1st Annual PSS Graduate Student Research Symposium

Date: April 22, 2019
Location: MCOM 0359

Program and Student Abstracts
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<td>Meet and sign in</td>
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<td>Lindsey Slaughter</td>
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<tr>
<td>8:50 AM</td>
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<td>9:00 AM</td>
<td>Exploring Variation in AFIS Length Distribution of 8 F2 Populations</td>
<td>Zach Hinds</td>
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<td>Research</td>
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<tr>
<td>9:15 AM</td>
<td>Coupling of Growth and Defense Potentials from Genetically Diverse Parents Configures a Transgressive Salt Tolerance Phenotype in Rice</td>
<td>Isaiah Pabuayon</td>
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<td>Joao Paulo Morais, Jake Sanchez</td>
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<td>9:30 AM</td>
<td>Characterization of Solanum lycopersicoides-derived introgression lines and identification of value added-traits for tomato improvement</td>
<td>Puneet Mangat</td>
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<td>9:45 AM</td>
<td>Forage yield and water use efficiency of sorghum, pearl millet, and corn under deficit irrigation</td>
<td>Bishwoyog Bhattarai</td>
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<td>10:00 AM</td>
<td>Genetic diversity analysis of silverleaf nightshade populations under herbicide stress</td>
<td>Joshua Singleton</td>
<td>MS</td>
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<td><strong>10:15 AM</strong></td>
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<td>10:30 AM</td>
<td>Dissolution of cotton cellulose in imidazolium-based ionic liquids: The effect of size and shape of cations</td>
<td>Niwanthi Dissanayake</td>
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<td>Jasmine Nepaune, Kris Petterson</td>
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<td>10:45 AM</td>
<td>Identification of novel sources of variation for the improvement of cold germination ability in upland cotton (Gossypium hirsutum)</td>
<td>Ritchel Gannaban</td>
<td>MS</td>
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<td>11:00 AM</td>
<td>Evaluation of root water uptake of cotton under deficit subsurface drip irrigation using HYDRUS (2D/3D) Model</td>
<td>Atinderpal Singh</td>
<td>MS</td>
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<td>11:15 AM</td>
<td>Impact of biochar on growth, physiology and yield of cucumber and sweet corn under deficit irrigation regimes.</td>
<td>Manpreet Singh</td>
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<td>11:30 AM</td>
<td>Conservation of a specialized bee-plant system involving Nama spp. Gray (Hydrophyllaceae) in the Southwestern U.S.</td>
<td>Aqeela Sehrish</td>
<td>PhD</td>
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<td>Time</td>
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<td>1:30 PM</td>
<td>Session 3</td>
<td>Trans-generational induction of epi-alleles by abiotic stress in Arabidopsis thaliana: a glimpse into the vast complexity of the plant epigenome and its contribution to the phenotype</td>
<td>Jake Sanchez</td>
<td>PhD</td>
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<td>1:45 PM</td>
<td>Session 3</td>
<td>Effects of Hail-netting on Gas Exchange and Production of Field Grown Malbec Grapevines (<em>Vitis vinifera</em>).</td>
<td>Trey Ruland</td>
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<td>Meagan Riley</td>
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<td>Crop response and weed control systems utilizing isoxaflutole in GLITP cotton</td>
<td>Delaney Foster</td>
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<td>Fate of nitrates in hydroponic leafy greens production using organic and inorganic nutrient formulations</td>
<td>Azeez Shaik</td>
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<td>3:00 PM</td>
<td>Session 4</td>
<td>Using the HVI fibrogram to improve yarn quality predictions</td>
<td>Abu Sayeed</td>
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<td>Session 4</td>
<td>Understanding Salinity Tolerance of Select Wildflower Species in a Hydroponic Setting.</td>
<td>Iryna Adrenko</td>
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<td>3:30 PM</td>
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<td>Determination of base saturation percentage in agricultural soils via portable X-ray fluorescence spectrometer</td>
<td>Ashmita Rawal</td>
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<td>Re-envisioning QTL dynamics in rice: Interaction of the drought-mediated yield penalty QTL qdty12.1 with its genetic background</td>
<td>Pushpinder Kaur</td>
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<td>4:15 PM</td>
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<td>4:30 PM</td>
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<td>Awards presentation, closing remarks</td>
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*Texas Tech University*

Department of Plant and Soil Science
Exploring Variation in AFIS Length Distribution of 8 F₂ Populations
Zach Hinds¹, Brendan Kelly¹,², and Eric Hequet¹
¹Texas Tech University, Department of Plant & Soil Science and ²Texas AgriLife Research

Abstract

Cotton fiber length distributions produced from the Advanced Fiber information System (AFIS) have been shown to better predict yarn quality compared to individual length parameters generated from the High Volume Instrument (HVI). The AFIS length parameters have the potential to provide breeders with additional information needed to select germplasm with improved spinning performance. However, the possibility of improving a trait through breeding only exists when there is genetic variation for the trait in question. In this study, 8 F₂ cotton populations, which were generated from crosses of obsolete cotton varieties, were explored using a multivariate statistical approach. The obsolete varieties were selected for this experiment because their development predates modern HVI testing, which may have contributed to a further reduced variation for fiber quality traits. Variation was seen both within a given population and across populations with the types of variation different for the two comparisons. These findings suggest that using the genetically diverse population of this experiment, there is variation in fiber length distributions that can be utilized by cotton breeders to genetically improve this important fiber quality parameter.
Coupling of Growth and Defense Potentials from Genetically Diverse Parents Configures a Transgressive Salt Tolerance Phenotype in Rice

