

# TEXAS A&M PLANT BREEDING BULLETIN

October 2018

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

**The graduate students in plant breeding and related majors developed and managed the first TAMU Gene Editing Symposium at Texas A&M University in October, 2018. The students handled all of the financial and organizational aspects of the symposium. They invited four outstanding scientists working in the area of gene editing and held a poster competition for graduate students in the College of Agriculture and Life Sciences. Invited presenting scientists were:**

## **Edward Cargill**



**Ed Cargill, Bayer CropScience asks a question of another speaker during the Gene Editing Symposium**

**E**d is currently the Applied Cell Biology Lead in Plant Biotechnology and a Science Fellow at Bayer Crop Science. He received his B.S. in Animal Science from the University of Nebraska-Lincoln, and his Ph.D. in Genetics from the Interdisciplinary Genetics Program at Texas A&M University. Dr. Cargill is currently leading a team of scientists working on genome editing and plant transformation.

**During his professional career, Ed has conducted research and provided leadership in the development of Monsanto's seed chipping**

**technologies, double haploid corn processes, and molecular detection methods. Dr. Cargill then transitioned to lead a team of discovery breeders at Monsanto that focused on breeding methodology, traits, phenotyping, and agronomic practices contributing to improvements in the breeding pipeline. As gene editing technology became prevalent, he began leading a team of breeders and scientists at the intersection of the Plant Breeding and Biotechnology organizations to develop and implement editing technology in the breeding pipeline.**

## **Joyce Van Eck**



**Dr. Van Eck explains a concept  
During the Gene Editing  
Symposium**



**Our four guest speakers (l to r):  
Bing Yang, UMO, Joyce Van Eck,  
Boyce Thompson Inst., Daniel Voytas,  
UMN, and Ed Cargil, Bayer CropSci.**

**Joyce Van Eck is an associate professor and director of the Center for Plant Biotechnology Research at the Boyce Thompson Institute in Ithaca, NY. She is also an adjunct faculty member of the Plant Breeding and Genetics Section at Cornell University. Joyce received her undergraduate degree in Plant Biology from the Pennsylvania State University, a M.S. from the University of Delaware, and a Ph.D. in Plant Breeding and Genetics from Cornell University.**

**The focus of research in the Van Eck laboratory is biotechnological approaches to the study of gene function and crop improvement. For her studies, she applies genetic engineering strategies, including gene editing, to food crops, such as grape,**

potato, and tomato, in addition to several model species (*Setaria viridis*, *Brachypodium distachyon*, and *Asclepias syriaca*).

## Daniel Voytas



**Daniel Voytas spoke on the use of geminivirus replicons as a means to increase the probability of precise genome modifications in gene editing.**

**D**an is a Professor in the Department of Genetics, Cell Biology and Development and the Director of the Center for Precision Plant Genomics at the University of Minnesota. Dr. Voytas graduated from Harvard College in 1984 and received his Ph.D. from Harvard Medical School in 1990. He conducted postdoctoral research at Johns Hopkins University's School of Medicine where he was a fellow of the Life Science Research Foundation. Prior to joining the University of Minnesota, Dr. Voytas was a professor at Iowa State University (1992-2008). Dr. Voytas is an elected Fellow of the American Association for the Advancement of Science. In addition to his position at the University of Minnesota, Dr. Voytas advises agricultural biotechnology companies on the use of new methods of genome engineering for crop improvement and serves as Chief Science Officer for Calyxt.

Specializing in molecular biology and genetics, Dr. Voytas' research focuses on genome modification using nucleases that recognize specific DNA sequences. In 2005, he co-founded the Zinc Finger Consortium, a group of academic scientists focused on creating open-source platforms for engineering zinc finger nucleases for targeted mutagenesis. His laboratory developed a superior class of

**sequence-specific nucleases – Transcription Activator-Like Effector Nucleases (TALENs) – which were heralded by Science magazine as one of the top ten scientific breakthroughs of 2012. Using Cas9/CRISPR-based nucleases, Dr. Voytas’ lab is currently optimizing methods for efficiently making targeted genome modifications in a variety of plant species. Recent advances in Dr. Voytas’ lab include the use of geminivirus replicons to dramatically increase the frequency of precise genome modifications.**



**Seth Abugho and Xiaoqing Shen “man” the registration table**

**Our speakers and graduate student organizing committee (l to r): Brendan Mormile (Plt Path), Karina Morales (Soil and Crop), Bing Yang, Joyce Dr. Van Eck, Daniel Voytas, Emily Boak (Hort), and Ed Cargil.**



## **Bing Yang**

**Dr. Yang is a professor of Plant Sciences with the College of Agriculture, Food & Natural Resources at the University of Missouri and a member and principle investigator at the Donald Danforth Plant Science Center. Bing received PhD degree in plant pathology at Kansas State University in 2000 and joined the Department of Genetics, Development, and Cell Biology at Iowa State University as an assistant professor in 2007.**

**Currently, Dr. Yang works on development and application of TALEN- and CRISPR-based genome editing technologies in crops such as rice, maize, wheat, sorghum and soybean. His research also focuses on basic understanding of host susceptibility/resistance to bacterial infection and using genome editing tools to engineer disease resistance in crop plants.**

**Three Texas A&M students were recognized for their poster presentations at the symposium. These were Anna Casto, PhD student in Molecular and Environmental Plant Sciences; April Demell, MS student in Plant Pathology; and Ranjita Thapa, PhD student in Soil and Crop Sciences. These three presented results of some outstanding research and their abstracts are below.**

