Joint Edgar McFadden Symposium/ Hard Winter Wheat Workers Workshop

Grapevine, TX - April 24 – 26, 2023
Organized by Texas A&M University, USDA-ARS, South Dakota State University, and the Hard Winter Wheat Improvement Committee

A. Speaker Abstracts (page 1-8)

Monday, April 24, 2022
5:00 p.m. Registration
5:30 p.m. – 7:00 p.m. Reception and poster set-up
7:00 p.m. – 8:00 p.m. The McFadden Address: Dr. Ed Souza, Global Head Wheat Breeding, BASF Corporation

"Thinking Like Edgar McFadden"

Dr. Edward Souza, BASF, Head of Global Wheat Breeding

Edgar McFadden is noted for developing "Hope" spring wheat and publishing the concept of the Puccinia Pathway. The latter is the observation of a progression of rust infection distributed from Mexico to Canada by wind and crop infection. It greatly affected his decisions as a scientist, and his choice in research. McFadden modeled thinking useful for tackling modern agricultural problems. 1) He had a clear overriding goal, develop rust resistance in wheat. 2) He was observant and prepositioned research and germplasm to take advantage of changing circumstances. 3) He distributed his best germplasm and information to enable rapid responses by others to emerging problems, such as stem rust race changes.

Rust resistance remains a large and important goal for the agricultural community. Seedling resistance often is rapidly overcome by race changes. Adult plant resistance is more stable than seedling resistance. But it requires a commitment to stacking traits. Breakdowns in rust resistance still can have widespread economic impact that can be difficult to predict. Prepositioning genes and germplasm is crucial for responding to other stress factors in the agricultural system. Changes in the environment happen more quickly than can be addressed by breeding alone. Resistance breeding needs to be leveraged with other agricultural initiatives in the areas, including climate change, ground water depletion, and soil health. Finally, many of the problems facing agriculture and society are exponential in their development, they have accelerating impact as they accelerate in scope. A single breeding program is linear and timebound in its development. Only by mimicking the types of linkage favored by McFadden can breeding programs reach exponential responses similar to the Green Revolution.

Tuesday, April 25

Edgar McFadden Symposium

- 8:30 AM: **KEYNOTE** – "Accelerating public plant breeding to respond to the demands of more and healthier food"
    - *Susanne Dreisigacker, Wheat Molecular Breeding Laboratory Head, CIMMYT*

Accelerating public plant breeding to respond to the demands of more and healthier food

Susanne Dreisigacker, International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico

Wheat is an essential component of global trade and food security, providing around 20 % of protein and calories consumed worldwide. The demand for wheat is projected to continue to grow over the coming decades, particularly in the developing world to feed an increasing population, and with wheat being a preferred food, continuing to account for a substantial share of human energy needs in 2050. The CIMMYT Global Wheat Program is one of the most important public sources of high yielding, nutritious, disease- and climate-resilient wheat varieties for Africa, Asia, and Latin America, and is therefore a central pillar for more resilient agri-food systems in these countries. To keep up with the pressing future demands of wheat production and to adapt to changing environmental factors, wheat breeders at CIMMYT are constantly turning to new and emerging technologies and breeding strategies to accelerate genetic gain. Approaches include re-defining current breeding pipelines in relation to the most relevant market segments, shortening breeding cycle with faster access of elite lines and data to partners, extended phenotyping networks, and using advanced genetics and genomics for rapid trait introgression. The presentation will give an overview of existing progress.

- 9:15 AM: "Redefining crop breeding strategy for effective use of nitrogen in major field crops"
    - *Dr. Ignacio Ciampitti, Kansas State University*

Redefining crop breeding strategy for effective use of N in major field crops

Ignacio A. Ciampitti

Department of Agronomy, Kansas State University, Manhattan, KS, United States

New insights for characterizing nitrogen (N) nutrition in major field crops are still relevant in order to better understand potential changes in the effective use of this nutrient over time and across different genotype by environment by management (GxExM) scenarios. Recent efforts demonstrated the need to redefine the determination of plant N status, focusing on the N nutrition index (NNI). The main goal on quantifying changes in plant N uptake relative to plant growth is to take into account the changes on nutrient uptake and provide a comparison under a fair level of crop biomass. For this purpose, studying changes in plant N concentration as plant ages is relevant to better understand the minimum amount of nutrient needed to maximize growth and to define scenarios under deficiency, sufficiency, or luxury nutrient consumption. Following this approach, more recent studies demonstrated the more universal N dilution model and helped to quantify the uncertainty on the estimation of the N needs for many major field crops.

From a breeding perspective, crop improvement for N use efficiency (NUE, yield to N supply ratio) is an elusive target for plant breeding programs, mainly focused on improving yields. A shift of paradigm to target more direct N gains is needed in order to produce a true change in the effective use of nutrients by crops and in order to reduce the overall dependency of fertilizer, with a consequent reduction in the overall environmental footprint of agriculture. This presentation provides new insights on the overall changes in NNI over time and the potential avenues for improving yields by directly targeting true N gains. Future breeding efforts could focus on translating this current knowledge to target relevant plant traits more directly linked to N gain (at comparable biomass levels) with a potential to improve yield and resiliency of the crop to changes in climatic conditions.

- 9:45 AM: **Discussion**
- 10:00 AM: **Coffee Break**
- 10:30 AM: "Current Status of Stem Rust"
    - *Dr. Yue Jin, USDA-ARS Cereal Disease Laboratory*
    - *Dr. Matt Rouse, USDA-ARS Cereal Disease Laboratory*

Stem rust update

Yue Jin and Matthew Rouse
USDA-ARS Cereal Disease Laboratory, St. Paul, MN 55108

Over the last two decades several countries have experienced a resurgence of stem rust after many decades of quiescence. This resurgence was caused by the evolution and continuing spread of the Ug99 race group and other highly virulent races that have caused severe epidemics. Through global surveillance, we have identified the sources of these virulent races and tracked their spread. Resistance, or a lack thereof, of elite breeding germplasm from breeding programs across the United States is assessed by screening at the seedling and adult plant stages. New strategies to reduce the vulnerability to stem rust in US wheat are now being emphasized. To bridge the gap between available genetic resources that provide resistance to highly virulent races and the vulnerability of conventional US wheat varieties, we backcross targeted resistance genes into advanced wheat breeding lines. Regions of the United States most vulnerable to stem rust epidemics (the northern Great Plains) and most influential in the initiation of epidemics (Texas and Gulf Coast) were prioritized in our prebreeding effort for stem rust resistance.

- 11:00 AM: "**Durable host plant resistance and gene stewardship"**
    - ***Dr. Bob Bowden, USDA-ARS, Manhattan, KS***

Wheat stripe rust, leaf rust, and stem rust are collectively the most important foliar diseases of wheat worldwide. Unfortunately, new resistant varieties are usually overcome by new races of the rust fungi within a few years after release. Fortunately, some varieties have shown durable resistance over many years of field production. I will discuss the two main strategies for breeding for durable resistance: gene stacks (pyramids) and adult-plant, slow-rusting resistance. I'll discuss pathogen population structure, phenotyping methods, new and/or important resistance genes, molecular markers, and some results of the cooperative applied rust research conducted by USDA and university cooperators. Finally, I will discuss the need for resistance gene stewardship to prolong the usefulness of our hard-won genetic resistance resources.