Isaiah Pabuayon¹, Ai Kitazumi¹, Harkamal Walia³, Rakesh Kumar Singh², Glenn B. Gregorio², Benildo G. de los Reyes¹

(1) Department of Plant and Soil Science, Texas Tech University, Lubbock, TX
(2) International Rice Research Institute, Los Baños, Laguna, Philippines; International Center for Biosaline Agriculture, Dubai, United Arab Emirates
(3) Department of Agronomy and Horticulture, University of Nebraska, Lincoln, NE

Mechanisms known to enhance the ability of plants to withstand ionic toxicity and osmotic stress due to salinity include the exclusion of toxic ions, osmolyte production, and radical scavenging. A multi-pronged approach combining these mechanisms is needed to maximize the physiological potential for tolerance in plant breeding. Through genetic recombination, shuffling of diverse parental genomes could lead to rare allelic combinations, further leading to novel phenotypes in the progenies that transgress the maximum potentials of both parents. A systems-level approach was used to elucidate the molecular basis of transgressive salt tolerance phenotypes across a panel of recombinant inbred lines (RIL) from a cross between salt-sensitive indica (cv. IR29) and salt-tolerant Aus (cv. Pokkali) rice parents. Digital phenotyping confirmed the transgressive properties of a minority of individuals from the RIL population and indicated that the superiority of a transgressive RIL was due to significant reduction in growth penalty under stress. Transcriptomic and metabolomics profiling revealed distinct mechanisms that configure unique tolerance properties across individual RILs. The positive transgressive RILs displayed better capacity for metabolic homeostasis than both parents, translating to significant reduction in the costs of metabolic adjustments associated with defenses to cellular and physiological dysfunctions brought about by stress. Apparently, the attribute came from the salt-sensitive parent IR29, previously selected for an ideotype with superior harvest index under optimal environments. In the salt-sensitive RILs, the high growth rates that appeared to have been inherited from the salt-tolerant parent Pokkali were unsustainable under stress conditions and led to substantial growth penalties. Comparative analysis of genetic networks across the comparative panel showed that optimal configurations leading to novel stress tolerance phenotypes involved an ideal coupling and uncoupling of multiple regulatory hubs (core genetic elements) and a multitude of trans-effect components (peripheral genetic elements), consistent with new paradigms associated with the Omnigenic Theory.
PSS Symposium: Abstract for Research Talk

Characterization of Solanum lycopersicoides-derived introgression lines and identification of value added-traits for tomato improvement

Puneet Kaur Mangat and Rosalyn B. Angeles-Shim*

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S. lycopersicoides is a diploid (2n = 24) nightshade relative of tomato that has been reported to have tolerance to low temperature as well as resistance to broadly group of pathogens. Monosomic alien addition lines (MAALs; 2n+1) of this wild species have been developed since the late 1990s. Despite the low transmission and instability of the additional chromosome, a great value in the synthesis of these pre-bred stocks can be found in the diploid introgression lines (DILs) segregating from the MAALs. In this study, we characterized 44 DILs segregating from S. lycopersicoides MAALs for alien chromosome introgression, drought tolerance, as well as for key morphological traits. A total of 366 S. lycopersicoides-specific indel and simple sequence repeat (SSR) markers designed based on our in-house sequence and structural analysis of the S. lycopersicoides genome were used for the molecular characterization of the DILs. The markers covered all the 12 chromosomes of tomato at a 3 Mb interval. Genotyping identified 71 unique alien introgressions in distinct combinations in all DILs. Variations in leaf type, fruit shape and locule number were observed between the progenies of different MAALs, as well as within progenies of same MAAL. Drought tolerance screening under a controlled environment indicate the tolerance of MAAL 2 progenies to at least a week of 0% moisture stress during the seedling stage. Previously mapped QTLs in the introgression regions validate chromosome introgressions in our DILs in correlation with the phenotype observed. For example, PTS gene has been mapped in chromosome 6 that coincides with a chromosome introgression in DIL5, which shows a serrated leaf pattern. Identification of wild introgressions combined with trait evaluation of the DILs will be important for the study of both single gene transfer and quantitative trait inheritance from S. lycopersicoides to the cultivated tomato.
Forage yield and water use efficiency of sorghum, pearl millet, and corn under deficit irrigation

Bishwoyog Bhattarai¹, Sukhbir Singh¹, Charles P. West¹, Calvin Trostle² and Glen L. Ritchie¹,²

¹Department of Plant and Soil Science, Texas Tech University, Lubbock, TX
²Texas A & M Agrilife Research and Extension Center, Lubbock, TX

