TEXAS A&M PLANT BREEDING BULLETIN

October 2019

TEXAS A&M UNIVERSITY--EDUCATING AND DEVELOPING PLANT BREEDERS WORLDWIDE TO ALLEVIATE HUNGER AND POVERTY THROUGH GENETIC IMPROVEMENT OF PLANTS

The plant breeding program in Soil and Crop Sciences graduated seven students in August, 2019; four PhD and three MS students. These students conducted original research across corn, cotton, rice, wheat, and sorghum. All performed exceptionally well during their collegiate careers. We wish these young scientists well in their continued academic careers or their professional careers and look forward to their successes.

Steven Anderson II: Ph.D. directed by Dr. Seth Murray

Title: Implementing unmanned aerial systems within a field-based maize (*Zea mays* L.) breeding program: Improving yield prediction and understanding temporal QTL expression of plant height

Abstract: Unmanned aerial system (UAS) technologies are becoming common place within field-based agriculture programs allowing breeders to evaluate greater numbers of genotypes, reducing resource inputs and maintaining unbiased data collection. A comprehensive evaluation was conducted focused on the implementation of UAS technologies within a field-based maize breeding program using the plant height phenotype as a proof of concept in implementation and validation. A robust data processing pipeline was developed to extract height measurements from RGB structure from motion (SfM) point clouds. The 95th percentile (P95) height estimates exceeded 70% correlation to manual ground truth
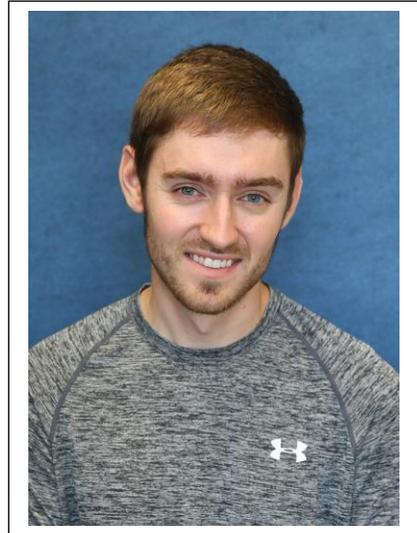
measurements across diverse germplasm groups of hybrid (F_1) and inbred lines. Sigmoidal functions were developed to model the overall growth and trajectory of hybrids (R^2: >98%; RMSE: < 14 cm) and inbreds (R^2: >99%; RMSE: < 4 cm). UAS-based height estimates demonstrated greater capacity to partition phenotypic variance to genetic components compared to manual measurements; function growth parameters (asymptote, inflection point, and growth rate) were explained by more than 70% of variance with genetics for the hybrid trials. UAS height estimates improved correlations to hybrid grain yield >1.5-fold similar to functional growth parameters. A ~4-fold improvement in indirect selection of hybrid grain yield was achieved using functional growth parameters compared to conventional manual terminal plant height (PHT_{TRML}). We expanded our implementation of UAS phenotyping to evaluate three inbred line mapping populations aimed at studying functional QTL and temporal QTL expression. Functional growth parameters identified 34 associations explaining 3 to 15% of the genetic variation. Height was estimated at one-day intervals to 85 days after sowing using the Weibull function, identifying 58 unique temporal peak QTL locations. Temporal QTL demonstrated all of the identified significant QTL had dynamic expression patterns. Consistent directions of additive effects were identified for the majority of QTL, although interval mapping of the entire linkage map demonstrated that directional changes in additive effect size are present throughout the growing season and throughout the genome. In all, UAS technologies improved phenotypic selection accuracy and have capacity to monitor traits on a temporal scale furthering our understanding of crop development and biological trajectories.

Tyler Foster: M.S. directed by Dr. Russell Jessup

Title: Development of novel perennial sorghum germplasm: Induced polyploidization and hybridization of *S. Bicolor* x *S. propinquum*

