

TEXAS A&M PLANT BREEDING BULLETIN

January 2018

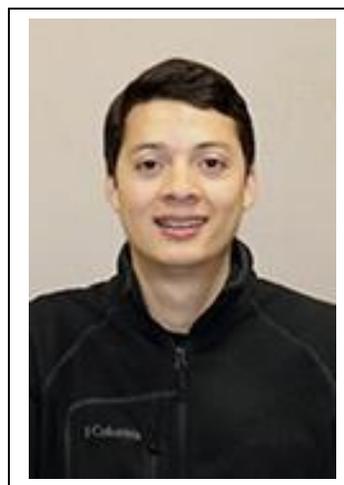
**TEXAS A&M UNIVERSITY--EDUCATING AND DEVELOPING PLANT BREEDERS
WORLDWIDE TO ALLEVIATE HUNGER AND POVERTY THROUGH GENETIC
IMPROVEMENT OF PLANTS**

The Department of Soil and Crop Sciences graduated three distance plant breeding students in Fall 2017 and we highlighted those students last month. This month, I want to highlight the six on-campus graduate students who received advanced degrees in plant breeding last month. After reviewing their abstracts I think that you will agree that these folks will make an impact in the world of plant breeding.

Francisco Gomez

Ph.D. dissertation title: QTL mapping of stem biomechanical traits and precision phenotyping in bioenergy sorghum. (Chair: William Rooney)

Abstract: Mechanical characterization is an important and now frequently used tool for phenotyping plants for crop improvement, e.g. lodging resistance. Mechanics of materials and structures in response to various external stimuli as well as information of basic building blocks that constitute the plants can be applied to study the Mechanical behavior of plant stems. The inherent mechanical properties of plant structures such as the stem are relevant to breeding strategies, aiming to tackle issues such as crop lodging due to stem or root lodging. While empirical tests of breaking strength and stiffness have been applied to plants, few of these studies consider the genetic background of the plants examined. In this study, we report for the first time on the mapping of QTL for mechanical traits in sorghum in three RIL mapping populations



from crosses between grain and sweet sorghum parents. The genetic architecture of biomechanical traits in the three RIL populations appear to be quantitative and pleiotropic. Six QTL affecting mechanical and morphological traits were detected; two of these QTL were consistently found in all populations and co-localized with previously cloned dwarfing genes *Dw1* and *Dw3*. These results suggest that dwarfing genes affect the mechanical properties of sorghum and ultimately their lodging resistance while also having a profound impact on the stem's morphology and geometry. Morpho-anatomical stem properties are major component affecting standability. However, phenotyping these traits is low throughput, and has been restricted by the lack of a high-throughput phenotyping platform that can collect both morphological and anatomical stem properties. X-ray computed tomography (CT) offers a potential solution, but studies using this technology in plants have evaluated limited numbers of genotypes. The platform and image analysis pipeline revealed extensive phenotypic variation for important morpho-anatomical traits in well-characterized sorghum genotypes at suitable repeatability rates. CT estimates were highly predictive of morphological traits and moderately predictive of anatomical traits. The image analysis pipeline also identified genotypes with superior morpho-anatomical traits that there were consistent with ground-truth based classification in previous studies. In addition, stem cross section intensity measured by the CT was highly correlated with stem dry weight density, and can potentially serve as a high-throughput approach to measure stem density in grasses.

Francisco currently is a post-doctoral research associate for the USDA-ARS in Raleigh, NC.

Yu-Ming Lin

M.S. thesis title: High-density SNP genotyping applied to interspecific germplasm in upland cotton (*Gossypium hirsutum* L.): (I.) CSB17 chromosome-specific RIL analysis and (II.)