Abstract

Corn (Zea mays L.) silage is a major feed ingredient of beef and dairy industries in the southern high plain (SHP) and relies on irrigation water from the Ogallala aquifer. With declining water levels of the Ogallala aquifer, it is difficult to sustain the increasing demand of corn silage in many areas of SHP. Forage sorghums (Sorghum bicolor L.) and pearl millet (Pennisetum glaucum L.) can be viable alternate to corn silage, when irrigation capacity is limited or even under rainfed condition. Hence, a field experiment was conducted during summer of 2018 at New Deal Research Farm of Texas Tech University to assess growth, yield, and water use efficiency (WUE) of forage sorghum, pearl millet, and corn under limited irrigation. The experiment was conducted in a split-plot design with three irrigation levels [I₁ (50 mm), I₂ (200 mm) and I₃ (350 mm)] as the main plot factor and five cultivars [P1498AM (corn), AF7401 and Silo700D (sorghum), and Epic and Exceed (pearl millet)] as the subplot factor with four replications. Stomatal conductance and leaf area index were the highest in I₂ and I₃ irrigation treatments compared to I₁, which indicate the higher CO₂ fixation and photosynthesis in I₂ and I₃ treatments. Plant biomass results were also aligned with stomatal conductance and leaf area index, and the highest plant biomass production was recorded in I₃ irrigation treatment. However, WUE was greater in I₂ irrigation treatment compared to I₁ and I₃. Within the cultivars, biomass and WUE were recorded the highest in AF7401 followed by Epic, and the lowest in P1498AM. Results indicate greater yield and WUE of sorghum and pearl millet compared to corn under deficit irrigation. However, research data from the year of 2019 will help us to reach at any concrete conclusions about this study.
**GENETIC DIVERSITY ANALYSIS OF SILVERLEAF NIGHTSHADE POPULATIONS UNDER HERBICIDE STRESS**

Joshua J. Singleton¹*, Ritchel B. Gannaban², Puneet Kaur Mangat², Rosalyn B. Angeles-Shim²

Department of Plant and Soil Science, College of Agricultural Sciences and Natural Resources, Texas Tech University, Lubbock, Texas 79409-2122, United States

*Solanum elaegnifolium* (silverleaf nightshade) is a member of the Solanaceae family and is native to central America. It is an aggressive, poisonous weed, that dramatically spreads from deep rootstocks with persistence. Silverleaf exhibits a large amount of morphological variation and harbors a high degree of resistance to several economically important pests, pathogens and herbicides. Increased infestation of weedy silverleaf nightshade exacerbates its position as a noxious agricultural weed having caused significant reduction of yield in crops worldwide. Successful populations of invasive weed species, indigenous or not to a region, rely on their vested levels of phenotypic plasticity and high genetic diversity in praxis of genetic adaptation to precipitate an infestation. The goal of our study is to assess the genetic variation in two populations of silverleaf subjected to herbicide pressure. To this end, we need to establish the genetic diversity of the *S. elaegnifolium* by first distinguishing transferability of related SSR markers and second use the markers that are transferable to elucidate the genetic diversity. From the acquisition of polymorphism information content and the generation of a dendrogram model we were able to deduce that herbicide resistance was not the cause of individual clustering, but there was significant variation/divergence within both the populations. The observed significant variation/divergence in population germplasms found between the heterogenous populations is entirely the product of obligate outcrossing that has resulted in an innate degree of variability. For an applicable, ergonomic control management strategy to be created we must first complete the aforementioned gaps in information that hinder further progress. Thus, this research propositions to elucidate molecular mechanisms that confer the genetic adaptability observed in *S. elaegnifolium* and then use the resulting information to create a simulation model that may better illustrate potential range expansion and population distribution of the species.
Dissolution of cotton cellulose in imidazolium-based ionic liquids: The effect of size and shape of cations
Niwanthi Dissanayake,1 Vidura D. Thalangamaarachchige2 Shelby Troxell,2 Edward Quitevis,*2 and Noureddine Abidi*1

1 Fiber and Biopolymer Research Institute, Department of Plant and Soil Science, Texas Tech University, Lubbock, TX 79403, USA.
2 Department of Chemistry and Biochemistry, Texas Tech University, Lubbock, TX 79409, USA.

*Corresponding author: Noureddine Abidi, E-mail: noureddine.abidi@ttu.edu, Tel: +1 (806) 834-1221.

Abstract

Cellulose is the most abundant, biopolymer on Earth. It has numerous applications in many industries and can be engineered into fibers, films, sponges, beads, and other cellulosic objects. Many of these applications require cellulose to be dissolved. However, cellulose is insoluble in water and most common solvents. Cellulose solvents used currently are not eco-friendly and non-recyclable. Moreover, these solvents have limitations including the toxicity, volatility, cost, and demand for high temperature and long time to dissolve cellulose. Recently, ionic liquids (ILs) emerged as promising solvents that can efficiently dissolve cellulose in mild conditions. During the past decade, the dissolution of cellulose in ILs has been extensively studied. However, the mechanism of cellulose dissolution, especially the role of IL cation in the dissolution process, is not well understood. In this study, we performed a systematic study to understand the effect of substituent groups at the cation in imidazolium-based ILs on cellulose dissolution. We synthesized a series of imidazolium-based ILs with acetate as the common anion; 1-heptyl-3-methylimidazolium acetate ([C7C1im][OAc]), 1-(cyclohexylmethyl)-3-methylimidazolium acetate ([CyhmC1im][OAc]), 1-benzyl-3-methylimidazolium acetate ([BnzC1im][OAc]), 1,3-dibenzylimidazolium acetate ([Bnz2im][OAc]), and 1-(2-naphthylmethyl)-3-methylimidazolium acetate ([NapmC1im][OAc]). In each dissolution experiment, 5% (w/w) ground cotton fiber was dissolved in the ILs below 100°C. The progress of the dissolution was monitored periodically with a polarized light microscope. We discovered that [BnzC1im][OAc] dissolved cotton cellulose more efficiently than the other four ILs. For the five ILs that were investigated, we find that the effect of the cation can be rationalized on the basis of both the size and shape of the cation. In addition to the dissolution, the cellulose was regenerated, and characterized by Fourier transform infrared (FTIR) spectroscopy and scanning electron microscopy (SEM).

