

TEXAS A&M PLANT BREEDING BULLETIN

February 2019

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

The students at Texas A&M University held their fifth annual Corteva Plant Sciences Symposium on 21 February at the Memorial Student Center. The event was well attended, as were the previous four, with 170 registrants. The leadership for this year's event expanded beyond plant breeding with Plant Pathology and Weed Science participating. The leaders, pictured below, did an outstanding job of organizing, obtaining financial contributions, inviting speakers, and general management of the event. Dr. Tabare Abadie, the originator of the Corteva Plant Sciences Event, attended this year's symposium and continues to give our students high marks for professionalism and dedication to the event.



From L to R: Roy Davis [Plant Pathology & Microbiology], Cynthia Sias (Weed Science), Jales Fonseca [Plant Breeding], Yu-Ya Liang [Plant Breeding], Nolan Bentley [Horticulture/Plant Breeding], Anil Adhikari [Plant Breeding], and Jeewan Pandey [Plant Breeding].

The theme of this year's Symposium was Plant Breeders, Assemble: How Interdisciplinary Teams are Working Together for Plant Improvement. Below are the invited scientists and their abstracts.



Dr. Robin Buell is a professor in the Department of Plant Biology at Michigan State University with research focused on genome biology of plants and pathogens. Robin's research involves crop plants (corn, rice, potato, sweetpotato), biofuels (switchgrass), and medicinal/herbal plants (periwinkle, mints, nightshade, ginseng,

***Camptotheca*) while her work with plant pathogens has focused primarily on bacteria and oomycetes.**

Title: *Evolution of potato: The world's most important vegetable crop*

Cultivated potato is a vegetatively propagated autotetraploid, a unique trait among major crop and model plant species. The assembly of characteristics that define cultivated potato relies on a complex balance of multiallelic loci with frequent epistatic interactions that are lost through sexual reproduction, with the result that most progeny are inferior to either parent as a consequence of inbreeding depression. We have uncovered a high degree of heterozygosity and rampant copy number variation that result in a highly heterogenous genome and a complex transcriptome with additive and non-additive gene expression. Using a panel of wild species, landraces, and cultivars, we have identified introgressions from wild species, loci under selection, and confirmed the single origin of domestication for this important food crop. Collectively, these results provide new foundations to begin to breed potato for improved agronomic traits to meet 21st century food security needs.

Dr. Jose Crossa is a member of the Biometrics and Statistics Unit at the International Maize and Wheat Improvement Center (CIMMYT). His substantive body of research and publications have addressed many areas of breeding and agronomic research, including genotype x environment, QTL x environment interactions, general breeding and experimental design, hybrids and heterotic patterns, and association mapping.



Title: Genomic and Deep Learning Models for Predicting Traits and Multiple Environments

In the last years several genomic-enabled predictions models have been developed for the prediction of a large number of unobserved phenotypes in different environments using dense molecular markers. Models include single and multi-traits, and single and multi-environments with the objective of increasing the prediction accuracy of the primary trait, grain yield, on unobserved individuals. Increase in prediction accuracy over the genomic best linear unbiased estimator (GBLUP) are achieved by means of the Gaussian kernel model with genomic \times environments interaction. Recently, we have developed models that incorporate other non-linear kernels that increase the prediction accuracy of genomic \times environment interaction over the Gaussian kernel by 5-10%. A Bayesian multi-trait-multi-environment model was described and used to efficiently exploit correlated traits and environments, thus producing and increasing the prediction accuracy by about 10-20% over the single-trait-single-environment model. However, due to the nature of the estimations process, this Bayesian model requires intense computing resources. In an attempt to speed up the prediction of the extensive number of unobserved phenotypes in large sets of multi-environments (big data) we have

been developing Deep Machine Learner (DL) models and methods. DL models with densely connected network architecture were compared with GBLUP on nine real genomic data sets. The DL appeared to be competitive, since they were better than GBLUP in 4 of the 9 data sets under a scenario that ignored covariates capturing genomic \times environment interactions. However, when genomic environment interaction was included, DL was not inferior in terms of prediction accuracy to GBLUP.

