

TEXAS A&M PLANT BREEDING BULLETIN -- January 2013

Our Mission: Educate and develop Plant Breeders worldwide.

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

A number of our Plant Breeding graduate students recently attended professional meetings and presented research data. The Beltwide Cotton Conferences met in San Antonio, TX on 7-10 January (http://www.cotton.org/beltwide/assets/website_documents/2013/2013-bw-online-booklet.pdf). The 2013 Plant and Animal Genome meetings were held in San Diego, CA from 12 January through 16 January (<http://www.intlpag.org/>). Complete schedules, abstracts, and some recordings of presentations can be found at the web sites above. Texas A&M Plant Breeding was well represented by these outstanding young men and women. The summaries below will give you a brief insight into the quality and quantity of research conducted.

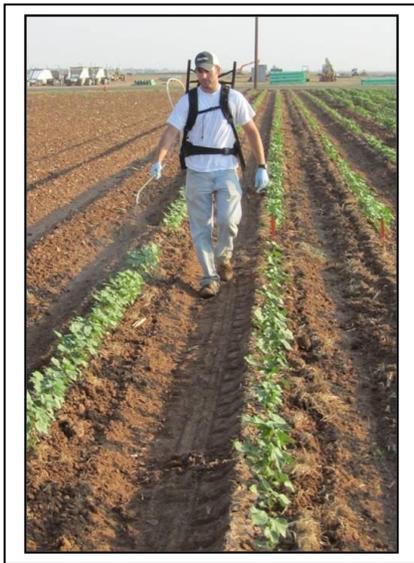
INHERITANCE AND STABILITY OF MUTATION-BASED HERBICIDE TOLERANCE IN COTTON (*Gossypium hirsutum* L.)

Trey Cutts (Ph.D. student with Jane Dever)

Mutant lines of upland cotton conferring tolerance of imidazolinone herbicides have been developed through mutation breeding using ethyl methanesulfonate (EMS) in three High Plains cultivars followed by selection pressure using imazamox herbicide. While previous studies have indicated that tolerance is controlled by a partially dominant gene in original mutated parents, little is known about the



inheritance of the trait during introgression. Therefore, inheritance studies have been initiated by selection of tolerant parental stocks and crossing these with an established cultivar (FM 958). Populations including parental lines, F₂, and F₃ non-selected generations, were evaluated in 2012 for early season imazamox herbicide injury from which heritability estimates were derived. Additionally, 2012 field studies also include a parental efficacy trial that evaluates treated and non-treated parents, and a parental equivalency trial that evaluates non-mutated and mutated parental cultivars to evaluate the imazamox tolerance stability. The mutation event that resulted in partial herbicide



resistance did not appear to harm plant growth and development, as yield and agronomic properties were substantially equivalent to non-mutated parent.

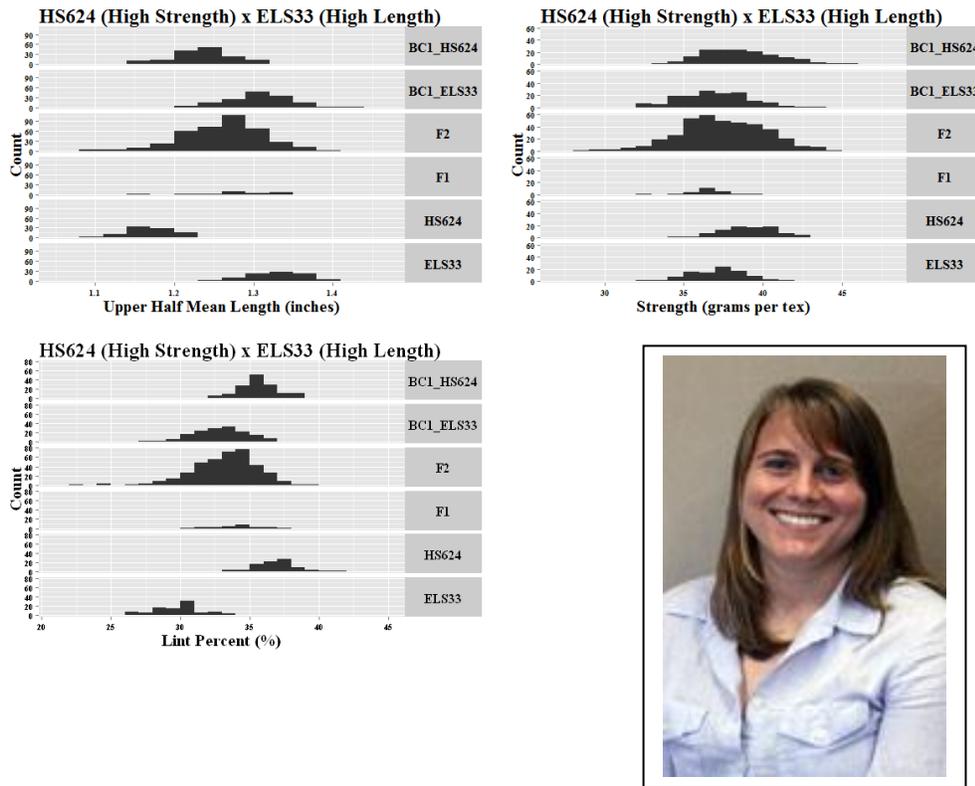
Yellowing of tolerant plants was evident 2 weeks post-application of herbicide, indicating current mutation events may not be commercially acceptable in terms of tolerance. The resistance trait is heritable, and non-transgenic herbicide resistance in cotton is possible with mutation events that provide more complete tolerance to target herbicide. More complete herbicide strategies, including mutation-based tolerance in combination with transgenic approaches can address effectively weed resistance issues.