Abstract: Plant polyploidization can provide valuable, novel phenotypes. In *Sorghum*, induced polyploidization is possible and relatively inexpensive. However, efficiency remains low and a consensus "best" method has yet to be determined. Some *Sorghum* species provide a unique opportunity to develop perennial cropping systems due to their interspecific hybridization compatibility

and phenotypic plasticity from annual to perennial life cycle. Due to their relatively close taxonomic relationship, *Sorghum bicolor* (L.) Moench x *S. propinquum* (Kunth) Hitchc. offer both valuable insights between annuals and perennials, as well as hybridization opportunities for the introgression of perenniality into a major cereal crop. Hybridization between these species also has potential to introgress other desirable alleles that have been lost through the domestication of *S. bicolor*. Our research identified transgressive segregation for height in a *Sorghum bicolor* x *S. propinquum* F_2 population. Perennial *Sorghum* hybrids (PSH) also were intermediate for days to maturity and tillering capacity; when compared to both parents. Experimental units overwintered through harsh winter conditions which allowed a stronger selection criterion for overwintering capacity than previous studies. Unfortunately, our novel method for inducing ploidy levels in *Sorghum* were unsuccessful. Thus, more research is still needed to improve this methodology. This thesis addresses induced polyploidy, wide hybridization, and perenniality in the genus *Sorghum* with the purpose of developing novel germplasm suitable for perennial cropping systems.

David Horne: Ph.D. directed by Dr. William Rooney
Title: Implementation of genomic and phenomic tools for introgression of reinstated sorghum conversion (RSC) germplasm

Abstract: Genotypic variance is necessary for trait improvement as limited diversity can reduce genetic gain in crop improvement. To maintain genetic diversity, a wealth of germplasm exists in the USDA-ARS sorghum [*Sorghum bicolor* (L.) Moench] collection, but most of the accessions are not adapted to temperate climates. Methodologies aimed at incorporating tropical germplasm have been evaluated extensively by public and private breeding programs due to their

beneficial alleles for improved agronomic performance. However, concerns as to how and when material from this program should be tested for its agronomic value have been expressed. Three different methodologies were conducted to assess partially converted, early-generation lines from the Reinstated Sorghum Conversion (RSC) program. Our first methodology was to investigate the utility of using markers for the identification of high levels of tropical genome recovery, while elucidating the relationship between marker data and agronomic performance. The utilization of markers to predict hybrid performance was not observed, nonetheless, the ability to prescreen lines with high amounts of tropical genome recovery proved useful. Expanding upon these results, the second methodology focused on the phenotypic evaluation of partially converted, early-generation lines. From the lines evaluated, I was able to release lines that combined agronomic productivity with greater genetic diversity as confirmed via genotyping-by-sequencing. These eleven parental germplasms are being released to provide new genetic diversity for forage and grain hybrid improvement programs. Finally, noticing the value of phenotypic observations and its implications on selecting valuable germplasm, I further investigated plant height using high-throughput phenotyping via unmanned aerial systems (UAS). Within both advanced and early generation sorghum trials, genotypic variation estimates were comparable to manual measurements with highly repeatable estimates of plant height, indicating the value of UAS in plant breeding programs.

Yuya Liang: Ph.D. directed by Dr. Endang Septiningsih

Title: Genetics and genomic studies for water-related stresses in rice (*Oryza sativa* L.)

Abstract: Rice is one of the most important crops that feeds more than half of the world's population. Along with the escalating problems with climate change, drought and submergence events have increased in recent years and have challenged the sustainability of rice production. This dissertation focused on these two water-related stresses, and studied the tolerance mechanisms underlying. Reproductive stage is the most water-sensitive period for rice cultivation, therefore the study was conducted to investigate the molecular and physiological responses of two rice genotypes, 'Rondo' and '4610', to drought stress during the reproductive stage under field conditions. Leaf samples were collected for RNA-Seq. Additionally, 10 agronomic traits and chlorophyll fluorescence were measured. The results showed that 4610 had better performance than Rondo under moderate drought stress conditions. The results indicated that 4610 had more stress responsive GO terms and several known genes families related to

drought stress were also identified in 4610 up-regulated DEGs, including the LEA proteins, HSPs, APXs, and GSTs. The second goal was to characterize the region of *qSub8.1*, a new submergence tolerance QTL during the vegetative stage of growth, which will enable us to develop suitable DNA markers and identify the gene(s) underlying *qSub8.1* for further functional characterization. Three rice varieties, Ciherang-Sub1, Ciherang, and IR64-Sub1, were sequenced with 150 bp pair-end WGS. The results showed that Ciherang-Sub1 genome is composed of 59% Ciherang, 24% of IR64-Sub1, and 17% of unknown sources; and the *qSub8* region is mainly from Ciherang with a few introgressed segments from IR64-Sub1 and unknown sources. There are challenges in conducting plant transformation and regeneration required to introduce the CRISPR reagents into the plant cell for gene-editing. Here, we used mature seeds as explants and reported a high-efficiency transformation and regeneration protocol for a recalcitrant *indica* rice cultivar Ciherang-Sub1 using article bombardment to deliver the CRISPR/Cas9 gene-editing vector. Our protocol successfully

gives an optimal condition for shoot regeneration with a 95% of regeneration rate and a 100% rate for root regeneration. Using this protocol, CRISPR gene-edited plants can be generated and validated within 12 weeks.