**Anna Casto (Molecular and Environmental Plant Sciences)**

**ABSTRACT: Meeting future energy demand requires efficient biomass feedstocks for biofuel production. Sorghum bicolor is a drought-resistant C4 grass that is a promising target for improvement as a biomass crop. Sweet sorghums can accumulate high concentrations of carbohydrates in their stems. However, in some cultivars, air spaces, or aerenchyma, form in the stem which limits the volume of sucrose that can accumulate and causes a dry stem phenotype. Aerenchyma first appear in the center of the stem near the top of fully elongated internodes. Aerenchyma then spread radially and basipetally as the internodes mature. A large main effect quantitative trait locus (QTL) modulating variation in stem aerenchyma formation was mapped to a region on chromosome 6 in three biparental populations derived from BTx623/IS320c, BTx623/R07007, and BTx623/Standard broomcorn. The locus was fine mapped to a gene encoding a NAC (NAM, ATAF1/2, and CUC2) family transcription factor (SbNAC<sub>D</sub><sup>+</sup>). Whole genome sequences and allele sequencing in various sweet sorghum genotypes revealed a single nucleotide polymorphism (SNP) in the first exon that causes a premature stop codon in genotypes with low aerenchyma formation. SbNAC<sub>D</sub> is induced in stem segments that are positioned to form aerenchyma. Transcriptomic analysis of stem tissue from SbNAC<sup>+</sup><sub>D</sub> or SbNAC<sub>d</sub> genotypes showed that genes involved in developmental programmed cell death are induced by SbNAC<sub>D</sub>. We**

**propose that SbNAC\_D is the D-gene identified by Hilton (1916) and that allelic variation in SbNAC\_D modulates the extent of aerenchyma formation in stems.**

**April DeMell**

**ABSTRACT: The CRISPR/Cas9 genome editing platform is a method for inducing double stranded breaks in a targeted genomic sequence using the RNA programmable Cas9 endonuclease. Viral vectors are rapid and robust heterologous gene expression tools capable of producing large quantities of RNA or protein products. Previously, we created a viral toolbox to transiently deliver the CRISPR/Cas9 components in high quantities. Here, we report the use of a single *Agrobacterium* launched Tobacco mosaic virus (TMV) vector, TRBO-G, containing a GFP substitution for the coat protein to target the highly conserved phytoene desaturase 3 (PDS) gene across multiple diverse *Nicotiana* species. The constructed Cas9 expression vector, pHCoCas9 was co-delivered with the Tomato Bushy Stunt virus (TBSV) RNA silencing suppressor P19, shown to increase vector expression. Three *Nicotiana* species were selected for further study from a screen based on vector expression, hypersensitivity response to P19, and genetic background. In *N. benthamiana*, editing of PDS3 was observed, increased by the presence of P19. Similar results were obtained when implementing these tools in *N. otophora* and *N. attenuata*. Developing flexible tools with the potential for targeted gene editing in multiple species could increase the efficiency of producing non-transgenic edited plants, and be used for functional genetic screens to interrogate conserved pathways and parallel gene function.**

**Ranjita Thapa**

**Rice is a staple food for more than half of the world's population. *Oryza sativa*, which belongs to the *Poaceae* family, has vast diversity in its panicle architecture. Panicle architecture directly influences the grain yield of rice. Development of breeding lines with improved grain yield potential is often the main focus of plant breeders. Panicle architecture varies from long to short panicles, sparse to dense panicles, or lax to compact panicles. Understanding the genetic basis of panicle architecture will significantly help on the development of**



**high yielding cultivars. The main objective of this study was to discover the genomic regions controlling various panicle traits - panicle length, primary branch length, secondary branch length, primary branch number, secondary branch number, and spikelet number per panicle. The field study was conducted in the Summer (March to September) of 2017 in Beaumont, Texas. The study included 203 accessions collected from different parts of the world. Seeds were sown following the direct seeding method using an experimental seed drill. Panicle traits were measured or counted manually. Spikelet number per panicle were counted using P-trap software. The rice panel, 203 accessions, was genotyped using the 7K rice SNP chip (Cornell University). A genome-wide association study was performed using the MLM(Q+K) model and GAPIT software. We found 5, 14, 10, 8, 5 and 7 markers significantly associated with panicle length, primary branch length, primary branch number, secondary branch length, secondary branch number and spikelet number per panicle, respectively. Many of these SNP markers are found to be co-localized with the genomic regions previously found to be controlling the traits.**



**Karina Morales opens the Texas A&M University Gene Editing Symposium**

**And the Symposium ends with a relaxing dinner.**



# Meetings of Interest 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>.

## **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

### **Available Courses**

**Spring Courses: January 14 – April 30, 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 – April 30, 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—April 30, 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 18, 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 19 – 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 – April 30, 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](mailto: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 – April 30, 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 18, 2019***

***Unit 2 – Recombinant DNA and Cloning*      *Cost - \$226.55***  
***February 19 – March 29, 2019***

***Unit 3 – Sequencing Genomes and Other Genomic Tools*      *Cost - \$226.55***  
***April 1 – April 30, 2019***

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

**January 14 – April 30, 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](mailto:leann.hague@tamu.edu) or (979) 845-6148.**

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

*January 14 – February 18, 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](mailto:cwsmith@tamu.edu) or 979.845.3450.**