***G. mustelinum* (Miers ex Watt) linkage mapping. (Chair: David Stelly)**

Abstract: The narrow genetic base of Upland cotton has slowed growth of its productivity as a crop and perhaps also its use in the world. The need to broaden genetic diversity of Upland cotton is urgent, especially given the contemporary need to improve competitiveness of the fiber attributes, productivity and sustainability. The advent of high-density high-throughput molecular marker genotyping in cotton using the CottonSNP63K array has revolutionized the resolution and accuracy of genetic analysis in cotton. In this study, the CottonSNP63K array is used to analyze two populations, one a set of interspecific chromosome-specific RILs and the other an early-generations interspecific mapping population, both at the 52-chromosome level. A chromosome linkage map was derived from 50 isogenic chromosome-specific recombinant inbred lines, which were derived from a cross between a disomic substitution line CS-B17 homozygous for *G. barbadense* '3-79' chromosome 17 and its recurrent parent TM-1. Fiber quality and Fusarium wilt race 4 resistance data on the lines were subjected to quantitative trait locus (QTL) analysis. Results indicated that the CS-RIL approach affords high sensitivity, in that it detected seven fiber quality QTLs in chromosome 17, whereas none had been found previously by analysis of conventional TM-1/3-79 populations. However, one lint% QTL was detected previously using a similarly interspecific population. A single locus accounted for multiple FOV4 resistance trait QTLs and corresponded to previous research. In this CS-RIL study, iii QTLs exhibited exceptionally high R² values and consistency across experiments, reflecting avoidance of genetic background noise and Gx_E interactions. The first high-resolution SNP-based genetic map between *G. hirsutum* and *G. mustelinum* was constructed from a 59 individuals of BC1F1 population. The map was highly collinear with the *G. hirsutum* – *G. barbadense* map and the *G. hirsutum* reference genome. In certain chromosomes, some markers exhibited segregation distortion. Co-segregation difference between genetic maps revealed possible chromosomal structure changes among species. Possible errors in the genome assembly were found by alignments of 1,996 low-specificity SNP markers to their homeologs in the reference genome. The genetic

map can help guide genome assembly corrections, and facilitate many sorts of future studies, e.g., genetic dissection of complex traits and marker-assisted breeding.

Lloyd Mbulwe

**Ph.D. dissertation title: Evaluating host-plant resistance against sugarcane aphid (*Melanaphis sacchari* (Zehntner)) in sorghum (*Sorghum bicolor* (L.) Moench).
Chair: William Rooney)**



Abstract: The sugarcane aphid (*Melanaphis sacchari* (Zehntner)) is an established and problematic pest on sorghum (*Sorghum bicolor* (L.) Moench) in the United States. The virulent pest on sorghum was initially identified in Southeast Texas and significantly affects production. Heavy infestation will decrease yield and quality of grain and forage sorghum. The aphid's sticky honeydew secretions cause harvest losses and clogging of combines. Using artificial and natural infestations, 500 lines from Texas A&M AgriLife Research were evaluated, including mechanisms of resistance and phenotypic traits useful for breeding. Resistant lines A/BTx3408 and A/BTx3409 were identified, and released to the public in 2016. Grain and forage sorghum hybrids produced using resistant lines also exhibited resistance. The resistant lines and hybrids produced from resistant sources were subsequently evaluated for their relative agronomic and breeding value. The performance of resistant hybrids was better than susceptible hybrids under sugarcane aphid infestation. The mechanisms of resistance were identified as antibiosis and antixenosis (non-preference). Some phenotypic traits also influenced aphid damage. Further investigation into the phenotypic, biochemical and genotypic traits responsible for conditioning sugarcane aphid resistance is planned through heritability and quantitative trait locus (QTL) mapping studies. This will enable more efficient selection of

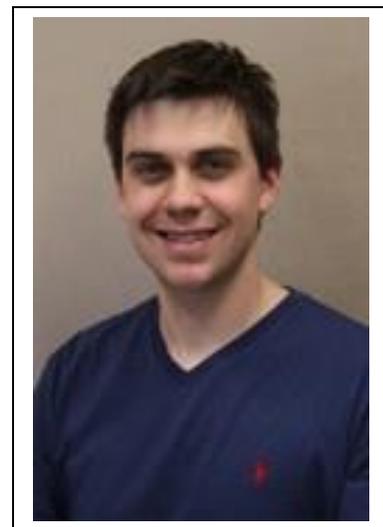
genotypes that maintain grain and/or forage yield and quality when subjected to aphid infestation.

Lloyd is director of the sorghum improvement program in Lusaka, Zambia for the Government of the Republic of Zambia. His Ph.D. studies were supported in part by a scholarship from the Zambia Agriculture Research Institute (ZARI) and research grants from the United Nations Environmental Program (UNEP), under a project called Ecosystems Based Adaptation for Food Security (EBAFOS-Zambia).