Fatma Betul Sade: M.S. directed by Dr. Amir Ibrahim
Title: Genotyype-by-floral characteristics interaction for hybrid wheat (*Triticum aestivum* L.) production in Texas

Abstract: The demand for agricultural and natural recourses is rising due to population growth. Hybrid technology is an effective way to increase yield potential and production of wheat (*Triticum aestivum* L.) to meet the demand of 9.7 billion people in 2050. Self-pollinated crops are challenging due to high seed production cost and the need to force them to behave as a cross-pollinated crop. Therefore, a compromise between heterosis and floral suitability often needs to be reached in hybrid wheat production. Recently, the interest in hybrid wheat has been renewed because of higher wheat prices, climate change, new technological developments in next-generation sequencing, and capability of predicting heterosis at the molecular level. In addition, the performance potential of hybrids increased due to more focused studies on wheat flower biology. It is apparent that the redesign of floral characteristics is a prerequisite for hybrid wheat breeding to achieve high outcrossing ability. Therefore, the purpose of this research was to 1) screen the Uniform Variety Trial (UVT) and Texas Elite (TXE) lines for desirable floral characteristics, and 2) characterize the best male and female candidates for inclusion in the Texas A&M AgriLife hybrid wheat crossing blocks. The lines were screened for floral characteristics such as days to heading, days to anthesis, anther extrusion, anther score, stigma exsertion, gape, and plant height in College Station and McGregor, TX for two years. The results of combined environment
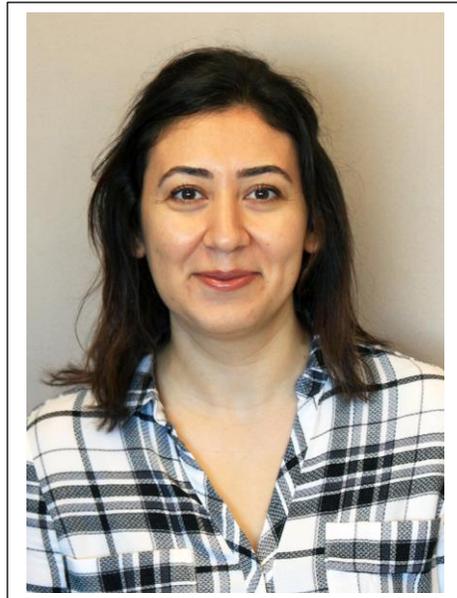
analyses indicated that genotypic variances were significantly different for all floral characteristics. Non-gender and male traits had high heritability estimates. The heritability of anther extrusion ranged from 0.82 to 0.87. The non-gender and male traits exhibited highly reliable genotypic coefficient of variance (GCV), while female traits had low GCV levels. The correlation between days to heading and anthesis; anther score and anther extrusion; as well as stigma exsertion and gape were positive and significant. The lines were screened for Rht-B1 and Rht-D1 height reduction genes. Five of the UVT lines had Rht-B1a/ Rht-D1b and only one of the TXE lines had it. The rest of the lines had Rht-B1b/ Rht-D1a genes.

Ranjita Thapa: Ph.D. directed by Drs. Endang Septiningsih and Michael Thomson

Title: Genome-wide association and expression studies for identification of QTLs and candidate genes underlying abiotic stress tolerance during germination state in rice

Abstract: Rice is one of the most important cereal crops feeding more than half of the world's population. Due to extreme climatic condition, different abiotic stresses like hypoxia stress and chilling stress have been the biggest threat to rice production. Direct sowing method is the most preferred way of planting in Asian countries and in the U.S. due to the lower cost of planting and less labor requirement. The major challenge associated with direct sowing is flash flooding that can happen immediately after sowing due to unpredicted rainfall. In this study, we evaluated more than 250 rice accessions belonging to different groups of rice for various traits related to chilling tolerance and hypoxia tolerance during the germination stage. Compressed Mixed Linear Model (CMLM) of GAPIT was used to conduct GWAS analysis for the identification of QTLs. From the GWAS study

