A PHENOTYPIC EVALUATION OF 61 MUTATED LINES OF TAM 94L-25

A Thesis

by

ISMAEL NINO BROWN

Submitted to the Office of Graduate Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

MASTER OF SCIENCE

December 2010

Major Subject: Plant Breeding

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Approved by:

Co-Chairs of Committee,	Wayne Smith
	Steven Hague
Committee Members,	James Starr
Head of Department,	David Baltensberger

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ABSTRACT

A Phenotypic Evaluation of 61 Mutated Lines of TAM 94L-25.

(December 2010)

Ismael Nino Brown, B.S., Texas A&M University

Co-Chairs of Advisory Committee: Dr. Wayne Smith
Dr. Steve Hague

Among the available methods of creating selectable variation, induced mutagenesis has been historically under-utilized in cotton improvement. Dick Auld showed that chemical mutagenesis could be used to enhance fiber length of a medium staple cotton cultivar without sacrificing yield. The goal of this project was to determine if mutagenesis could be used to improve the fiber quality of a germplasm line already considered to be at the upper-limits of fiber length.

Seed of TAM 94 L-25 were treated with EMS in 2001 and the M_2 generation was produced at Lubbock, Texas in 2002. More than 1200 M_3 plants were grown at College Station, Texas in 2004, harvested individually, and HVI fiber properties determined. The top and bottom 1 % for UHML, strength, and elongation were selected and the seeds of these individuals planted as an M_4 progeny row nursery in 2005. Approximately ten individual plants per progeny row were harvested for re-evaluation of fiber parameters. From the approximately 1600 individual TAM 94L-25 M_4 plants harvested in 2005, 61 were selected and subsequently treated as pure lines. Agronomic performance trials were conducted on 61 of those TAM 94L-25 M lines along with the M_0 check and two commercial cultivar checks, Fiber Max 832 and Phytogen 355, in 2008 and 2009 in

College Station and Weslaco, Texas. Within-boll yield components were examined for 13 representative mutant lines and the three checks.

TAM 94L-25 averaged 751 kg lint ha^{-1}, 31.1 mm UHML, 303 kN m kg^{-1} fiber bundle strength, and 6.0% elongation. The 61 mutant lines yielded from 366 to 932 kg lint ha^{-1}, exhibited UHML from 24.3 to 34.9 mm, fiber bundle strengths of 261 to 333 kN m kg^{-1}, and elongations from 5.4 to 8.1%. Seed surface area of the TAM 94L-25 M-lines was between 99 and 124 mm^2, and fibers per unit seed surface area from 123 to 168 fibers mm^{-2}. The M_0 parent, TAM 94L-25 averaged 125 mm^2 $seed^{-1}$, and 128 fibers mm^{-2}. The data presented herein demonstrate that EMS-induced mutagenesis was successful in creating TAM 94L-25 M-lines with superior fiber and yield traits to that of the non-mutated, high fiber quality parent, TAM 94L-25.

DEDICATION

I would like to dedicate this thesis to my beautiful wife, Emily, and dear son, Aiden.

ACKNOWLEDGEMENTS

I would like to take this opportunity to thank my committee co-chairs, Drs. Wayne Smith and Steve Hague, and committee member, Dr. Jim Starr, for their guidance and insight. I would like to especially thank Dr. Smith for giving me the opportunity to work at the Cotton Improvement Lab and for being such a great mentor and boss. My years spent working at the CIL for Drs. Smith and Hague were an absolute pleasure, and I will miss the lab dearly.

Thank you to the student workers at the Cotton Improvement Lab who were always so willing to work hard and provide much needed levity when circumstances permitted. They are a great group of people and I am proud to have worked with every one of them. A special thanks to Dawn Deno, who was not only a great co-worker, but a dear friend of whom I am forever grateful to have known.

Thank you to my parents for teaching me the value of family, honesty and hard work. There is no better example than the way they live their lives. Thank you also to my brother who has always looked out for me and been my best friend. Thank you to my grandparents for their subtle encouragements to attend A&M, and everything they have done for me. I will always be thankful for the time I was able to spend with my grandparents in College Station.

Finally, thank you to my loving wife, Emily, for the encouragement and love she has shown me during this process, and to my little buddy, Aiden, for the joy he brings to my life.

NOMENCLATURE

TAM 94L-25 M-lines	Mutant lines of TAM 94L-25
M-#	Mutant line designation; the number following the letter is an arbitrarily assigned identifier
EMS	Ethyl methane sulfonate
FM 832	Fiber max 832
PSC 355	Phytogen 355
MS	Mean squares
DF	Degrees of freedom
LYLD	Lint yield
TLYLD	Square-root transformed lint yield
SGLP	Saw-ginned lint percent
HVI	High volume instrument
MIC	Micronaire
UHML	Upper half mean length
UNIF	Uniformity index
STR	Fiber bundle strength
ELONG	Elongation
AFIS	Advanced fiber information system
HGLP	Hand-ginned lint percent
LN	Length by number
FINE	Fineness

FIB/SD	Fibers seed^{-1}
SUR/SD	Surface area seed^{-1}
FIB/MM	Fibers millimeter^{-2}

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INTRODUCTION

Gossypium hirsutum (upland cotton) has long been prized for its high lint yield and ease of geographic adaptability. It is grown extensively in the southern United States from California to North Carolina and all over the world. The cotton industry has changed a great deal in recent years with textile producers moving operations overseas and textile production technology advancing very quickly. Higher yarn processing speeds requires a high quality fiber for efficient production. American producers of cotton must compete in a global economy of countries that produce excellent cotton. Because the market in the US is largely an export market of the raw material, the success of American producer exports depends largely on the quality of the cotton produced.

Technological advances in processing as well as market tastes have contributed to the demand of a higher quality fiber. Long, fine fibers create higher strength yarns and better quality textiles {Perkins, 1984 #95}. Better fiber strength and elongation are becoming increasingly important in processing of today's textiles {May, 2000 #96}. Longer fibers, with higher strengths and greater elongation are the material of choice for spinners because the fibers can be processed into yarn cheaper due to less waste in the processing {Bradow, 2000 #94}. It is imperative then, that cotton breeders focus on improving fiber quality as well as yields.

Cotton has been selectively bred for thousands of years. Modern, scientific plant

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This thesis follows the style of the Journal of Crop Science.

breeding has occurred only in the last century, but during this time, incredible advances have been made in fiber yields per hectare. Yields have nearly doubled since the 1950s. Fiber yields ranged from 302 to 522 kg ha^{-1} during that decade, and total production reached as high as 15 million bales {, 2010 #100}. The early 2000s saw total production reach as high as 20 million bales a year on half the acreage. National average yields routinely reach as high as 900 kg ha^{-1} {USDA, 2010 #100}. The 2009 cotton crop produced only 12.2 million bales, 97% of which was upland cotton, and was worth 3.7 billion dollars. National average Upper Half Mean fiber length (UHML) for 2009 was 28.1 mm, and fiber bundle strength (STR) averaged 285 kN m tex^{-1}. Texas averages ranged from 26.8 mm to 28.4 mm for UHML, and 278 to 290 kN m tex^{-1} for STR, at the four classing offices in the state {USDA, 2010 #100}.

Yield, defined in this paper as kilograms (kg) lint per hectare (ha), has been the driving force in modern cotton breeding, and one possible explanation for the lack of fiber quality improvement. The intense breeding for this trait might have narrowed genetic diversity to such a point that fiber quality gains have become difficult.

GENETIC DIVERSITY

It has been often suggested within the literature that the domestication of the crop from its wild Mexican, photo-periodic progenitors and modern plant breeding has severely narrowed the genetic base of the cultivars currently grown globally and within the US. *G. hirsutum* exists in nature throughout both Central and South America. These wild relatives

of the crop are bushy perennials, produce little fiber, and are photoperiod sensitive. Indigenous peoples of the Mexican-Guatemalan border region are believed to have selected plants that had a more annual growth habit, and flowered during the long days of summer {Hutchinson, 1947 #70}. These then became established in the Mexican highlands and served as the primary introduction source of US Upland cotton {Wendel, 1992 #51}. Iqbal suggests that this selection could have produced a severe "genetic bottleneck" on the inherent diversity of cultivated Upland cotton grown in the US, as many of the current cultivars can be traced back to these Mexican accessions {Iqbal, 2001 #18}. This theory of genetic similarity has been given further credibility by a large body of molecular studies using varying molecular methods {Rahman, 2002 #71;Rana, 2005 #64;Liu, 2000 #66;Iqbal, 1997 #50}

Several methods of introducing variation exist, but it is often suggested that exotic, wild material be introduced into breeding populations to increase diversity and therefore variation of the progeny. Due to the photoperiodism of some of these tropical brethren, however, they are not readily available for use in breeding programs within the US or other non-tropical locales. To combat this, some public programs use back crossing schemes to introduce day-neutrality into tropical accession lines {McCarty, 1996 #19}. These day-neutral, tropical lines and inter-specifics, can then serve as an invaluable source of novel genes for lint yield, fiber quality, and stress and pest resistance {Zeng, 2007 #89;McCarty, 2006 #63;Meredith Jr, 1991 #90}. The draw-back to this is, of course, the length of time necessary to produce these day-neutral lines, the retention of unfavorable linkage groups, and the loss of favorable alleles. Compounding this, of course, is the fact that once

day-neutrality has been reached, it takes further backcrossing to introduce the desired traits into a commercially acceptable cultivar.

Inter-specific hybridization is also an important method of introducing diversity to *G. hirsutum*, and has been used with some success. Although these methods work and are useful, they have produced few, if any, commercially grown cultivars with widespread popularity. The time it takes to produce commercially viable cultivars descendent from backcross populations is simply too long. By the time the desired trait has been introduced into a high yielding variety, another entity has long since produced a higher yielding variety. Although an important tool, backcross breeding may not be the most efficient method of introducing variation into a breeding pool.

Although theoretically, there should still be plenty of genetic diversity within closely related species and wild relatives to provide us with the genes necessary to boost fiber quality and yields, the process is difficult and time consuming. The gains attained are often over-shadowed by the massive debt incurred in other traits. Fiber quality my increase dramatically, but the yield of the plant, or the agronomic characteristics of the plants may become undesirable. A situation where breeders could take adapted cultivars and tweak one or two traits quickly without disrupting the beneficial linkage groups would be the desired course of action.

MUTATION BREEDING

The use of mutagens on organisms as a method of altering their genetic make-up has been around for a long time. The pioneering work done by HJ Muller on *Drosophila*

in the late 1920s and 1930s lead to great insights into the nature of radiation mutagenesis. Mutation work quickly branched out to include crop species such as barley and maize (Stadler, 1928a; Stadler, 1928b), and has grown to become an invaluable tool in genetic research and breeding. Point mutations and deletion mutations have led to the discovery of several genes in many species. Much of the molecular genetic work being done in several crops relies on these types of mutations to discover allelic locations by disrupting coding regions and locating where the change occurred and matching that to the phenotype.

In addition to being used for gene discovery, mutation can also be used in creating novel genetic variation within populations. Mutations are what drive evolution, but they only occur within a population at very low rates. The use of mutagenic agents increases the rate of mutation. Radiation such as x-rays and gamma-rays typically produce deletion type mutations, which are usually single nucleotide deletions along the organism's genome. Chemical mutagens such as ethyl methanesulfonate (EMS), cause point mutations by nucleotide substitutions. These are almost exclusively G/C to A/T conversions and occur at random along the target organism genome (Greene et al., 2003). A point mutation only alters a coded protein within the amino acid sequence in which it occurs, whereas a nucleotide deletion can alter an entire reading frame.

EMS has been shown to be a more efficient and effective mutagen due to its high plant mutation and survival rate (Favret, 1960). The higher survival rate results in higher recovery of mutants.

Mutation has not been used extensively in upland cotton breeding. Auld, however, has produced several papers and released several lines (Auld and Bechere, 2000; Auld et

al., 1998; Auld et al., 2009; Bechere et al., 2009; Herring et al., 2004; Key et al., 1998; Krifa et al., 2007; Peabody et al., 2002) that were the fruits of induced mutagenesis.