DISTRIBUTIONS OF FIBER LENGTH AND STRENGTH IN F₂ AND BC₁F₁ GENERATIONS

Kari Hugie and Kolbyn Joy (Ph.D. students with Wayne Smith)

A generation means analysis recently conducted by Kolbyn Joy with the Cotton Improvement Lab, Texas A&M AgriLife Research, evaluated high volume instrumentation (HVI) upper half mean length (UHML) and fiber bundle strength using five genotypes that represented a wide genetic base. Genotypes included TAM B182-33 ELS, an upland extra-long staple line, TAM 94L-25 M24, an upland genotype derived through mutation breeding with exceptional UHML, 06 WE 62-4, an experimental upland line with exceptional strength, 04 SID 84-2, an interspecific derived line, and Tamcot 22, a conventional cultivar with moderate fiber length and strength. Distributions of UHML, fiber bundle strength,

and lint percent were compared between the F₂ and backcross (BC₁F₁) generations of 10 of the derived families. The distributions indicate that one BC generation to the high parent (i.e., fiber length or fiber strength) increased the frequency of desirable phenotypes compared to the F₂ distribution while maintaining useful variation among other fiber traits (Figure 1). These data suggest that one BC to a desirable phenotype within a standard pedigree breeding program in upland cotton may be useful to cotton breeders in the improvement of fiber length and strength.



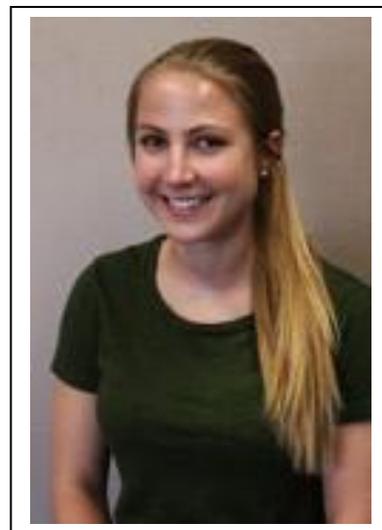
STABILITY ANALYSIS OF UPLAND COTTON IN TEXAS

Whitney M. Jones (M.S. student with Wayne Smith)

Plant breeding programs traditionally strive to improve cotton genotypes in terms of yield and overall quality by improving specific traits. The goal of this study was to evaluate the stability of several experimental lines of upland cotton exhibiting two significantly improved traits, upper half meal length (UHML) and fiber bundle strength. Eight experimental lines (four with exceptional UHML and four exceptional strength) were compared with three current cultivars, FM 832LL, Tamcot 22 and DP 491, for stability of

UHML and strength across several environments in Texas. Trials were planted at seven locations (College Station, Corpus Christi, Commerce, Lubbock, Thrall, and Weslaco) in 2010 and 2011 resulting in 11 environments, defined as a growing season per location. Utilizing regression analysis, the stability of each genotype for UHML and fiber strength across these 11 environments was quantified using the b_i , or slope, value. The stability of the experimental lines was considered different and unusual if their b_i values were greater or less than that of the check b_i value +/- standard error. Experimental UHML lines performed exhibited $b_i > 1.0$ while the control cultivars ranged from 0.96 to 1.12, suggesting that these exceptional UHML lines preformed better than the cultivars when grown in the more favorable environments.

The exceptional UHML lines were similar to the control cultivars in terms of strength stability across these 11 environments, i.e., they had similar b_i values. The exceptional strength lines performed similar in terms of UHML stability with the exceptional strength lines and the controls having b_i values indicating better performance in more favorable environments. However, two of the four exceptional UHML lines were less stable across environments. Overall, the results of this



study indicated that breeders should have little concern about stability of exceptional UHML or fiber bundle strength in upland cotton grown in Texas. Data may provide researchers with guidelines for performance testing resource allocation as well.