In modern agriculture and plant breeding the use of hyperspectral cameras provide hundreds of reflectance data at discrete narrow bands in many environments. These bands often cover the whole visible light spectrum and part of the infrared and ultraviolet light spectra. Since vegetation indices only use some wavelengths (referred to as bands), authors have proposed using all bands simultaneously as predictor variables for the primary trait grain yield; results of several multi-environment maize and wheat breeding trials indicated that using all bands produced a more accurate prediction. However, until now, these prediction models have not accounted for the effects of genotype \times environment ($G \times E$) and band \times environment ($B \times E$) interactions incorporating genomic or pedigree information. In this study, we propose Bayesian regression models that take into account all available bands, genomic or pedigree information, the main effects of lines and environments, as well as $G \times E$ and $B \times E$ interaction effects. The data set comprised wheat lines from the Global Wheat Program of CIMMYT evaluated for grain yield in three environments (Drought, Irrigated and Reduced Irrigation). The reflectance data were measured in 250 discrete narrow bands ranging from 392 to 851 nanometers (nm). The proposed Bayesian functional regression models were implemented using two types of basis: B-splines and Fourier. Results of the proposed Bayesian functional regression models, including all the wavelengths for predicting grain yield, were compared with results from conventional models with and without

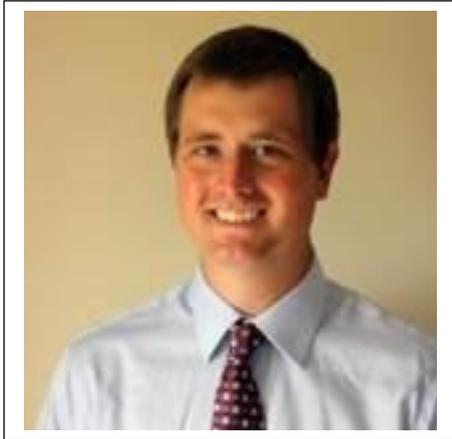
bands. Models with B×E interaction terms were the most accurate models.



Dr. Laura Mayor assumed responsibilities for sorghum breeding with Corteva in 2011. She has established a molecular breeding strategy for eastern Kansas and the High Plains markets. Laura focuses on improved yield, stalk strength, sugarcane aphid tolerance, and cold tolerance using new phenotyping and molecular technologies.

Title: Sorghum hybrid development in a commercial setting

The Corteva Sorghum research department has been providing elite commercial hybrids to farmers for the last 50 years. To this end, our research and crop platform teams align objectives and breeding targets according to current markets and available resources. This information becomes the framework or blueprint for our commercial breeding programs. During the hybrid development process, the latest phenotyping and genotyping technologies are implemented to efficiently increase our genetic gain by developing superior parental lines and creating the best possible hybrid combinations among those parents. As an example, current efforts in molecular breeding and precision phenotyping provide breeders with more effective tools throughout the creation, evaluation, and selection process, thus providing hybrids with higher yield, improved resistance to diseases, better standability, and enhanced drought tolerance.



Dr. Matthew Rouse is a Plant Pathologist with USDA-ARS Cereal Disease Lab and Adjunct Associate Professor in the Department of Plant Pathology at the University of Minnesota. Matt's research mission is to reduce losses in wheat and barley to major diseases, including stem rust and leaf rust. Matt has contributed

towards solutions to the threat of Ug99 and other emerging virulent races of the stem rust pathogen. In the fight against Ug99, Matt has conducted research in Kenya, Ethiopia, and in a biocontainment facility at the University of Minnesota.