TAM 94L-25

TAM 94L-25, the germplasm line used in this mutation experiment, was released by the Cotton Improvement Lab, Department of Soil and Crop Sciences, Texas A&M University (Smith, 2003). With the goal of improving fiber length and bundle strength, this line was developed through traditional cross hybridization and pedigree selection. TAM 94L-25 resulted from an individual plant selected in the segregating F_3 population of a cross between TAM $87G^3$-27 (Smith and Niles, 1994) and TAM $87O^3$-37, an unreleased breeding line developed by Niles. In 19 irrigated and 18 non-irrigated test trials grown in several locations across Texas and one plot in Oklahoma between 1996 and 1998, the High Volume Instrument (HVI) Upper Half Mean Length (UHML) of the fibers averaged 31mm and 29mm respectively. An HVI Micronaire (MIC) reading of 4.4 units was acceptably fine and no different than the commercial checks included in the test.

TAM 94 L-25 is a cotton germplasm with above average fiber quality. Yield potential of the line is not worthy of a cultivar, however, it has been an integral parent in the pedigree of several germplasm lines released by the Cotton Improvement Lab at Texas A&M University with commercially competitive yields (Smith et al., 2008; Smith et al., 2009). One of the goals of this project was to ascertain the ability of mutagenesis to improve upon a trait already considered at the upper-limits of breeding potential for upland cotton. TAM 94L-25 was chosen for its excellent fiber, and acceptable yield.

OBJECTIVES

The objectives of this project were to determine if the Auld et al. (1998) method of crop mutagenesis could be used to further improve yield and fiber quality of a cotton germplasm line with exceptional fiber quality. To accomplish this we assessed 61 putative TAM 94L-25 M-lines for yield and fiber quality characteristics to identify exceptional variants. Within-boll yield components were also examined for variants with improved traits.

MATERIALS AND METHODS

PROJECT HISTORY

Two kg of TAM 94L-25 seeds were treated at Texas Tech University in 2001, with ethyl methane sulfonate (EMS), a mutating agent, at three to five times the LD_{50} {Auld, 1998 #39}. The resulting M_1 and M_2 generations were grown at the Texas Tech University Research Farm in Lubbock, Texas in 2001 and 2002. About 1300 M_3 plants were grown at College Station, Texas in 2004. These plants were individually hand harvested, the seed cotton saw-ginned on a laboratory 10 saw gin, and the fiber tested at the Fiber and Biopolymer Research Institute (FBRI) in Lubbock, Texas using High Volume Instrument (HVI) analysis. The top and bottom 1 % for Upper Half Mean Length (UHML), fiber bundle strength (STR), and elongation (ELONG) were selected and the seeds of these individuals were planted in a M_4 progeny row nursery in 2005. Approximately ten individual plants per progeny row were harvested for re-evaluation of fiber parameters. Fifty normal, full size bolls were hand harvested from 128 rows of TAM 94L-25 M_0 generation planted within the F_4 progeny row nursery to serve as checks for base line fiber properties. Seed-cotton from these individual plants and the TAM 94L-25 M_0 boll samples were ginned on a laboratory 10-saw gin and fiber analyzed for HVI fiber properties at the FBRI in Lubbock, TX. From the approximately 1600 individual TAM 94L-25 M_4 plants harvested in 2005, 63 were selected and subsequently treated as pure lines.

As noted in the introduction, the premise of this research was based on results reported by Auld {Auld, 1998 #39;Auld, 2000 #30} that treatment with EMS provided the

opportunity to select for improved UHML. The 63 lines selected for additional evaluation contained individual lines with [1] longer UHML, [2] shorter UHML, [3] higher strength and/or [4] greater elongation. These 63 TAM 94L-25 $M_{4:5}$ lines, along with the M_0 TAM 94L-25 were grown in a progeny row nursery at College Station and Weslaco, Texas in 2007 to increase seed supply and verify fiber properties. Twenty-five boll samples were hand harvested from each progeny row, ginned on a laboratory 10-saw gin, and evaluated for HVI fiber properties at the FBRI in Lubbock, TX. Seed from the 63 lines were retained for field trials in 2008. Two lines were discarded based on poor seed yield in 2007.

YIELD TRIALS

In 2008 and 2009, 61 TAM 94 L-25 $M_{4:6,6}$ progeny lines, along with TAM 94L-25 M_0 and two commercial check cultivars, Fiber Max 832, and Phytogen 355, were grown in a randomized complete block design with four replications at two locations. Phytogen 355 was selected due to its high yield potential in south-central Texas, and Fiber Max 832 was included because of its good fiber quality and high yield potential. The trial was planted at two locations, College Station and Weslaco, TX. Each plot was two rows x 1.02 m x 10.1 m at Weslaco, and two rows x 1.02 m x 13.1 m at College Station. Soil type at the Texas A&M Research Farm near College Station, TX was a Ships clay loam. Soil at Weslaco was a Raymondville clay loam. Planting was accomplished with a John Deere MaxEmerge planter with plot cone-planters. Furrow irrigation provided supplementary water requirements, and each field was fertilized pre-season and again at first to mid-bloom stage of growth with 25.4 kg N ha^{-1}. Herbicide and insecticide applications were

made as needed throughout the season. One row of each plot was harvested using a one-row spindle picker modified for research plot harvest. Twenty-five mature, open bolls were hand harvested from the non-machine harvested row in reps one and three before harvest. Bolls were selected on an arbitrary basis from the fruiting zone and along the entire row to ensure a thorough representation of the fiber quality distribution. Boll samples from lines previously selected for determination of within-boll yield components, described below, were hand harvested from the second rep also. Boll samples were ginned on a laboratory 10-saw gin, and fiber samples of at least 40 g were sent to the FBRI in Lubbock for HVI analysis.

WITHIN BOLL YIELD COMPONENTS

A selected subset of the 61 TAM 94L-25 M lines was used to determine the impact of a putative mutation event on the relationship of HVI fiber quality characteristics and within boll yield components of fibers seed^{-1} and fibers per seed surface area. To accomplish these objectives, lines were selected based on individual plant fiber properties, and in 2008 and 2009, sub-samples were taken from the yield trial plot boll samples for hand ginning and AFIS fiber analysis. This procedure was carried out in College Station in 2008 and 2009, but only in 2009 at Weslaco. These samples were hand ginned to minimize fiber damage that would affect the fiber length readings and therefore the total number of fibers calculation.

From each boll sample harvested per plot, eight locks, insuring 50 seeds, were arbitrarily selected in each of the selected lines for hand ginning, along with each of the

control cultivars. Each sample was carefully hand ginned by one individual to minimize variation in technique. Fibers were sent to the FBRI at Lubbock for AFIS analysis. Seed cotton, fuzzy seeds, and lint were weighed to minimize possible recording mistakes. True lint percent was determined as [lint wt. / seed cotton wt) * 100].

Sulfuric acid (95%, industrial grade) was used to remove the linters, the fibers still clinging to the seed after ginning. Thirty delinted seeds were then scanned using a modified computer scanner (Epson Perfection 3200 Photo) and seed surface area determined using the WinSeedle™ {Regents Instruments, #101} software/scanner platform. Each sample of 30 seeds was scanned, then re-randomized on the scanning surface and scanned again for a total of three scans.

The WinSeedle™ program takes a series of measurements from the scanned images, measuring the lengths of each seed as well as the width at the widest point. It then calculates a center line for each seed, which serves as an axis for the program to apply three different cross-sectional shapes to create three different three-dimensional surface area estimates of the seed. For cotton seed the closest approximation would be a circular cross-section as opposed to the ellipsoidal or oval choices in the computer program. Surface area values used in this experiment were based on a circular cross-section. The average number of fibers per unit surface area was calculated using the data collected from the AFIS readings of each sample and the average seed surface area determined in the Winseedle program. The equation used to determine the total number of fibers per sample was:

$$1{,}000{,}000\ (Lwt/Fn) / (L_{(n)}*0.0254)$$

where Lwt is the total weight of the fiber sample in grams, Fn is the AFIS fineness reading in millitex (milligrams per kilometer), and $L_{(n)}$ is the mean fiber length by number reading from AFIS in inches. Multiplying by the 1,000,000 constant is for unit conversion. Fineness is given in mg km^{-1}, so the fiber sample weight must be converted to mg by multiplying by 1000. Multiplying by 1000 again then converts kilometers to meters. $L_{(n)}$ is given in inches, so it must be converted to meters by multiplying by 0.0254. The resulting number is then number of fibers per sample.

Fibers $seed^{-1}$ is determined by dividing the total number of fibers per sample by the total number of seed per sample. The fibers per seed values for each sample were divided by the average seed surface area for each sample to determine fibers per unit seed surface area.

STATISTICAL ANALYSES

Yield trials were conducted in 2008 at College Station and in 2009 in College Station and Weslaco. Bartlett's Test for Homogeneity of Variances was applied to the data to ensure equal and proportionate variances. The yield data variances were found not to be homogeneous, and the data were transformed with a number of standard transformation factors. Although square root transformation resulted in the best distribution and therefore used in the analysis of variance, none of the transformations resulted in homogeneous variances. Yield means and analysis parameters were corrected to original units in all tables. Bartlett's Test indicated that HVI data variances were homogeneous.

Analyses of variances were conducted using the SAS/STAT® software, Version 9.1.3 of the SAS System for Windows {SASInstitute, 2002-2003 #104}. PROC GLM, or the general linear model, was used to analyze the data. Years, location, and genotypes were considered fixed effects. Means were separated by Bayes' LSD at k=100, which approximates the 5% probability level. Significant interactions were evaluated as described by Smith {Smith, 1978 #3}.

Surface area and AFIS data were analyzed similarly to the yield and HVI data. Bartlett's Test for Homogeneity revealed a few environments where variances were not homogeneous. Because seed surface area determinations were only made in one of the two years at Weslaco, location years were analyzed as environments. This allowed for a balanced test. Environments and genotypes were considered fixed effects for the general linear model. No significant interactions were observed between environment and genotype for any of the traits considered.

RESULTS AND DISCUSSION

YIELD AND HVI FIBER PROPERTIES

Yield Parameters

Bartlett's Test for homogeneity of variances was conducted on the original yield data for each location and year (Table 1). Variances for lint yield were found not to be homogeneous in either year at College Station and in 2008 for Weslaco, and thus yield data were transformed by the typical arithmetic transformations in an attempt to homogenize the data. Of those used, square root transformation produced the fewest significant environments. The chi square values for the transformed data were significant for two of the location years as opposed to three in the non-transformed data. The transformed data was therefore used in the analysis of variance.

The analysis of variance indicated that all sources of variation were significant for lint yield and lint percent (Table 2). Significant interaction sources of variation for genotype x year and genotype x location suggests that it is statistically inappropriate to separate means of main effects (year, location, and genotype), and the standard strategy is to separate genotypic means within each year and within each location. However, such methodology does not allow the identification of genotypes that are responding the same to year or location and which genotypes are responding differently. This could be important information in a plant breeding program where stability of genotypic response would be meaningful information when deciding which genotypes to keep or discard.

Table 1. Homogeneity of variance chi-squares of yield and HVI fiber traits for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX.

	College Station		Weslaco	
Source	2008	2009	2008	2009
TLYLD	83.4**	77.6	187.9**	68.0
LYLD	82.8**	84.6**	102.5**	65.6
SGLP	52.0	74.0	68.1	55.6
MIC	33.5	34.6	30.2	30.4
UHML	21.3	44.8	30.0	31.1
UNIF	57.4	57.8	49.1	36.3
STR	66.1	44.9	44.9	53.1
ELONG	41.4	37.2	39.7	31.8

** Significant at the 0.01 probability level

Table 2. Analysis of variance mean squares (MS) for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX. Genotype by year interaction (G x Y), genotype by location interaction (G x L), and genotype by year by location interaction (G x Y x L).

	TLYLD		SGLP	MIC	UHML	UNIF	STR	ELONG
Source of Error	df	MS	df	MS	MS	MS	MS	MS	MS
Year	1	2963**	1	322**	6.1**	1026**	331**	1124**	646**
Error A	6	31	2	0.2	0.8	2.5	0.2	0.5	0.4
Location	1	12586**	1	8.6	7.9	78**	212**	421**	27.2**
Error B	6	45	2	9.7	3.5	4.0	0.6	2.2	0.1
Genotype	63	172**	63	28.5**	7.5**	57.8**	4.0**	25.1**	3.2**
G x Y	63	46**	63	2.7**	0.6**	3.3**	1.1	2.8**	0.3**
G x L	63	10**	63	2.1**	0.5**	1	1.4**	2.1	0.1
G x Y x L	63	13**	63	1.9**	0.5**	1	1.0	2.1	0.1
Error C	755	5	252	1.1	0.3	0.8	0.9	1.7	0.1

** Significant at the 0.01 probability level

Smith (1978) described methodology to separate interaction elements and to identify genotypes responding similarly or differently to environments. This methodology separates interaction elements, described as the difference between treatments (in this case genotypes), using a modified error standard deviation in the calculation of an LSD. Instead of calculating an error standard deviation of the difference of two treatment means, the formula calculates the error standard deviation of the difference of four treatment means, thus $s=\sqrt{(4*ems)/r}$. This standard deviation value is used in the formula for calculating the LSD of choice, a Bayes LSD (or Waller or Waller/Duncan) as reported herein. This method allows breeders to recognize patterns or genotypes that might have interacted differently to years or locations. In the research reported herein, it was considered important to know whether or not the mutated TAM 94 L-25 lines reacted differently to changes in environment than the parent or check cultivars.