Brian Pfeiffer

**Ph.D. dissertation title: The improvement of grain sorghum productivity, black pericarp color, and protein digestibility.
(Chair: William Rooney)**

Abstract: Sorghum [*Sorghum bicolor* (L.) Moench] is an important cereal crop for the semiarid regions of the world. The improvement of sorghum grain production and sorghum grain quality are essential for the future of the crop. This study explores the genetic gain of hybrid sorghum breeding programs and investigates the nature of two important grain quality traits. A multi-environment trial was conducted that included hybrids ranging from the 1950s to today. Genetic yield gains in grain sorghum are increasing at approximately .008 t ha⁻¹ annually and many other physiological traits have demonstrated changes as well. Also, a F5 recombinant inbred line (RIL) population segregating for black and red pericarp color was evaluated in two Texas environments in the summer of 2017. Heritability and repeatability estimates were calculated and secondary plant metabolite biosynthesis genes were explored using RNAseq. The black pericarp trait appeared to be moderately heritable. Many of the same genes involved in 3-deoxyanthocyanidins (3-DOA) production in leaf tissue during fungal invasion appeared upregulated in black



pericarp sorghum versus red pericarp sorghum. Finally, sorghum grain protein digestibility was investigated in a biparental mapping population and evaluated in two environments for two years. A near-infrared spectrometry (NIR) calibration curve for *in-vitro* protein digestibility was developed to assist the phenotyping of this important quality trait. The protein digestibility trait was highly heritable and a significant genotype x environment effect was observed. Understanding key components of genetic gains in yield and other traits, as well as factors involved with important quality traits will benefit sorghum production in the future.

Brian currently is a sorghum breeder for Innovative Seed Solutions in Bishop, Texas

Nancy Wahl

**Ph.D. dissertation title: Identification of genetic components for resistance to aflatoxin production in pre-harvest maize.
(Chair: Seth Murray)**

Abstract: Aflatoxins, produced by the fungus *Aspergillus flavus*, often contaminate preharvest maize (*Zea mays* L.) grain under heat and drought stresses, and pose serious health hazards to humans and livestock. Since 2003, a multi-environmental trial of public breeding maize (*Zea mays* L.) hybrids across multiple programs in the southeastern United States has evaluated accumulation of aflatoxin following inoculation with the fungus, *A. flavus*. The Southeast Regional Aflatoxin Trial (SERAT) was formed to identify public germplasm with the most consistent resistance to aflatoxin accumulation and agronomic traits in different environments. Yield and agronomic traits were evaluated in 13 locations, aflatoxin in four, from 2006 to 2015. The 295 experimental hybrids that included tropical and subtropical derived germplasm exhibited lower average levels of aflatoxin and lower average yield



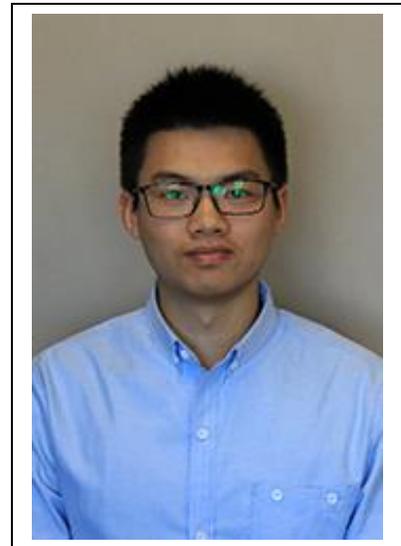
versus commercial checks. However, the 13 top-performing experimental hybrids identified in SERAT yielded as much or exceeded check averages, and had aflatoxin levels significantly lower than check averages.

A second study was conducted to investigate changes in differential gene expression (DGE) during seed morphogenesis and maturation in the "aflatoxin resistant" inbred line TX772 when challenged by *A. flavus* through two different methods of ear inoculation; non-wounding (silk channel) and wounding (side needle) in reference to a non-inoculated control. Grain maturity had the largest effect on RNA-Seq DGE, however, within each stage of development, similar up-regulation in expression from either inoculation method was observed. A larger number of fungal reads were observed in side-needle inoculated samples and a correlation of .65 between fungal read percentages and aflatoxin were found. Sixteen genes previously associated with resistance to pathogens were identified among the transcripts differentially expressed (DE) at $p \leq .05$, $FDR \leq .10$, and fold change ≥ 2.0 over all stages. Others not directly associated with resistance but differentially expressed included six zeins, and eight enzymes controlling carbohydrate metabolism. This study confirmed previously implicated candidate genes for resistance and identified new pathways to control *A. flavus* by investigating a unique maize genetic background.