- 11:30 AM: “The Challenge of Wheat Stem Sawfly”
    - *Dr. Jeff Bradshaw, University of Nebraska, Lincoln*
    - *Dr. Esten Mason – Colorado State University*

Breeding for resistance to the wheat stem sawfly

Dr. Esten Mason – Associate Professor and Wheat Breeder

Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO

Abstract: The wheat stem sawfly (*Cephus cinctus* Norton) was identified in North America almost 150 years ago and was first documented infesting the native grasses of Colorado in 1872. By 1910, damage had been reported in spring wheat production of Montana and North Dakota before expanding into winter wheat growing areas in Colorado, Nebraska, and Wyoming. Damage from sawfly occurs through a reduction in kernel weight due to larval feeding in the stem and lodging of wheat at harvest due from formation of a hibernaculum for overwintering. Annual losses are estimated at $350 million in North America and $50 million in Colorado. Beyond yield, cutting of stems negatively impacts residue retention and water capture in dryland production systems of the high plains. The CSU Wheat Breeding Program began introgressing resistance to sawfly in 2011, focusing on the *Qss.msub*-3BL locus conferring stem-solidness. The locus was later cloned, with *Sst1* encoding a *TdDof* transcription factor, which when present as three tandem repeats, inhibits programmed cell death of the pith tissue. The first CSU semi-solid stemmed cultivar, Fortify SF, was released in 2019. Additional hard red winter wheat releases include Amplify SF and Fortress in 2021, with Windom SF, a hard white wheat released in 2022. The breeding program employs a combination of phenotypic (stem solidness and cutting) and genomic selection to build yield and quality around the *Sst1* locus. Additional types of resistance, including antibiosis and antixenosis, both in hexaploid and wild wheat ancestors are being identified and utilized in the program.

- 12:00 PM: **Lunch**
- 1:30 PM: “Managing Wheat for Plant Health in Changing Environments”
    - *Dr. Amanda de Olivera Silva, Oklahoma State University*
- 2:00 PM: “Economics of Wheat Quality”
    - *Dr. Cory Walters, Center for Agricultural Profitability, University of Nebraska, Lincoln*

Shane Roberts, Kathleen Brooks, Lia Nogueira and Cory Walters, University of Nebraska, Lincoln, NE

This study empirically examines the role of conventional and end-use wheat quality characteristics as well as transportation costs on the pricing of U.S. hard red winter wheat (HRWW) utilizing a hedonic price analysis framework, detailed quality characteristic data as well as location matched price data. We find evidence that multiple conventional quality characteristics and multiple end-use quality characteristics (milling and baking) have a statistically significant and economically important effect on the price of U.S. HRWW. This evidence suggests that, although U.S. HRWW producers are not directly paid premiums or discounts for end-use quality characteristics, they can be paid indirectly through regional HRWW prices. We also evaluate the role of information about conventional and end-use quality characteristics on price as harvest progresses. Results suggest that as harvest progresses, prices are updated to reflect changes in wheat quality. Results suggest revisions to U.S. policy on standard grade factors to improve transparency between characteristics farmers are paid for on grade sheets and characteristics millers and bakers value.

- 2:30 PM: "Genomics of Utilization of Ancient Relatives"
  - *Dr. Eduard Akhunov, Kansas State University Dept of Plant Pathology*
  - *Dr. Allan Fritz, Kansas State University Dept of Agronomy*

Wild relatives of wheat serve as a wheat genetics goldmine, but much effort is required to extract the gold from the dross. These efforts are need to enable the wheat community to address future challenges related to food security, climate change, functional quality, health and nutrition and sustainability/regenerability. Recent efforts by the Wheat Genetics Resource Center and allied programs at K-State and the USDA-ARS have focused on mobilization of diversity of wild emmer and Aegilops tauschii. Introgression efficiencies below expectation were observed in most populations derived from Ae. tauschii. Transfer of alien segments in pericentromeric regions was most strongly suppressed.
To date, potentially valuable variation has been identified for protein content, protein quality, wheat stem sawfly, wheat streak mosaic virus and response to abiotic stress. Beyond screening for key traits, there is a need for strategic approaches to retain diversity for future challenges. Shorter- and longer-term strategies will be discussed, as well as the importance of introgressing diversity into different backgrounds and evaluating materials in a wide range of conditions. Future efforts would also benefit from tools to enhance recombination, especially as we seek to exploit genetic resources beyond the primary gene pool.

- 3:00 PM: **Coffee Break**
- 3:30 PM: "Designing a hybrid wheat program in the public sector"
  - *Dr. Amir Ibrahim, Texas A&M University*
  - *Dr. Katherine Frels, University of Nebraska-Lincoln*

Designing a Hybrid Wheat Program in the Public Sector

Amir M.H Ibrahim[1*], Katherine Frels[2], Anil Adhikari[1], P. Stephen Baenziger[2], Bhoja R. Basnet[3], Susanne Dreisigacker[3], Jackie C. Rudd[4], Betul Sade[1], Jordanna Tadlock[1], Brandon Gerrish[1], Nithya Subramaniam[1], Gigi Opeña[1], Shuyu Liu[4]

[1]Department of Soil and Crop Science, Texas A&M University, College Station, TX, 77843
[2]Department of Agronomy and Horticulture, University of Nebraska, Lincoln, NE, 68583
[3]International Maize and Wheat Improvement Center (CIMMYT), Mexico City, Mexico
[4]Texas A&M AgriLife Research, Amarillo, TX, 79106
[*]Corresponding author: amir.ibrahim@tamu.edu

Hybrid wheat (*Triticum aestivum* L.) is a promising technology aimed at increasing yield potential to meet future global food demand. However, for its commercial success, a cost-effective seed production system, satisfactory anther extrusion, pollen flow, stigma receptivity, and adequate heterosis are essential. In this presentation, we discuss the need in the public sector to develop the tools and knowledge for a hybrid wheat program. Our program focuses on chemical hybridization agents to induce female parent sterility and F_1 seed production for research and breeding purposes. However, we have ongoing work on cytoplasmic male sterility (CMS) system with a focus on mapping and utilizing the fertility-restoring genes (*Rf* genes) for cost-effective F_1 seed production. We will also present the genetic control and genotype-by-environment interaction associated with the male and female floral traits and using the F_2 yield as a proxy for the F_1 hybrid performance, which offers a quick and efficient approximation of the F_1 hybrid performance available to virtually every wheat breeder. In addition, genetic control of yield and its components, general and specific combining ability, and the concept of heterotic pools, will be discussed. We evaluated yield heterosis in diverse environments. We will also discuss the use of trancriptome analysis to characterize differences between parent lines and corresponding hybrids that exhibit positive or negative yield heterosis.

- 4:00 PM: "Using next-gen sequencing to finding out what viruses we are really facing in the wheat field"
    - *Dr. John Fellers, USDA-ARS HWWGRU*

What viruses are really in the wheat field?