Genotypes responded differently to years as indicated by the significant genotype x year interaction source of variation (Table 2). Thirty-four of the TAM 94 L-25M lines responded similarly to the 2008 and 2009 growing seasons as did TAM 94 L-25 (Tables 3 and 4). However, most of the mutation lines and the parental TAM 94L-25 responded differently than FM 832 or PSC 355. Assuming that the response of the parental TAM 94L-25 and the two commercial checks indicates stability, there were 21 TAM 94L-25M lines with deltas different ($p<0.05$) than at least one of the controls and thus were not stable across these two years. Four TAM 94L-25M lines (39, 50, 45, and 49), exhibited deltas 2.9 to 3.8 times larger than the delta for the TAM 94L-25 parent. These lines, however, in 2008 had poor lint yields, ranging from 237 to 410 kg ha^{-1} and in 2009 ranged

Table 3. Genotype x location and genotype x year interactions of square-root transformed yield data (TLYLD) for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX.

Genotype x Year				Genotype x Location			
Genotype	2009	2008	Δ	Genotype	W	CS	Δ
M-39	26.3	15.6	10.7	M-9	30.6	20.8	9.8
M-50	24.5	14.5	9.9	M-16	27.5	17.8	9.7
M-45	27.1	19.1	8.0	M-29	30.7	21.1	9.7
M-49	23.0	15.1	8.0	M-52	26.7	17.1	9.6
M-36	24.4	16.8	7.6	M-22	31.2	21.8	9.4
M-52	25.6	18.2	7.5	M-46	28.2	18.9	9.3
M-5	25.3	18.2	7.2	M-53	31.2	22.1	9.1
M-32	24.4	17.3	7.1	M-13	29.9	21.0	8.9
M-13	28.9	22.0	6.8	M-24	31.8	22.9	8.8
M-55	24.1	17.3	6.8	M-56	31.0	22.2	8.7
M-4	26.5	19.9	6.6	M-51	27.0	18.4	8.7
M-43	24.5	17.9	6.6	M-20	25.1	16.6	8.4
M-7	23.2	16.6	6.5	M-2	30.0	21.6	8.4
M-42	23.1	16.7	6.4	FM 832	36.0	27.6	8.4
M-6	21.7	15.4	6.3	M-14	28.7	20.4	8.3
M-21	22.5	16.3	6.3	M-5	25.9	17.6	8.3
M-11	28.4	22.3	6.1	M-40	25.9	17.7	8.2
M-61	24.5	18.5	6.0	M-63	27.7	19.5	8.2
M-12	26.3	20.4	6.0	M-36	24.6	16.6	8.0
M-41	22.7	16.9	5.8	M-6	22.4	14.7	7.7
M-10	27.4	21.7	5.7	M-12	27.2	19.5	7.7
M-37	24.1	18.6	5.5	M-43	25.1	17.3	7.7
M-35	20.7	15.4	5.2	M-59	27.3	19.6	7.7
M-53	29.3	24.1	5.2	M-8	30.3	22.6	7.7
M-46	26.0	21.0	5.0	M-25	31.1	23.5	7.6
M-34	23.9	19.1	4.8	M-58	32.1	24.6	7.5
M-51	25.1	20.3	4.8	M-34	25.2	17.7	7.5
M-9	28.0	23.3	4.7	M-10	28.3	20.8	7.5
M-33	24.7	20.2	4.5	M-23	32.5	25.2	7.3
M-40	23.9	19.6	4.3	M-54	30.9	23.6	7.3
M-44	23.7	19.4	4.3	M-39	24.6	17.4	7.2
M-60	24.7	20.6	4.0	TAM 94 L-25	29.5	22.3	7.2

Table 3 continued

Genotype x Year				Genotype x Location			
Genotype	2009	2008	Δ	Genotype	W	CS	Δ
M-62	26.4	22.7	3.8	M-17	27.1	20.0	7.1
M-63	25.4	21.8	3.6	M-26	32.0	24.9	7.1
M-54	28.9	25.5	3.4	M-4	26.7	19.7	7.0
M-14	26.1	22.9	3.3	M-15	25.8	18.8	7.0
TAM 94 L-25	27.3	24.5	2.8	M-32	24.3	17.4	6.9
M-16	24.0	21.2	2.8	M-7	23.3	16.5	6.8
M-19	23.0	20.4	2.6	M-55	24.1	17.3	6.7
M-57	27.5	25.0	2.5	M-31	31.1	24.4	6.7
M-38	23.8	21.3	2.5	M-27	31.3	24.7	6.6
M-20	22.1	19.6	2.4	M-38	25.7	19.3	6.4
M-8	27.7	25.3	2.4	M-3	31.2	24.8	6.4
M-15	23.4	21.2	2.2	M-30	32.0	25.6	6.3
M-2	26.3	25.2	1.1	M-41	22.9	16.6	6.3
M-27	28.5	27.5	1.0	M-28	31.2	25.0	6.1
M-17	23.7	23.4	0.3	M-19	24.6	18.7	5.9
M-18	21.9	21.6	0.3	M-37	24.3	18.5	5.8
M-56	26.7	26.5	0.1	M-21	22.3	16.5	5.7
M-29	25.8	26.0	-0.2	M-62	27.4	21.7	5.7
M-1	28.1	28.3	-0.2	M-42	22.7	17.1	5.6
M-22	26.4	26.6	-0.2	M-45	25.9	20.3	5.6
M-26	28.3	28.6	-0.4	M-44	24.3	18.8	5.5
M-58	28.1	28.5	-0.4	M-35	20.8	15.4	5.4
M-3	27.8	28.2	-0.4	M-1	30.9	25.5	5.4
M-59	23.1	23.8	-0.7	PSC 355	34.8	29.4	5.4
M-24	26.7	28.0	-1.3	M-60	25.1	20.1	5.0
M-28	27.3	28.9	-1.6	M-33	24.8	20.1	4.8
M-25	26.3	27.9	-1.6	M-49	21.4	16.7	4.6
M-31	26.8	28.6	-1.8	M-57	28.6	24.0	4.6
FM 832	30.9	32.7	-1.8	M-11	27.4	23.2	4.2
M-30	27.7	29.9	-2.3	M-61	23.4	19.5	3.9
M-23	27.2	30.4	-3.2	M-18	23.5	19.9	3.6
PSC 355	30.5	33.7	-3.3	M-50	21.3	17.7	3.6
		Mean	3.1			Mean	6.3
		BLSD	2.8			BLSD	3.8

Table 4. Transformed lint yield (TLYLD) means expressed in original units (kg/ha) for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX.

2009		2008		Weslaco		College Station	
Genotype	TLYLD (kg/ha)	Genotype	TLYLD (kg/ha)	Genotype	TLYLD (kg/ha)	Genotype	TLYLD (kg/ha)
FM 832	1069	PSC 355	1275	FM 832	1453	PSC 355	969
PSC 355	1040	FM 832	1200	PSC 355	1356	FM 832	853
M-53	961	M-23	1039	M-23	1185	M-30	736
M-54	938	M-30	1004	M-58	1153	M-1	729
M-13	934	M-28	934	M-26	1145	M-23	710
M-27	909	M-31	919	M-30	1145	M-28	702
M-11	901	M-26	918	M-24	1131	M-26	695
M-26	895	M-58	910	M-27	1096	M-3	690
M-58	887	M-1	898	M-53	1093	M-27	684
M-1	885	M-3	893	M-22	1090	M-58	676
M-9	881	M-24	878	M-3	1090	M-31	665
M-3	865	M-25	873	M-28	1088	M-57	646
M-30	858	M-27	848	M-25	1084	M-54	622
M-8	858	M-22	791	M-31	1083	M-25	619
M-57	850	M-56	790	M-56	1074	M-11	604
M-10	840	M-29	756	M-1	1070	M-24	590
M-28	836	M-54	728	M-54	1067	M-8	574
TAM 94 L-25	835	M-8	717	M-29	1058	TAM 94 L-25	557
M-23	832	M-2	713	M-9	1049	M-56	554
M-45	824	M-57	702	M-8	1030	M-53	549
M-31	806	TAM 94 L-25	671	M-2	1008	M-22	530
M-24	800	M-53	650	M-13	1003	M-62	528
M-56	796	M-59	633	TAM 94 L-25	974	M-2	521
M-4	789	M-17	614	M-14	921	M-29	497
M-62	784	M-9	610	M-57	915	M-13	493
M-22	779	M-14	587	M-10	896	M-10	484
M-39	778	M-62	576	M-46	888	M-9	483
M-12	778	M-11	556	M-63	858	M-14	465
M-2	777	M-13	544	M-16	846	M-45	462
M-25	775	M-63	531	M-11	843	M-60	454
M-14	766	M-10	527	M-62	841	M-33	452
M-46	759	M-18	522	M-59	833	M-17	449
M-29	747	M-38	509	M-12	831	M-18	444

Table 4 continued

2009		2008		Weslaco		College Station	
Genotype	TLYLD (kg/ha)	Genotype	TLYLD (kg/ha)	Genotype	TLYLD (kg/ha)	Genotype	TLYLD (kg/ha)
M-52	737	M-16	506	M-17	823	M-4	436
M-63	722	M-15	504	M-51	819	M-59	430
M-5	718	M-46	494	M-4	800	M-61	428
M-51	705	M-60	476	M-52	798	M-12	427
M-33	683	M-12	466	M-45	754	M-63	425
M-60	681	M-19	465	M-40	751	M-38	419
M-61	673	M-51	462	M-5	751	M-46	399
M-43	671	M-33	458	M-15	746	M-15	397
M-50	670	M-4	445	M-38	742	M-44	397
M-32	669	M-20	432	M-34	714	M-19	393
M-36	666	M-40	431	M-60	709	M-37	382
M-37	652	M-44	423	M-20	705	M-51	378
M-55	651	M-45	410	M-43	704	M-16	353
M-16	645	M-34	408	M-33	691	M-34	352
M-40	642	M-37	389	M-19	680	M-50	352
M-34	639	M-61	382	M-39	679	M-40	349
M-38	632	M-52	370	M-36	678	M-5	347
M-17	630	M-5	370	M-44	663	M-32	340
M-44	630	M-43	360	M-37	662	M-39	338
M-15	615	M-55	335	M-32	662	M-43	337
M-7	601	M-32	335	M-55	649	M-55	336
M-59	597	M-41	318	M-18	620	M-52	329
M-42	596	M-36	316	M-61	615	M-42	327
M-49	595	M-42	313	M-7	608	M-49	314
M-19	593	M-7	310	M-41	589	M-20	310
M-41	577	M-21	297	M-42	577	M-41	310
M-21	569	M-39	274	M-6	565	M-36	308
M-20	546	M-35	267	M-21	556	M-21	307
M-18	535	M-6	267	M-49	513	M-7	305
M-6	529	M-49	255	M-50	507	M-35	265
M-35	480	M-50	237	M-35	483	M-6	243
Mean	738	Mean	555	Mean	846	Mean	469
CV	31.7	CV	11.9	CV	23.1	CV	18.9
BLSD		BLSD		BLSD		BLSD	

from 595 to 823 kg ha^{-1}, which was only 19% of the highest yielding check, PSC 355. This response could be due to some cause other than genetic response to an improved growing environment. Although no plant stand data were collected, plant populations in the 2008 plots appeared more erratic than in 2009. The improvement, or higher lint yield as indicated by negative deltas in Table 3, in 2009 yields for the 13 TAM 94L-25 M lines responding differently ($p < 0.05$) to the two years of this experiment than TAM 94L-25 may represent genotypes that respond positively to improved growing environments since both commercial checks, FM 832 and PSC 355, responded to years with higher yields in 2009 also.