Together these two studies provide new insights into germplasm and genes to further reduce aflatoxin in a field environment.

Nancy was an officer in the Crop Science Student Organization during her time with us and completed a 6-month co-op with Monsanto Company from June - December 2017 in soybean breeding.

Runhsi Xie



M.S. thesis title: Evaluation of leaf protein content, extraction, and purification in Napiergrass (*Pennisetum purpureum* Schumach.) (Chair: Russell Jessup)

Abstract: As protein deficiency is still a major health issue in the less developed portion of the world, novel sources of protein need to be identified. Grasses in the genus *Pennisetum*, such as napiergrass, can be a potential alternative protein source. The robust growth nature of grass provide abundant biomass, as well as enough protein to supply both livestock and human diets. However, plants are difficult to utilize as protein sources due to both non-digestible fiber fractions and antiquality factors (phytates, tannins, etc.). Therefore, feasible approaches are needed to further estimate and purify the leaf proteins. The objectives of this research are, first, to identify the potential relationship between leaf proteins and chlorophyll content index (CCI) for developing indirect tools for leaf protein quantification; and secondly, to further evaluate methods of leaf protein extraction and purification techniques, including heat coagulation (HC), mild alkali extraction (AL), and mild alkali extraction with the novel utilization of activated carbon (ALC). The percentage of crude protein in napiergrass was found to decrease sequentially at 30, 60, and 90 days of growth in this study. Trends of decreasing crude protein content between napiergrass parent group and both its self-pollinated progeny group and its F₁ hybrid progeny group were also identified. Two spectroscopic methods were used in this experiment, and both have reported low r² values (the highest r² = 0.477) for the correlation between crude protein content of napiergrass and CCI at three harvest dates. Neither heat coagulation nor mild alkali extraction method improved the extractability of leaf protein. Activated carbon column treatment effectively removed anti-quality factors (tannins) detected for this experiment. However, the

utilization of activated carbon also caused lower protein yield in the final purified product.

Runshi has initiated his Ph.D. studies with with Dr. Mengmeng Gu in the Department of Horticultural Sciences at Texas A&M.

Congratulations to Runshi, Nancy, Brian, Lloyd, Yu-Ming, and Francisco!

Meetings of Interest Meetings of Interest

National Association of Plant

Breeders, NAPB will hold their annual meeting at the University of Guelph, Ontario, Canada August 7 – 10, 2018. More information will be available soon at <https://www.plantbreeding.org>.

American Society of Agronomy and the Crop Science Society of America's annual meeting will be in Baltimore, MD, November 4 – 7. More information at <https://www.acsmeetings.org/>.

Distance Plant Breeding at Texas A&M

Distance Plant Breeding at Texas A&M

Distance Plant Breeding Program and Continuing Education courses available for Fall 2017

(<https://scsdistance.tamu.edu/available-courses>)

Continuing Education

Available Courses

Spring Courses: January 16 – May 8, 2017

To fully participate in our continuing education courses, students should have:

- **High speed internet connection and updated browsers, including Internet Explorer and either Chrome or Firefox**
- **Common plug-ins (e.g. Adobe Reader, Flash Player, Virus Protection, Java, etc.)**
- **Speakers and Webcam with microphone**
- **Skype**
- **Ability to either scan or fax course documents to the instructor**

Spring 2018

Plant Breeding Fundamentals – Full Course (3 Units) – Cost \$679.65

January 16 -May 8, 2018

Introduction to the field of plant breeding for students without a plant breeding background. Includes common plant breeding terminology and introduction of concepts. Genetic improvement of crops by hybridization and selection; special breeding methods and techniques applicable to naturally self-pollinated, cross-pollinated and asexually reproduced plants.

Basic Plant Breeding - Full Course (3 Units) - Cost - \$679.65

January 16-May 8, 2018

Basic Plant Breeding can be taken as an entire course (all three units) or each unit can be taken individually. For participants in our Professional Certificate in Plant Breeding and Genetics, completion of all three units is required.

