This might mean that the recommended irrigation treatment lowers neonicotinoid concentrations by removing seed treatments over time, which would lead to diminished efficacy and pest control.

Student/Presenter: Arjun Kafle, Ph.D. student, Horticulture

Format: Poster presentation

Effect of deficit irrigation and biochar application on growth, physiology, yield, and water productivity of cucumber in West Texas

Arjun Kafle^{1*}, Sukhbir Singh¹, Manpreet Singh¹, Glen Ritchie¹, Sanjit Deb¹, Catherine Simpson¹, Veronica Acosta-Martinez²

¹ Department of Plant and Soil Science, Texas Tech University, Lubbock, TX

² Agriculture Research Service, USDA, Lubbock, TX

Abstract: A rapid decline in water table of the Ogallala Aquifer has drawn attention to water-conserving strategies such as deficit irrigation (DI) in West Texas region. Cucumber (*Cucumis sativus*), a mild water-stress tolerant vegetable, can thrive in the hot climate; however its production under water-limited conditions is less understood in this region. Additionally, soil amendments like biochar are gaining popularity mostly in water-scarce regions, however its application under DI remains understudied in this region. Therefore, the aim of our study is to compare the integrated effect of DI and biochar rates on the growth, physiology, yield, and water productivity of cucumber in West Texas. A field study was conducted in 2021 at Quaker Research Farm, Texas Tech University where experimental units were randomized four times in a split-plot design involving four irrigation levels as main plot [I1(100% crop evapotranspiration (ETc) replacement from crop establishment to mid-season-100% ETc replacement from mid-season to maturity), I2 (80%ETc-60%ETc), I3 (60%ETc-80%ETc), I4 (40%ETc-40%ETc)] and three biochar rates [0 t/ha, 15 t/ha, and 20 t/ha] as a sub-plot factor. Leaf Area Index under I4 significantly dropped compared to I1, I2, and I3. Stomatal conductance and photosynthesis remained comparable among all irrigation treatments. The number of fruits/ha and yield (t/ha) were significantly higher in I1 compared to I2, I3, and I4. The observed yield reduction values were 15%, 20%, and 53% in I2, I3, and I4, respectively compared to I1. Water productivity was similar among I1, I2, and I3 with a significant reduction in I4. The biochar rates did not influence growth, physiology, yield, and water productivity of cucumber which might be because of its early year of application. Results suggest that DI can be effectively practiced for sustainable production of cucumber and help in saving a huge amount of water in West Texas.

Student/Presenter: Arjun Ojha Kshetry, PhD Student, IGCAS, TTU

Format: Poster Presentation

Tissue-culture-free genetic transformation and gene-editing in plants

Arjun Ojha Kshetry, Vikas Devkar, Luis Herrera Estrella, and Gunvant B. Patil

Institute of Genomics for Crop Abiotic Stress Tolerance (IGCAST), Department of Plant & Soil Science, Texas Tech University, Lubbock, TX.

Email: arjun.ojha@ttu.edu , Corresponding Author: gunvant.patil@ttu.edu

Abstract

Gene editing technologies, especially CRISPR/Cas have revolutionized basic and applied biological research within a decade of its development. It has been profoundly used in crop engineering research thereby transforming the pace of plant breeding and trait discovery. However, the delivery of gene editing reagents and regeneration of the edited progeny are the biggest hurdles in efficient genetic engineering and crop improvement. Current delivery methods and regeneration are largely dependent on tedious, lengthy, and costly *in vitro* (tissue culture) processes. Moreover, plant regeneration and genetic transformation are highly genotype-dependent and therefore, only very few of all plant species can be genetically modified. Therefore, the development of efficient genotype-independent plant transformation and gene-editing methods in several recalcitrant crops including cotton, soybean, sorghum, common bean, etc. is important in applying this technology for crop improvement. To overcome these challenges, we have created a synthetic cascade to express genes called developmental regulators that are involved in stem cell activity, rapid tissue differentiation, and the regeneration process. This system is successfully tested *in vivo*, without a need for tissue culture in the model plant *Nicotiana benthamiana* (tobacco), and applied in tomato with successful results. Our data suggested the successful development of robust technology for gene-editing and regeneration of gene-edited plants as we envisioned.