Genotypes also responded differently to the two locations (Table 2). Separating these interaction elements, or deltas, indicated that the TAM 94L-25M lines responded similarly ($p < 0.05$) to these locations as the check cultivars, Fibermax 832 or PSC 355 (Tables 3 and 4). The TAM 94L-25M lines 39, 50, 45 and 49, which exhibited the largest deltas for genotype x year and responded differently ($p < 0.05$) to years than the controls, were distributed throughout the array of location x genotype deltas. In fact, TAM 94L-25M lines 45, 49, and 50 were among the numerically lowest deltas for this interaction. No check or mutant lines reacted significantly more disproportionately than TAM 94 L-25 to location for lint yield. The mean separations for this interaction suggest nothing biologically meaningful.

Although significant interactions mandate that one should look at individual years and individual locations within years when making selections among these TAM 94L-25M lines, an evaluation of overall genotypic means could be informative, although statistically

inappropriate. Lint yield within years across locations and within locations across years are shown for the reader's information in Table 4, while the square root transformed data with deltas and mean separation of the deltas are shown in Table 3. The genotype x year interaction is the most troubling from a selection perspective since several TAM 94L-25M lines were different ($p < 0.05$) than the parental line and the commercial controls, which could have been caused by the large number of highly variable genotypes or variation in seed quality. Planting seed for 2008 were produced in 2007 and that for 2009 was produced in 2008. The 2008 planting seed was of much lower germination quality (data not shown) than that for 2009 and therefore any differences in environmental stress could have impacted plot populations and productivity more than location differences averaged across years.

Mean lint yields ranged from 366 kg ha^{-1} for TAM 94L-25M-35 to 1155 kg ha^{-1} for PSC 355 when averaged over years and locations (Table 5). The two commercial checks, FM 832 and PSC 355, yielded significantly higher than any of the mutant lines. The non-mutated parent check, TAM 94L-25, averaged 751 kg ha^{-1}, which is significantly lower than the commercial check cultivars as well as the highest yielding mutant lines. Nine mutant lines yielded significantly higher than the TAM 94L-25 parent and 36 yielded lower, suggesting that treatment with EMS did result in mutation events resulting in changes in yield potential. Of the better yielding mutation lines, 12 had higher ($p<0.05$) UHML, 10 showed improved elongation values, two exhibited improved UI, and three had improved strength (Table 6). The three mutated lines with improved strength also had improved length but were not different than the parental strain in overall means for UI or

Table 5. Saw-ginned lint percent (SGLP) means for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX. Genotype means are shown averaged for each year, and averaged for each location. Transformed Lint Yield (TLYLD) shown for comparison.

		SGLP				
Genotype	TLYLD	Weslaco	College Station	2008	2009	Overall Mean
	kg/ha	%	%	%	%	%
PSC 355	1155	38.5	39.0	38.9	38.5	38.7
FM 832	1133	37.6	37.3	36.9	38.0	37.5
M-23	932	35.4	35.3	34.4	36.2	35.3
M-30	930	33.2	34.1	32.8	34.5	33.6
M-26	906	36.1	36.9	35.8	37.3	36.5
M-58	899	32.2	31.6	30.3	33.5	31.9
M-1	891	34.4	34.3	34.3	34.5	34.4
M-28	884	33.4	33.8	32.6	34.6	33.6
M-3	879	34.9	33.8	33.7	35.0	34.3
M-27	878	35.7	36.2	35.3	36.7	36.0
M-31	861	33.5	33.2	32.9	33.8	33.4
M-24	838	34.0	34.6	33.4	35.2	34.3
M-54	830	31.2	30.3	29.7	31.7	30.7
M-25	820	34.8	33.8	33.1	35.5	34.3
M-53	798	34.0	33.7	32.2	35.5	33.9
M-56	793	34.0	33.3	32.5	34.8	33.6
M-8	786	34.6	33.1	33.5	34.2	33.9
M-22	785	36.4	37.1	36.4	37.1	36.8
M-57	774	33.4	31.8	30.7	34.6	32.6
M-29	751	32.7	33.6	31.7	34.6	33.2
TAM 94 L-25	751	35.4	34.9	34.0	36.3	35.1
M-2	744	34.8	33.3	33.5	34.7	34.1
M-9	739	34.6	33.3	33.8	34.0	33.9
M-13	726	38.1	38.2	37.7	38.6	38.1
M-11	718	36.2	35.6	34.7	37.1	35.9
M-62	676	31.4	31.9	30.3	33.0	31.7
M-10	675	34.1	33.2	33.3	34.1	33.7
M-14	674	35.7	38.2	36.6	37.3	37.0
M-63	623	32.6	30.0	29.7	32.9	31.3
M-17	622	35.3	36.9	35.7	36.5	36.1
M-46	619	34.1	33.9	31.8	36.2	34.0
M-59	615	31.9	31.5	29.6	33.8	31.7

Table 5 continued

Genotype	TLYLD	SGLP				
		Weslaco	College Station	2008	2009	Overall Mean
	kg/ha	%	%	%	%	%
M-12	612	33.5	32.9	33.0	33.3	33.2
M-4	605	36.5	36.7	36.2	37.1	36.6
M-45	599	31.4	31.4	30.5	32.3	31.4
M-51	577	32.3	30.7	30.4	32.6	31.5
M-60	574	31.0	30.3	29.4	31.8	30.6
M-16	573	33.5	32.9	33.2	33.2	33.2
M-38	569	34.0	35.1	34.3	34.8	34.5
M-33	565	32.6	32.9	32.1	33.5	32.8
M-15	558	34.8	34.0	34.4	34.5	34.4
M-52	538	33.9	33.7	32.9	34.7	33.8
M-40	531	35.8	35.0	35.1	35.7	35.4
M-5	530	35.8	37.6	36.5	36.9	36.7
M-18	528	34.5	32.5	32.9	34.0	33.5
M-19	527	34.7	34.2	34.3	34.6	34.4
M-44	522	32.0	31.5	30.4	33.1	31.8
M-61	517	33.1	32.5	31.8	33.8	32.8
M-34	517	36.5	35.2	35.3	36.4	35.9
M-37	512	34.6	35.3	35.4	34.6	35.0
M-43	504	30.3	30.3	28.2	32.4	30.3
M-39	494	31.0	30.3	29.7	31.6	30.6
M-32	488	35.6	36.8	35.6	36.7	36.2
M-20	488	35.4	36.3	34.9	36.8	35.8
M-55	480	34.0	32.4	31.8	34.5	33.2
M-36	475	34.6	32.0	31.9	34.7	33.3
M-7	444	35.7	36.3	35.6	36.5	36.0
M-42	443	33.4	32.7	32.0	34.1	33.1
M-41	438	33.7	32.5	33.2	33.0	33.1
M-50	426	35.6	35.6	35.6	35.5	35.6
M-21	422	34.3	34.1	33.9	34.6	34.2
M-49	407	34.6	33.6	33.0	35.1	34.1
M-6	387	34.4	33.6	33.4	34.7	34.0
M-35	366	34.2	36.2	33.9	36.5	35.2
Mean	574					34.1
BLSD	79					1.0
CV	8.99					3.20

Table 6. Lines that exhibited lint yields equivalent to or higher than TAM 94 L-25, and their associated fiber characteristics for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX.

Genotype	TLYLD	SGLP	MIC	UHML	UNIF	STR	ELONG
	kg/ha	%	n/a	mm	index	kN m/kg	%
PSC 355	1155	38.7	5.0	28.4	84.1	283	8.1
FM 832	1133	37.5	4.6	30.3	84.2	303	6.5
† M-23	932	34.4	4.0	32.9	82.9	299	6.5
† M-30	930	34.1	3.8	34.1	83.2	316	6.3
† M-26	906	34.3	3.9	33.6	83.2	314	6.2
M-58	899	36.6	4.0	29.4	82.3	275	7.3
M-1	891	36.7	3.9	29.5	82.4	275	7.9
† M-28	884	34.0	3.9	34.3	84.0	312	6.3
M-3	879	36.0	4.2	29.8	83.1	285	7.4
† M-27	878	33.9	3.9	33.8	83.6	312	6.4
† M-31	861	33.9	3.8	34.2	83.2	312	6.3
† M-24	838	33.7	3.8	34.9	83.7	322	6.4
M-54	830	35.9	4.0	30.6	82.3	299	5.7
† M-25	820	33.2	3.8	34.8	83.0	321	6.3
M-53	798	38.1	4.9	27.1	80.9	271	6.4
M-56	793	37.0	4.0	29.2	82.6	277	7.5
M-8	786	34.4	4.2	31.8	82.9	300	6.1
M-22	785	33.2	4.0	32.9	83.3	316	6.1
M-57	774	36.1	3.8	29.4	82.5	270	7.5
M-29	751	33.5	4.1	32.8	83.5	311	6.1
TAM 94 L-25	751	34.4	4.4	31.1	82.9	303	6.0
M-2	744	35.8	4.0	29.3	82.3	277	7.4
M-9	739	34.2	4.5	32.6	83.9	311	5.7
M-13	726	36.8	4.5	31.2	83.1	296	6.2
M-11	718	35.3	4.3	31.1	82.9	297	6.0
M-62	676	34.3	4.0	29.7	82.2	277	5.4
M-10	675	34.3	4.2	31.5	82.6	296	5.9
M-14	674	36.5	4.5	31.5	83.0	295	6.2
Mean	643	34.0	4.2	31.0	83.1	302	6.3
BLSD	89	1.0	0.16	0.6	0.9	11	0.3

† - Lines selected for further advancement within the improvement program

elongation. Recalling that the initiating idea for this research was to evaluate the Auld {Auld, 1998 #39} chemical mutation system to determine if it would create lines with improved UHML as reported for HS 200, several lines indeed exhibited significant improvement. Note that six of the TAM 94L-25M lines, 23, 30, 26, 28, 27, and 31, averaged higher lint yield than TAM 94L-25 and UHML exceeding TAM 94L-25 and Fibermax 832. Six TAM 94L-25M lines, 30, 28, 27, 31, 24, and 25, approach extra long staple status, defined as 34.9 mm (USDA-AMS, 2005).

Bartlett's Test for Homogeneity indicated that lint percent values, determined from hand harvested boll samples as described in the materials and methods section above, were normally distributed (Table 1). Lint percent varied ($p<0.01$) across years and genotypes, and genotypes responded differently to years and locations (Table 2).

Four TAM 94L-25M lines, 7, 18, 41, and 61, responded differently to years than at least one control cultivar or their non-mutated parent (Table 7). Average lint percents across locations for the TAM 94 L-25M lines changed no more than the checks. This probably resulted from the fact that the Bayes' t-value is associated with the analysis of variance F value and the F value for genotype x location was 1.8 while the F value for genotype x year was 2.35, which would result in a smaller Bayes' t-value and thus a smaller absolute value of Bayes' LSD. It is intuitive that one places more confidence in mean separation when F is larger, but this independence of Bayes' LSD and the error mean square apparently produced this inability to separate these particular means. The deltas for 47 TAM 94L-25M lines numerically exceeded either one of the control cultivars or TAM

Table 7. Genotype x location and genotype x year interactions of saw-ginned lint percents for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX.

