GENETIC IMPROVEMENT OF UPPER HALF MEAN LENGTH AND SHORT

FIBER CONTENT IN UPLAND COTTON, *GOSSYPIUM HIRSUTUM*

A Dissertation

by

BENJAMIN MICHAEL BEYER

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

DOCTOR OF PHILOSOPHY

August 2012

Major Subject: Plant Breeding

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ABSTRACT

Genetic Improvement of Upper Half Mean Length and Short Fiber Content in

Upland Cotton, *Gossypium hirsutum.* (August 2012)

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Desired base upper half mean length (UHML) of upland cotton (*G. hirsutum*) in the U.S. has been set a 27.0 mm and is shorter than the standard set by the international community. Upland cotton genotypes from China, South Africa, West Africa, and the U.S. were test crossed to an extra long staple upland (ELSU) and a short staple upland (SSU) and selected genotypes that included both ELSU and MSU phenotypes were crossed in a half-diallel mating scheme to estimate general combing ability (GCA) effects and specific combining ability (SCA) effects. A recombinant inbred line (RIL) population was established to determine the narrow sense heritability (h^2) of AFIS short fiber content by weight (SFCw) and lower half mean length (LHML) and to estimate SFCw using HVI fiber properties.

Obsolete cultivars from China are not likely sources for UHML improvement, cultivars from Africa and the U.S. could harbor alleles not being used in current elite short staple cultivars or modern ELSU cultivars. Two ELSU

lines used in this study derived through interspecific hybridization with *G. barbadense* could contain alleles for UHML improvement in modern ELSU cultivars developed without any apparent *G. barbadense* introgression. A third line D&PL 45-867, might contain alleles for UHML improvement in long staple upland cotton genotypes.

Narrow sense heritability estimates indicated a much higher heritability of LHML than AFIS SFCw. Correlation between AFIS SFCw and LHML did not agree with previous studies when using an ELSU X MSU cross. Further study is needed to understand this complex relationship.

DEDICATION

I would like to dedicate this dissertation to my family. I want to thank my parents for their love and support during my Ph.D. tenure. I also want to thank my brother and sister-in-law for their support. And also my lovely wife for her love and support.

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ACRONYMS

US – United States of America

ELS – Extra Long Staple

ELSU – Extra Long Staple Upland

LSU – Long Staple Upland

MSU – Medium Staple Upland

HVI – High Volume Instrument

AFIS – Advanced Fiber Information Systems

UHML – Upper Half Mean Length

ML – Mean Length

LHML – Lower Half Mean Length

UI – Uniformity Index, HVI

SFC – Short Fiber Content

SFCw – Short Fiber Content by Weight, AFIS

FBRI – Fiber and Biopolymer Research Institute, Lubbock, TX

RIL – Recombinant Inbred Line

DP491 – Deltapine 491, Monsanto, Co.

FM832 – FiberMax 832, Bayer Crop Science

MX2010 – Tecoman, Colima, Mexico in 2009-10

CS2010 – College Station, TX in 2010

CS2011 – College Station, TX in 2011

G – Genotype

E – Environment

GxE – Genotype X Environment Interaction

GCA – General Combining Ability

GCAxE – General Combining Ability X Environment Interaction

SCA – Specific Combining Ability

SCAxE – Specific Combining Ability X Environment Interaction

P – Parents

C – Crosses

P vs. C – Parents vs. Crosses

PxE – Parents X Environment Interaction

CxE – Crosses X Environment Interaction

(P vs. C)xE – (Parents vs. Crosses) X Environment Interaction

L – Line

T – Tester

LxT – Line X Tester Interaction

LxE – Line X Environment Interacton

TxE – Tester X Environment Interaction

LxTxE – Line X Tester X Environment Interaction

MSE – Mean Square of Error

S.E. – Standard Error

CV – Coefficient of Variation

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CHAPTER I

INTRODUCTION

Upland cotton, *Gossypium hirsutum* L., is a crop that produces spinnable fibers and is a major crop in 14 of the 17 cotton producing states of the United States (US) (Cotton Incorporated, 2009). During the period of 2009 to 2011, the US on average produced 15.3 million bales per year and exported 11.6 million bales per year (National Cotton Council, 2012). Because cotton is now being traded in a global market, producers in the US must compete with producers around the world. While yield has always been the primary trait of interest by producers, fiber quality quickly is becoming of major importance in order to maintain global competitiveness. This is evident also by the increase in demand for the high quality fibers produced by pima, *G. barbadense* L., fibers (Cline, 2009).

The quality of cotton is dependent upon the cultivar, environmental conditions during the growing season, harvest methods, and ginning methods (Anthony, 1999). While improvements have been made in the way cotton is handled from harvesting to ginning, genetic improvement of fiber quality will provide the highest return per dollar invested. New sources of alleles coding for improved fiber quality are needed along with improved conventional or molecular techniques for understanding inheritance and epistatic interactions.

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This dissertation follows the style of Crop Science.