Presenter: FNU **Pallavi**, Ph.D. student, Plant Molecular Biology
Format: Poster presentation

Deciphering the dynamics of sugarcane aphid resistance mechanism in sorghum

FNU Pallavi¹, Vikas Devkar¹, Gunvant Patil¹, Yinping Jiao¹

¹Texas Tech University, Lubbock, Texas

Melanaphis sorghi (Theobald), the sorghum sugarcane aphid (SCA), is a destructive pest that has been impeding all commercial varieties of sorghum in the U.S. since 2013 leading to great extent of yield loss. SCA resistance has been discovered in the greenbug [*Schizaphis graminum* (Rondani)] resistant Tx2783 line. A clear understanding of the inheritance, function, mechanism of the genes that confer resistance in these resistant sources in TX2783 is necessary for having long-lasting resistance and transfer the resistant source to the susceptible commercial cultivars. Previous mapping experiments have identified a major QTL *RMESI* located on chromosome 6 (SBI-06) in a 3.0 Mb genomic region. The exact causal gene/variants and the resistance mechanisms are still elusive. My research focuses on finding the causal gene in resistant Tx2783 line using metabolomics, genomics, and molecular biology approaches. We did global metabolome analysis of resistant R, (Tx2783) and susceptible S, (Btx623) genotypes and found several compounds more abundantly present in the resistant genotype, might be responsible for conferring resistance. Based on comparative expression analysis and genomic organization between R and S lines we identified 3 putative candidate genes. The mutant population of Tx2783 was created to dissect the genetic mechanism of SCA resistance. Mutants losing resistance have been identified to study causal mutations using whole genome sequencing compared to wild type. Bulk segregant analysis will be performed with Tx2783 (Mutant) x WT F₂ individuals to know exact causal mutations. Further, validation of candidate gene will be performed by CRISPR/Cas9 mediated gene knockout and/or over-expression.

Student/Presenter: Hector Rogelio Najera Gonzalez, Ph.D. student, Institute of Genomics for Crop Abiotic Stress Tolerance

Format: Poster

Development of a chemical switch to improve phosphorus assimilation and usage efficiency in plants

Hector-Rogelio Najera-Gonzalez ¹ & Luis Herrera-Estrella ¹

¹Department of Soil and Plant Science, Texas Tech University, Lubbock, TX, USA.

Abstract: Phosphorus (P), together with Nitrogen (N) and Potassium (K) are the main nutrients required by plants to grow and develop correctly. Usually, these nutrients are supplemented to the soil in agricultural fields to maintain high yields. However, phosphorus presents a particular problem because it gets rapidly fixed in the soil as it reacts with soil cations forming complexes unavailable for plant uptake. Organic P compounds are also not readily absorbed in the plant unless the inorganic phosphate (Pi) is released previously through the action of microbe metabolism or plant excreted enzymes. In Pi limited conditions, plants activate genetic, biochemical, metabolic, and physiologic changes globally called the phosphate starvation response (PSR), which increase Pi scavenging and utilization efficiencies. Transcriptional activation of most of these responses is mediated by the transcriptional activator PHR1, which under sufficient Pi conditions is inactivated by binding of the repressor SPX1. When Pi is depleted, SPX1 releases PHR1, which then activates transcription of PSR genes, including *SPX1*. In this project we tested a diverse set of 10,000 molecules to evaluate their ability to modify PSR. We found several molecules that consistently activate or repress the PSR reporter gene *SPX1* independent of Pi concentration in the growing media. With this information we will continue to investigate mode of action of active molecules and verify if they directly act on the PHR1/SPX1 master regulatory complex or if they act over a different known or unknown upstream regulating pathway. We aim to better understand Pi sensing and regulation in plants to ultimately be able to modify it either chemically or genetically to improve phosphorus uptake and usage efficiency in crops.

Allelopathic cover crops for palmer amaranth control in a semi-arid organic system

Lauren E. Selph¹, Katie L. Lewis^{1,2}, and Paul B. DeLaune³

¹Texas Tech University

²Texas A&M AgriLife Research – Lubbock, Texas

³Texas A&M AgriLife Research – Vernon, Texas

Format: Poster Presentation

Weed management is a top concern for Texas producers who are considering organic transition. Since mechanical weed management counteracts potential benefits of organic management, the use of allelopathic cover crops for alternative weed control has been suggested. This study sought to evaluate weed control using conventional and unconventional allelopathic cover crops at two sites (Vernon and Lamesa) in the Texas southern high plains in 2021 and 2022. Crop rotations were continuous cotton, cotton/peanut, cotton/sesame, and cotton/wheat/forage. Cover crop treatments were rye at 17 kg ha⁻¹ and 34 kg ha⁻¹, rye/fenugreek/fennel mix at 17 kg ha⁻¹, and fenugreek/fennel mix at 17 kg ha⁻¹ arranged in a randomized complete block design with three replications. Weed cover was evaluated by visual weed assessment and by biomass collection in a 1 m² area (Vernon only).