John Fellers, Nar Ranabhat, Carla Redila, Mary Guttieri, and Jessica Shoup Rupp
USDA-ARS, Manhattan, KS

Dept of Plant Pathology, Kansas State University, Manhattan, KS

The wheat mosaic complex (WMC) is a major plant disease caused by three viruses, Wheat streak mosaic virus (WSMV), Triticum mosaic virus (TriMV), and High plains wheat mosaic Emaravirus are transmitted by the wheat curl mite. There are three known resistance genes available to breeders, Wsm1, Wsm2 and Wsm3 and each are in various stages of release in new varieties. It has been assumed that these were major viruses present in the field and thus breeders have been selecting varieties based on visual and antigen based assays. With the advent next generation sequencing, this assumption can now be tested. A three year field survey of Kansas was conducted and infected samples were tested using Illumina and ONT technology. Multiple viruses were found in several samples and the discovery of Brome mosaic virus in Kansas. These findings can aid in the process of selection of resistant varieties.

- 4:30 PM: **Flash and Dash** *(Coordinated by Dr. Shuyu Liu, Texas A&M and Dr. Mary Guttieri, USDA-ARS)*
- 5:00 PM: **Poster Session** *(Coordinated by Dr. Shuyu Liu, Texas A&M and Dr. Mary Guttieri, USDA-ARS)*
- 6:00 PM: **Adjourn**

Wednesday, April 26

Hard Winter Wheat Workers Workshop

- 6:30 AM – 8:00AM: Breakfast
- 8:15 AM: **Welcome/Announcements/Awards**
- 8:30 AM: "Mixograph Replacement"
    - *Andrew Green, North Dakota State University*

Breeding for Wheat Quality Without the Mixograph

Andrew Green
Shahidul Islam, North Dakota State University, Fargo, ND
Senay Simsek, Purdue University, West Lafayette, IN

The announcement of the discontinuation of Mixograph production caused many wheat breeders to wonder how to quickly analyze quality data in a fast-moving breeding program. Prior to this announcement, the NDSU spring wheat breeding program began working with Solvent Retention Capacity and the GlutoPeak instrument as a replacement for the Mixograph. A large project was initiated using grain samples from 50 released varieties of hard red spring wheat, which were grown at four diverse locations across two years. These samples were milled in duplicate on both the Quadrumat Jr. and Buhler mills, and a full quality evaluation panel was completed. Data collected included SRC with multiple reagents, GlutoPeak, Mixograph, Farinograph, Glutomatic, and baking evaluations. Good prediction models have been identified using as few small-scale tests as possible to approximate the data from the Mixograph. Perhaps more importantly, these tests have been predictive of the Farinograph and bake tests. Data will be presented on using Quadrumat Jr. milled samples to predict Buhler milled quality responses, which would be similar to the procedure a breeding program might use. Multiple types of analysis were used to develop and test predictive models, including linear regression, and machine learning. Results were verified with a coincidence of selection analysis to mimic a breeding program advancing experimental lines and comparing what would be advanced vs. discarded.

- 9:00 AM: "Options for replacing the Perkin Elmer/Perten Single Kernel Characterization System in breeding and agronomy applications"
    - *Dan Brabec, USDA-ARS Center for Grain and Animal Health Research, Manhattan, KS*

Overview of Wheat Hardness Testing and Single Kernel Characterization System

Daniel Brabec,
USDA-ARS-Center for Grain and Animal Health Research,
Manhattan, KS

Wheat hardness is one of the basic parameters of wheat classification. For instance, a wheat sample could be classified as hard red winter (HRWW) or soft red winter (SRWW). Many growing regions tend to have predominantly either hard varieties or soft varieties. Prior to the mid-1980s, wheat hardness was determined from a bulk sample with several types of grinding and sifting devices. In 1984, a new HRW variety from Kansas was classified as SRW at the export terminals in the gulf which created some marketing issues. The Federal Grain Inspection Service organized research efforts to develop instruments to objectively measure wheat hardness. By the early 1990s, USDA-ARS engineers had developed an instrument which could determine a hardness index value from a small sample of wheat, 300 seeds in ~4 minutes. The basic seed handling and electronic technologies of this single seed instrument was officially transferred to Perten Instruments. Over the next 20 years, more than 250 single kernel characterization instruments (SKCS) were manufactured and sold. In 2019, Perkin-Elmer's acquired Perten Instruments. Support for the SKCS units has continued through a contractor, John Kennedy of Kennedy Technical Services. John Kennedy has verbally committed to supporting the service of the SKCS systems for the next 3-5 years. After that period, the future of the SKCS is uncertain because of the potential lack of availability of part and repair services. Discussions are being considered for either alternate support for wheat hardness instruments or potential of newer technologies to work in the capacity which wheat breeders and industry might need for measuring wheat hardness characteristics.

- 9:30 AM: **Panel discussion**
    - Integrating Diversity: *Dr. Jackie Rudd, Texas A&M*
    - Resiliency: *Dr. Sunish Sehgal, South Dakota State University*
- 10:30 AM: **Break**
- 10:45 AM: **Hard Winter Wheat Improvement Committee Meeting** *(Chaired by Dr. Amir Ibrahim, Texas A&M)*
- 11:45 AM: **Depart for McGregor, TX, lunch provided for attendees**
- 2:00 PM: **Winter Wheat Breeders' Field** – *McGregor, TX and Adjourn*
- 4:00 PM: **Depart for Hotel**

B. Poster abstracts (Arranged by first then last names)

1. Graduate student poser abstracts (Page 9-17)

1) Introgression of improved root biomass traits into wheat hybrids

Abdullah, A.M.H. Ibrahim, Qingwu Xue, Jackie C. Rudd, Nithya Rajan, Shuyu Liu, Department of Soil & Crop Sciences/ Texas A&M University, College Station, Texas

Hybrid wheat root system is the major plant organ for water and nutrient acquisition. An initial wheat root study with Winrhizo scanner showed that entries with high root surface area but narrow root angle are associated with past drought tolerance in Texas, while those with wide angle can perform best in normal growing conditions. In hybrid field experiment, a commercial heterosis upto 8.3% in grain yield was obtained from diverse parents selected from male and female diverse groups. These hybrids showed promising yield at Greenville and McGreger, texas with grain yield upto 4412 Kg ha-1 as compared to best performing commercial varieties 'TAM-304' (4075 Kg ha- 1) and 'Gallagher' (3981 Kg ha-1). Among 130 hybrids produced, a subset of 50 better performing hybrids and parents was subjected to one month old plant root studies scanned with Winrhizo. The results showed a significant positive correlation of grain yield with initial root angle and negative correlation with root length. For root traits of two months old plants, the same entries have been grown into deep pots under controlled environmental conditions. Also, the same set has been grown under field conditions for scanning with Ground penetrating Radar. For genotyping, the KASP markers (HapB3-2, HapB6-1, HapA2-2) for major QTLs existing on chromosome 5B related to root biomass shall be used followed by screening with 25K SNP chip for genomic studies.

