

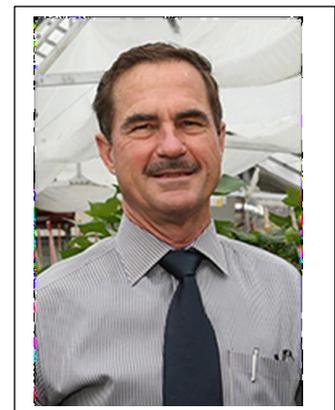
TEXAS A&M PLANT BREEDING BULLETIN

January 2019

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

Texas A&M Department of Soil and Crop Sciences had six plant breeding and genetics graduate students present comments and posters about their graduate research at the 2019 Beltwide Cotton Conferences held recently in New Orleans, LA. Before I introduce you to these outstanding young men and women, I want to first remind you that our student led Corteva Agriscience Plant Sciences Event 2019 Plant Breeding Symposium will be held on campus on Thursday, 21 February, in the Memorial Student Center. Information on their outstanding slate of speakers can be found at <http://plantbreedingsymposium.com/>. The event will be our 5th consecutive plant breeding symposium and our students do a fantastic job of developing, organizing, and conducting this event. I hope that many of you can join in person on 21 February and the many of you can join electronically through the webinar connection.

Secondly, I want to congratulate Dr. David Stelly who was recognized with the 2018 Cotton Biotechnology Award at the Plant and Animal Genome meetings in San Diego. David was selected as the recipient of the 2018 Cotton Biotechnology Award for his contributions known all over the world covering cytogenetics, chromosome substitution lines, and the widely used 63K SNP Chip genotyping tool. The Cotton Biotechnology Award, endowed by a gift from Dr. Norma Trolinder in 2000, has been presented on six previous occasions to a scientist or group of



scientists for outstanding biotechnology research in cotton and is administered by the Agricultural and Environmental Research Department at Cotton Incorporated. Congratulations Dr. Stelly.

The six plant breeding and genetics students presenting research at the Beltwide Cotton Conferences this month were:



Drutdaman Bhangu is a Ph.D. student directed by Wayne Smith in our cotton quality breeding program. He is expected to complete his degree by the end of 2019.



Luis De Santiago is a Ph.D. Genetics major under the direction of David Stelly in our cotton genetics and cytogenetics program. He is expected to complete his degree in 2020.



Christian Hitzelberger is an M.S. student in plant breeding directed by David Stelly. He is expected to complete his degree during 2019.



Alexandra Ullrich will complete her M.S. plant breeding degree under the direction of Wayne Smith in 2019 and remain with his cotton breeding program for a Ph.D. degree that she will complete in 2021.



Kubra Velioglu is an M.S. plant breeding student under the direction of David Stelly. She will complete her M.S. degree requirements in 2020.



Wenzhuo Wu is an M.S. plant breeding student under the direction of Steve Hague in his cotton breeding program. She expects to graduate in 2019 and pursue a Ph.D. degree.

These folks are conducting some outstanding research and are developing into outstanding scientists. Their poster abstracts are below.

Drutdaman Bhangu **(Third Place Winner for Ph.D. Presentation and Poster)**

TITLE: Novel Gene Based Breeding vs Field Based Breeding in Improving Fiber Quality Traits

ABSTRACT: The U.S. produced just over 20,000,000 bales (480 pounds each) of cotton in 2017 with 99% of that production being upland cotton (*Gossypium hirsutum*) and only 1% being pima cotton (*G. barbadense*). Pima is often referred to as Extra Long Staple (ELS) with grade # 1 having upper half mean length (UHML) of 1.375 inches (35 mm) or more and fiber bundle strength equal to or greater than 37.5 g/tex. Upland cotton will exhibit UHML in the 1.06 to 1.14-inch range and fiber bundle strengths of 27 to 31 g/tex. Upland cotton is higher yielding than pima in most areas of the world and improving the fiber quality of upland could improve the product portfolio for upland, improve the competitive position of upland cotton relative to non-natural fibers, and help maintain markets for American upland cotton. YunHua Liu, Post Doc, and Hongbin Zhang, Plant Genomics & Systems Biology, collaboratively with Wayne Smith, cotton breeder, at Texas A&M University identified over 400 genes associated with UHML and over 1000 associated with strength and proposed Gene-based Breeding, GBB, based on not only gene allele selection but also on expression profiles of the genes controlling the targeted trait(s). The research reported herein used two segregating populations [F2: 13P-54

Extra Long Staple (ELSU) // 11K-13 ELSU / NMSI 1331] and F3: 11K-13 ELSU / 06WE-621 Extra Strength Upland (ESU)] to compare phenotypic selection with GBB selection. The F2 population is considered an interspecific cross with NMSI (New Mexico Sea Island) 1331 contributing 25% of the alleles in the population while the F3 population does not contain any *G. barbardense* in its pedigree. Eleven of the UHML and eleven of the Strength markers that were expected to be the most informative were used and those GBB-marker (SNP predicted) identified selections were compared with selections based strictly on field and High Volume Instrument fiber phenotype selections. **COMCLUSIONS: [1] the correlation between the SNP predicted and the HVI predicted selections were more highly correlated in the interspecific population than the intraspecific population, suggesting that a population with higher polymorphism for UHML may be better suited to Gene based breeding; [2] a poor correlation between the SNP predicted and the HVI predicted strength was observed in both populations, suggesting a lack of robustness of the limited SNP markers used in this study for strength; and [3] the low number of markers used in this study are not conclusive enough to use in an applied breeding program to select for UHML or fiber bundle strength compared with current phenotypic selection.**