At Vernon, no differences in ground cover or biomass were observed between treatments in either year, but visual weed control was significantly greater in 2022 than 2021. Severe weather or delayed planting could have contributed to enhanced weed control in 2022. At Lamesa differences were observed because of cover crop and crop rotation, but these diminished between June and August measurements. At both sites, weed pressure was so overwhelming that the use of allelopathic cover crops alone were insufficient to adequately control palmer amaranth.

Student/presenter: Leonidas D'Agostino, PhD. student, Plant and Soil Science

Format: Poster presentation

Developing single nucleus transcriptome technology for the study of soybean root nodulation

Leonidas D'Agostino , Lenin Yong-Villalobos, Luis Herrera-Estrella and Gunvant B. Patil

Institute of Genomics for Crop Abiotic Stress Tolerance (IGCAST), Department of Plant & Soil Science, Texas Tech University, Lubbock, TX

Abstract: Beneficial microbes, especially rhizobium, offer a sustainable solution for improving nutrient uptake in legume crops and the research community understands a substantial amount about the processes involved in nitrogen fixation in legumes. Root nodules are exogenous organs formed through the symbiotic relationship between legume plants and the bacterial group rhizobium. Once formed, these nodules fix atmospheric nitrogen into usable ammonia for the plant, essentially replacing the need for nitrogen fertilizer application. However, the complexity of signal reception, metabolic-flux, nodule development, N-fixation, and nutrient uptake at the 'sub-cellular level' is elusive and not investigated in soybean or any other legume. In this project, we aim to capture the temporal and subcellular expression differences in relation to the nodule's growth stages (immature, mature, post-maturity) through a process known as single-cell transcriptomics. To do so, soybean genotype (Williams 82, reference genome) is inoculated with rhizobia to induce nodulation. Nodules are then collected at three stages and nuclei are extracted. These nuclei are processed through the 10X genomics single cell pipeline in order to generate a barcoded library made up of the individual cells. The transcriptional map generated from this data will help us to understand the dynamics of the gene-regulatory network and nitrogen fixation processes at a single cell level. On a larger scale, this project will provide in-depth understanding of symbiosis between rhizobium and soybean and will provide sustainable solutions to improve nutrient uptake in soybean and other legumes.

Student/Presenter: Mylea C. Lovell, Ph.D. student, Institute of Genomics for Crop Abiotic Stress Tolerance

Format: Poster

Synthetic tetraploidization as a strategy to face abiotic stresses in crops

Mylea C. Lovell¹, Alfonso Carlos Barragan Rosillo¹ and Luis Herrera-Estrella¹
¹Texas Tech University, Department of Plant and Soil Science

Polyloid plants are common in nature; and, many modern diploid organisms arose from polyloid ancestors. During environmental upheavals in the evolutionary timeline, polyloids often proved more fit and better survived adverse conditions. Genome doubling events were also key during the domestication of modern crops. There is currently interest in applying the benefits of genome doubling to modern breeding strategies. However, there is little known about how recent genome doubling events affects phenotypic diversity. Here, we use RGB imaging of two diploid and two tetraploid lines of *Arabidopsis thaliana* (Arth) to examine plant size, mean red, blue and green color, plant size, plant coverage, and average color. Our plant materials originate from two Arth lines with a tetraploid and diploid example for each. The Wa-1 line is a natural tetraploid; its diploid, Wa-1 (2X), is a result of recent diploidization. Col-0 is a natural diploid and its tetraploid, Col-1(4X) is a result of recent tetraploidization. Fifty-four plants of each ploidy level were grown in a growth chamber set at 22C, 50%RH and a 12-hour photoperiod with 90 umols of light during the day period. RGB images were collected using the LemnaTec PhenoAlxpert HTC at 25 DAP. Image processing was completed using LemnaGrid, LemnaExperiment and LemnaAnalysis software. Data was analyzed using Xcel. Our initial results show that Wa-1 was larger and covered more area than any of the other three ploidy level combination. However, there was no difference in size or coverage between Col-1 and Col-1 (4X). These differences suggest that halving the genome may have stronger impacts on plant size and coverage than those resulting from doubling the genome. This supports previous studies which show stronger responses of polyloids during prehistoric climate changes. Further exploration of ploidy events' immediate impact on plant phenotype will improve and inform future plant breeding technologies.