2) Candidate selection signatures of sign epistasis are observed in the KSU wheat breeding program

Augusto Tessele, Kansas State University, Manhattan, Kansas Geoffrey Morris, Colorado State University, Fort Collins, Colorado Eduard Akhunov, Kansas State University, Manhattan, Kansas Blaine Johnson, University of Nebraska, Lincoln, Nebraska Marshall Clinesmith, Syngenta Agriscience, Junction City, Kansas Allan K. Fritz, Kansas State University, Manhattan, Kansas

In wheat breeding, additive gene action is assumed to underpin complex agronomic traits, but oftentimes the cross of elite lines leads to poor breeding populations. Although this observation is not supported by the additive model, epistasis could explain such phenomena. As the effects of epistasis influence agronomic performance, selection signatures are expected to be found in breeding populations. We divided 40 wheat breeding populations into discovery and validation sets and analyzed the interchromosomal linkage disequilibrium within and across populations. Interactions that presented strong LD (>0.9) were used for further investigation. The existence of linkage drag flanking the candidate interacting regions was analyzed. All interactions presented some level of linkage drag and were further investigated. To distinguish selection signatures of epistasis from additive gene action, we analyzed the allele frequency of the interacting loci. Interactions presenting contrasting alleles in high frequency and off-combinations at low frequencies were deemed appropriate for further analysis. In the discovery set, all interactions presented the sign epistasis allelic frequency, however four failed the predictions in the validation set. Then we analyzed the allelic frequency of the candidate interactions in the breeding program. Out of the 19 initial candidate interactions, 15 presented opposing allelic combinations in very high rates in preliminary yield trails and off-combinations absent or in very low frequency in elite yield trials. In conclusion, we have found strong evidence of selection signatures of epistasis in wheat breeding populations, which has implications on important breeding decisions, such as germplasm management and parental selection.

3) Diversification of FHB resistance QTL in winter wheat germplasm

Bhanu Dangi, Gideon Francois Marais
North Dakota State University, Fargo, North Dakota

Fusarium Head Blight (FHB) is a devastating small grain disease that infects the floral heads and reduces grain yield and quality. Integrated FHB management relies strongly on the availability of FHB resistant cultivars. This study aims to expand FHB resistance QTL available for breeding and has two parts. First, four testers were crossed with 14 winter wheat (WW) lines in a line X tester mating design. The parents and 56 F1 were evaluated for FHB type II resistance in a greenhouse. ANOVA revealed highly significant genetic differences for FHB disease severity (DS), general (GCA) and specific (SCA) combining ability. ND Noreen showed the strong GCA, and its hybrid with 18Nord103 had the lowest DS and strongest SCA among the F1. Several other promising parents and F1 were found. F2 hybrids from the four best families will be tested in 2023/24 to initiate inbred line development. The second aspect of this study is to transfer Fhb7 (on a Thinopyrum elongatum-derived translocation) through modified backcrosses. Following a cross and backcross to four WW genotypes, 80 F1 and controls were genotyped using the Illumina 90K SNP array and STS marker WGC-2315 in order to confirm the marker. Using the phenotypically best progeny, a second (three WW parents) and third backcrosses (six WW parents) were conducted to recover ±93.8% of WW genetic background. B3F1 are being marker analyzed. Following F2 marker selection, single seed descent inbreeding will be initiated to establish genetically diverse resistant germplasm that can be employed in future WW crossing blocks.

4) Clodinofop Propargyl and Fenoxaprop-P-ethyl Nanoherbicides: Preparation, Characterization and Effect on Growth, Yield, and management of weeds of Wheat

Bilal Ahmad Khan1,2*, Muhammad Ather Nadeem2, Muthukumar Bagvathiannan1*, Hesham Oraby3

1 Department of Soil and Crop Sciences, College Station, Texas A&M TX 77843, United States
2 Department of Agronomy, College of Agriculture, University of Sargodha 40100, Pakistan.
3 Deanship of Scientific Research, Umm Al-Qura University, Makkah 24381, Saudi Arabia

*** Correspondence: Bilal Ahmad Khan (bilalahmadkhan678@gmail.com); muthu@tamu.edu**

With an emphasis on more sustainable agriculture, nanoformulations have been employed to enhance the delivery of fertilizers, insecticides, and growth regulators. Nanoherbicides has focuses on improving efficiency through targeted distribution and lowering environmental risk. This study aimed to investigate the effect of Clodinofop Propargyl and Fenoxaprop-P-ethyl nanoherbicides on growth, yield, and weed management in wheat under field conditions. Chitosan-based nanoherbicides were characterized using FT-IR, and XRD. The FT-IR analysis of both nanoherbicides matched the standard parameters. The XRD results confirmed the existence of (2θ) peak at 29.83 related to 176 anatase form in the the clodinofop propargyl nanoherbicide and 30.55 related to 74 anatase form in the fenoxaprop-p-ethyl one. The nanoherbicides were sprayed at 3-4 leaf stage of the targeted weeds. Six different doses (D0= Weedy Check, D1= Normal herbicides at recommended dose, D2= Nanoherbicides at the recommended dose of normal herbicides, D3= 05-fold lower dose of nanoherbicides, D4= 10-fold lower dose of nanoherbicides and D5= 15-fold lower dose of nanoherbicides) were used. Maximum weed control efficacy, growth and yield related parameter, minimum weed density, weed fresh and dry biomass, and weed index were tested. Both recommended dose of commercial herbicides and 10-fold lower dose of nanoherbicides produced similar negative effects on growth and yield related parameters of the studied weeds. The results revealed that the use of those nanoherbicides could be effective in 100% control of weeds under investigation. Nanoherbicides can be an essential solution for weed management due to associated nanoformulation efficiency in comparison with the conventional formulations.

5) A Diallel Study to detect Genetic Background Variation for FHB Resistance in Winter Wheat

Bipin Neupane*, Gideon Francois Marais, North Dakota State University, Fargo, ND

Fusarium head blight (FHB) is a serious disease of winter wheat. Resistance breeding programs rely heavily on a limited number of larger-effect FHB resistance QTL that have been identified, mapped, and associated with nearby markers. In addition, smaller-effect (background) resistance QTL may contribute moderate levels of “native” resistance, yet these QTL are generally poorly characterized. The overall resistance of a genotype is determined by the combined action of characterized as well as uncharacterized resistance QTL. FHB resistance can be improved by integrating, known larger-effect QTL through marker-aided introgression into genotypes with significant background resistance. This study aimed to identify and utilize well-adapted, advanced hard red winter wheat breeding lines with useful background FHB resistance QTL. A diallel trial consisting of 11 parents and 55 non-reciprocal F1 hybrids was tested for Type II FHB resistance in a replicated greenhouse experiment. Data were first analyzed following the Griffing analysis. Significant differences were detected among entries for disease severity (DS), general combining ability (GCA) and specific combining ability (SCA). The ratio of GCA:SCA effects suggested that additive QTL effects were of primary importance. The Hayman analysis provided additional

information on the genetic nature of the resistance QTL. Eight F1 hybrids with the lowest DS resulted from crosses among the best general combiners. F2 of the latter crosses were compared in a second-greenhouse FHB trial to identify possible **transgressive segregates.** An arbitrary threshold DS of 14% was used to select a manageable number of the most promising F2 plants for continued line development.