Luis M. De Santiago **(First Place Winner for Ph.D. Presentation and Poster)**

TITLE: Recombination Rates in Interspecific and Intraspecific Cotton Mapping Populations

ABSTRACT: Recombination is crucial for genome stability by ensuring proper chromosome segregation and can increase genetic diversity by generating novel allele combinations during meiosis. Recombination also allows for the localization of markers, such as single nucleotide

polymorphisms (SNPs) and simple sequence repeats (SSRs), through linkage mapping and effects the pattern of linkage disequilibrium between markers and alleles. The rate and distribution of recombination within the genome is important for the creation of novel alleles within cotton hybrids and influences the rate at which the co-inheritance of favorable and non-favorable alleles occurs (linkage drag). In this study, the recombination rates within 2 intra- and 3 inter-specific cotton mapping populations are assessed. Five high-density, SNP-based genetic maps were aligned to the *G. hirsutum* v2 sequence assembly (unpublished) and recombination rates across chromosomes were calculated using linear regressions of 1 mega base (Mb), non-overlapping windows with a minimum of 4 SNPs per window. Significant differences in recombination rates between mapping populations are observed.

J Christian Hitzelberger (Second Place Winner in M.S. Presentation and Poster)

TITLE: Development and Characterization of Chromosome Segment Substitution Lines

ABSTRACT: Genetic improvements of Upland cotton (*Gossypium hirsutum* L.) must be continuous if the crop is to remain biologically and economically viable, e.g., competitive to synthetic fibers, resistant to most diseases and pests, profitable to produce, and be environmentally sustainable. The notoriously low genetic diversity found among Upland cottons constrains opportunities for improvements by breeding based on conventional elite-by-elite crosses. Fortunately, each related wild AD-genome species harbors about 80,000 genes and so introgression of a wild species germplasm can significantly increase the breadth of variation available among Upland cottons. However, for most genes, it is virtually impossible to

predict whether a variant would be helpful, neutral or deleterious in Upland cotton genetic background. The history of wide-cross introgression into cotton has shown us we need more scientific and methodical approaches to effectively harness the genomes of wild species. One such method involves the breeding of Chromosome Segment Substitution Lines (CSSLs) by modified backcross-inbreeding. Each CSSL cotton would be marker-selected to contain one to several small subchromosomal introgressed alien segments but otherwise isogenic for *G. hirsutum*. Panels of CSSLs would be chosen by marker-based selection such that they collectively "capture" all or most of an alien genome. We report here progress toward a *Gossypium hirsutum* (TM-1) panel of CSSLs containing germplasm from *Gossypium mustelinum*, a wild Brazilian cotton species. These CSSLs will provide a powerful tool for introgression and characterization of *G. mustelinum* germplasm; it will significantly expand the isogenic platform, which also includes Chromosome Substitution Lines. Fiber data (HVI) were obtained from late backcross hybrid generations to look for any exceptionally strong dominant or codominant effects. The CSSLs (BC5Sn lines) will be high-density genotyped and tested for fiber (HVI, APHIS) and other traits.

Alexandra Ullrich

TITLE: Utilization of Novel Alleles Found in Obsolete Germplasm for the Improvement of Upland Cotton

ABSTRACT: Narrowing genetic variability is a developing issue in upland cotton (*Gossypium hirsutum*). In many cases novel alleles for the improvement of fiber quality traits, especially for fiber length and strength, are sought in other cultivated species (*G. barbadense*) or in wild relatives (e.g. *G. mustelinum*). Each of the options can be difficult to intercross or tend to bring along detrimental alleles which require

pre-breeding efforts to make useful breeding populations. This study seeks to find positively associated fiber quality alleles in obsolete elite cultivars found within the USDA germplasm collection and other sources by using 127 lines backcrossed to modern, Extra Long Staple Upland germplasm line TAM B182-33 which is representative of the TAMU cotton breeding program. Analysis will be conducted on F2 progeny grown in 2018, 2019 and 2020 at three locations for compatibility with this line. In this way, novel variation could be found that could be readily used or used with comparatively little preparation in continued trait advancement within the TAMU program. A structural analysis will also be conducted in 2019 and 2020 using six cultivars selected on the basis of their backcross performance, three found to be high performing and three found to be low performing, as well as their genetic distance from each other. This analysis will help in the understanding of the additive, dominance, and epistatic effects within the population and how the germplasm may be best utilized.