Reference

Genetic diversity analysis of upland cotton (*Gossypium hirsutum*) germplasm and EMS-induced mutants for cold germination improvement

Ritchel B. Gannaban, Junghyun Shim, Benildo G. delos Reyes, and Rosalyn B. Angeles-Shim  
Department of Plant and Soil Science, Texas Tech University, Lubbock, TX 79410

Cotton production in the Southern High Plains is perpetually challenged by extreme temperature fluctuations during the start and end of the cropping season. While chemical treatments have been used to mitigate the negative impacts of cold stress, breeding of cold tolerant varieties remain the most economical approach to ensure the production stability of early-planted cotton. This study aims to identify genetic variation that can improve cold germination ability of upland cotton. Twenty-six accessions from the *Gossypium* Diversity Reference Set (GDRS) and 20 EMS-induced mutants of cotton were genotyped using 105 simple sequence repeats (SSR) markers. Allelic information, genetic distances, and clustering were generated using the GenAlEx 6.5 and MEGA 10.0 software. Cold germination ability screening was carried out at 12, 15, and 30°C, with or without hydropriming. The parameters used to evaluate cold germination ability included germination percentage (GP), germination index (GI), mean daily germination (MDG), peak value (PV), germination value (GV) and mean germination time (MGT). Of the 105 SSRs tested, 22 were polymorphic. Polymorphism information content (PIC) for each locus ranged from 0.04-0.50, with an average PIC of 0.26. The high PIC indicates the presence of high genetic variation within the test germplasm. Clustering based on genetic similarities grouped the test materials into five major clades. Two major clades separately grouped the EMS mutants and most of the GDRS accessions. Three smaller clades were composed of 2-3 genotypes or landraces each. The observed clustering was highly reflective of the selection pressure that imposed on the materials were subjected to for many generations. GP, GI, MDG, PV and GV increased whereas MGT decreased with increasing temperature. Imbibition treatment significantly improved germination of GDRS lines at 12 and 15°C. The genetic variation available within the GDRS germplasm and EMS mutant lines can be used to improve cold germination ability.
Evaluation of root water uptake of cotton under deficit subsurface drip irrigation using HYDRUS (2D/3D) Model

Atinderpal Singh and Sanjit Deb
Department of Plant and Soil Science, Texas Tech University, Lubbock, TX 79409

Abstract
Water availability is one of the major constraints in irrigated cotton (Gossypium hirsutum L.) production system in the Southern High Plains (SHP) of the United States, where erratic rainfall and droughts are increasing pressure on the depleting Ogallala aquifer to support intensive agricultural production in the SHP. Evaporation from soil and transpiration from the crops are affected by the root zone water dynamics, and hence, water balance in agricultural systems requires concurrent knowledge of water flow and root water uptake (RWU). An enhanced understanding of spatial and temporal patterns of RWU of cotton under semi-arid conditions is of great importance for efficient use of irrigation water in the SHP. Despite its importance, there remains a paucity of quantitative information on spatial and temporal patterns of RWU of cotton, particularly under deficit subsurface drip irrigation. Therefore, the objective of this study was to simulate patterns of multidimensional RWU in a semiarid subsurface drip-irrigated cotton field using HYDRUS (2D/3D) numerical model. A field study consisted of four levels of deficit subsurface drip irrigation was conducted over two consecutive cotton growing seasons (2017-2018) to evaluate spatial and temporal RWU. HYDRUS simulations, which agreed with measured volumetric water contents and soil temperatures at different soil depths in the root zone during model calibration (2017 growing season), were used to predict root zone soil water dynamics, and compensated and non-compensated RWU under four different levels of subsurface drip irrigation during model validation (2018 growing season). Overall, the results of the simulation, validated against measured data at a cotton field, suggest that HYDRUS (2D/3D) could be an effective tool for managing enhanced RWU in a deficit drip-irrigated cotton production system.
Impact of biochar on growth, physiology and yield of cucumber and sweet corn under deficit irrigation regimes.

Manpreet Singh and Sukhbir Singh

Department of Plant and Soil Science, College of Agricultural Sciences and Natural Resources, Texas Tech University, Lubbock, Texas 79409-2122