Title: *Integrating Pathology and Breeding for Wheat Resistance to Stem Rust*

Wheat varieties around the world have been protected from stem rust disease by several stem rust resistance genes since the Green Revolution in the 1960s. In 2004, a wheat stem rust epidemic in Kenya surprised the global wheat community including Dr. Norman Borlaug. The cause of the epidemic was a strain of the stem rust pathogen recently detected in Uganda called Ug99. Ug99 possessed virulence to the stem rust resistance genes that had protected wheat for decades. After Borlaug's advocacy to address Ug99, substantial progress was made in identifying effective wheat stem rust resistance genes and releasing resistant wheat varieties. However, the stem rust pathogen continued to rapidly change and overcome the newly released varieties. Single-race field nurseries were deployed in Ethiopia in order to address this dynamic pathogen. These nurseries facilitated the identification of varieties and breeding lines with resistance to the latest emerging strains. Overall, the genetic basis of resistance in wheat varieties was still limited. Linkage blocks of

multiple effective stem rust resistance genes were constructed and backcrossed into advanced germplasm to facilitate the utilization of genetic resources in breeding. International and interdisciplinary collaboration allowed for plant pathologists to equip wheat breeders to address stem rust.

Dr. Bill Rooney is Regent's Professor and Borlaug-Monsanto Chair in Crop Improvement at Texas A&M University. He has led our sorghum improvement program since 1995 that aims to enhance the productivity and profitability of grain, forage, and bioenergy sorghums.



Title: Exploring genomic prediction for crop improvement: Broadening the reach of evaluation

Breeding technology is evolving and the introduction of technology into the process is specific to each crop and breeding program. Public breeding programs continue to serve an important role in the plant breeding industry through research, education, and development. Using our sorghum program as a model, I hope to demonstrate the role of a public breeding program in crop improvement. Compared to other major U.S. field crops, the rate of genetic gain in grain sorghum (*Sorghum bicolor* L. Moench) has been slower due to a combination of factors, some of which are reduced research and development investment, shifting production environments, and regularly changing priorities in traits and trade-offs between traits. These issues are likely to continue, and as such, existing sorghum breeding programs must adopt new technologies to increase the rate of genetic gain in yield. Several new and developing

technologies have the potential to increase the rate of gain. Doubled haploid technology will reduce the time to produce new hybrids for evaluation. Chemical gametocide technology is essential for doubled haploid deployment and could facilitate the testing new seed parents prior to sterilization. Genomic selection offers the potential to pre-select inbred lines and hybrids with greater genetic potential prior to field evaluation. High-throughput phenotyping has the potential to evaluate hybrids rapidly and efficiently. In addition, genetic transformation and gene editing have the additional potential to impact specific traits in ways previously not possible. If these technologies - which combine efficiency, speed, and effective selection – are effective, then rates of genetic gains in sorghum should increase and new traits previously not available can be integrated into production.



Attendance at the fifth annual TAMU Plant Breeding Symposium, a Corteva Plant Sciences Event

In addition to these terrific speakers, the symposium featured presentations by three Corteva Travel Scholarship winners: Bal Maharjan, a M.S. candidate in Plant Biotechnology at the University of Arkansas-Pine Bluff; Gina Sideli, a Ph.D. candidate in Horticulture and Agronomy at the University of California-Davis; and Alexander Susko, a Ph.D. plant breeding candidate from the University of Minnesota. The organizing committee selected three additional students for oral presentations: Ammani Kyanam, a Ph.D. candidate in Plant Breeding with Bill Rooney, Ranjita Thapa, a Ph.D. candidate in Plant Breeding with Endang Septiningsih, and April DeMall, a M.S. candidate in Plant Pathology with Herman Scholthof. The poster competition this year featured 32 posters.

You can view abstracts from the student speakers at <http://plantbreedingsymposium.com/>. Student poster winners were Stephany Toinga (Molecular and Environmental Plant Science), Aditi Raju (Biology), and Lauren Fedenia (Horticulture). Our students did another excellent job of developing and leading the fifth annual Corteva Plant Breeding Symposium. We congratulate the organizing committee, volunteers, and participants in another successful event. We also appreciate the sponsors who made this event possible.



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>.

Distance Plant Breeding at Texas Distance Plant Breeding at Texas

A&M

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.