	SGLP				SGLP		
Genotype	2008	2009	Δ	Genotype	CS	W	Δ
		%				%	
M-61	31.8	36.2	4.3	M-6	30.0	32.6	2.6
M-41	29.6	33.8	4.2	M-16	32.0	34.6	2.6
M-18	28.2	32.4	4.2	M-29	32.5	34.5	2.0
M-7	30.7	34.6	3.9	M-7	31.8	33.4	1.7
M-32	32.2	35.5	3.4	M-55	32.4	34.0	1.6
M-6	29.7	32.9	3.2	M-43	30.7	32.3	1.6
M-42	30.3	33.5	3.2	M-30	33.3	34.8	1.5
M-46	31.7	34.6	2.8	M-27	33.1	34.6	1.5
M-16	31.9	34.7	2.8	M-31	33.3	34.6	1.3
M-49	30.3	33.0	2.7	M-51	35.3	36.5	1.2
M-55	31.8	34.5	2.7	M-40	32.5	33.7	1.2
M-60	33.9	36.5	2.6	M-26	33.8	34.9	1.1
M-19	30.4	33.1	2.6	M-10	33.8	34.8	0.9
M-54	34.7	37.1	2.5	M-34	33.6	34.6	0.9
M-10	33.1	35.5	2.5	M-24	33.2	34.1	0.9
M-50	29.4	31.8	2.4	M-20	30.3	31.2	0.9
M-36	32.5	34.8	2.3	M-8	34.0	34.8	0.8
M-35	34.0	36.3	2.2	M-28	33.6	34.4	0.8
M-43	30.4	32.6	2.2	M-52	35.0	35.8	0.8
M-5	32.0	34.1	2.1	M-5	32.7	33.4	0.7
M-34	33.0	35.1	2.1	M-15	30.3	31.0	0.7
M-21	31.8	33.8	2.1	M-36	33.3	34.0	0.7
M-20	29.7	31.7	2.0	M-22	32.9	33.5	0.7
M-15	29.7	31.6	2.0	M-50	30.3	31.0	0.7
M-17	32.6	34.6	2.0	M-21	32.5	33.1	0.7
M-2	34.9	36.8	1.9	M-42	31.6	32.2	0.6
M-39	32.9	34.7	1.9	M-25	32.9	33.5	0.6
M-62	33.4	35.2	1.8	M-35	34.9	35.4	0.5
M-11	34.4	36.2	1.8	M-54	35.6	36.2	0.5
M-44	30.5	32.3	1.8	TAM 94 L-25	34.2	34.7	0.5
M-59	32.8	34.5	1.7	M-19	31.5	32.0	0.5
M-14	35.8	37.3	1.5	M-41	31.5	31.9	0.4

Table 7 continued

	SGLP				SGLP		
Genotype	2008	2009	Δ	Genotype	CS	W	Δ
		%				%	
M-45	32.1	33.5	1.4	M-12	33.2	33.5	0.4
M-63	35.3	36.7	1.4	M-32	33.7	34.0	0.3
M-26	33.7	35.0	1.3	M-39	33.7	33.9	0.3
M-28	33.4	34.7	1.3	FM 832	37.3	37.6	0.2
M-30	33.5	34.7	1.2	M-61	33.9	34.1	0.2
M-51	35.3	36.4	1.2	M-9	34.1	34.3	0.2
M-4	35.6	36.8	1.2	M-23	34.3	34.4	0.1
M-29	32.9	34.0	1.1	M-11	35.3	35.4	0.1
FM 832	36.9	38.0	1.1	M-37	35.6	35.6	0.0
M-53	37.7	38.6	0.9	M-18	30.3	30.3	0.0
M-58	36.2	37.1	0.9	M-44	31.4	31.4	0.0
M-3	35.6	36.5	0.9	M-53	38.2	38.1	-0.1
M-12	32.9	33.8	0.9	M-58	36.7	36.5	-0.2
M-24	33.3	34.1	0.8	M-17	33.8	33.4	-0.3
M-57	35.7	36.5	0.8	M-45	33.0	32.6	-0.3
M-27	33.5	34.2	0.7	M-63	36.2	35.7	-0.5
M-13	36.4	37.1	0.7	M-49	31.9	31.4	-0.5
M-9	33.9	34.6	0.7	PSC 355	39.0	38.5	-0.5
M-52	35.1	35.7	0.6	M-62	34.6	34.0	-0.6
M-56	36.7	37.3	0.6	M-3	36.3	35.7	-0.6
M-33	34.3	34.8	0.5	M-38	35.3	34.6	-0.7
M-1	36.5	36.9	0.4	M-13	37.1	36.4	-0.8
TAM 94 L-25	34.3	34.6	0.3	M-14	36.9	36.1	-0.8
M-25	33.0	33.3	0.3	M-2	36.3	35.4	-0.9
M-23	34.3	34.5	0.2	M-46	33.6	32.7	-1.0
M-31	33.8	34.0	0.2	M-59	34.1	33.2	-1.0
M-8	34.4	34.5	0.1	M-33	35.1	34.0	-1.2
M-22	33.2	33.2	0.0	M-4	36.8	35.6	-1.2
M-37	35.6	35.5	-0.1	M-57	36.9	35.3	-1.6
M-40	33.2	33.0	-0.2	M-1	37.6	35.8	-1.7
PSC 355	38.9	38.5	-0.4	M-60	36.2	34.2	-2.0
M-38	35.4	34.6	-0.8	M-56	38.2	35.7	-2.5
		Mean	1.59			Mean	0.3
		BLSD	2.75			BLSD	2.9

94L-25, but the differences in response to location were similar to those of the checks ($p<0.05$).

The response of TAM 94L-25M lines relative to lint percent is similar to their lint yield response, i.e., year had a greater impact than did locations effects (Tables 3 and 7). This similarity suggests that the response is not due to variation in seed germination quality leading to variation in plot plant population since the boll samples were hand harvested and should have represented only mature and morphologically normal bolls, although plant population, and thus seed quality, still could have impacted yield more than lint percent. Regardless of such speculation, it appears that there are several of the TAM 94L-25M lines that are not as stable across years as their parent genotype. A second conclusion from these data is that environmental variation across years is more important for plant breeders to measure than across locations, at least within this limited study. Within the TAM 94L-25M lines in Table 6, lint percents ranged from about 33 to about 38 while FM 832 averaged about 39% lint and TAM 94L-25 averaged only 34%. Within these selected TAM 94L-25M lines, the EMS treatment and subsequent selection for UHML, fiber strength, and fiber elongation did not result in a decreased lint percent.

Fiber Properties

Bartlett's Test for Homogeneity of variances revealed no significant chi-square values for any of the testing environments thereby substantiating pooling the error for combined analysis (Table 1). The analysis of variance for HVI fiber quality traits produced significant mean square values for all main effects which included year, location,

Table 8. Genotype x location and genotype x year interactions, and overall means of HVI Micronaire (MIC) for 61 TAM 94 L-25 M- lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX.

	MIC				MIC				MIC
Genotype	2008	2009	Δ	Genotype	CS	W	Δ	Genotype	Overall mean
		n/a				n/a			n/a
M-44	4.6	4.1	0.5	M-1	4.2	3.7	0.5	M-42	5.1
M-13	4.7	4.3	0.4	M-11	4.5	4.1	0.4	PSC 355	5.0
M-53	5.1	4.7	0.4	M-4	4.2	3.9	0.3	M-53	4.9
M-37	5.0	4.6	0.4	M-8	4.4	4.1	0.3	M-43	4.8
M-33	4.5	4.2	0.4	M-56	4.1	3.8	0.3	M-37	4.8
M-32	4.6	4.3	0.3	M-57	4.0	3.7	0.3	M-63	4.7
M-49	4.5	4.2	0.3	M-23	4.2	3.9	0.3	M-35	4.6
M-8	4.3	4.1	0.2	M-10	4.4	4.1	0.3	FM 832	4.6
M-5	4.3	4.0	0.2	M-60	4.3	4.0	0.3	M-52	4.5
M-22	4.1	3.9	0.2	M-36	4.5	4.3	0.3	M-9	4.5
TAM 94 L-25	4.6	4.3	0.2	M-44	4.5	4.2	0.3	M-13	4.5
M-9	4.6	4.4	0.2	M-2	4.1	3.9	0.2	M-14	4.5
M-15	4.1	3.9	0.2	M-49	4.5	4.3	0.2	M-59	4.5
M-35	4.7	4.5	0.2	FM 832	4.7	4.5	0.2	TAM 94 L-25	4.4
M-39	4.2	4.0	0.2	M-30	3.9	3.7	0.2	M-32	4.4
M-31	3.9	3.7	0.2	M-13	4.6	4.4	0.2	M-12	4.4
M-4	4.1	4.0	0.2	M-7	4.1	3.9	0.2	M-50	4.4
FM 832	4.6	4.5	0.2	M-28	4.0	3.9	0.2	M-61	4.4
M-7	4.1	3.9	0.2	M-9	4.6	4.4	0.1	M-36	4.4
M-25	3.9	3.8	0.2	M-46	4.4	4.3	0.1	M-38	4.4
M-28	4.0	3.9	0.2	M-50	4.5	4.3	0.1	M-49	4.4
M-40	4.0	3.9	0.2	M-62	4.1	4.0	0.1	M-33	4.4
M-12	4.5	4.3	0.1	M-22	4.1	3.9	0.1	M-34	4.4
M-59	4.5	4.4	0.1	M-45	4.2	4.1	0.1	M-44	4.4
M-56	4.0	3.9	0.1	M-58	4.1	4.0	0.1	M-46	4.4
M-42	5.1	5.0	0.1	M-59	4.5	4.4	0.1	M-11	4.3
M-1	4.0	3.9	0.1	M-63	4.8	4.7	0.1	M-55	4.3
M-11	4.3	4.3	0.1	M-15	4.0	3.9	0.1	M-3	4.2
M-16	4.3	4.2	0.1	M-39	4.2	4.1	0.1	M-8	4.2
M-29	4.1	4.1	0.1	M-25	3.9	3.8	0.1	M-10	4.2
M-52	4.6	4.5	0.1	M-32	4.5	4.4	0.1	M-16	4.2
M-2	4.1	4.0	0.1	M-3	4.3	4.2	0.1	M-51	4.2

Table 8 continued

	MIC				MIC				MIC
Genotype	2008	2009	Δ	Genotype	CS	W	Δ	Genotype	Overall mean
		n/a				n/a			n/a
M-36	4.4	4.4	0.1	M-5	4.2	4.1	0.1	M-45	4.2
M-19	4.1	4.1	0.0	M-14	4.5	4.4	0.1	M-60	4.2
M-51	4.2	4.2	0.0	M-26	4.0	3.9	0.1	M-5	4.1
PSC 355	5.1	5.0	0.0	M-52	4.6	4.5	0.1	M-19	4.1
M-38	4.4	4.4	0.0	TAM 94 L-25	4.5	4.4	0.1	M-39	4.1
M-26	3.9	3.9	0.0	M-12	4.4	4.4	0.0	M-29	4.1
M-30	3.8	3.8	0.0	M-19	4.1	4.1	0.0	M-17	4.1
M-3	4.2	4.2	0.0	M-24	3.8	3.8	0.0	M-4	4.0
M-10	4.2	4.2	0.0	M-53	4.9	4.9	0.0	M-23	4.0
M-23	4.1	4.0	0.0	M-6	3.9	3.8	0.0	M-54	4.0
M-34	4.4	4.4	0.0	M-21	3.9	3.9	0.0	M-62	4.0
M-50	4.4	4.4	0.0	M-41	4.0	4.0	0.0	M-2	4.0
M-55	4.3	4.3	0.0	M-27	3.9	3.9	0.0	M-58	4.0
M-45	4.2	4.2	0.0	M-31	3.8	3.8	0.0	M-18	4.0
M-6	3.8	3.9	0.0	M-40	3.9	3.9	0.0	M-22	4.0
M-20	3.9	4.0	0.0	M-54	4.0	4.0	0.0	M-7	4.0
M-24	3.8	3.8	0.0	M-61	4.4	4.4	0.0	M-15	4.0
M-57	3.8	3.8	0.0	PSC 355	5.0	5.0	0.0	M-41	4.0
M-63	4.7	4.8	0.0	M-16	4.2	4.2	0.0	M-56	4.0
M-54	4.0	4.1	0.0	M-29	4.1	4.1	0.0	M-1	3.9
M-14	4.4	4.5	-0.1	M-18	4.0	4.0	0.0	M-20	3.9
M-60	4.1	4.2	-0.1	M-38	4.3	4.4	-0.1	M-28	3.9
M-43	4.8	4.9	-0.1	M-37	4.7	4.8	-0.1	M-40	3.9
M-46	4.3	4.4	-0.1	M-20	3.9	4.0	-0.1	M-21	3.9
M-18	3.9	4.1	-0.1	M-34	4.3	4.4	-0.1	M-26	3.9
M-58	4.0	4.1	-0.1	M-17	4.0	4.2	-0.2	M-27	3.9
M-17	4.0	4.2	-0.2	M-35	4.5	4.6	-0.2	M-6	3.8
M-21	3.8	4.0	-0.2	M-43	4.7	4.9	-0.2	M-25	3.8
M-27	3.8	4.0	-0.2	M-33	4.3	4.5	-0.2	M-31	3.8
M-61	4.3	4.5	-0.3	M-42	5.0	5.2	-0.2	M-24	3.8
M-62	3.9	4.2	-0.4	M-51	4.1	4.3	-0.3	M-57	3.8
M-41	3.8	4.2	-0.4	M-55	4.1	4.5	-0.4	M-30	3.8
		Mean	0.1			Mean	0.1	Mean	4.2
		BLSD	0.5			BLSD	0.5	CV	4.3

and genotype except for location for mic (Table 2). The genotype x year interaction was significant for all HVI parameters except UI, while genotypes responded similarly to location relative to UHML, strength, and elongation. The genotype x year x location interaction was significant only for micronaire.