Water scarcity has become a major concern for the sustainability of contemporary farming systems, especially in arid and semi-arid regions such as Southern High Plains (SHP) of the US. As a result, drought adaptive strategies for saving water and sustaining crop productivity are requisite. Deficit irrigation (DI), a strategy of applying water lesser than the evapotranspiration (ET) demand of a crop, is commonly practiced in dry areas, with major emphasis on maximizing water use efficiency (WUE). However, considering the water stress sensitivity of the fast-growing vegetable crops like cucumber and sweet corn, some additional agronomic strategies might be useful for successful practice of DI in vegetables. The ability of biochar to retain enormous amount of water elucidates its potential as a soil amendment to mitigate drought stress by increasing plant available water. The studies examining the effects of biochar on the performance of vegetable crops and water availability to the plants under open field conditions are limited. The current research is planned to investigate the efficacy of DI and biochar as an integrated approach to save water and sustain vegetable productivity in water-limited regions. Multi-year field experiments will be conducted to study the effects of DI-biochar interactions on growth, physiology, WUE and yield of cucumber and sweet corn. A split-plot design will be used to allocate three irrigation treatments (100% ET<sub>c</sub>, 80% ET<sub>c</sub> and 60% ET<sub>c</sub>) to the main plot and three biochar treatments (control: 0 t ha<sup>-1</sup>, hardwood: 14 t ha<sup>-1</sup>, softwood: 14 t ha<sup>-1</sup>) to the sub-plots, with four replications of each experimental unit. Integration of DI and biochar may prove to be a viable approach for sustainability of vegetable production in semi-arid SHP.
CONSERVATION OF A SPECIALIZED BEE-PLANT SYSTEM INVOLVING *Nama* spp. Gray (Hydrophyllaceae) in the Southwestern U.S.

Aqeela Sehrish, Scott. D. Longing

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Abstract

In the Southern High Plains semi-arid grasslands, large-scale clearing for agriculture has contributed to decreased grassland acreage, with potential impacts to pollinators and their resources. Protecting pollinators and their habitats is an important aim for sustainable agriculture, while a broader and concurrent aim in pollinator conservation should include a focus on native bees and native plant-specialization, especially in regions such as the southwestern U.S. that supports high bee biodiversity. The proposed series of field and laboratory studies will address a specific plant-bee system endemic to the southwestern U.S. The gypsophile plant *Nama* spp. and its associated bee communities (with a focus on *Sphecodosoma pratti* Crawford) are the center of the proposed basic and applied investigations to advance what is known about this specialized system and to inform strategies for ecological restoration and conservation in agricultural lands. The objectives of the current and proposed research include to 1) determine germination requirements and greenhouse and field cultivation of *Nama* spp., 2) using cultivated and wild *Nama* plants, quantify local and landscape conditions influencing bee/insect communities and behaviors of specialized bees, 3) in laboratory soil mesocosms, observe and quantify foraging behaviors of *S. pratti* and related soil and plant conditions, and 4) Determine toxicity and exposure of *S. pratti* to common agrochemicals across highly-variable landscapes. The overall goal of the research is to better understand this endemic specialized plant-pollinator system to support species’ monitoring and integration with conservation actions to support native solitary bees.

*Keywords*: *Nama hispidum*, *Sphecodosoma*, Bee-plant system, Restoration
Trans-generational induction of epi-alleles by abiotic stress in Arabidopsis thaliana: a glimpse into the vast complexity of the plant epigenome and its contribution to the phenotype

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DNA methylation is an epigenetic mechanism by which plants and animals regulate genomic activity. In particular, DNA methylation serves to repress gene expression, which is spatio-temporally regulated and could be permanent. Because most plant and animal genomes contain transposable elements that could harm the integrity of the genome, methylation of these sequence repeats serves to tame their activities. Beyond these permanent methylation states, there are other methylation states within the euchromatic regions that serve to give the genome its “flexibility” with respect to its interaction with a dynamic environment. The dynamic nature of the genic response, via DNA methylation, serves as a type of “organismal memory.” It is logical to assume that the DNA methylation states that are present in modern day crop plants were established during the course of domestication, further directed selection by breeding, or perhaps in the wild ancestors of crops that preceded domestication. An emerging question involves the heritability of methylation marks that arise due to environmental perturbations in the form of biotic and abiotic stresses. In this proof of concept study, we seek to answer the following questions in the plant model Arabidopsis thaliana (ecotype Col-0): (1) Can epi-alleles be created by selection pressure mediated by recurrent exposure to abiotic stress during the vegetative stage? (2) If yes, how many successive generations of recurrent pressure will be required to effectively “fix” the induced epi-alleles so as to have a measure of constitutive stress resiliency? (3) Will each successive application of abiotic stress be additive in terms of epi-allele induction and “fixation”? (4) What epigenetic mechanisms are involved in the stable creation and transgenerational transmission of epi-alleles? Our research questions will be addressed through an integrative approach that includes functional genomics, reverse genetics, and comparative cellular physiology and biochemistry.
Effects of Hail-netting on Gas Exchange and Production of Field Grown Malbec Grapevines (*Vitis vinifera*). Kenneth Ruland¹*, Thayne Montague¹,², Pierre Helwi², and Matthias Bougreay¹. Department of Plant and Soil Science, Texas Tech University, MS 2122, Lubbock, TX 79409-2122¹, Texas A&M University AgriLife Research and Extension Center, 1102 E FM 1294, Lubbock, TX 79403². (trey.ruland@ttu.edu)

