

# TEXAS A&M PLANT BREEDING BULLETIN

January 2014

**Our Mission:** Educate and develop Plant Breeders worldwide

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

## STUDENTS AT TRISOCIETIES IN TAMPA, FL

Our Plant Breeding Students have several professional opportunities to present and discuss their research data with other scientists and graduate students on the national and international stage. Several Plant Breeding students from Soil and Crop Sciences attended the 2013 International TriSocieties (Agronomy/Crop Science/Soil Science) annual meeting in Tampa Florida in November 2013. Below are abstracts or summaries of their research presentations. It's obvious that our plant breeding scientific future will be in good hands.

**Brijesh Angira (Dirk Hays, chair)**

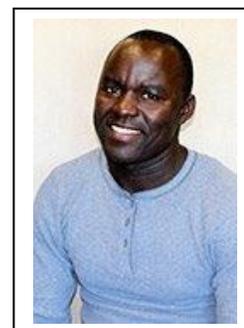
**Title: Genetic and Physiological Studies of Heat Tolerance in Cowpea**

Brijesh's objectives were to [1] Identify genetic variability for heat tolerance in cowpea; [2] Understand inheritance of heat tolerance in cowpea; and [3] Improve heat tolerant cowpea through hybridization and selection. A few of his results to date are [1] Significant genetic variability exist among available Texas A&M AgriLife cowpea germplasm and other available cultivars; [2] Significant differences were found among the genotypes tested for yield potential when heat stressed; [3] excessive heat primarily affected pollen fertility, which affected pod set and eventually seed yield; and [4] genotype IT98K-589-2 produce more ethylene compare to genotype IT98K-205-8 under non-stress conditions, which leads to flower drop and eventually reduction in pod set.



**Joseph Awika (Dirk Hays, chair)**

**Title: QTL for leaf wax is a precursor to effective staygreen related responses in grain setting and filling in sorghum under heat and drought stress**



Based on screening for rate of senescence and green leaf area at maturity, four major QTLs for staygreen in sorghum have been shown to individually effect tolerance to post flowering drought-induced senescence. Possible genetic interaction between QTL for leaf wax and QTL for staygreen under drought was identified. By elucidating the intervening physiological architecture and effects of this interaction in response to a combination of elevated heat and drought levels, we determined that the two genomic loci collectively mediate seed development and yield. We used four staygreen near isogenic lines and the recurrent parent in four controlled treatments of heat, drought, drought-heat, and normal to obtain data relative to various physiological parameters during the vegetative growth period to grain maturity. Data indicated that efficiency of photochemical functionality and of staygreen genomic loci is phenology- depended, and is a function of healthy leaf temperature depression. Further, temperature depression is tightly modulated by stomatal conductance and leaf waxiness. Depending on plant development phase, stomata conductance and wax act both antagonistically and in a compensatory manner to mediate temperature depression which strongly correlates with quantum yield of photosynthetic chemistry from embryo formation to pollination, and at mid to late grain filling. Isolines that failed this delicate balance under drought-heat and under drought, show significantly reduced seed number, shriveled seed, and low transpiration-based and seed-based water use efficiencies. We conclude that these results suggest staygreen 1, 2, 3, and 4 strategies interact differently with leaf wax to repackage the way plants respond to drought, heat or a combination of both stresses. Results could be used to discriminate staygreen related heat and drought tolerance. We also speculate that a major gene(s) in wax biosynthetic pathway is pleiotropic to functional staygreen regulatory factors and could be important in seed development.

**Trevis Huggins (Dirk Hays, chair)**

**Title: The Association of Yield Stability with Epicuticular Leaf Wax Across Diverse Environments in Wheat**



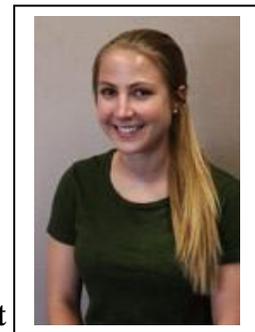
A 180 RIL wheat population (Halberd x Len) was used to investigate the effects of water deficit and high temperature on epicuticular wax load (EWL) and its effects on yield stability. Leaf epicuticular wax load was significantly higher in water deficit conditions compared to irrigated conditions. In fact, the environment with the highest temperature resulted in the highest leaf epicuticular wax load. It was concluded that the effect of epicuticular wax on yield stability

varies across diverse environments, with some lines producing consistent epicuticular wax load across environments, whereas others varied by environment. Epicuticular wax load significantly and negatively correlated with kernel number per spike, single head weight, and thousand kernel weight under both water deficit and high temperature stress. This association suggests that increased epicuticular wax load results in an increase in these yield component values. The significant and positive correlation between epicuticular wax and grain yield under water deficit suggest that increased epicuticular wax load may increase grain yield. QTL mapping identified numerous yield stability segments co-localizing with epicuticular wax and canopy temperature QTL on chromosomes 1B, 2B, and 7A. The Halberd parent exhibited greater yield stability than the Len parent.