conducted for chilling stress tolerance, we identified 41 QTLs associated with different chilling indices like low temperature germinability, germination index, coleoptile growth under cold condition, plumule length at 4 d recovery, and plumule growth rate after cold germination. Of 41 QTLs identified in the whole panel, 14 QTLs were potentially colocalized with known genes/QTLs and 27 QTLs were found to be novel. From the GWAS analysis of hypoxia stress tolerance traits, there were 24 significant SNPs identified to be associated with different traits measured under hypoxia stress. Out of the 24 significant SNPs discovered in the whole panel, 11 QTLs were found to be potentially colocalized with previously identified candidate genes underlying flooding tolerance mechanism in rice. From the phenotypic evaluation of the whole panel for chilling stress tolerance and hypoxia stress tolerance, two lines with contrasting phenotypes under each stress condition were selected and used for global gene expression analysis. The results of these transcriptomics studies have provided new insights of underlying biological processes, molecular functions and cellular components related to the phenotypic differences of the contrasting lines. The findings of our study will help in identification of promising candidate genes underlying hypoxia stress and chilling stress tolerance and will eventually assist rice breeding program to develop improved tolerant rice cultivars.

Wenzhuo Wu: M.S. directed by Dr. Steve Hague

Title: High-throughput phenotyping that improves the efficiency of a cotton plant breeding system

Abstract: Unmanned Aerial Vehicles (UAVs) play an important role in agricultural research because they facilitate high-throughput phenotyping (HTP). Cotton (*Gossypium spp.*) is the world's leading natural textile fiber crop, and breeding programs that enhance the efficiency of growing the crop are important to the viability of the cotton industry. The effectiveness of plant breeding programs is improved when researchers have the ability to quickly evaluate important traits in a field environment. The ability to identify cotton plant height and boll count across a field an serve as an important tool in predicting plant growth and yield. In order to capture a three-

dimensional (3D) view of field plots, which is believed to be helpful in estimating yield and crop development parameters, sensors mounted on UAVs must have access to a view of the ground. However, cotton planted in solid rows can obscure this view. Canopy closure prevents sensors from measuring plant architecture and boll-loads three dimensionally from the mid-growing season until the crop is defoliated. Therefore, this project was initiated to compare solid vs. skip-row planting patterns in terms of predicting yield and fiber quality since skip rows would allow UAV sensors to capture more ccurate 3D data from plots. The purposes of this project were to (1) use UAVs to characterize genotype x row pattern interaction and how location and year affect that interaction, (2) evaluate the ability of UAVs to predict plant height and yield, (3) compare the accuracy of UAV-derived data from different planting patterns and (4) use images processed from UAVs to standardize data for every single row to predict yield performance. Two UAVs were used for red, green, and blue (RGB) data collection and multispectral data collection. Five cotton genotypes were grown in a skip versus solid row-pattern at Weslaco, College Station and Corpus Christi in 2017 and 2018. Yield and fiber qualities were measured for all treatments. UAVs were flown across the field bi-weekly to estimate plant height, canopy cover, canopy volume, vegetation indices, open boll count and boll area over different growing stages. Without extreme weather influence, lint yield and fiber quality were not affected by Genotype X row-spacing effects. Also, year and location did not influence that interaction. In addition, yield and plant height estimations were improved when cotton was planted in a skip-row pattern. Single row rating based on orthomosaic images and 3D point cloud images correlated with yield performance. Therefore, to take full advantage of UAV data, cotton breeding programs need to plant early generation lines (progeny rows) in skip rows that allow sensors to have access to the view of the ground and capture 3D images. This can be accomplished without compromising the efficiency and accuracy of the breeding program.

Publications by Soil & Crop Sciences Plant Breeding Faculty

Third Quarter, 2019

Cason & Rooney: J.M. Cason, C.E. Simpson, W. L. Rooney, and J. A. Brady. 2019. First Report of Successful Hybridization Between *Arachis vallsii* and *Arachis dardani*. *Agrosystems, Geosciences & Environment* 2:190013.