Student/Presenter: **Sanjida Sultana Keya**, Ph.D. Student, Institute of Genomics for Crop Abiotic Stress Tolerance, Department of Plant and Soil Science

Format: **Poster presentation**

Presentation title: **Exogenous salicylic acid helps to mitigate saline stress in cotton**

Presentation authors: ¹**Sanjida Sultana Keya**, ²Mohammad Golam Mostofa, ¹Md. Mezanur Rahman, ¹Lam Son-Phan Tran

Author affiliations: ¹Institute of Genomics for Crop Abiotic Stress Tolerance (IGCAST), Department of Plant & Soil Science, TTU; ²MSU-DOE Plant Research Laboratory, Michigan State University, East Lansing, Michigan.

Abstract

Cotton (*Gossypium* spp.) is a crucial industrial crop, particularly grown for fiber; however, its growth, development, and yield are substantially restricted by high salt stress. Salicylic acid (SA) is a crucial phytohormone, exhibiting a multifarious array of roles in the enhancement of plant growth, progression, and resilience to stress. In the current investigation, we provided persuasive evidence on the potential roles of exogenous SA in promoting salinity tolerance in cotton plants by investigating various morphological, biochemical, and physiological features. Our results showed that pre-application of SA to the root zones of cotton plants led to a substantial enhancement of plant biomass, individual leaf area, net photosynthetic rate, stomatal conductance, transpiration rate, water-use-efficiency, and chlorophyll, carotenoid, and relative water contents in leaves, resulting in better growth performance of cotton under salt stress. SA pretreatment further diminished the salinity-induced accumulation of hydrogen peroxide, and the elevated levels of electrolyte leakage and malondialdehyde in the leaves of cotton plants. The SA-pretreated cotton plants experienced reduced oxidative burden because of improved antioxidant defense systems, as manifested by the enhanced activities of catalase, ascorbate peroxidase, peroxidase, and the levels of total flavonoids. Furthermore, the pre-treatment with SA resulted in a remarkable elevation in the levels of total free amino acids and total soluble sugars in salt-stressed plants, indicating that SA utilized these compounds for optimal osmotic regulation in the plant tissues amidst adverse saline conditions. Importantly, the pre-treatment with SA resulted in substantial inhibition of Na⁺ uptake and a remarkable increase in the uptake of K⁺, Mg²⁺, and Ca²⁺ in both roots and leaves of cotton plants. Together, our findings suggest that SA pretreatment could be an effective strategy to increase the resiliency of cotton plants toward salinity, thereby enabling better performance of cotton plants in saline-prone areas.

Student/Presenter: Zhiyuan Liu, Ph.D. student, Crop Science

Format: Poster presentation

Develop PACE markers for waxy-sorghum Marker-Assisted Selection

Zhiyuan Liu¹, Melinda K. Yerka², Yinping Jiao¹

1, Institute of Genomics for Crop Abiotic Stress Tolerance, Department of Plant and Soil Science, Texas Tech University, Lubbock, TX, 79409 USA

2, Department of Agriculture, Veterinary & Rangeland Sciences, University of Nevada, Reno; 1664 N Virginia St, Reno, NV 89557

Abstract: Sorghum is the fifth crop around the world and the US is the largest producer. Waxy sorghum is consisted of almost all amylopectin compared to the wild type which contains 75 percent amylopectin and 25 percent amylose. Mutations of GBSS (granule-bound starch synthase) are considered as the reason for waxy sorghum because it is the sole enzyme responsible for amylose synthesis. Pedersen et al. (2004) first categorized waxy sorghum as wx-a and wx-b type based on whether the GBSS is entirely (wx-a) or partially (wx-b) unfunctional. Later, wx-a was identified as a large insertion mutation and wx-b was known as containing an SNP mutation by Sattler et al. (2009). However, an efficient way to identify waxy sorghum remains lacking. Here we developed markers being able to identify wx-a and wx-b sorghum quickly and economically in various genetic backgrounds. We characterized the wx-a insertion as a 5.1kb Ty1-Copia retrotransposon and designed markers to identify the insertion and SNP in waxy lines. The markers were validated by sequencing and applied to breeding populations. Genotypes were consistent with their amylose content except for 4 lines because the breeding population is still segregating. Our results show how PACE markers can be designed and applied in large breeding populations even if there is a large insertion. We anticipate our markers to help breeders identify waxy sorghums in the early stage efficiently without dissecting the embryo. Furthermore, it can be applied to broad sorghum varieties background.