6) Quantitative Trait Loci for Hessian fly Resistance in Wheat Mapped Across Multiple Environments

Ellen Melson, Amir M.H. Ibrahim, Texas A&M University/AgriLife Research, College Station, Texas
David D. Drake, AgriLife Extension, Commerce, Texas
Shuyu Liu, AgriLife Research, Amarillo, Texas
Russell Sutton, AgriLife Research, Commerce, Texas

Hessian fly (Mayetiola destructor) is a pest of wheat (Triticum aestivum L.) found across most wheat producing areas of the world. This pest causes significant loss of yield in infested fields due to poor fall growth and spring lodging. The most effective control measure is integrated pest management including resistant varieties. Knowing the presence and location of resistance genes in the wheat genome is an important tool in breeding new resistant varieties, pyramiding resistance genes, and determining the effectiveness of specific genes in environments across wheat growing areas. A 186 recombinant inbred line (RIL) mapping population of wheat, ('TAM 113'/'Gallagher') was genotyped with 8,075 single nucleotide polymorphisms (SNPs). The population was field phenotyped in two major wheat growing areas of Texas, the Blacklands and South/Central Texas as well as in a greenhouse. Greenhouse and field data showed two major quantitative trait loci (QTL) for Hessian fly resistance on the short arm of the 1A chromosome with PVE of 23.01% (QHf.tamu-1A.9) and 31.82% (QHf.tamu-1A.13). An additional 5 QTL were mapped to 1AS in different greenhouse and field screenings. QTL were also mapped to 3B, 5A, and 2D. The 2D QTL (QHf.tamu-2D.36) which has a PVE of 22.4% from 'Gallagher', was previously mapped to a half-sibling 'Iba', and appears to be related to adult resistance.

7) Analysis of Hessian fly (Mayetiola destructor) Biotype and Virulence in Texas

Ellen E. Melson, Amir M. H. Ibrahim, Texas A&M University/AgriLife Research, College Station, TX
Ming-Shun Chen, USDA-ARS, Manhattan, KS
Shuyu Liu, Texas A&M AgriLife Research, Amarillo, TX
David R. Drake, Texas A&M AgriLife Extension, Commerce, TX
Russell Sutton, Texas A&M AgriLife Research, Commerce, TX

Hessian fly is an important pest of wheat worldwide and of particular importance in Texas and the southeastern United States. Texas is the highest wheat producing state that is severely impacted by this insect. The most effective control in these areas is an integrated pest management program beginning with resistant varieties of wheat. Hessian fly populations are genetically diverse and can rapidly become virulent to resistance genes that are widely deployed in a region. Knowing the current virulence status of regional fly populations is important for wheat breeders and producers. In this study, Hessian fly pupae were collected in the northeastern and central Texas regions. A biotype analysis for each region was conducted at the USDA-ARS Hessian fly Research Laboratory in Manhattan, Kansas. This analysis showed that resistance genes H12, H13, H20, H22, H25, H26, H28, H29, H32, H33, H34, and Hdic are highly effective in these regions. Texas fly populations have increased in virulence in the past 10 years and are now considered the most virulent biotype L or vH3, vH5, vH6, vH7/H8, vH9, vH10, vH14, vH15, vH23, vH24, vH31, and vH35/H36.

8) Is Chinese Spring Enough? A Comparison of Alignment of Whole Genome Sequencing of Elite Great Plains Wheat Germplasm to Alternative Reference Genomes

Kyle Parker, Zhen Wang, Yahya Rauf, Jackie Rudd, Shuyu Liu*, Texas A&M Agrilife Research And Extension Center, Amarillo, Texas
Amir M. H. Ibrahim, Department of Soil and Crop Sciences, Texas A&M University, College Station, Texas

In this era of genomics, the question comes to arise, is my reference genome ideal for my material? In this study 32 publicly available elite Great Plains hexaploid wheat (Triticum aestivum L.) germplasm lines with whole genome sequencing ranging from 5-20x's coverage were aligned to three reference genomes, Chinese Spring V2.1 (CS), Jagger (JG), and a custom Synthetic reference (DT). The Synthetic reference is an 'in silico' hybridization of SvevoV1 (Triticum turgidum subsp. durum) reference, and AL 7/8 V5 Aegilops tauschii reference. The collinearity of each reference was compared, resulting in percentage of colinear genes ranging from 66.88% to 75.42% for the JG/DT and CS/DT, respectively. Alignments were compared utilizing alignment, coverage, and discovered variant statistics. There were significant differences between supplementary aligned reads, properly paired reads, reads with mapping quality (MQ) of 0, alignment error rate, percentage of reference alleles, percentage of heterozygous calls, and percentage of missing alleles. For most metrics, CS and JG performed significantly better than the DT reference. However, for percentage of reads with MQ of 0, error rate, percentage of reference alleles, and percentage of missing alleles, JG performed significantly better than the other references. Initially the DT reference called the most variants, followed by CS and JG, however after filtering, JG retained the most variants, followed by CS and DT. The result of this study reveals reference bias that can affect downstream analysis by the position and the type of variants identified.

9) Genomic Prediction and Selection Of Advanced Breeding Lines In Texas Hard Winter Wheat Breeding Programs

Kyle Parker, Jackie C. Rudd, Jason Baker, Shannon Baker, Zhen Wang, Yahya Rauf Shuyu Liu*, Texas A&M Agrilife Research And Extension Center, Amarillo, Texas; Paul St. Amand, Guihua Bai, Amy Bernardo, USDA-ARS, Hard Winter Wheat Genetics Research Unit, Manhattan, Kansas
Amir M. H. Ibrahim, Geraldine B. Opena, Bryan E. Simoneaux, Department of Soil and Crop Sciences, Texas A&M University, College Station, Texas

Wheat (Triticum aestivum L.) is a staple crop grown in forty-two out of fifty states in the U.S.A. As the changing climate increases the severity and occurrence of extreme weather, breeders must continue to breed more resilient, high-quality, and adapted wheat cultivars. In this study, 931 Texas A&M Agrilife Research breeding lines were evaluated for grain yield in 11 environments across two years and six locations, each year by location was considered a single environment. The number of evaluated lines varied in each growing season. In 2021 and 2022, 559 and 534 lines were evaluated, with 162 lines shared in both years. Grain yield was predicted by utilizing single environment data through Genomic Best Linear Unbiased Predictor (GBlup), Bayesian Ridge Regression (BRR), Bayesian Lasso (BL), and Random Forest (RF). Under the five-fold cross-validation scheme, single environment prediction accuracy was represented by the average Pearson's correlation coefficient value, which ranged from 0.34 for 22BI to 0.74 for 21EI in the GBlup model. RF was significantly the lowest prediction model, while the other single environment models demonstrated nominally similar results. Predictions made across years or to unknown environments were proven to have lower accuracies ranging from 0.08 – 0.34 and -0.16 – 0.57. When utilizing a multi-environment model, 5-fold cross validation for each individual environment ranged from 0.83-0.98. Sparse testing schemes of predicting unknown genotypes in known environments showed accuracies ranging from 0.25 – 0.43. These results demonstrated that in wheat breeding, genomic prediction can be most effective in sparse testing or predicting partially damaged fields.