S K. Velioglu

TITLE: Genome-wide Spaced Simplex SNP Assays for Marker-based Interspecific Germplasm Introgression and Genetic Manipulation in Cotton

ABSTRACT: The cotton industry is a major contributor to the United States economy amounting to over \$75 billion annually. Thus, even small improvements in cotton quality and yield have significant ramifications. Genomic molecular markers are critical to many types of genetic analysis and manipulation. Single-nucleotide polymorphisms (SNPs) are the most abundant type of marker and most amenable to high-throughput technologies. Marker-assisted selection (MAS) utilizing SNPs is an effective way to manipulate agriculturally and economically important genes and genome regions, e.g., for genes

that enhance yield, pest resistance, and drought tolerance. Here, we report on SNPs for efficient introgression (transfer) of wild species germplasm into an Upland cotton genetic background, and subsequent manipulation, analysis, dissection and breeding. We report nearly 400 SNP assays for loci that are approximately evenly spaced across the genome. The SNPs were chosen to distinguish upland cotton, *G. hirsutum*, from other tetraploid cotton species (*Gossypium mustelinum*, *Gossypium tomentosum*, *Gossypium barbadense*), as well as their corresponding F1s). Only biallelic SNPs were used for this project, and most were derived from 18,000 mapped interspecific SNPs on the commercially available high-density CottonSNP63K array that discriminate between *G. hirsutum* and non-*G. hirsutum* cotton species. The SNPs were selected for primer design using BatchPrimer3 v1.0 software and tested to give comprehensive genome coverage. Our initial target was about 15-cM spacing using “Kompetitive Allele Specific” PCR (KASP) or “PCR Allelic Competitive Extension” (PACE) assays. A minimum of 10 markers per chromosome have been successfully assayed. These will be useful for a number of types of breeding and research applications where targeted genotyping is needed and will be especially helpful if large numbers of samples need to be screened using low-cost DNA preps, for which PCR-based assays such as KASP and PACE are generally compatible.

Wenzhuo Wu (Third Place Winner for M.S. Presentation and Poster)

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 which facilitate high-throughput phenotyping (HTP). Cotton (*Gossypium* spp.) is the world’s leading natural textile fiber crop. The ability to identify cotton plant height and boll count

across a field can serve as an important tool in predicting plant growth and yield. But precision farming has created a critical need for plant density. In order to capture a three-dimensional view of field plots, sensors mounted on UAV's must have access to a view of the nearby soil level, but cotton planted in solid rows can obscure this image. Canopy closure prevents the sensor from measuring plant architecture and boll-loads three dimensionally especially during mid-growing season. Therefore, this project was initiated in 2017 to compare solid vs. skip-row planting patterns in terms of predicting yield and fiber quality since skip row would allow UAV sensors to capture more accurate 3-dimensional data from plots. The research objectives of this project were to 1) evaluate the ability of UAVs to predict plant height and yield; 2) determine if there are genotype X row-spacing effects that would change the decision making process of a cotton plant breeder. Two UAVs were used for RGB data collection and multispectral data collection. Five cotton genotypes were grown in a skip versus solid row-pattern at three locations in 2017 and 2018. Yield and fiber qualities were measured for all treatments. UAVs were flown across the field bi-weekly basis to estimate canopy height, canopy cover, canopy volume, vegetation indices, and boll count and boll area over different growing stages. There were no genotype X row-spacing effects for fiber traits at any location. Genotype X row-spacing effects were minimal for lint yield. Yield and plant height estimations were improved when cotton planted in skip-row pattern. 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 reach the soil level and capture 3-D images. This can be done without compromising the efficiency and accuracy of the breeding program.

Meetings of Meetings of Interest

National Association of Plant Breeders, NAPB will hold their annual meeting at the University of Georgia, August 25-29, 2019. More information will be available soon at <https://www.plantbreeding.org>.

5th Annual Texas A&M Plant Breeding Symposium—21 February 2019

Now accepting travel scholarships for graduate students to attend, speak, and present research posters. Symposium theme is “Plant Breeders, Assemble: how interdisciplinary teams are working together for crop improvement.”

Speakers will be **Dr. Jose Crossa**, statistician from CIMMYT; **Dr. Matt Rouse**, plant pathologist from UMN & USDA; **Dr. Robin Buell**, genomicist from MSU; and **Dr. William Rooney**, sorghum breeder from Texas A&M University.

More information at

**<http://www.plantbreedingsymposium.com> or contact
pbsymposium@gmail.com.**

Distance Plant Breeding at Texas Distance Plant Breeding at Texas



Available Courses

Spring Courses: January 14 – May 10, 2019

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 2019

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

January 14 – May 10, 2019

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 14—May 10, 2019

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 14 – February 15, 2019

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 18 – March 29, 2019

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 1 – May 10, 2019

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 14 – May 10, 2019

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 14 – February 15, 2019

Unit 2 – Recombinant DNA and Cloning *Cost - \$226.55*
February 18 – March 29, 2019

Unit 3 – Sequencing Genomes and Other Genomic Tools *Cost - \$226.55*
April 1 – May 10, 2019

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

January 14 – May 10, 2019

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.**

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.

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

January 14 – February 15, 2019

Refresher course in host plant resistance breeding and selections.

Other Academic and Continuing Education courses in plant breeding and related disciplines that will be available during other semesters include Advanced Plant Breeding; Crop Production; Selection Theory.

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.