Micronaire

All of the TAM 94L-25M lines responded no differently ($p<0.05$) than at least one of the control genotypes in this study to the effect of years or locations when the interaction was analyzed, although the analysis of variance indicated significant interactions with both (Tables 2 and 8). Since the evaluation of the significant interaction terms involving micronaire resulted in the conclusion that years and locations had little impact on the expression of this fiber trait, micronaire was averaged across years and locations (Table 8).

Micronaire ranged from 3.8 for TAM 94L-25M line 30, to 5.1 for TAM 94L-25M line 42. PSC 355 and mutant line 42 had the highest mic values, suggesting coarse fibers and/or a high maturity level, which is typical for PSC 355. TAM 94L-25 exhibited a micronaire of 4.4, which would generally be considered as acceptably mature and of acceptable fineness. Thirty-seven TAM 94L-25M lines averaged lower ($p<0.05$) mic than the parental line, which was not different than FM 832 and lower than PSC 355. Additional Advanced Fiber Instrumentation System (AFIS) data are needed on these mutation lines to determine if these lower mic values represent immaturity or actual finer yet mature fibers. Finer fibers within upland cotton combined with longer UHML and

strength could be instrumental in maintaining the competitiveness of the American cotton producer. All TAM 94L-25M lines except line 42 averaged mic values within the acceptable range of 3.5 – 4.9 that indicates mature, well developed fibers with industry acceptable secondary cell wall development.

Upper Half Mean Length

Years, locations and genotypes were all significantly different for UHML, as was the interaction of genotype x year (Table 2). Five TAM 94L-25M lines, 16, 26, 20, 17, and 18, responded differently (k=100) to years than either commercial cultivar or the parental TAM 94L-25 (Table 9). The UHML of these five TAM 94L-25M lines exhibited a greater reduction in UHML in 2009, averaged across both locations, than any of the control cultivars or many of the remaining TAM 94L-25M lines. It is tempting to speculate that the level of decrease in UHML from 2008 to 2009 was greater for genotypes with longer UHML than those with shorter UHML. While these data do not definitively support that assumption, the data do suggest that trend. Additional research is necessary to determine if upland cotton genotypes with long or extra long UHML are more susceptible to variation in growth environments than those with shorter UHML.

Averaged over years and locations, UHML ranged from 24.4 to 34.9 mm (Table 9). The M_0 parent and FM 832 averaged 31.2 and 30.2 mm respectively, while PSC 355 was shorter (k=100) at 28.4 mm. The UHML of the controls were similar to values reported elsewhere (data not shown) and thus supports the assumption that the UHML reported for the TAM 94L-25M lines are accurate. Twenty-three of the TAM 94L-25M lines averaged

Table 9. Genotype x year interaction and overall means of Upper Half Mean Length (UHML) for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX.

	UHML				UHML
Genotype	2008	2009	Δ	Genotype	Overall mean
		mm			mm
M-16	34.5	30.4	4.2	M-24	34.9
M-26	35.6	31.5	4.1	M-25	34.8
M-20	35.2	31.2	4.0	M-28	34.3
M-17	34.2	30.5	3.7	M-31	34.2
M-18	35.1	31.5	3.6	M-30	34.1
M-23	34.6	31.1	3.5	M-27	33.8
M-24	36.6	33.1	3.4	M-2□	33.6
M-46	32.7	29.3	3.4	M-15	33.5
M-29	34.5	31.1	3.4	M-18	33.3
M-6	34.1	30.8	3.3	M-19	33.2
M-45	33.3	30.0	3.2	M-20	33.2
M-55	31.9	28.8	3.2	M-5	33.0
M-60	31.8	28.6	3.1	M-22	32.9
M-34	30.9	27.9	3.0	M-23	32.9
M-22	34.4	31.4	3.0	M-29	32.8
M-21	34.0	31.1	3.0	M-9	32.6
M-28	35.8	32.8	3.0	M-21	32.5
M-30	35.6	32.6	3.0	M-6	32.4
M-5	34.4	31.6	2.9	M-7	32.4
M-14	32.9	30.0	2.9	M-16	32.4
M-15	34.9	32.1	2.8	M-17	32.4
M-25	36.2	33.4	2.8	M-41	32.1
M-10	32.9	30.1	2.8	M-8	31.8
M-41	33.5	30.7	2.8	M-45	31.7
M-27	35.1	32.4	2.7	M-10	31.5
M-36	31.9	29.1	2.7	M-14	31.5
M-19	34.5	31.9	2.7	M-12	31.3
M-13	32.6	29.9	2.7	M-13	31.2
M-31	35.5	32.8	2.7	TAM 94 L-25	31.1
M-8	33.0	30.5	2.5	M-11	31.1
M-54	31.8	29.3	2.5	M-46	31.0
M-62	31.0	28.5	2.5	M-59	30.9

Table 9 continued

	UHML				UHML
Genotype	2008	2009	Δ	Genotype	Overall mean
		mm			mm
M-7	33.7	31.2	2.4	M-40	30.7
M-11	32.3	29.8	2.4	M-33	30.7
M-58	30.6	28.2	2.4	M-54	30.6
M-40	31.9	29.6	2.3	M-36	30.5
M-51	29.5	27.2	2.2	M-55	30.4
M-57	30.5	28.3	2.2	FM 832	30.3
FM 832	31.4	29.3	2.1	□-4	30.3
M-56	30.3	28.2	2.1	M-39	30.3
M-9	33.6	31.6	2.0	M-60	30.2
M-4	31.2	29.3	2.0	M-32	30.2
M-2	30.2	28.3	1.9	M-38	30.1
M-38	31.1	29.2	1.8	M-44	30.0
M-59	31.8	30.0	1.8	M-3	29.8
M-12	32.1	30.5	1.7	M-62	29.7
TAM 94 L-25	31.9	30.4	1.5	M-37	29.6
M-63	29.9	28.4	1.5	M-1	29.5
M-33	31.4	30.0	1.4	M-42	29.4
M-43	29.9	28.6	1.3	M-34	29.4
M-3	30.5	29.2	1.3	M-58	29.4
M-32	30.8	29.5	1.3	M-57	29.4
M-52	29.2	27.9	1.3	M-2	29.3
M-39	30.9	29.7	1.2	M-43	29.2
M-44	30.6	29.4	1.2	M-56	29.2
M-53	27.7	26.5	1.2	M-63	29.2
M-61	29.3	28.2	1.1	M-35	29.1
PSC 355	28.8	27.9	1.0	M-61	28.7
M-1	29.8	29.1	0.7	M-52	28.6
M-42	29.8	29.1	0.7	M-51	28.4
M-50	24.5	24.1	0.4	PSC 355	28.4
M-49	24.5	24.1	0.4	M-53	27.1
M-35	29.0	29.1	-0.1	M-49	24.3
M-37	29.5	29.7	-0.3	M-50	24.3
		Mean	57.76	Mean	31.0
		BLSD	1.45	BLSD	0.6
				CV	2.31

longer (k=100) UHML than the longest control, TAM 94L-25, and 26 were significantly shorter. Thirty of the TAM 94L-25M lines had longer UHML than Fibermax 832, the quality standard among currently available cultivars in south Texas. Eleven of the 25 better yielding TAM 94L-25M lines in Table 6 have UHML exceeding (k=100) TAM 94L-25, the longest control. Six of these also yielded significantly higher than TAM 94L-25.

Length Uniformity Index

The analysis of variance for HVI UI indicated significant differences among years, locations and genotypes (Table 2). Location x genotype was the only significant interaction. The UI for these genotypes were higher numerically when averaged over years for Weslaco than for the College Station location (Table 10). However, the deltas for most genotypes across locations were not different (k=100) and all were not different than at least one of the controls. When averaged over all locations and years, seven TAM 94L-25M lines had higher UI than the non-mutated parent, which was lower than either of the commercial cultivars, and two had lower UI than TAM 94L-25. Of the selected TAM 94L-25M lines in Table 6, only one averaged lower UI, line 53 which also had lower UHML, and one averaged higher UI, line 9. Treatment with EMS appears to have had little impact on UI.

Uniformity index was not used as a selection criterion, but rather a tool for which to see if lines were acceptably uniform for fiber length and as further proof that mutations actually occurred. None of the mutation lines exhibited unacceptable UI.

Table 10. Genotype x location interaction and overall means of HVI Uniformity Index (UNIF) for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX.

	UI				UI
Genotype	CS	W	Δ	Genotype	Overall mean
		%			%
M-30	81.5	84.8	3.4	FM 832	84.2
M-17	81.0	84.2	3.2	M-18	84.2
M-39	81.3	84.0	2.7	PSC 355	84.1
M-24	82.5	85.0	2.6	M-36	84.1
M-20	82.1	84.6	2.5	M-7	84.0
TAM 94 L-25	81.7	84.1	2.4	M-12	84.0
M-44	81.3	83.7	2.4	M-28	84.0
M-31	82.1	84.4	2.4	M-33	84.0
M-16	82.0	84.3	2.3	M-9	83.9
M-58	81.2	83.4	2.3	M-15	83.8
M-18	83.1	85.3	2.2	M-46	83.8
M-12	82.9	85.1	2.1	M-5	83.8
M-19	82.7	84.8	2.1	M-19	83.7
M-2	81.3	83.2	1.9	M-24	83.7
M-46	82.9	84.8	1.9	M-43	83.7
M-14	82.1	84.0	1.8	M-27	83.6
M-59	82.6	84.5	1.8	M-32	83.6
M-5	82.9	84.7	1.8	M-35	83.6
M-54	81.5	83.2	1.8	M-38	83.6
M-6	82.6	84.4	1.7	M-59	83.5
M-7	83.1	84.9	1.7	M-6	83.5
M-9	83.1	84.8	1.7	M-29	83.5
M-40	82.1	83.7	1.6	M-37	83.4
M-25	82.3	83.8	1.6	M-63	83.4
M-33	83.2	84.7	1.6	M-45	83.4
M-51	80.5	82.1	1.6	M-20	83.4
M-15	83.1	84.6	1.5	M-22	83.3
M-62	81.4	82.9	1.5	M-34	83.3
M-23	82.2	83.5	1.4	M-21	83.3
M-45	82.7	84.1	1.3	M-41	83.3
FM 832	83.5	84.9	1.3	M-31	83.2
M-50	81.2	82.5	1.3	M-16	83.2

Table 10 continued

Genotype	UI			Genotype	UI
	CS	W	Δ		Overall mean
		%			%
M-57	81.9	83.1	1.2	M-26	83.2
M-28	83.4	84.5	1.1	M-30	83.2
M-35	83.1	84.1	1.1	M-3	83.1
M-32	83.1	84.1	1.0	M-13	83.1
M-29	83.0	84.0	1.0	M-14	83.0
M-43	83.2	84.2	1.0	M-25	83.0
M-8	82.5	83.4	0.9	M-8	82.9
M-13	82.7	83.6	0.9	M-60	82.9
M-1	82.0	82.9	0.9	TAM 94 L-25	82.9
M-56	82.1	83.0	0.9	M-4	82.9
M-61	82.4	83.2	0.8	M-11	82.9
M-21	82.9	83.7	0.8	M-23	82.9
M-34	82.9	83.7	0.8	M-40	82.9
PSC 355	83.7	84.5	0.8	M-61	82.8
M-4	82.5	83.2	0.7	M-55	82.8
M-26	82.8	83.5	0.7	M-39	82.7
M-63	83.1	83.8	0.7	M-10	82.6
M-10	82.3	83.0	0.7	M-17	82.6
M-3	82.8	83.5	0.7	M-56	82.6
M-38	83.3	83.9	0.7	M-44	82.5
M-52	81.8	82.4	0.6	M-57	82.5
M-27	83.4	83.9	0.6	M-1	82.4
M-11	82.6	83.1	0.5	M-54	82.3
M-49	81.6	82.1	0.5	M-2	82.3
M-41	83.1	83.5	0.4	M-58	82.3
M-60	82.7	83.1	0.3	M-42	82.2
M-42	82.1	82.3	0.3	M-62	82.2
M-55	82.7	82.8	0.1	M-52	82.1
M-37	83.4	83.5	0.0	M-49	81.9
M-36	84.2	83.9	-0.3	M-50	81.9
M-53	81.1	80.7	-0.4	M-51	81.3
M-22	83.6	83.0	-0.7	M-53	80.9
		Mean	1.3	Mean	83.1
		BLSD	3.0	BLSD	0.93
				CV	1.13

Fiber Bundle Strength

Years, locations, and genotypes varied ($p < 0.01$) in strength and the analysis of variance indicated that genotypes did not respond the same to the two years of this experiment (Table 2). When fiber strengths of each genotype averaged over locations in 2009 were subtracted from their 2008 averages, only two of the TAM 94L-25M lines, 42 and 46, appear to have responded differently (k=100) to years than PSC 355, four responded differently than FM 832, and 12 exhibited deltas different (k-100) than TAM 94L-25 (Table 11). Thus, all of the TAM 94L-25M lines responded similarly to years as at least one of the controls.