10) Utilizing Unmanned Aerial Systems to Evaluate the Temporal Effects of Drought on the Phenology of Winter Wheat Cultivars in the Texas Panhandle

Kylie Diaz, Brock Blaser, Guillermo Marcillo, West Texas A&M University, Canyon, Texas
Mahendra Bhandari, Jose Landivar Scott, Texas A&M AgriLife Research, Corpus Christi, Texas
Shannon Baker, Jason Baker, Jackie Rudd, Texas A&M AgriLife Research, Amarillo, Texas

Unmanned aerial system technology is challenging the boundaries of precision agriculture by providing a cost-effective means of capturing high-spatiotemporal data for wheat breeding nurseries. A 2-year field study was conducted in Bushland, TX from 2021-2022 to evaluate the temporal effects of drought on canopy growth of winter wheat. RGB and multispectral sensors were flown weekly over 40 winter wheat advanced breeding lines in irrigated and dryland environments. Geospatial data products were processed from raw UAS images and used to extract canopy characteristics (CC, CH, CV) and vegetations indices (NDVI, NDRE, ExG). Temporal trends in UAS indices represented four distinct physiological stages: stand establishment, canopy growth/tillering, anthesis/heading, and senescence; CH and CV followed a sigmoidal curve. Positive correlations were observed between ExG and NDRE with yield in the 2021 dryland environment ($R2 = 0.30$ and $R2 = 0.26$, $p = <0.01$), while in irrigated environments, CV ($R2 = 0.33$) and NDRE ($R2 = 0.36$) exhibited the strongest positive correlations with grain yield. UAS-based parameters demonstrated the highest correlation to grain yield around anthesis for both irrigated environments and slightly earlier in the season for the 2021 dryland environment. RGB sensors were found to be a proficient tool for monitoring plant health. Highest-yielding genotypes possessed a genetic propensity to put on biomass more quickly after winter dormancy. These same genotypes also had a delayed senescence, resulting in a longer grain-filling period, demonstrating the utility of temporal UAV data as a selection tool for breeding nurseries.

11) Identifying Leaf Rust Resistance and End-Use-Quality QTLs in a HRW Wheat Population

Luke G. Whiteley, Luke Whiteley, Amir Ibrahim, Shuyu Liu, Thomas Isakeit, Jackie C. Rudd, Texas A&M University, College Station, Texas and Texas A&M AgriLife Research, Amarillo, TX.

We seek to identify leaf rust (Puccinia triticina) resistance and end-use-quality quantitative trait loci (QTLs) in the T44 mapping population. The T44 population was derived from a cross between ‘TAM 114’ and ‘TAM 204’ and is composed of 244 recombinant inbred lines and 225 doubled haploid lines. This bi-parental population was grown in three locations: McGregor, Castroville, and Amarillo, Texas. The QTLs for major resistance genes to leaf rust will be identified using a field-scoring method where 0 will indicate a completely resistant phenotype, and 9 will indicate a fully susceptible phenotype. For end-use-quality, we will utilize four laboratory techniques to identify the main components that predict bread-making quality. Sodium dodecyl sulfate (SDS) sedimentation will be used to identify gluten strength and, thereby, dough strength. Single Kernel Characterization System (SKCS) will be used to evaluate kernel quality based on weight, diameter, hardness, moisture content, and class (hard, soft, mix). Near-Infrared Reflectance Method (NIR) will be utilized to determine the protein content of the recovered flour. Finally, the mixograph method will be employed to ascertain dough qualities related to mixing and bake absorption. Our final objective is to identify individuals within the T44 population that combine the elite agronomic, leaf rust resistance, and bread-making qualities of TAM 114 with the broad biotic resistance and superior forage performance of TAM 204 to produce exceptional grain-and-grazing lines.

12) Yield Predictions using High Throughput Phenotyping with UAS Platform

Russ Garetson, Amir Ibrahim, Mahendra Bhandari, Sorin Popescu, Jackie Rudd Texas A&M University, College Station, Texas

There has been a growing interest in using high throughput phenotyping to predict crop yields. High throughput phenotyping involves using advanced technologies such as remote sensing, unoccupied aerial vehicles (UAVs), and sensors to collect large amounts of data on crops quickly and efficiently. This data can then be analyzed using machine learning and other statistical techniques to predict yield and identify factors that influence crop performance. In the 2021-2022 season College Station and McGregor replicated wheat breeding blocks UVT, TXE, and SRPN were flown with a multispectral UAV and visible spectrum UAV. Vegetation indices and canopy attributes were calculated and analyzed using a neural network predictive model in JMP Pro 16. The training model and validation model for College Station were shown to have R2 of 0.7 and 0.55, respectively. In McGregor the training model and validation model have shown a R2 of 0.84 and 0.73, respectively. Therefore, using high throughput with UAS platform can lead to reliable yield predictions with significant potential to improve a breeding program efficiency and higher selection accuracy.

13) Exploring novel genetic alleles for improving wheat yield and quality using synthetic derived lines by genome wide association studies

Zhen Wang, Kyle Parker, Yahya Rauf, Smit Dhakal, Qingwu Xue, Jackie C. Rudd, Jason Baker, Shannon Baker, Shuyu Liu*, Texas A&M AgriLife Research, Amarillo, TX;
Amir M. H. Ibrahim, Dirk B. Hays, Department of Soil and Crop Sciences, Texas A&M University, College Station, TX;
Shuhao Yu, Department of Horticulture and Landscape Architecture, Oklahoma State University, Stillwater, OK;
Chenggen Chu, Northern crop science laboratory, USDA-ARS, Fargo, ND;
***Correspondence: Shuyu.Liu@ag.tamu.edu**

During the evolution of bread wheat (Triticum aestivum L.), genetic diversity was significantly reduced due to the polyploidization and domestication caused genetic bottleneck. As the artificial reproduction of that process, synthetic hexaploid wheat (SHW) built up the bridge for deriving the novel genetic variation from diploid and tetraploid wheat. In current study, two adapted Texas hard red winter wheat cultivars TAM 111 and TAM 112 were designated as recurrent parents and backcrossed with 21 SHWs to generate a set of 298 BC1F6 synthetic derived wheat lines (SDLs), and then evaluated in nine environments across Texas high plains for 35 traits including yield, end-use quality, kernel, and other agronomic traits. A set of 10,7653 single-nucleotide-polymorphisms (SNPs) from Genotyping-by-sequencing (GBS) were used for genome-wide-association studies (GWAS) and genomic predictions. GWAS identified 767 consistent QTLs on all 21 wheat chromosomes and several QTLs were colocalized with known genes such as Gli-B1, Glu-D1, and Pina/b. Novel QTLs were identified on chromosome 2B at 58 Mb, 4A at 670 Mb, 4B at 66 Mb and 211 Mb, 5A at 534 Mb, and 7D at 46 Mb, with increasing alleles from SHWs for kernel weight and size, spike and tiller weight, and plant height, while increasing alleles for yield, spike number, harvest index, and quality traits were from adapted cultivars. Linkage disequilibrium (LD) analysis determined three candidate genes within the selected major QTLs on 2B at 58Mb and on 4A at 666 Mb for kernel weight, and on 4B at 72 Mb for yield, plant height, and spike weight. Genomic prediction using G-BLUP model showed prediction accuracy varied significantly for different traits, and up to 0.60 and 0.48 under within and across population scenario, which suggested significant environment influence on prediction accuracy. Results from current study provided comprehensive understanding on the genetic resources in SHW, which will facilitate the gene cloning and functional characterization, marker-assisted selection, gene pool enrichment and breeding application.