The ultimate evaluation of fiber quality is the quality of yarn that can be produced. The fundamental problem that breeders face is that maximum genetic gain from selection occurs from single plant selections in the F_2 or F_3 generation which doesn't provide enough for spinning (Braden, 2005). Breeders must rely on estimates, i.e., correlations, of the relationship between fiber properties and yarn properties.

Fiber length is typically a good indicator of cotton fiber quality and producers can receive a premium for longer fibers (Braden and Smith, 2004). Length also is related to strength and fineness characteristics. Long and strong fibers are desired by processors because they allow increased spinning speeds which correspond to increased production and decreased cost per unit.

Fiber length in cotton is a heritable trait controlled by multiple genes. Because of the narrow genetic base of current elite commercial cultivars, genetic variation might not be present for continued improvement of fiber quality (Paterson et al., 2004; Percy et al., 2006). Possible sources for improving current elite lines can be found in primary germplasm resources that include foreign cultivars and obsolete cultivars in the national germplasm collection (Percy et al., 2006). Knowing the inheritance and genetic variation for fiber length is essential to the improvement of UHML and reduction of short fiber content in upland cotton.

This project used a total of 29 cultivars collected from China and Africa in addition to seven US cultivars that represented different cotton production

regions or germplasm pools in testcross *per se* performance with a short staple cultivar and a recently released ELSU germplasm line to determine GCA and SCA of potential parents for improved UHML. A second study was a half diallel mating design using a long staple upland (LSU) germplasm line and a recently release ELSU germplasm line along with three confirmed ELSU accessions from the United States Department of Agriculture (USDA) Cotton Collection to determine GCA and SCA. Broad sense heritability (H^2) estimates for UHML were obtained from the testcross and diallel studies. Lastly, individual plants were selected in the $F_{2:3}$ generation of a 'DP491'(PVP 200100159, PI 618609)/ELSU cross. Seed of each plant was increased to the $F_{3:5}$ generation and planted in a replicated design. Fiber data were obtained to determine the narrow sense heritability (h^2) of Advanced Fiber Information System (AFIS) Short Fiber Content by Weight (SFCw) and Lower Half Mean Length (LHML) measurements from High Volume Instrument (HVI) data. Regression equations to determine AFIS SFCw from HVI data were developed. Pearson's correlation coefficients (r) were obtained between the regression equations and AFIS SFCw and other HVI measured fiber properties. The data obtained will be of importance to plant breeders to develop ELSU cottons with improved spinning properties.

Objectives

The objectives of the research described herein are:

1) determine general combining ability (GCA), specific combining ability (SCA), and broad sense heritability (H²) estimates for fiber length among a cohort of medium staple genotypes from China, Africa, and the U.S. when crossed to TAM B-182-33 ELS and Tamcot CAMD-E, a short staple obsolete upland cultivar;

2) determine GCA and SCA for fiber length parameters among three confirmed USDA accessions, TAM B182-33 ELS, and TAM 94L-25;

3) evaluate heritability and equations used to estimate short fiber content using HVI parameters in an $F_{3:5}$ population derived from DP491/TAM B-182-39 ELS.

CHAPTER II

REVIEW OF LITERATURE

Cotton Fiber Development

Cotton (*Gossypium sp.*) fibers are single cell growths that arise from epidermal cells on the outer integument of ovules within developing bolls (Basra and Malik, 1984). The fiber is ultimately a hair or trichome that elongates up to 1000-3000 times longer than its diameter and is one of the purest forms of cellulose.

Cotton fibers consist of two distinct types; longer fibers that have commercial value because they can be spun into yarns and made into textiles, and the extremely short fibers called linters that have little commercial value (Basra and Malik, 1984). Fiber development consists of four phases; initiation, elongation, secondary wall thickening, and maturation (Naithani et al., 1982; Basra and Malik, 1984). While initiation and maturation are distinct steps, a study by Gibson and Johan (1969) found an overlap between the elongation and secondary cell wall thickening phases.

Stewart (1975) documented the beginning states of the development of cotton fibers. Prior to antheis, the ovules of developing cotton squares are anatropous. However, the ovules begin to form stomata on the surface beginning one week before anthesis, primarily on the chalazal end. While fiber initials can form anywhere from a day before to two days past anthesis (dpa) (Basra and Malik, 1984), Stewart (1975) noted that they first form on the crest of

the funiculus on the morning of anthesis. This is followed by the formation of initials around the lateral circumference of the ovule. Within a few hours, initials will form at the chalazal end and is finished at the micropylar end. In this area, fiber initials can continue to occur up to four days past anthesis. Linters typically begin to form at four dpa (Joshi et al., 1967; Zhang et al., 2007).