As with other HVI data, the interaction of genotype and year does not appear to prohibit looking at overall genotypic means for fiber strength. When averaged over all locations and years, 45 of the 61 TAM 94L-25M lines exhibited stronger (k=100) fibers than PSC 355 and 16 had stronger fibers than Fibermax 832 and TAM 94L-25, which were not different (Table 11). Sixteen TAM 94L-25M lines had lower strength than the non-mutated parent. Fiber bundle strength ranged from 261 to 333 kN m kg^{-1}. Mutant lines 22, 24, 25, and 30 exhibited exceptional fiber length as well as bundle strengths greater (k=100) than the three check lines (Table 6). Treatment with EMS may have effected variation that lead to the development of these lines with exceptional combinations of fiber quality.

Elongation

Elongation of fibers is measured in the HVI process of determining strength (personal communication with E. Hequet). A given weight of fibers is held within clamps

Table 11. Genotype x year interaction and overall means of HVI Fiber Bundle Strength (STR) for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX.

	STR				STR
Genotype	2008	2009	Δ	Genotype	Overall Mean
	kN m/kg				kN m/kg
M-42	336	279	57	M-35	333
M-46	335	279	56	M-18	329
M-35	360	306	53	M-12	328
M-44	330	279	51	M-15	324
M-36	345	297	48	M-34	324
M-6	332	288	44	M-41	323
M-41	345	302	44	M-43	323
M-55	321	277	43	M-24	322
M-62	298	255	42	M-25	321
M-32	338	296	42	M-36	321
M-17	330	290	40	M-21	318
M-45	334	294	40	M-32	317
M-16	329	291	38	M-22	316
M-8	319	281	38	M-30	316
M-10	314	277	37	M-7	316
M-20	327	291	36	M-37	316
M-5	324	289	34	M-45	314
M-33	329	295	34	M-26	314
M-21	335	301	34	M-31	312
M-23	316	283	33	M-27	312
M-39	327	294	33	M-28	312
M-54	316	283	33	M-33	312
M-19	328	295	33	M-19	311
M-38	323	292	31	M-9	311
M-11	312	282	30	M-29	311
M-43	338	308	30	M-39	310
M-58	290	260	30	M-6	310
M-51	282	254	29	M-16	310
M-37	330	301	29	M-17	310
M-25	335	307	28	M-20	309
M-27	326	299	27	M-38	308
M-18	342	315	27	M-42	307

Table 11 continued

Genotype	STR 2008	STR 2009	STR Δ	Genotype	STR Overall Mean
		kN m/kg			kN m/kg
M-22	330	303	27	M-40	307
M-59	312	284	27	M-46	307
PSC 355	297	270	27	M-5	306
M-52	294	267	27	M-44	304
M-40	320	294	27	TAM 94 L-25	303
M-49	275	248	27	FM 832	303
M-34	337	310	26	M-8	300
M-26	327	301	26	M-23	299
M-4	303	278	25	M-54	299
M-7	329	304	25	M-55	299
M-57	282	257	25	M-59	298
M-24	334	310	24	M-11	297
M-63	303	279	24	M-13	296
M-56	289	266	24	M-10	296
M-14	307	284	23	M-14	295
M-53	282	259	23	M-63	291
M-31	323	302	22	M-4	291
M-28	323	301	22	M-61	286
FM 832	313	292	22	M-3	285
M-50	283	262	21	M-60	285
M-3	296	275	21	PSC 355	283
M-29	320	301	18	M-52	281
M-15	332	315	17	M-2	277
M-30	325	307	17	M-56	277
M-61	294	277	17	M-62	277
M-60	293	277	16	M-58	275
M-12	334	321	12	M-1	275
TAM 94 L-25	308	298	10	M-50	273
M-9	316	306	9	M-53	271
M-13	300	291	9	M-57	270
M-2	281	274	8	M-51	268
M-1	277	273	3	M-49	261
		Mean	29	Mean	302
		BLSD	28	BLSD	11
				CV	4.2

set 3.175 mm apart and force is added to determine the amount of force to break the fibers. The distance that the fibers stretch before breaking, expressed as a percent of 3.175 mm , is called elongation. The problem with this measurement is that there are no calibration standards, so using multiple machines or comparing across machines is impossible. Therefore, all elongation data reported in the literature is suspect.

Years, locations, and genotypes varied significantly in elongation, and genotypes did not respond the same to each year of the experiment (Table 2). TAM 94L-25M line 21 was the only mutant line that responded differently to years than the parent germplasm line, TAM 94L-25 (Table 12). These data suggest that the interaction of genotypes and years is not biologically meaningful. This conclusion is supported by the size of the mean squares in Table 2 where the mean square for genotype x year is less than 0.05% of that for tear and only about 8% of that for genotype. This minor interaction suggests that treatment with EMS had no effect on fiber elongation.

Averaged over years and locations, PSC 355 had the highest elongation with 8.1% with TAM 94L-25M line 5 having numerically the lowest elongation at only 5.4% (Table 12). As noted above, drawing conclusions from elongation data probably should be avoided. However, a plethora of data (not shown) suggest that in Texas environments, PSC 355 will usually exhibit better elongation than Fibermax 832, which will exhibit better elongation than TAM 94-25. The distribution in Table 12 of elongation means averaged across years and locations suggest that treatment with EMS effected variation for this trait, with a few mutation lines having better (k=100) elongation than TAM 94L-25 and one line, 1, being not lower in elongation mean than PSC 355. However, again caution

Table 12. Genotype x year interaction and overall means of HVI Elongation (ELONG) for 61 TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 and 2009 at College Station and Weslaco, TX.

	ELONG				ELONG
Genotype	2008	2009	Δ	Genotype	Overall Mean
		%			%
PSC 355	9.8	6.5	3.3	PSC 355	8.1
M-21	7.9	5.0	2.9	M-1	7.9
M-60	8.2	5.3	2.9	M-56	7.5
M-3	8.8	6.0	2.8	M-57	7.5
M-54	7.1	4.3	2.8	M-2	7.4
M-58	8.7	5.9	2.8	M-3	7.4
M-32	8.0	5.3	2.7	M-50	7.4
M-59	7.2	4.5	2.7	M-49	7.3
M-30	7.6	4.9	2.7	M-58	7.3
M-35	7.8	5.2	2.6	M-4	7.1
M-57	8.8	6.2	2.6	M-61	6.9
M-37	7.9	5.3	2.6	M-38	6.9
M-33	7.8	5.3	2.6	M-51	6.8
M-2	8.7	6.1	2.6	M-34	6.8
M-8	7.4	4.8	2.5	M-60	6.8
M-14	7.4	4.9	2.5	M-32	6.6
M-53	7.6	5.1	2.5	M-37	6.6
M-61	8.2	5.7	2.5	M-33	6.5
M-63	7.3	4.8	2.5	M-35	6.5
M-4	8.3	5.8	2.5	FM 832	6.5
M-24	7.7	5.2	2.5	M-45	6.5
M-38	8.2	5.7	2.5	M-23	6.5
M-1	9.1	6.7	2.5	M-43	6.5
M-28	7.5	5.1	2.4	M-21	6.4
M-49	8.5	6.1	2.4	M-24	6.4
M-26	7.3	5.0	2.3	M-36	6.4
M-29	7.3	5.0	2.3	M-52	6.4
M-23	7.6	5.3	2.3	M-27	6.4
M-52	7.6	5.3	2.3	M-44	6.4
M-25	7.4	5.2	2.2	M-53	6.4
M-27	7.5	5.3	2.2	M-42	6.3
M-42	7.4	5.2	2.2	M-25	6.3

Table 12 continued

	ELONG				ELONG
Genotype	2008	2009	Δ	Genotype	Overall Mean
		%			%
M-31	7.4	5.2	2.2	M-28	6.3
M-56	8.6	6.4	2.2	M-30	6.3
M-51	7.9	5.7	2.2	M-31	6.3
M-12	7.1	5.0	2.1	M-13	6.2
M-10	6.9	4.8	2.1	M-26	6.2
M-43	7.5	5.4	2.1	M-14	6.2
M-20	6.6	4.5	2.1	M-29	6.1
TAM 94 L-25	7.0	5.0	2.1	M-46	6.1
M-13	7.2	5.2	2.1	M-8	6.1
M-7	6.6	4.5	2.1	M-22	6.1
M-9	6.8	4.7	2.1	M-12	6.1
M-22	7.1	5.1	2.1	M-63	6.1
M-36	7.5	5.4	2.1	TAM 94 L-25	6.0
M-62	6.5	4.4	2.0	M-11	6.0
M-5	6.4	4.4	2.0	M-39	5.9
M-11	7.0	5.0	2.0	M-10	5.9
M-41	6.7	4.7	2.0	M-59	5.8
M-55	6.6	4.6	2.0	M-19	5.8
M-6	6.4	4.5	2.0	M-9	5.7
M-44	7.3	5.4	2.0	M-54	5.7
M-50	8.3	6.4	2.0	M-15	5.7
M-15	6.6	4.7	1.9	M-40	5.7
M-19	6.8	4.9	1.9	M-16	5.7
M-40	6.6	4.7	1.9	M-41	5.7
FM 832	7.4	5.6	1.8	M-55	5.6
M-18	6.3	4.6	1.8	M-7	5.5
M-45	7.4	5.6	1.8	M-17	5.5
M-17	6.4	4.7	1.7	M-20	5.5
M-34	7.6	5.9	1.7	M-6	5.4
M-39	6.7	5.1	1.7	M-62	5.4
M-16	6.5	4.9	1.6	M-18	5.4
M-46	6.9	5.3	1.6	M-5	5.4
		Mean	2.2	Mean	6.33
		BLSD	0.8	BLSD	0.297
				CV	5.32

must be urged and firm conclusions avoided. There appears to be an inverse relationship of UHML and elongation in these TAM 94L-25M lines which would be consistent with many years of observations in breeding plots (personal communication with W. Smith, 2010).

SEED SURFACE AREA AND FIBERS PER UNIT AREA OF SEED SURFACE

Bartlett's Test for Homogeneity of Variances was conducted on the hand-ginned boll samples taken from a subset of TAM 94L-25M lines, plus controls, and the associated within boll yield component measurements taken from those boll samples. Chi-square value comparison revealed that the variances in Environment 1 (College Station, 2008) were non-homogeneous for Length by Number (L(n)), Surface Area $Seed^{-1}$, or Fibers mm^{-2} (Table 13). Variances were not homogeneous for hand-ginned lint percent at Environment 2 (College Station, 2009), or for Surface Area $Seed^{-1}$ at Environment 3 (Weslaco, 2009). All typical transformation methods were attempted on the data, but none resulted in more homogenous variances. The non-homogeneity of variances was therefore ignored for the purposes of this thesis and a combined analysis of variance was used.

Genotypes and environments were significantly different ($p<0.05$) for hand ginned lint percent (Table 14). None of the genotypes showed any differential interactions with the different environments. These boll samples were hand ginned in order to minimize breakage of fibers in the saw ginning process that could contribute to erroneous information when used to calculate within boll yield components. As was expected, the hand ginned lint percents were similar to those of the saw ginned in that the two

Table 13. Homogeneity of variance chi-squares for seed surface area and relevant AFIS fiber traits for 12 representative TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 at College Station, and 2009 at College Station and Weslaco, TX.