14) Characterizing novel resistance alleles using synthetic hexaploid wheat and synthetic derived wheat by genome wide association studies

Zhen Wang, Kyle Parker, Yahya Rauf, Smit Dhakal, Qingwu Xue, Jackie C. Rudd, Jason Baker, Shannon Baker, Shuyu Liu*, Texas A&M AgriLife Research, Amarillo, TX;
Amir M. H. Ibrahim, Dirk B. Hays, Department of Soil and Crop Sciences, Texas A&M University, College Station, TX;
Shuhao Yu, Department of Horticulture and Landscape Architecture, Oklahoma State University, Stillwater, OK;
Chenggen Chu, Northern crop science laboratory, USDA-ARS, Fargo, ND;
***Correspondence: Shuyu.Liu@ag.tamu.edu**

Bread wheat (Triticum aestivum L.) is one of the most important cereal crops that closely related to the food security. However, wheat production in the United States was seriously threated by the biotic stresses from arthropods such as greenbug (GB), Hessian fly (HF), and wheat curl mite (WCM). Genes cause host plant resistance are able to efficiently protect wheat from the virulence of arthropods and synthetic hexaploid wheat (SHW) is a major genetic resource carries novel genes for arthropods resistance. To characterize the underlying genetic composition, a panel of 209 SHWs and 298 synthetic derived lines (SDLs) were evaluated for GB, HF, and WCM resistance and genotyped using genotyping-by-sequencing (GBS) for genome-wide association studies (GWAS). The GB associated QTL on 7D at 599.8 Mb known for resistance gene Gb3 was detected in both SDLs and SHWs. Two HF associated QTLs on 3D at 569.7 – 578.5 Mb known for H24/H26/H32 was only detected in SDLs. Linkage disequilibrium (LD) analysis determined the deletion of RGA4 in Ae.tauschii is a potential causation for the resistance of Gb3 and a gene annotated for leucine-rich repeat receptor-like serine/threonine-protein kinase was determined as the candidate gene of the 3D QTL for HF. Moreover, a set of five, four, and one novel QTLs for GB, HF, and WCM were detected in SHWs. Novel QTLs for GB on 5D at 79.7 Mb, for HF on 5D at 540.8 Mb, and for WCM on 3D at 5.4 Mb each explained phenotypic variation up to 37.6 %, 25.3%, and 10.3%, respectively. The results from current study paved way for diagnostic marker development and gene cloning, which will further facilitate the high-efficient utilization of SHWs in the development of resistant wheat germplasms.

2. Postdoc poser abstracts (Page 18-21)

15) Plant traits to increase wheat yield under dryland conditions in the Texas High Plains

Andrea Leiva Soto[1], Qingwu Xue[1], Xuejun Dong[2], Shuyu Liu[1], Jackie C. Rudd[1], Amir M. H. Ibrahim[3], Kirk Jessup[1], Jason Baker[1], Shannon Baker[1]
[1] Texas A&M AgriLife Research and Extension Center, Amarillo, Texas
[2] Texas A&M AgriLife Research and Extension Center, Uvalde, Texas
[3] Department of Soil and Crop Sciences, Texas A&M University, College Station, Texas

Drought is the main constraint for agriculture in the Texas High Plains and is the leading cause of decreases in wheat yield. Thus, selecting wheat (*Triticum aestivum* L.) varieties with increased drought tolerance under dryland conditions is key. The objective of this study was to investigate the plant traits reflecting improvements in yield performance in dryland wheat. A long-term field experiment has been conducted in 16-20 genotypes under dryland conditions at Bushland, Texas. The present study analyzed the data from 2019/2020 growing season under extreme drought conditions. The experiment followed a randomized complete block design with 3 replications. Measurements included plant height, percent greenness, leaf rolling score, leaf dry matter content (LDMC), specific leaf area (SLA), stem, head, and total biomass at anthesis and maturity, number of spikes, seeds per spike, 1000-kernel weight (TKM), and harvest index (HI). Wheat yield was linearly and positively related to plant greenness, spike weight at maturity, seeds per spike, and HI. Similarly, plant greenness was positively related to seeds per spike and HI. In contrast, leaf rolling score measured during grain filling was linearly and negatively related to yield, seeds per spike, HI, and plant greenness. The findings of this study showed that newer varieties had higher yields, better plant greenness during grain filling, more seeds per spike, and lower leaf rolling scores. Plant greenness and leaf rolling score may be important traits to screen drought tolerance for the Texas High Plains.

16) Intensifying Dryland Wheat Systems with Guar in the U.S. Southern Great Plains Increased Production and Profitability

Rajan Shrestha, Texas A&M University, Department of Soil & Crop Sciences, College Station, TX
Curtis B. Adams, Texas A&M AgriLife Research, Research and Extension, Vernon, TX
Francisco Abello, Texas A&M AgriLife Extension Service, 7101 TAMU College Station, TX
Paul B. DeLaune, Texas A&M AgriLife Research, Research and Extension, Vernon, TX
Calvin Trostle, Texas A&M AgriLife Extension Service, 7101 TAMU College Station, TX
Nithya Rajan, Texas A&M University, Department of Soil & Crop Sciences, College Station, TX
Srinivasulu Ale, Texas A&M AgriLife Research, Research and Extension, Vernon, TX

Waltram Ravelombola, Texas A&M AgriLife Research, Research and Extension, Vernon, TX

Guar [Cyamopsis tetragonoloba (L.) Taub.], is a summer legume with heat- and drought-tolerance properties, that is produced in the U.S. Southern Great Plains but is often restricted to a catch crop or substitute crop following cotton failures. This is despite the large domestic market for guar gum and the opportunity to diversify regional cropping systems with guar. To address this, a systems research study (2018-2021) was conducted near Chillicothe, TX to evaluate the integration of guar into no-till dryland winter wheat (Triticum aestivum L.) systems. Treatments included integrated wheat-guar systems: WG1.3; 1.33 crops yr-1 and WG2; 2 crops yr-1, including guar (G1) and wheat (W1) monocrop systems. Results showed that crop rotation sequence was critical in determining seasonal guar yields, with negative yield impacts on guar immediately following wheat. The average seasonal guar yield was greatest in G1 and WG1.3 (1.01 and 0.96 Mg ha-1, respectively), followed by WG2 (0.64 Mg ha-1). Seasonal wheat yield averaged 2.31 Mg ha-1 across years, with no differences among systems. Cumulative system yield was greatest for WG2 <W1/WG1.3 <G1. Similarly, average annual net income was as follows: G1 < W1 < WG1.3 < WG2, which ranged from US$ 62.7 - 213.0 ha-1 year-1. Although overall production and net income were somewhat greater for WG2 than WG1.3, seasonal risks of crop failure were lower for the WG1.3 system under the regional climate. Soil analysis showed that guar enhanced soil NO3-N at varying levels among systems, particularly following wet seasons and in less intensive systems.