Data summary: Stability of four upland cotton germplasm lines exhibiting exceptional fiber bundle strength and for lines exhibiting exceptional upper half mean length, and three cultivars when grown at seven locations in 2010 and 2011 in Texas.

Cultivar	Trait	$b_i \pm se$ of UHML	$b_i \pm se$ of Strength
06WE 62-4	Strength	1.01	1.30
06WE 62-19	Strength	1.06	1.27
06WE 62-21	Strength	0.95	1.29
06WE 62-32	Strength	1.00	1.24
03 B-182-31-06-18	Length	1.31	0.83
TAM B182-33 ELS	Length	1.29	1.18
TAM C-147-42 ELS	Length	1.27	1.02

TAM C-155-22 ELS	Length	1.22	1.13
FM 832	Cultivar	0.96 ± 0.09	1.22 ± 0.15
DP 491	Cultivar	0.96 ± 0.06	1.38 ± 0.16
Tamcot 22	Cultivar	1.12 ± 0.08	1.26 ± 0.18

BREEDING TOWARDS INCREASED RESISTANCE TO COTTON FLEAHOPPER (Hemiptera: Miridae)

Laura Ann McLoud (Ph.D. student with Steve Hague)

Twenty parental lines were screened for resistance to the cotton fleahopper in an effort to evaluate their breeding value for use in a breeding program designed to move resistance traits from wild-type lines into high yielding lines. Three families of potentially resistant, wild-type lines (18 genotypes) and two high-yielding lines were screened for resistance to cotton fleahopper under field infestation levels in College Station and Corpus Christi in 2012. Genotypes within the three families exhibited pubescences ranging from no or almost no foliar trichomes (smooth) to very hairy (dense foliar trichomes); of the high-yielding lines, one was smooth and one was hairy (moderate level of foliar trichomes). Square-mapping was the primary tool by which plant responses to cotton fleahopper feeding pressure was monitored. Overall, the wild-type lines showed significantly less square loss than either of the high-yielding lines, despite harboring more fleahoppers than the high-yielding lines, similar to previously reported research. Within phenotype groups, the wild-type lines significantly outperformed the smooth and hairy high-yielding lines in terms of square loss. These data suggest that the wild-type lines have resistance to cotton fleahoppers and have significant breeding value. Development of generations to determine breeding behavior and heritability of this resistance have been initiated and will be reported at a later date.



Data summary: Percent square loss under natural cotton fleahopper infestation at College Station, TX in 2012, when plants were treated with an insecticide to control cotton fleahopper or not treated.

Untreated

Smooth		Hairy		Very Hairy	
Genot.	% loss	Genot.	% loss	Genot.	% loss
07V45	57.8 a	06WE14	32.7 a	GH04	16.4 a
GH02	44.1 b	GH02	17.3 ab	GH02	15.8 a
GH07	34.0 bc	GH07	15.9 b	GH07	13.3 a
GH04	32.2 c	GH04	14.0 b		

Treated

Smooth		Hairy		Very Hairy	
Genot.	% loss	Genot.	% loss	Genot.	% loss
07V45	41.3 a	06WE14	32.6 a	GH07	21.9 a
GH04	35.2 ab	GH04	16.0 b	GH02	13.5 a
GH07	33.8 ab	GH07	15.6 b	GH04	12.4 a
GH02	27.1 b	GH02	11.9 b		

TRANSGRESSIVE SEGREGATION FOR FIBER PROPERTIES OF THREE SELECTED POPULATIONS IN COTTON

Benjamin Meritt (M.S. student with Wayne Smith)

Improved fiber quality adds value to U.S. upland cotton and makes U.S. cotton more competitive in global markets. Improving characteristics such as fiber length, strength, uniformity and elongation will allow American cotton to be used for a wider range of end products. The issue currently, however, is that breeders must develop a more efficient methodology to improve selection of these characteristics. This study was developed to observe two equivalent generations of a breeding scheme in order to monitor selection opportunities for these desirable fiber traits via comparison of transgressive segregation. A simple pedigree and then pedigree plus backcross system was used that allowed us to look

at the F₃ and BC₁F₂ generations of three populations derived from the following crosses: Tamcot 22/TAM B182-33 ELS, Tamcot 22/ 06WE62-4, and Tamcot 22/04SID84-2).