Vineyards on the Texas High Plains produce 80 percent of wine grapes grown in Texas (about 7,091 metric tons of grapes). Although conditions are favorable for grape production, early season hail events may result in heavy yield losses, while late season hail events may result in damaged foliage and fruit, causing losses in fruit quality along with yield loss. High Plains grape growers have recently begun turning to hail-netting to negate hail event risks. As hail-netting is comprised of a fine plastic mesh, concerns over grape production and ripening have risen. Objectives of this study were to conduct a two growing-season study to evaluate effects of hail-netting on vine gas exchange, fruit ripening, and fruit production. Results presented here are preliminary results after the first growing season. This experiment was conducted on seven year old, own-rooted *Vitis vinifera* ‘Malbec’ grapevines in a commercial vineyard located in Brownfield, Texas. Treatments consisted of experimental blocks with fruit-zones and foliage covered by hail-netting, and control blocks left uncovered. Throughout the season, fruit-zone shortwave radiation, vapor pressure, and air temperature were measured. Photosynthesis and gas exchange measurements were taken twice monthly. At harvest, production measurements included total yield, average berry weight, and average cluster weight. Fruit-zone sensor data indicate shortwave radiation was reduced by roughly 25 percent in treatment fruit-zones covered by hail-netting. Sensor data also indicates no difference in fruit-zone vapor pressure or air temperature between treatment and control vines. Fruit yield data was not affected by application of hail-netting. As yield and berry weight parameters were unaffected, preliminary data indicate growers may consider hail-netting as an effective method to prevent hail damage, and preserve vine production.
**Presentation Title:** Soil microbial dynamics in playas of the Southern High Plains

**Authors:** Meagan Riley* and Lindsey Slaughter

**Abstract**

Playas are a common feature in semi-arid environments of the western U.S., with over 20,000 playas located in the Southern High Plains (SHP) of Texas alone. These ephemeral wetlands serve as an important habitat for wildlife, as recreational areas for human activity, sites for stormwater retention, and provide a source of recharge for the Ogallala Aquifer. Despite our heavy dependence on and interactions with playas, we know surprisingly little about soil biogeochemical dynamics in these systems. No studies to date have characterized soil microbial communities and activities in these wetlands. In this ongoing study, we characterized soil microbial communities and activity within and across three ephemeral playa wetlands in Lubbock, TX. Playas were classified according to their predominant surrounding land development (residential, urban parking lot, or rangeland), and subdivided into three zones (inner playa, outer playa, and bank). Twenty samples were collected from each location in a fishnet grid pattern. We measured microbial biomass, community composition, and selected chemical and physical soil properties of each sample. Non-metric multidimensional scaling ordinations were used to compare the community composition between the playas and playa zones. Selected results were spatially analyzed in ESRI ArcGIS. The findings of this study revealed that each playa is a unique habitat with distinct microbial communities, partially distributed within distinct zones. Further research will continue to reveal how soil microbial community dynamics vary across playa basins and how these dynamics are altered by land use, which will impact how land managers, producers, and urban residents interact with these ecosystems in the future.
Title: Crop response and weed control systems utilizing isoxaflutole in GLITP cotton

In recent decades glyphosate resistant weeds such as kochia (*Kochia scoparia*), Palmer amaranth (*Amaranthus palmeri*), and tall waterhemp (*Amaranthus tuberculatus*) have threatened cotton (*Gossypium hirsutum*) production in Texas, forcing producers to utilize other herbicide modes of action to control these weeds. The newest herbicide tolerant traits on the market include cotton tolerant to synthetic auxins such as 2,4-D and dicamba. The use of these herbicides has become controversial because of off-target movement. There is a critical need for novel herbicide modes of action to control herbicide resistant weeds while at the same time minimizing off-target movement. *P*-hydroxyphenylpyruvate dioxygenase (HPPD) inhibitors are the newest herbicide class of chemistry discovered in the 1980’s. These herbicides could have a significant impact on weed management for Texas growers. HPPD inhibitors are currently labelled for use in field corn (*Zea mays*); however, BASF Corporation recently developed an HPPD-tolerant cotton which will allow producers to use Balance Pro (isoxaflutole) in cotton production. This trait received US approval for deregulation by APHIS and will be studied under BASF Stewardship Procedures in 2019. It is referred to as “GLITP” because of stacked genes that express tolerance to glyphosate, glufosinate, isoxaflutole, and two insecticides. In 2019, proposed research in collaboration with BASF will examine cotton response to isoxaflutole applied preemergence and early postemergence (EPOST) in several weed management systems. Four different application timings will be examined to determine effective “systems” for season-long crop tolerance and weed management. Applications will be made at-planting (preemergence), EPOST, late postemergence, and at flowering and will include different combinations of isoxaflutole and other herbicides commonly used in cotton production. Data collection will include visual crop injury, weed control, plant stand, lint yield, and fiber quality. Efficacy trials to determine optimum application timings and effective tank-mix partners using other common herbicides also will be conducted.
Fate of nitrates in hydroponic leafy greens production using organic and inorganic nutrient formulations