17) Host plant resistance alters virus titer in source plants and vectors

Saurabh Gautam, Entomology Department, Texas A&M AgriLife Research, 6500 W Amarillo Blvd, Amarillo, TX 79106
Senthilraja Chinnaiah, Entomology Department, Texas A&M AgriLife Research, 6500 W Amarillo Blvd, Amarillo, TX 79106
Fekede Workneh, Plant Pathology Department, Texas A&M AgriLife Research, 6500 W Amarillo Blvd, Amarillo, TX 79106
Charles Rush, Plant Pathology Department, Texas A&M AgriLife Research, 6500 W Amarillo Blvd, Amarillo, TX 79106,
Kiran R. Gadhave, Entomology Department, Texas A&M AgriLife Research, 6500 W Amarillo Blvd, Amarillo, TX 79106

Wheat streak mosaic (WSM) is caused by the Wheat streak mosaic virus (WSMV) and Tricticum mosic virus (TriMV), both of which are transmitted by the wheat curl mite (WC). Management of the disease has primarily focused on an integrated pest management approach that combines host plant resistance with cultural practice. However, limited knowledge is available on the effects of resistant wheat cultivars on disease epidemics and the WSMV and TriMV ratio in infected plants and mites. To study both aspects, we conducted field studies with three wheat cultivars i.e., TAM 304 (susceptible), Joe (resistant, Wsm2 gene), and Breakthrough (resistant, Wsm1 gene) at Texas A&M AgriLife Research, Bushland. The experimental field was planted to the cultivar panel in three replications. After initial symptoms developed plants and mites were sampled to determine the ratios of WSMV and TriMV titers as a baseline. As disease started to develop on the field edges, sampling of plants and mites was done weekly until the end of the

season. Samples were tested by qPCR to quantify the titer ratios of viruses and compared with the baseline data. Data showed both genes restricted WSM spread in the field. Also, both genes significantly lowered the WSMV accumulation in infected plants and mites feeding on them. However, similar trends were not observed for TriMV. Taken together our data suggests that HPR worked against only one component (WSMV) of WSM. Therefore, it is very likely that TriMV may become a dominant virus in the WSM disease complex.

18) Genome-wide Association for Seed Traits and Biomass in Wheat Doubled Haploid Lines

Yahya Rauf1, Kyle Parker1,2, Zhen Wang1,2, Jackie C. Rudd1, Qingwu Xue1, Amir M. H. Ibrahim2, Jason Baker1, Shannon Baker1, Shuyu Liu1*
1Texas A&M AgriLife Research and Extension Center, Amarillo, TX
2Department of Soil and Crop Sciences, Texas A&M University, College Station, TX
***Correspondence: Shuyu.Liu@ag.tamu.edu**

Genetic improvement in wheat yield is the most focused research area for breeding community to ensure food security and sustainable production. Biomass and grain traits are considered key contributors to enhance crop yield. A set of 264 doubled haploid (DH) lines mainly derived from TAM 114 and TAM 204 were developed at the AgriLife Research Center in Amarillo, which mostly carried widely adopted and improved cultivars in their pedigree from the Southern Great Plains. Lines were evaluated in two field environments (Bushland-irrigated & Bushland-dryland) planted in alpha lattice design during the 2020 crop season. Seed traits including seed length, width, area, perimeter, and 1000 Kernel weight were collected using the SeedScan G4010. We used genotyping-by-sequencing (GBS) as a genotyping platform for the DH lines. The genomic libraries were sequenced on Illumina NovaSeq to generate paired end reads of 150 bp. For single nucleotide polymorphism (SNP) calling, sequences were aligned to the IWGSC RefSeq genome assembly v2.1 using the Burrows Wheeler Aligner. The SNP filtration was performed at 50% missing data and 5% minor allele frequency. Finally, a set of 595,456 polymorphic markers were retained for genetic analysis. To investigate the marker trait association and the genomic regions, genome-wide-association study (GWAS) analysis was conducted in GAPIT. Three SNP makers in chromosomes 1A, 2B, and 4B were significantly associated with at least two traits while two SNP markers on chromosomes 2A and 2B were associated with three or more traits. The significant marker trait associations might be representing some known/major genes which need further confirmation.

19) Exploring Novel Alleles in Synthetic and Synthetic Derived Wheat Lines for Rust Resistance

Yahya Rauf, Zhen Wang, Shuhao Yu, Kyle Parker, Jackie C. Rudd, Qignwu Xue, Shuyu Liu*, Texas A&M AgriLife Research and Extension Center, Amarillo, TX;
Amir M. H. Ibrahim, Department of Soil and Crop Sciences, Texas A&M University, College Station, TX;
Yue Jin, USDA-ARS, Cereal Disease Lab, Saint Paul, MN
***Correspondence: Shuyu.Liu@ag.tamu.edu**

Wheat rusts are air-borne fungal pathogens causing huge economic losses around the world. The rapid evolution and especially recently evolved highly aggressive races adopted to higher temperature in Europe, Africa, Middle East, and Asia have quickly overcome several resistance genes in the adopted cultivars. The narrow basis of rust resistance in modern cultivars emphasizes the need for identifying new sources of resistance in wheat wild relatives. This study used two association mapping panels; a set of 209 synthetic hexaploid lines (SHL) developed by the wheat wide crosses program at CIMMYT and 298 BC1F2:7 synthetic derived lines (SDL) involving 21 SHL and two well adopted cultivars (TAM 111 & TAM 112) from the Southern Great Plains. Both populations were genotyped using genotyping-by-sequencing (GBS) and the genomic libraries were sequenced on Illumina Hiseq 2500 to generate paired end reads. The SHL panel was evaluated for stem rust (SR) seedling resistance against three races, while SDL panel was screened in two environments each for leaf (LR) and stripe rust (YR) in the Texas nurseries. Genomic analysis was conducted to find out the marker-trait associations using four models (Blink, FarmCPU, MLM, MLMM) in Genome Association and Prediction Integrated Tool. Preliminary results suggested that SDL panel has 13 and 17 significant markers associated with LR and YR resistance, respectively. Based on single race assays for SR, we postulate that SHL panel harbors Sr13 gene conferring resistance against TTKTT (Sr31, Sr24, and SrTmp virulence) and some other unique sources of resistance.

3. Other abstracts

20) Physiological Mechanisms for Improving Drought Tolerance and Water Use Efficiency in Winter Wheat

Qingwu Xue1, Shuyu Liu1, Jackie C. Rudd1, Amir M. H. Ibrahim2, Kirk Jessup1, Jason Baker1, Shannon Baker1

1 Texas A&M AgriLife Research and Extension Center, Amarillo, Texas, USA
2 Department of Soil and Crop Sciences, Texas A&M University, College Station, Texas, USA

Hard red winter wheat is a major food crop in the US Southern Great Plains. Due to the semi-arid climate with highly variable annual precipitation, drought is the most common stress for reducing wheat yield and water use efficiency (WUE). We have conducted field studies at Bushland, TX since 2010. The objectives are (1) understand physiological mechanisms for improved drought tolerance; (2) identify plant traits conferring drought tolerance; (3) develop phenotyping tools for screening drought tolerance in the field. Each year, 20 hard red winter wheat genotypes were grown under both dryland and irrigated conditions. The genotypes include a historic check cultivar, new released cultivars, and advanced experimental lines. Wheat yield varied significantly among the years under water-limited conditions. For dryland wheat, higher yield and WUE are generally associated with greater soil water storage at planting and as well growing season precipitation. The newer cultivars or more drought tolerant genotypes had greater biomass at anthesis, more seeds per spike and higher 1000-kernel weight under drought. In addition, new drought tolerant cultivars were able to extract more water from deeper soil profile (particularly between jointing and maturity) and maintained cooler canopy temperature than drought susceptible ones. Remobilization of stem carbon reserves also contributed to yield under dryland conditions. We have evaluated different sensors and platforms for field

phenotyping. The Unmanned Aerial System (UAS) based platform showed more promise for high-throughput phenotyping under field conditions.