

TEXAS A&M PLANT BREEDING BULLETIN

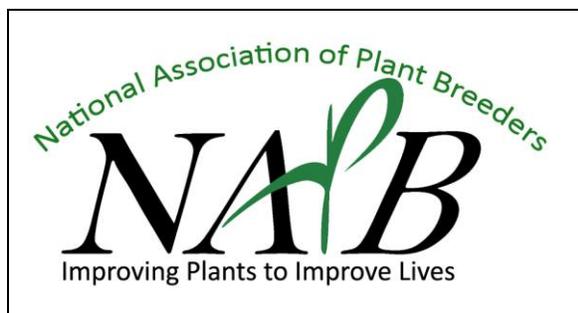
August 2014

Our Mission: Educate and develop Plant Breeders worldwide

Our Vision: Alleviate hunger and poverty through genetic improvement of plants

Four outstanding plant breeding students received Ph.D. degrees from Texas A&M University in August 2014. John Gill (Bill Rooney, Chair) is employed as a corn breeder with Agriliant in Champaign, IL; Yun-Hua Liu (Hongbin Zhang and Wayne Smith, Co-chairs) is a post doc in Dr. Zhang's lab; Sean Thompson (Dirk Hays, Chair) is a post doc with Dr. Creighton Miller in Horticulture at TAMU; and Xiuting Zheng (Dave Stelly, Chair) is a post doc with the USDA-ARS in College Station. Three outstanding students received their M.S. degrees in Plant Breeding. Rasha Al-Azzawi (Steve Hague, Chair) currently is anticipating her husband's degree completion at Texas A&M; Brian Pfeiffer (Bill Rooney, Chair) will remain with Dr. Rooney's sorghum breeding program to pursue a Ph.D.; and Bryan Simoneaux (Amir Ibrahim, Chair) is employed as an Agricultural Research Technician with Dr. Ibrahim and will pursue his Ph.D. also. We congratulate these young men and women on their accomplishments to date and look forward to their continued success and contributions to the field of plant breeding.

The National Association of Plant Breeders met in Minneapolis, MN on August 5 through 8. Texas A&M University and Texas A&M AgriLife Research were well represented by faculty and graduate students. Four graduate students presented plant breeding research posters and two professors were invited to speak at the event. The student's abstracts are presented below, followed by the abstracts for presentations made by Dr. Seth Murray as recipient of the NAPB Young Scientist award for 2013 and Dr. Jane Dever's invited presentation at the NAPB's "Private Breeding Perspective" workshop.





Comparison of Mapping Population Design and Analysis of Blue Aleurone in a 4-way Maize Cross

Adam L. Mahan, Seth C. Murray, Patricia Klein

Traditional mapping populations involve the use of recombinant inbred lines (RILs) produced from a bi-parental cross. An increase in the number of parents, as well as the use of intermating can increase the detectable recombination, thus making it possible to map traits with increased resolution. It is also a goal to determine population design effects on the ability to identify improved progeny for breeding purposes. To compare multiple mapping population designs, an unprecedented, 1246 line, 4-way maize population was developed. This population consists of five separate F₅ or F₆ subpopulations consisting of bi-parental and 4-way RILs, as well as 4-way RILs with 1, 2, or 3 generations of intermating. The population has been sequenced on an Illumina HiSeq platform yielding 103,370 informative SNP markers. As a test case, association mapping methodology accurately detected the *Y1* allele for yellow endosperm on chromosome 6, confirming that genotypic data was accurate and that association mapping methods are an effective method of analysis for populations with greater than two parents. Observed kernel colors across the population include 23% blue, 31% white, 33% yellow, and 13% segregating. The ~25% blue indicates two alleles are necessary for blue aleurone in this population and that both blue parents have both genes. Future work includes genetic map construction of the 4-way population, and genetic mapping of recombination modifiers and the blue aleurone trait.