Tamcot 22 is a high yielding, average quality cultivar, TAM B182-33 ELS is an extra long

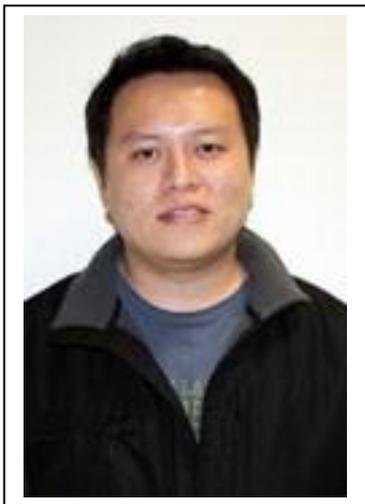


staple germplasm release, 06WE62-4 is a breeding line with exceptional fiber strength, and 04SID84-2 is a breeding line with exceptional length and strength derived from an interspecific cross of *Gossypium hirsutum*/*G. barbadense* biotype Sea Island. We observed fiber characteristics using High Volume Instrument analysis, and our results for 2011 did not suggest any pattern associated with

transgressive segregation by family. The majority of the positive transgressive segregates were contained in the BC₁F₂ generation that was backcrossed to the high quality parent, either TAM B182-33 ELS, 06WE62-4, or 04SID84-2.

GENETICS OF FIBER ELONGATION IN UPLAND COTTON

Eng Hwa Ng (Ph.D. student with Wayne Smith)



Fiber elongation is one of the key components in determining overall yarn quality. Elongation in U.S. cotton (*G. hirsutum*) has remained largely neglected due to [1] absence of monetary incentives for growers to produce high elongation cotton, [2] lack of research interests among breeders, and [3] absence of a reliable and repeatable fiber testing system for elongation. This study was conducted to [1] dissect gene action involved in fiber elongation

via generation means analysis (GMA) for five distinctive upland parents, [2] to predict gain from selection, and [3] to determine the possible effective factors, i.e., the number of genes in which the parents differed, involved in fiber elongation within the GMA families.

Sources of variation for fiber elongation across the six generations studied within each

GMA family were significant and Hayman's estimates indicated that gene actions for fiber elongation is predominantly additive. Estimated gains from selection for fiber elongation at 20%, 10% and 5% selection intensity averaged at 0.6%, 0.7% and 0.8%, respectively. Estimates of effective factors governing elongation in some of the GMA families in the study also suggested good diversity of elongation genes between parents.

RESOLVING TIGHT LINKAGES AROUND REN^{LON} BY MAS FOR HIGH-RESOLUTION RECOMBINATION IN CHROMOSOME 11 OF UPLAND COTTON

Xiuting Zheng (Ph.D) and Kevin Hoegenauer (M.S.) (students with David Stelly)



The reniform nematode (*Rotylenchulus reniformis*) resistance gene Ren^{lon} was introgressed into *Gossypium hirsutum*, a natural allotetraploid that is produced commercially worldwide, from *G. longicalyx*, a non-cultivated diploid, by Dr. A.A. Bell, USDA, ARS, College Station, TX. Two resistance lines, Lonren-1 and Lonren-2, have been released from the original introgression work. However, the Lonren materials often show abnormal or stunted growth in fields heavily infested with reniform nematodes, although the reniform nematode population is reduced, thus reducing the impact of reniform nematodes the following crop year. If the nematode population is low or it has been repressed by growing Lonren-1 or Lonren-2, then the Ren^{lon} gene functions as hoped, suppressing reniform nematode numbers and normal plant growth is observed. From a breeding standpoint, the plant growth stunting problem associated with the Lonren materials needs to be resolved, which would make the material more valuable as parental material in developing resistant

cultivars. To attack this issue, we have created a large population (~10,000s seeds) from different resistance families of Lonren and 70,000s *G.longicalyx* SNPs by RNA-seq. These SNPs have been aligned to the alien segment region by D5 genome assembly. Some SNPs have been tested and found to be linked with *Ren^{lon}*. The next step is to make a high-resolution map for the resistance gene region using SNP makers. This will result in additional Lonren lines for MAS and better characterize this chromosome region, since numerous nematode and fungal resistance loci, and some fiber quality genes are known to reside in this region. A large population will be screened with closest SNP makers in an attempt to separate the resistance loci from those associated with plant stunting, assuming that the stunting is due to linkage drag. A high-through put DNA extraction method that is non-destructive and based on seeds has been developed for this effort.

Reminder: NAPB Annual Meeting, 2-5 June 2013 in Tampa, FL

Visit <http://www.plantbreeding.org/napb/Meetings/pbccmeeting2013.html> for information on the seventh annual meeting of The National Association of Plant Breeders. The annual meeting is an opportunity for breeders and allied scientists to stay updated on recent innovations in plant science and to discuss public policy issues relevant to plant breeding. The meeting also provides an important venue for graduate students to present their research, meet with potential employers, and become acquainted with plant breeding graduate students from other universities. This year's meeting will be hosted by the University of Florida.

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eLearning at Texas A&M University: <http://elearning.tamu.edu>

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