**Whitney Jones (Wayne Smith, chair)**

**Title: Genetic Gain through Breeding for Resistance to *Pythium ultimum* in Cotton Seedlings**

*Pythium ultimum*, a pathogen included in the Cotton Seed Disease Complex (CSDC), is one of the most prevalent soilborne pathogens of cotton in the United States. Symptoms of the disease include poor plant stands due to pre- and post-emergence damping off and seed rot, seedling root rot, hypocotyl lesions and stunting that delays growth. Previous studies indicate that breeding programs utilizing single plant selections have been successful in achieving resistance and partial resistance to some CSDC pathogens for other crop species and cotton respectively. The research objectives of this study were to evaluate genetic gain achieved through individual plant selections and to produce cotton germplasm that is resistant to *P. ultimum*. Three potentially resistant, high-tannin lines (originally bred for insect resistance) and two high-yielding checks were screened for *P. ultimum* resistance under greenhouse conditions conducive to disease. Two generations of individual selection produced C<sub>1</sub> and C<sub>2</sub> test lines. A range of resistance from complete susceptibility (phenotypic rating of 6) to fully resistant (phenotypic rating of 0) was demonstrated within the C<sub>2</sub> test lines. Individual test lines have been selected for germplasm release as highly *P. ultimum* tolerant.



**Laura Masor (Dirk Hays, chair)**

**Title: Screening for drought tolerance among cowpea (*Vigna unguiculata* L. Walp) genotypes**

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; i.e. by reducing total biomass and grain yields. Differing



physiological mechanisms have evolved in cowpea that confer tolerance to water stress, which vary among genotypes. The goal of this study was to investigate the effect that water deficit has on osmotic regulation, photosynthetic capacity and biomass accumulation among cowpea genotypes, and also determine which drought screening potting method is more effective at partitioning experimental effects. Five genotypes of cowpea were sown in a split-split plot design in pots and plastic boxes in a greenhouse setting.

Water was withheld from half of the plants to simulate drought conditions. Stomatal conductance, photosystem II quantum yield and biomass accumulation were recorded at predetermined time points. Some differences among genotypes, treatments and time of measurement, as well as screening potting method were highly significant.

### **Suheb Mohammed (Dirk Hays, Chair)**

#### **Title: The role of leaf epicuticular wax in improved adaptation to drought**

The objectives of this study were: [1] Investigate genotypic alterations in leaf epicuticular wax content during drought stress; [2] Identify the role of increased leaf epicuticular wax in improving physiological function and yield stability during drought stress; and [3] Define QTLs associated with increased leaf wax, improved physiological function and yield stability during heat and drought stress using the Len X Halberd RIL population. Data suggested the following conclusions: [1] Wax inheritance is low (0.12) and canopy temperature is moderately heritable at 0.40; [2] 19% to 30% higher wax content was found in non-irrigated wheat compared to irrigated plants; [3] Yield potential and yield stability index was improved by higher wax content and cooler canopy; [4] Stable and co-localized QTLs were identified for potential yield, drought stress index, canopy temperature, and leaf epicuticular wax; and [5] 'Halberd' parent contributed more genes for wax load and cooler canopy to improve yield stability across RILs than the 'Len' parent.



**Silvano Assanga Ocheya (Shuyu Liu and Amir Ibrahim, co-chairs)**

**Title: Identification of SNP markers linked to Drought Tolerance in TAM111 Wheat**

The objectives of the current study were [1] map tightly linked single nucleotide polymorphic markers (SNP) for drought tolerance in wheat; [2] introgress drought tolerance QTLs in the background of stem rust resistant spring wheat lines; and [3] validate the QTL for wheat streak mosaic virus (WSMV) in wheat. A bi-parental mapping population was developed by crossing CO90296-2 x 'TAM111'. CO96029-2 has resistance to WSMV and high yield in a high performance environment. The F<sub>1</sub> were advanced to F<sub>2</sub> and single seed descent used to advance the lines to the F<sub>8</sub> generation. The family structure was comprised of 217 recombinant inbred lines (RILs), which were genotyped using 90,000 SNP markers and phenotyped across three environments in the USA (one drought stress and two well-watered environments). The environments include Etter, TX, Hays, KS and Aberdeen, ID. A total of 1420 polymorphic SNP markers based on Genome Studio analysis were used for linkage and QTL analysis using JoinMap and MapQTL, respectively.



Preliminary findings show common putative QTLs for grain yield on chromosome 2A and 5B for all three environments. One common QTL for grain yield was mapped on chromosome 6B for two of the three environments used in the analysis. Several QTLs for 1000 kernel weight and kernel number per head were mapped on chromosome 5B and 2A. One QTL for 1000 kernel weight was co-localized with QTL for grain yield on chromosome 5B. The R<sup>2</sup> for the QTLs ranged from 5.9-9.2 %. The SNP markers linked to novel QTL for drought tolerance could be utilized for marker assisted breeding for drought tolerance in wheat.