Azeezahmed Shaik and Sukhbir Singh

Hydroponic plant production is regarded as more sustainable and economically feasible than conventional cultivation, and perhaps the most intensive method of crop production with efficient use of water and inorganic nutrients. However, the excessive use of inorganic nutrients in hydroponic production systems especially Nutrient Film Technique (NFT), not only raises the risk of higher nitrate accumulation in edible parts, but also increases environmental pollution through nutrient solution leachate, which contains higher concentrations of nitrates and phosphates. Organic fertilizers in hydroponic reduce nitrate concentrations in edible parts and nutrient leachate compared to inorganic fertilizers, because organic fertilizers are typically lower in nitrate nitrogen. Moreover, market for organic food continues to expand in the US, which attracts the greenhouse growers for exploring the use of organic nutrient sources in hydroponic vegetable production. However, the greenhouse growers face many challenges like unbalanced pH and electrical conductivity (EC) levels, while using liquid organic formulations compared to conventional inorganic soluble fertilizers in hydroponic crop cultivation. Keeping these points in view, a multiple greenhouse experiments are designed to evaluate the effects of different organic and inorganic nutrient formulations on growth and development of lettuce, basil, kale, and Swiss chard with an emphasis on plant nitrate accumulation and amount of nutrients (nitrates, phosphates, etc.) left in hydroponic nutrient leachate at the end of each experiment. All the experimental units will be replicated three times in factorial randomized complete block design for few experiments and remaining in split plot design. Research results might help growers to produce sustainable leafy greens with effective use of inputs and minimum environment pollution.

**Key words:** Leafy Greens, Nutrient Film Technique (NFT), Plant Nitrate Uptake, Nitrate Leachate, Organic Nutrient Formulations
USING THE HVI FIBROGRAM TO IMPROVE YARN QUALITY PREDICTIONS

Speaker: Abu Sayeed

Abstract

Within-sample variation in cotton fiber length impacts processing performance and yarn quality. Excessive within-sample variation in fiber length can slow processing and contribute to imperfections in the yarn structure. HVI length parameters, Upper Half Mean Length and Uniformity Index, are based on the fibrogram measurement principle. In this experiment, we demonstrate that the fibrogram contains more information than is captured by current HVI length parameters, and this information is useful for predicting yarn quality. We extracted additional information from the fibrogram, and used this information to predict yarn quality. These results were then compared with the yarn quality predicted by standard HVI length parameters. Our experiment shows that the fibrogram holds important information that improves the prediction of yarn quality that is not captured by standard HVI length measurement protocols. The results also show that the additional length information extracted from the fibrogram is at least as good at explaining variation in yarn quality as the AFIS length distribution by number. This was demonstrated on three sets of samples representing a range of sample types. This approach suggests it should be possible to capture important information about within-sample variation in fiber length using the fibrogram.
Understanding Salinity Tolerance of Select Wildflower Species in a Hydroponic Setting. Iryna Andrenko*1, Cynthia McKenney1, Thayne Montague1,2, and Russell Plowman1, Department of Plant and Soil Science, Texas Tech University, Lubbock, TX 79409-21221, Texas A&M University AgriLife Research and Extension Center, 1102 E FM 1294, Lubbock, TX 794032 (iryna.andrenko@ttu.edu)

Water quality and quantity are critical issues in many locations around the world. Use of reclaimed water for landscape irrigation can conserve potable water, and possibly reduce landscape fertilizer applications. A potential concern of using alternative water sources is elevated salt levels, which can have adverse effects on plant growth and aesthetic appearance. After establishment, the majority of Texas native wildflowers are known to be hardy, easy to maintain, and drought tolerant. In addition, native wildflowers provide wildlife habitat, and support native pollinators. However, information on salinity tolerance of many Texas wildflower species is lacking. In this study, two hydroponics experiments (March-May 2017, and February-April 2019) were conducted to determine salt tolerance of three native wildflowers: sleepy daisy (*Xanthisma texanum*), standing cypress (*Ipomopsis rubra*), and gaura (*Gaura villosa*). Seedling plants were suspended in a hydroponic solution using a randomized complete block design with a control (municipal Lubbock tap water with nutrition solution 3dSm⁻¹) and three salinity treatments: 5dSm⁻¹, 7dSm⁻¹, and 10.4dSm⁻¹; with NaCl:CaCl₂ = 2:1. Sixty days after salinity treatments were initiated, visual rating, fresh weight, and length measurements were recorded on root and shoot tissue. To determine tissue percent Ca, Na, and Cl concentration, shoot and root tissue were dried and powdered for tissue analysis. Results of the first trial indicate survival percentage for *X. texanum*, *G. villosa*, and *I. rubra* were 100, 90, and 77 respectively, with greatest mortality rates at the highest salinity treatment. Ion concentrations of root and shoot tissue were affected by salinity levels and varied among species. Standing cypress and gaura could be identified as moderately salt tolerant species (up to 7dSm⁻¹). Whereas, sleepy daisy is salt tolerant (up to 10.4dSm⁻¹). Although additional research is needed, these native Texas wildflowers appear to have great potential in landscapes utilizing poor quality irrigation water.
**Presentation Title:** Determination of base saturation percentage in agricultural soils via portable X-ray fluorescence spectrometer

**Authors:** Ashmita Rawal\textsuperscript{a}, Somsubhra Chakraborty\textsuperscript{b}, Bin Li\textsuperscript{c}, Katie Lewis\textsuperscript{d}, Maria Godoy\textsuperscript{e}, Laura Paulette\textsuperscript{f}, David C. Weindorf\textsuperscript{a}, \textsuperscript{⁎}