Unit 1 - Introduction to Basic Plant Breeding Cost - \$226.55

January 16 – February 16, 2018

Introduction to Basic Plant Breeding provides a review of plant reproduction, genetic variation, gene banks, germplasm preservation, gene segregation, the power of selection and its role in plant breeding, and an introduction to intellectual property and its role in the life of a plant breeder. This unit is designed to prepare the participant to explore the genetics and methodologies employed by plant breeders of self and cross pollinated crop species in units two and three of Basic Plant Breeding.

Unit 2 - Breeding Self Pollinated Crops Cost - \$226.55

February 19 – March 30, 2018

The frequency of any specific heterozygous locus will be reduced by 50% for every generation of selfing, resulting in a mixture of homozygous lines within any natural population. Phenotypic selection within heterozygous generations will lead to homozygous or near homozygous germplasm lines or cultivars under self-pollination. This unit is designed to communicate plant breeding methodologies that take advantage of the genetic consequences of natural or forced self-pollination in agronomic crops. Topics will include: [1] the basics of segregation, [2] breeding methodologies, [3] the grain sorghum conversion program-an example of backcrossing in a different direction, [4] review of a commercial soybean cultivar development program, and [5] a review of the types of genetic releases from Texas A&M AgriLife Research.

Unit 3 - Breeding Cross Pollinated Crops Cost - \$226.55

April 2 – May 8, 2018

Topics covered include: quantitative genetics and plant breeding, effects of selection on Hardy Weinberg Equilibrium, mating designs with cross pollinated

crops, breeding methods for cross pollinated crops, deviations from Mendelian ratios, genetic male sterility and hybrid seed production, seed certification and types of release.

Recommended textbooks are “Breeding Field Crops” by J.M. Poehlman and D.A. Sleper, and “Principles of Cultivar Development” by W.F. Fehr. A final exam will allow the participant to assess their grasp of topics covered. Participants in the Plant Breeding and Genetic Certificate Program must score 70% on the final exam for each unit.

This is a "self-paced" course and is available for viewing for a limited time. Time commitment is individual student driven. Few outside assignments are made. Students should view each lecture, review all previous lectures and be prepared to discuss any issues that are unclear. Each unit has a printable note set and most units have a set of review questions that can be used as a tool to check your comprehension and grasp of unit concepts. Feel free to contact the instructor, Dr. Wayne Smith, by e-mail (cwsmith@tamu.edu) or phone (979-845-3450) with any questions you have or if you need additional information.

Analysis of Complex Genomes – Full Course (3 Units) – Cost - \$679.65 January 16-May 8, 2018

Genome structure, organization and function of model organisms and higher eukaryotes; theory and methodology of genetic and physical mapping, comparative genomics, sequencing, sequence analysis and annotation; emphasis on understanding the function of complex genomes, genome-wide expression analysis, genetic and epigenetic mechanisms; X-inactivation, imprinting, gene silencing, transposons, genome duplication and evaluation. Requires an in-depth and working knowledge of basic and advanced plant breeding concepts.

***Unit 1 – DNA Marker Technology and Genetic Mapping Cost - \$226.55
January 16 – February 16, 2018***

***Unit 2 – Recombinant DNA and Cloning Cost - \$226.55
February 19 – March 30, 2018***

***Unit 3 – Sequencing Genomes and Other Genomic Tools Cost - \$226.55
April 2 – May 8, 2018***

Quantitative Genetics and Plant Breeding - Full Course (3 Units) - Cost - \$679.65

January 16-May 8, 2018

Applied aspects of quantitative genetics in plant breeding; examination of methodologies to analyze quantitative variation in crop species; genetic phenomena

(inbreeding, heterosis and epistasis); quantitative trait loci (QTL) mapping and marker-assisted selection (MAS); genotype by environment interaction, heritability multiple traits and selection theory with implications in plant breeding. Requires an in-depth and working knowledge of basic and advanced plant breeding concepts.

Introduction to Host Plant Resistance (1 Unit) - Cost - \$226.55

January 19 – February 19, 2016

Host plant resistance programs from the standpoint of the plant breeder.

Other Academic and Continuing Education courses in plant breeding and related disciplines that will be available during other semesters include Host Plant Resistance; Crop Production; Selection Theory; Marker Assisted Selection; Genomic Analysis; Field Crop Diseases; Field Insects; Essential Nutrients in Crop Growth; and others. 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.

Distance Degrees in Plant Breeding

M.S. and Ph.D. degree programs at Texas A&M.

Visit <https://scsdistance.tamu.edu/plant-breeding-distance-education/> for details.

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