Molecular Mapping of Drought Tolerance Genes in Cowpea (*Vigna unguiculata* [L.] Walp)

Laura Masor, Dirk Hays

Cowpea (*Vigna unguiculata* L. Walp) is a leguminous crop that many people around the world rely on to meet their basic nutritional needs. Both humans and

livestock consume the protein and fiber-rich grain and vegetative matter of the cowpea plant. Water stress affects this crop like many other crops, by reducing total biomass and grain yields. Genotypes of cowpea have been identified that contain genes that confer tolerance to drought. In order to map the genes controlling the drought tolerance, a recombinant inbred line (RIL) population has been created from the parental genotypes IT98K-476-8 and 'Green Eye Cream' (GEC). This population is being phenotypically analyzed for drought stress response. Genotyping of the population is in process by double digestion restriction site-associated DNA sequencing (ddRAD-seq), and the genes controlling the drought tolerance will be mapped using the resulting SNPs. These genes, once identified and cloned, will aid in the understanding of drought tolerance and development of molecular plant breeding tools that can be applied to this and closely related species.

Cotton Fleahopper (*Pseudatomoscelis seriatus*) Damage in *Gossypium hirsutum*: Breeding Efforts Towards Increased Resistance

Laura Ann McLoud, Steve Hague

Cotton fleahopper (*Pseudatomoscelis seriatus*) (Hemiptera: Miridae) is a piercing-sucking insect that has emerged as a major pest in the Texas cotton industry over the past decade. Cotton fleahopper feeding results in square abscission

and damage and subsequently, yield-loss. Previous studies in *Gossypium hirsutum* indicate that plant trichome density plays an important role in conferring resistance to cotton fleahopper, but the mechanism of resistance remains largely unknown. Six potentially resistant lines and two high-yielding lines were screened for resistance to cotton fleahopper under field infestation levels. In this project, three lines (GH18-3, GH15-2, GH20-1) found to be resistant in field-screening and one susceptible line (TAM07V-45) were subjected to cotton fleahopper feeding pressure, and RNA was isolated from squares collected from each of the plants for RNA sequencing. RNA was isolated using a Spectrum™ Plant Total



RNA Kit and sequenced in four lanes of 100bp SE Illumina HiSeq2000. Results will only be presented for line GH18-3 in this presentation. Expression analysis of line GH18-3 found 1,139 significant differentially expressed genes between the fed-on and not-fed-on conditions. Of those, 11 genes involved in plant immunity and defense were found to be significantly upregulated in plants exposed to cotton fleahoppers, suggesting the possible role of plant immune response in conferring resistance to the cotton fleahopper.

Flow Cytometry and a Thioredoxin-like Gene: Useful Tools to Identify *Poa arachnifera* x *Poa pratensis* Interspecific Hybrids

Meghyn Meeks, Ambika Chandra

Hybrid bluegrasses are growing in popularity in the southern United States for their visual appeal and competitive heat and drought tolerances to tall fescue.

However, the phenotypic assessment of

Poa arachnifera x *Poa pratensis* hybrids can be time

consuming and sometimes unreliable. Here we demonstrate the utility of flow cytometry and the *trx* gene as useful tools in the identification of true hybrids. Replicated samples were taken from one gram of fresh plant tissue and analyzed using flow cytometry to determine diploid (2C) DNA content for each of 19 *P. arachnifera* and 4 *P. pratensis* genotypes, as well as 5 interspecific hybrids from two *P. arachnifera* x *P. pratensis* pedigrees. Flow cytometry results show that interspecific hybrids have an intermediate nuclear DNA content to each of their polyploid parents. Furthermore, we observed a wide range of nuclear DNA content within *P. arachnifera* suggesting a possible variation in the chromosome numbers in the species. Additionally, the *trx* gene was amplified through polymerase-chain-reaction in the *P. arachnifera*, *P. pratensis*, and hybrid genotypes. Sequencing and phylogenetic analyses of the *trx* alleles shows that *P. arachnifera* x *P. pratensis* hybrids inherit allele sequences from both parents. One unique 851bp allele was found to be uniformly present among 19 male and female *P. arachnifera* ecotypes as well as interspecific hybrids but completely absent in examined *P. pratensis*. Thus, the discovered



851bp allele can not only be used to prove *P. arachnifera* inheritance in hybrids, but also to distinguish *P. arachnifera* from *P. pratensis* genotypes. This allele is characterized by a 163 bp insertion within the intron region that folds to form a hairpin loop. Results of the miRBase search show sequence similarity of the hairpin loop stem structure with micro RNA from sorghum, wheat, rice, and barley, suggesting a potential role as a precursor to a micro RNA.