**Sean Thompson (Dirk Hays, chair)**

**Title: Estimating Wheat Root Biomass Using Ground Penetrating Radar**

In response to predicted climate change, crop scientists have increased their efforts to adapt crops to heat and drought stressed environments. Increasing root biomass is a principal focus since it permits access to deep water and balances evaporative demand at high vapor pressure deficit. However, direct selection for roots is not yet feasible at a breeding scale due to the high cost of current methodologies and a lack of high throughput tools. Ground penetrating radar (GPR) is a remote sensing technology that has been successfully used in evaluation of coarse tree root biomass. Incorporating ground

penetrating radar into current crop phenotyping methodologies could potentially provide a long awaited solution to high throughput phenotyping for roots under realistic field conditions. Ground penetrating radar was used in evaluation of wheat root biomass in vertisol type soils and compared with traditional sampling methods. Using a Geophysical Survey System Incorporated SIR-20 GPR, a replicated field trial of wheat consisting of 10 lines was evaluated for below ground biomass non-destructively at 80 cm intervals, using a signal frequency of 1.6 GHz, to ensure resolution within the first 2.5 cm of soil. Three-dimensional reconstruction and data analysis was made using GPR-SLICE v7.0 software. Root biomass was determined destructively from 5 cm x 1.2 m soil core samples divided into 4 equal depth profiles. Dry weight root biomass measurements of each depth profile



were compared to the ground penetrating radar signal returned for each plot. Ground penetrating radar spatially predicted root mass presence or absence ( $r^2 = 0.28$ ,  $n = 4620$ ,  $p < 0.0001$ ).

**Sean Thompson (Dirk Hays, chair)**

**Title: You go to the field: U.S. Borlaug Fellows in Global Food Security**

When asked how do you become a successful wheat breeder, Dr. Norman E. Borlaug replied, “Well, you go to the field. You go to the field again, and then you go to the field. When the wheat plants start to talk to you, you know you have made it.” The Nobel Peace Prize, the Congressional Gold Medal, and the Presidential Medal of Freedom were awarded to Dr. Borlaug for saving the lives of over one billion through his efforts. An example of how Borlaug’s legacy continues today is through the U.S. Borlaug Fellows in Global Food Security Program at Purdue University’s Center for Global Food Security, providing graduate students the opportunity to “go to the field” and become successful scientists in their own right. Funded by USAID, the Borlaug Fellowship provides graduate students the opportunity to collaborate with agricultural scientists in developing nations. The program fosters connections between scientists internationally, while furthering research and developing community around important agricultural themes, such as production, natural resource conservation, and development. With a focus on interdisciplinary and cross-cultural experiences, students benefit from the ability to practice their science on the ground in an international setting, preparing them to become important members of the global scientific community. Here doctoral candidate Sean M. Thompson of Texas A&M University was given the opportunity to “go to the field” during the 2013 field season in partnership with the International Maize and Wheat Improvement

Center (CIMMYT). The primary objective of Thompson's project, *Estimating Wheat Root Biomass Using Ground Penetrating Radar*, is to define the capability of the non-destructive high-throughput tool to phenotype below ground crop biomass, in the context of higher yield and quality stability in wheat during drought stress. Research was conducted in Ciudad Obregon, Sonora, Mexico at CIMMYT's Norman E. Borlaug Experiment Station.

### **Continuing Education in Plant Breeding at Texas A&M University**

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 open for enrollment are (<https://scsdistance.tamu.edu/purchase/>):

#### **Basic Plant Breeding: W. Smith**

**Unit 1: Introduction to Plant Breeding (13 January)**

**Unit 2: Self Pollinated Crops (24 February)**

**Unit 3: Cross Pollinated Crops (28 March)**

#### **Quantitative Genetics and Plant Breeding: S. Murray**

**Unit 1: (13 January)**

**Unit 2: (24 February)**

**Unit 3: (28 March)**

#### **Analysis of Complex Genomes: H. Zhang**

**Unit 1: DNA Marker Technology and Mapping (13 January)**

**Unit 2: Recombinant DNA and Cloning (24 February)**

**Unit 3: Sequencing Genomes and other Genomic Tools (28 March)**

#### **Host Plant Resistance: W. Smith**

**Unit 1: Introduction to HPR (13 January)**

**Unit 2: HPR to Diseases (24 February)**

**Intellectual Property and Plant Breeding: R. Jessup**

**Unit 1: Intro to IP, International Treaties & Patents (13 January)**

**Unit 2: IP Documentation (24 February)**

**Unit 3: IP Transfer and Enforcement (28 March)**

**Other Continuing Education courses in plant breeding and related disciplines that will be available include Host Plant Resistance; 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](mailto:leann.hague@tamu.edu) or (979)845-6148.**

**Distance Plant Breeding MS and PhD degree programs at Texas A&M. Visit <https://scsdistance.tamu.edu/plant-breeding-distance-education/> for details.**

**National Association of Plant Breeders 2014 Annual Meeting in Minneapolis MN on August 5 – 8. Visit [www.plantbreeding.org](http://www.plantbreeding.org) for details.**

**Please direct comments concerning this bulletin to Wayne Smith, [cwsmith@tamu.edu](mailto:cwsmith@tamu.edu) or 979.845.3450.**