**Abstract:** Soil base saturation percentage (BSP) plays an important role in the assessment of soil taxonomic classification and soil fertility. Conventionally, soil BSP measurement methods are fraught with many drawbacks such as being time consumptive, destructive to the samples, and can lead to the underestimation of true cation exchange capacity (CEC). Recently, proximal sensors such as portable X-ray fluorescence (PXRF) spectrometry have proven to be effective for rapid physicochemical analysis of soils. In this study, we proposed and examined a PXRF-based method to predict BSP using 300 soil samples from agricultural lands across six states in the USA; Colorado, California, Minnesota, Nebraska, Oklahoma, and Texas. An Olympus Vanta series PXRF analyzer was employed to measure Mg, Ca, and K for BSP prediction. Predicted BSP was validated against measured BSP using four different multivariate models [generalized additive model (GAM), multiple linear regression (MLR), random forest (RF), and regression tree (RT)] via R 3.5.1. Predictive model performance was assessed via root mean squared error (RMSE), coefficient of determination ($R^2$), residual prediction deviation (RPD), and the ratio of performance to interquartile (RPIQ) range. While predicting BSP, models exhibited validation $R^2$ and RPDs as follows: GAM = 0.58, 1.6; MLR = 0.45, 1.4; RF = 0.62, 1.6; RT = 0.68, 1.8, respectively. Soil CEC was also predicted using a similar approach, with similar and moderate predictive performance; GAM produced $R^2$ and RPD of 0.69, 1.8, respectively, relative to laboratory data. This study demonstrated that PXRF elements can be used to predict BSP with fair accuracy for the range of agricultural soils examined. Therefore, PXRF could offer advantages for faster and in-situ analysis of base elements and soil classification. As such, further study and enhancement of the approach outlined herein on a wider array of soils is warranted to establish the wider applicability of this technique.
Soil Physiochemical Properties and Carbon Sequestration of Urban Landscapes in Lubbock, TX

Manish Sapkota, Joseph Young, Cade Coldren, Lindsey Slaughter, and Scott Longing

Abstract

Organic matter accumulation and carbon sequestration are ecosystem services provided by urban landscapes. These characteristics are expected to increase over time, but little is known about the effects management or the semiarid climate on these factors. The objective of this study was to evaluate physiochemical attributes of urban soils established under turfgrass landscapes of different ages. Soil samples were obtained from 10 locations within each home age category: old homes (1950-1970), middle-aged homes (1971-1990), newer homes (1991-2010), and newest homes (2011-present) as well as city managed parks encompassing all age ranges. Soil texture, bulk density, extractable nutrients, pH, soil organic matter (SOM), soil organic carbon (SOC), and total nitrogen (TN) were determined for each soil sample. Bulk density and pH were highest in newest homes and lowest in oldest homes, but no differences in CEC, P, K, Mg or Ca were identified. Increasing home or park age increased SOM, SOC, and TN with similar accumulation rates for homes and parks. This result suggests management practices may not effect accumulation rates. In Principal Component Analysis, SOM, SOC, and TN contributed most to PC1 (36.2%) and bulk density and soil pH for PC2 (22.5%). Interestingly, East oriented home lawns had higher accumulation rate of SOM compared to other home orientations, which may indicate a benefit from reduced sun intensity to promote more rapid SOM accumulation. These findings support previous research that limiting C intensive management practices (mowing, fertility, pesticide applications, etc.) would not alter SOM or SOC accumulation rate in a semiarid environment, but would reduce the C footprint of the urban landscape.
Re-envisioning QTL dynamics in rice:
Interaction of the drought-mediated yield penalty QTL \textit{qDTY12.1} with its genetic background

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The \textit{qDTY12.1} is large-affect QTL in rice, responsible for yield maintenance under drought stress. Marker-assisted backcrossing was utilized to introgress \textit{qDTY12.1} in elite varieties to improve their performance under drought stress. However, it was found that presence of critical \textit{qDTY12.1} allele did not necessarily result in yield maintenance under drought, as observed in the sibling backcross introgression lines in the genetic background of the elite \textit{indica} cultivar IR64. It was hypothesized that the effect of \textit{qDTY12.1} is dependent upon the synergistic and antagonistic interactions with other genes in its genetic background. To investigate the possible trans-regulation of genes within \textit{qDTY12.1} by other peripheral genes/alleles in the genetic background, we performed the very first transcriptomic characterization across the \textit{qDTY12.1} minimal comparative panel consisting of two sibling backcross introgression lines in IR64 genetic background with contrasting yield under drought stress, \textit{i.e.}, Low Penalty BIL (LPB, superior) and High Penalty BIL (HPB, inferior), original \textit{qDTY12.1} donor parent Way Rarem, and recurrent parent IR64.

To accomplish our objective, we identified a critical candidate gene within \textit{qDTY12.1}, Os12g0465700 (Decussate) with unique expression at booting stage and relevant function in reproductive growth and grain yield. We also generated a genetic circuit unique to the LPB exhibiting optimal alliances between \textit{qDTY12.1}-encoded Decussate gene and trans-acting genes from the genetic background. The network model of the Decussate gene in LPB that is specific to booting stage was inter-linked through yield related-attributes and assumed to play important roles in yield maintenance by regulating the sink-source balance through the cytokinin signaling pathway. We also validate that Decussate gene is crucial for yield maintenance under drought stress by conducting a separate drought study in heterologous model system, \textit{Arabidopsis thaliana}. To our knowledge, this is the first example of trans-regulation of \textit{qDTY12.1} function and an evidence for QTL X genetic background interaction.

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\textbf{Type of Talk:} Full Research talk (mid-stage to completed research)