Chandra: Manuel Chavarria, Benjamin Wherley, James Thomas, Ambika Chandra, and Paul Raymer. 2019. Salinity Tolerance and Recovery Attributes of Warm-season Turfgrass Cultivars. *American Society for Horticultural Science 54:9.*

Ibrahim & Rudd: Bin Peng, Xuejun Dong, Qingwu Xue, Clark B. Neely, Thomas Marek, Amir M. H. Ibrahim, Guorong Zhang, Daniel I. Leskovar, Jackie C. Rudd. 2019. Root morphological traits of winter wheat under contrasting environments. *Journal of Agronomy and Crop Science* https://doi.org/10.1111/jac.12360

Ibrahim & Rudd: Jackie C. Rudd, Ravindra N. Devkota, Amir M. Ibrahim, Jason A. Baker, Shannon Baker, Russell Sutton, Bryan Simoneaux, Geraldine Opena, Daniel Hathcoat, Joseph M. Awika, Lloyd R. Nelson, Shuyu Liu, Qingwu Xue, Brent Bean, Clark B. Neely, Robert W. Duncan, Brad W. Seabourn, Robert L Bowden, Yue Jin, Ming-Shun Chen, and Robert A. Graybosch. 2019. 'TAM 204' Wheat, Adapted to Grazing, Grain, and Graze-out Production Systems in the Southern High Plains. *Journal of Plant Registrations* doi:10.3198/jpr2018.12.0080crc.

Murray: Steven L. Anderson II, Seth C. Murray, Lonesome Malabo, Colby Ratcliff, Sorin Popescu, Dale Cope, Anjin Chang, Jinha Jung, and J. Alex Thomasson. 2019. Prediction of Maize Grain Yield before Maturity Using Improved Temporal Height Estimates of Unmanned Aerial Systems. *The Plant Phenome Journal* 2:190004.

Murray: Robert J. Arnold, Alejandra Ochoa, Chris R. Kerth, Rhonda K. Miller, and Seth C. Murray. 2019. Assessing the impact of corn variety and Texas terrior on flavor and alcohol yield in new-make bourbon whiskey. *PLOS* https://doi.org/10.1371/journal.pone.0220787

Rathore: Steffen Hagenbucher, Michael Eisenring, Michael Meissle, Keerti S. Rathore and Jörg Romeis. 2019. Constitutive and induced insect resistance in RNAi-mediated ultra-low gossypol cottonseed cotton. *BMC Plant Biology* 19:322.

Rathore: Yves Carrière, Alex J. Yelich, Ben A. Begain, Virginia S. Harpold, Gopalan C. Unnithan, Jae H. Kim, Lolita G. Mathew, Graham P. Head, Keerti S. Rathore, Jeffrey A. Fabrick, and Briuce E. Tabashnik. 2019. Gossypol in cottonseed increases the fitness cost of resistance to Bt cotton in pink bollworm. *Crop Protection* https://doi.org/10.1016/j.cropro.2019.104914

Rooney: Ulises Aranda-Lara Alfonso López-Benítez, Antonio Flores-Naveda, Víctor M. Zamora-Villa, Luis A. Rodríguez-del-Bosque, W.L. Rooney. 2019. Susceptibility of Sorghum Hybrids to the Sugarcane Aphid, *Melanaphis sacchari*, in Central Mexico. *Southwestern Entomologist* 44(3): 771-774.

Septiningsih: Yoichiro Kato, Bertrand C. Y. Collard, Endang M. Septiningsih, and Abdelbagi M. Ismail. 2019. Increasing flood tolerance in rice: combining tolerance of submergence and of stagnant flooding. *Annals of Botany* mcz118, https://doi.org/10.1093/aob/mcz118

Septiningsih: Sharmistha Ghosal, Carlos Casal Jr., Fergie Ann Quilloy, Endang M. Septiningsih, Merlyn S. Mendioro, and Shalabh Dixit. 2019.

Deciphering Genetics Underlying Stable Anaerobic Germination in Rice: Phenotyping, QTL Identification and Interaction Analysis. *Rice* 12:50.

Meetings of Interest

American Society of Agronomy-Crop Science Society of America-Soil Science Society of America will hold their annual meeting November 10 – 13, 2019 in San Antonio, Texas. More information available at https://www.acsmeetings.org/.

National Association of Plant Breeders, NAPB will hold their annual meeting at the University of Nebraska, August 16-19, 2020. More information will be available soon at https://www.plantbreeding.org.

Distance Plant Breeding at Texas A&M Graduate Degrees

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Please direct comments concerning this bulletin to Wayne Smith, cwsmith@tamu.edu or 979.845.3450.

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For more information visit https://scsdistance.tamu.edu/ or contact LeAnn Hague, Distance Education Coordinator in Soil and Crop Sciences at leann.hague@tamu.edu or (979) 845-6148.