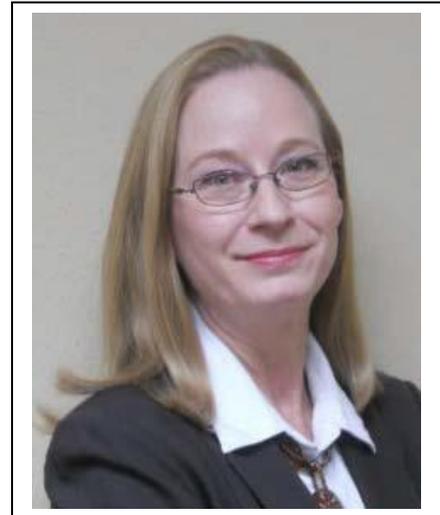
Private Breeding Perspectives Workshop

Panelist: Dr. Jane Dever

Title: Public and Private Breeding Experience: Contrasting and Complementary Opportunities

Plant breeding conducted in any venue has common activities. Each major activity or component -- objective setting, germplasm resources, methodology, testing, advancement decisions, financial resources, germplasm value, and breeding program evaluation – will have

special circumstances depending on the nature of the breeding program. Considerations for these activities based on public or private, academic or business, are discussed along with types of opportunities associated with breeding training and experience in both the public and private sector.

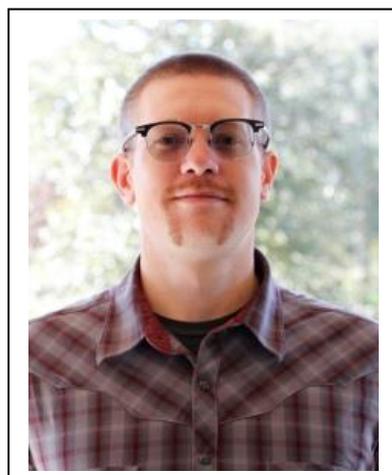


Early Career Award: Dr. Seth Murray

Title: Plant Breeding Approaches and Technologies For Challenges in Agriculture: A View from a Texas Maize Breeding Program

Over the last century, plant breeding and agronomic technologies have vastly improve

yield and reduced the amount of land needed to produce a unit of grain for many crops, with maize (*Zea mays* L.) as a prime example. Agriculture will be challenged in the future



with decreasing availability of inputs, an increasing need for food safety and security, and increasing needs in the provision of ecosystem services, all under a changing climate. While the yield of maize continues to increase in the Midwest it has remained stagnant under the more stressful (hotter, drier) conditions in Texas over the last 15 years. These conditions exacerbate *Aspergillus flavus*/aflatoxin contamination and drought stress, which are predicted to become more frequent even in the Midwest Corn Belt. In the TAMU maize breeding program and in our molecular quantitative genetic studies (linkage and association mapping) we have identified exotic diversity useful for improvement of yield, yield under dryland conditions and for reducing aflatoxin. Yet a number of challenges remain in how we confirm these lines and alleles, incorporate them and get them adapted by industry and growers. More broadly, current limiting factors to improve the speed and efficiency in exotic germplasm introgression, phenotypic plant breeding and molecular genetic discovery can be improved. Increasing the number of effective recombination events through traditional methods and the cycling of gametes *in vitro* (COGIV), both appear promising with recent improvements in genomics technologies. To meet increasing demands on sustainable agricultural production, applying these and other technologies will allow breeding of perennial maize and sorghum, long-lived perennial crops, and even algae.

Continuing and Distance Education in Plant Breeding at Texas A&M

Continuing education course modules in plant breeding and genetics, and related disciplines are available from Texas A&M University to clientele interested in gaining new information in plant breeding or simply seeking refresher courses. This program is designed for individuals employed in private industry, CGIAR centers, government agencies, non-government organizations, and other agriculture professionals who need and desire additional knowledge and training in plant breeding but who are not interested in an additional academic degree. A professional certificate can be a part of this program. No campus visit is required. Course modules currently available can be found at [\(https://scsdistance.tamu.edu/continuing-education-courses/\)](https://scsdistance.tamu.edu/continuing-education-courses/).

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

Texas A&M University offers MS Thesis Option, MS non-thesis option, and PhD Plant Breeding degrees at distance. For details, visit <https://scsdistance.tamu.edu/plant-breeding-distance-education/>.

Meetings

ASA/CSSA/SSSA International Annual Meeting in Long Beach, CA, November 2-5. Visit <https://www.acsmeetings.org/> for details.

National Association of Plant Breeders Annual Meeting in Pullman, WA—July, 2015. Visit www.plantbreeding.org for details.

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