	College Station		Weslaco
Source	2008	2009	2009
HGLP	17.7	24.0**	9.2
LN	26.8**	6.5	14.8
FINE	18.8	12.0	13.1
FIB/SD	21.0	10.4	16.2
SUR/SD	24.7**	10.8	23.5**
FIB/MM	25.3**	17.5	10.8

** Significant at the 0.01 probability level

Table 14. Analysis of variance mean squares for seed surface area and relevant AFIS fiber traits for 12 representative TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 at College Station, and 2009 at College Station and Weslaco, TX.

Source	df	HGLP	LN	FINE	FIB/SD	SUR/SD	FIB/MM
Environment	2	3.6**	16.1**	20	1071*	535**	235*
Error A	6	0.20	0.4	88	153	28	24
Genotype	14	2.3**	3.3**	397**	598**	644**	135**
Environment*Genotype	28	0.20	0.3	77	161	36	12
Error B	84	0.30	0.3	56	117	41	19

*, ** Significant at the 0.05 and 0.01 probability level, respectively

commercial checks had the highest lint percents (Tables 5 and 15). TAM 94 L-25 was intermediate in hand ginned lint percent, with three mutant lines having significantly higher lint percents, and the rest of the mutants having similar lint percent to that of the non-mutated parent.

Significant differences ($p<0.01$) among genotypes for AFIS Length by Number (LN) are noted in Table 14. The three Environments had a significant effect on the LN, but no interaction of environment x genotype was detected. TAM 94L-25M lines 22 and 17 had longer UHML than TAM 94L-25 (Table 9), but were not different than the M_0 parent in LN. Lines 34, 35 and the commercial check FM 832 were shorter than TAM 94L-25 according to HVI length, but no different according to AFIS Length by number. Such differences are not unusual since the two measurements are using a different array of fibers to determine length, with HVI using the longest 50% and Ln measuring the average length of all fibers in the sample. However, differences in ginning, hand-ginned versus saw-ginned, could have impacted these measurements of fiber length.

Table 15 verifies the array of the subset chosen for this portion of the thesis in that two TAM 94L-25 lines, 25 and 36, were significantly longer in LN than TAM 94L-25 which was not different than FM 832 and both were significantly longer than PSC 355. Conversely, one TAM 94L-25M line, 50, was significantly shorter than PSC 355 and three were not different.

Significant differences were detected among genotypes for fiber fineness ($p<0.01$), but not for Environments (Table 14). PSC 355 had the coarsest fibers as indicated by AFIS fineness (Table 15). The majority of the mutant lines exhibited fiber fineness

Table 15. Genotype means of seed surface area and relevant AFIS fiber traits for 12 representative TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a TAM 94L-25 check grown in 2008 at College Station, and 2009 at College Station and Weslaco, TX.

Genotype	HGLP	Genotype	LN	Genotype	FINE	Genotype	SUR/ SD	Genotype	FIB/SD	Genotype	FIB/ MM
	%		in		millitex		mm^2		count $seed^{-1}$		count mm^{-2}
PSC 355	39.7	M-25	1.02	PSC 355	190	TAM 94 L-25	125	M-50	17,059	M-2	168
FM 832	39.3	M-36	0.99	M-35	181	M-25	124	M-2	16,592	PSC 355	150
M-2	38.9	M-22	0.96	M-34	179	M-11	118	M-51	16,326	M-3	149
M-3	38.4	TAM 94 L-25	0.96	FM 832	177	M-35	117	TAM 94 L-25	15,992	M-51	148
M-11	37.5	M-11	0.96	TAM 94 L-25	176	M-36	117	M-11	15,848	M-50	147
M-51	37.2	M-17	0.95	M-51	176	M-50	117	M-3	15,322	FM 832	143
M-10	36.9	FM 832	0.95	M-50	175	M-17	115	M-25	15,229	M-11	135
M-35	36.9	M-34	0.94	M-36	174	M-34	114	M-17	15,148	M-10	133
M-36	36.8	M-10	0.94	M-11	173	M-10	114	M-35	15,044	M-17	132
M-34	36.4	M-35	0.93	M-3	171	M-22	114	M-10	15,017	M-22	131
TAM 94 L-25	35.8	M-3	0.90	M-10	171	M-51	111	FM 832	15,015	M-35	129
M-17	35.8	PSC 355	0.88	M-17	168	FM 832	105	M-36	14,923	M-36	128
M-22	35.6	M-2	0.87	M-2	168	M-3	103	M-22	14,781	TAM 94 L-25	128
M-50	34.6	M-51	0.87	M-22	167	M-2	99	PSC 355	14,180	M-34	124
M-25	34.5	M-50	0.77	M-25	162	PSC 355	95	M-34	14,111	M-25	123
Mean	37.0		0.93		174		113		15,373		138
BLSD	1.5		0.05		7		6		1,007		12
CV	4.47		6.23		4.29		5.72		7.05		9.88

readings that were similar to that of TAM 94 L-25 or FM 832, although a few of the mutant lines had significantly finer fiber such as lines 17, 2, 22, and 25. TAM 94L-25 M-25 was one of the four mutant lines in Table 6 that averaged significantly longer UHML and strength. The fiber for line 25 seems to be strong, long, and apparently quite fine, the combination of which might prove to be valuable for yarn production. Although mutant line 25 might not have cultivar-worthy yield potential, it could serve as a valuable source of genes in the germplasm and breeding stocks.

Genotypes differed ($p<0.01$) in seed size as indicated by seed surface area (Table 14). Seed surface area also was different among Environments. TAM 94L-25 and mutant line 25 had the largest (k=100) seed of those tested and all mutant lines except TAM 94L-25M-2 and -3 were larger than FM 832 and PSC 355 (Table 15). This large seed size no doubt is a major contributing factor to the low lint percent expressed by the parent and mutant lines. It is interesting that only one of the mutant lines tested had a similarly sized seed as TAM 94 L-25. Since small seeds are often associated with high yields, this was to be expected. Mutant line 3 was among the higher yielding mutants (Table 6).

Total number of fibers seed^{-1}, shown in Table 15, varied from 17,059 fibers per seed for mutant line 50 to 14,111 for mutant line 34. PSC 355 and FM 832 were among the lines with the fewest fibers seed^{-1}, however, they were also the smallest seed of those tested. Surface area available for fiber development was much less, probably resulting in the low total fiber count. TAM 94L-25 had a relatively high number of fibers per seed with 15,992 fibers per seed as well as the largest seed.

Fibers per unit surface area, given in this work as fibers mm^{-2}, are shown in Table 15. While the two commercial checks had high values, mutant line 2 had the highest number of fibers per unit seed surface area. This is interesting, since mutant line 2 also had one of the smallest seeds of the mutant lines tested and one of the highest total numbers of fibers $seed^{-1}$. This would suggest a possible candidate for high yield, but this was not the case in this evaluation. Mutant line 2 actually yielded about the same amount of lint ha^{-1} as the TAM 94 L-25 check (Table 5). However, this combination of quality and lint density per unit of seed surface could be an excellent candidate for breeding purposes and certainly deserves additional research. Mutant lines 3, 51, and 50 were equivalent to the high yielding check, PSC 355, for fibers mm^{-2}. Mutant line 3 yielded higher than TAM 94 L-25 in the yield trial, but lines 50 and 51 did not. The remaining eight mutant lines had similar numbers of fibers mm^{-2} to TAM 94 L-25.

CORRELATIONS

It has been suggested in the literature that fibers per unit seed surface area are positively correlated with yield {Worley, 1974 #78}, and negatively correlated with some HVI fiber quality parameters {Coyle, 1997 #80}. Recall that one of the goals of this project was to determine if mutation could affect these relationships.

In an attempt to glean relationships based on seed size, total number of fibers per seed, and fibers per unit seed surface area, the data were correlated with relevant HVI and AFIS fiber traits, and yield data (Table 16). Significant correlations were found for several of the traits.

Table 16. Pearson Correlation Coefficients of within-boll yield components and discussed yield and fiber traits for 12 representative TAM 94 L-25 M-lines, two commercial checks, Phytogen 355 (PSC 355) and Fiber Max 832 (FM 832), and a non-mutated TAM 94L-25 check grown in 2008 at College Station, and 2009 at College Station and Weslaco, TX.

	FIB/SD	FIB/MM	SUR/SD
TLYLD	0.05	0.36**	-0.43**
SGLP	-0.03	0.43**	-0.57**
MIC	-0.16	0.04	-0.21*
UHML	-0.35**	-0.52**	0.36**
UNIF	-0.35**	-0.15	-0.13
STR	-0.41**	-0.64**	0.42**
ELONG	-0.21*	-0.06	-0.11
HGLP	0.20*	0.59**	0.62**
LN	-0.54**	0.41**	-0.64**
FINE	-0.28**	-0.11	-0.14
FIB/SD		0.68**	0.01
FIB/MM	0.68**		-0.72**
SUR/SD	0.01	-0.72**	

*, ** Significant at the 0.05 and 0.01 probability level, respectively

Surface Area Seed^{-1}

Seed surface area, or seed size, was significantly correlated with several measured traits, although most of these correlations, such as yield (r= -0.4), micronaire (r= -0.2), UHM length (r=0.35), bundle strength (r=0.4), and length by number (r= 0.4) were weak (Table 16). The R2 values ranged from 0.04 to 0.189 for these traits, meaning that surface area per seed only explained 4 to 18.9% of the association seen in those traits. The other fiber quality parameters, uniformity, elongation, and fineness, were unaffected by over-all seed size. The fibers per unit surface area, hand and saw-ginned lint percent and lint yield were negatively correlated with seed size. As seed size increases, those traits that are either directly or closely associated with lint yield goes down. This is a fairly intuitive result, i.e., that the more energy devoted to the seed means less energy devoted to fiber development. That fiber length and strength increased with seed size is interesting and has also been shown in the work of Stewart and Kerr {Stewart, 1974 #82}.

Fibers seed^{-1}

Total number of fibers per seed was not correlated with total lint yield, saw-ginned lint percent, micronaire, or surface area per seed (Table 16). It is interesting that the total number of fibers per seed had no affect on the yield nor was it associated with surface area per seed. Worley et al. (1974) suggest that lint per seed impacts lint yield, however, they were dealing with the mass of fiber, or lint index, as opposed to count. A weak, positive correlation (r=0.2) existed for total fibers per seed and hand-ginned lint percent. Fineness, micronaire, uniformity, length by number, fiber bundle strength, and elongation were

negatively associated with total number of fibers per seed, suggesting that fiber quality may decrease as number of fibers per seed increases. It is interesting to note that although some of the relationships may be weak (r= -0.2 to -0.54), all fiber quality parameters were negatively associated with total fibers per seed. So as the total number of fiber per seed increased, fiber quality went down in this study. A strong, positive correlation existed between fibers mm^{-2} area and number of fibers $seed^{-1}$ (r=0.68).

Fibers mm^{-2}

Fibers mm^{-2} was not correlated with micronaire, uniformity, elongation, or fiber fineness (Table 16). A strong positive correlation existed between fibers mm^{-2} and fibers $seed^{-1}$ (r=0.68), as would be expected since as the concentration of fibers increases per unit seed surface area, total fibers per seed increases. However, fibers mm^{-2} was negatively associated with total seed surface area. These data suggest that the smaller the seeds, the greater the number of fibers produced per unit of seed surface area. The correlation between fibers mm^{-2} and lint yield (r= 0.36), saw-ginned lint percent (r= 0.43), and hand ginned lint percent were positive (r= 0.59). This too is an expected result and it should go without saying that as fibers per unit seed surface area goes up, so should yield and the yield component lint percent. Worley et al. (1974) suggested that although it might play a small role, fibers per unit surface area is an important component of yield.

CONCLUSIONS

The purpose of this experiment was to analyze the effectiveness of Auld's (1998) cotton mutation technique to improve further upon a germplasm line with fiber traits already considered to be at the upper bounds of those available and to see if yield could be improved without sacrificing lint quality or conversely. From the analyses of these data it was evident that:

- Mutation was successful in producing selectable variation within the TAM 94L-25 mutant population.
- Mutation had little to no effect on fiber Length Uniformity or Elongation.
- Mutation did affect Lint Yield, Upper Half Mean Length, Micronaire, Fiber Bundle Strength, Seed Surface Area, and Fibers mm^{-2}.
- EMS-induced mutagenesis was successful in producing TAM 94L-25 mutated lines with higher yield and better fiber quality than the non-mutated parent line.

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