Following initiation of fiber development, elongation immediately begins (Basra and Malik, 1984). Stewart (1975) described the beginning of the elongation with the initials becoming rounded and expanding, thus resembling a balloon. At this stage, the developing fibers on the chalazal end expand more rapidly than the other initials. Furthermore, elongation happens as a tangent to the ovule in the direction of the micropyle. On the second dpa, fiber elongation becomes more evident with directional growth occurring at the top of the funiculus. Following this stage, the fibers will begin to grow together and take on spiral growth as they continue to elongate. The fibers will continue to elongate for 27-30 days dpa under optimum conditions (Schubert et al., 1973). The fiber lengths obtained during elongation are a result of the rate of elongation and the elongation period (Gipson and Joham, 1969), which also varies among genotypes (Basra and Malik, 1984). The rate of elongation is determined by environmental conditions and dpa (Gipson and Joham, 1969). Gipson and Johan (1969) showed fiber elongation is highly temperature dependent from zero to 15 dpa when developing bolls were subjected to temperatures below 21.1C. Temperatures below 21.1C resulted in significantly slower rates. The

authors also noted that the maximum elongation/day occurred at 10-15 dpa. Once bolls were 15 dpa, elongation rates were constant regardless of night time temperature and continued until the end of elongation.

As elongation cycle ends, secondary cell wall thickening begins (Basra and Malik, 1984). Secondary cell wall thickening however may begin prior to cessation of elongation (Benedict et al., 1973; Schubert et al., 1973, 1976; Meinert and Delmer, 1977; Beasley, 1979; Naithani et al., 1982; Basra and Malik, 1984) and occurs evenly over the entire fiber and not at specific regions (Basra and Malik, 1984). Upon maturation the secondary cell walls will be comprised of up to 94% cellulose. The thickness of the secondary cell walls and the angle at which they spiral ultimately affect their strength and thus their ability to withstand fiber breakage during harvesting, ginning, and cleaning.

When secondary cell wall thickening is complete, the ovary wall will begin to dry and split along lines in the surface tissue of the boll (Basra and Malik, 1984). This will leave seeds and fibers exposed to the elements and the remaining fluids in the boll will evaporate. Fiber maturity is determined traditionally by the amount of secondary cell wall thickening that occurs. Fully mature fibers will have a thick secondary wall and thin lumen. This makes the fibers stronger and more resistant to breaking during harvesting and processing. On the other hand, if the fibers are not mature, they will have thinner secondary walls and not spin as well because they will not twist and bind together during

spinning. Furthermore, the fibers will entangle and produce small knots known as neps.

The type of cotton fibers desired by yarn spinners are long, strong, fine, and mature fibers because they produce stronger and finer yarns (Basra and Malik, 1984). Because of the impact the environment has on fiber development, potential cultivars should be tested for adaptation prior to adoption by producers in order to determine the potential for fiber quality.

Fiber Quality

Cotton fiber quality is at its peak when the bolls are still on the plant (Anthony, 1994; Anthony 1999). The fiber quality however will depend upon the cultivar, environmental conditions during the growing season, weathering of the open bolls prior to harvest, harvest method, and ginning procedures (Anthony, 1999). The primary fiber quality parameters are length, fineness, length distribution, and strength (Hsieh, 1994). The fiber properties that are important depend upon the spinning system used and will have impacts on the yarn strength, thick and thin places, and feel and attractiveness of the yarn produced. Furthermore, the fiber properties are determined by both genetic and environmental factors.

Cotton Harvesting

The two means of harvesting cotton in the U.S. are by mechanical spindle picker harvest and stripping (Anthony, 1999). It is estimated that 75% of the cotton in the U.S. is harvested with the mechanical spindle picker and the

remaining 25% is harvested with the mechanical stripper (Mayfield et al., 1999).

The primary difference in the harvested product between mechanically picked

and stripped cotton is the amount of trash. About 1500 pounds of picked

seedcotton is required to make a 480 pound bale of lint and whereas 2200

pounds of seedcotton is required under stripper harvest. The difference is due

to the amount of trash in the seedcotton. Picker harvested cotton will contain

approximately 120 pounds of trash in the 1500 pounds of seedcotton versus

approximately 800 pounds of trash in the 2200 pounds of stripped seedcotton.

However, modern cotton strippers utilize onboard trash extractors in order to

reduce the amount of trash in the harvested seedcotton (Anthony, 1999).

Ginning Procedures

Prior to the mechanization of cotton harvesting, the only machinery

needed were a gin stand and a press to form bales (Mayfield et al., 1999). The

modern saw type ginning system now includes seedcotton cleaning and drying,

ginning, lint cleaning, and bale pressing. The optimum moisture of seedcotton to

maintain fiber quality is six to seven percent (Anthony, 1999). Furthermore, the

amount of cleaning of seedcotton should be kept to a minimum in order to

preserve the fiber quality.

A saw gin uses a set of circular saws between ginning ribs that do not

allow seed to pass through (Mayfield et al., 1999). Fibers are caught on the

teeth of the saw blades and pulled free of the seeds as the blade passes

through the ribs. The seeds then drop to an auger system for removal from the

gin stand while the fibers are doffed from the saw blades by brushes that spin at a faster speed and opposite direction to the saw blades. Ginned fibers then pass through one or two lint cleaners. Lint cleaners remove any remaining fine trash but reduce fiber quality by breaking fibers. One lint cleaner is used in the ginning process and a second is only used if further cleaning is needed. Finally, the lint is compressed into bales and wrapped completing the saw ginning process.

Extra long staple (ELS) or Pima cotton (*G. barbadense*) in the U. S. is ginned on rotary-knife roller gin stands that use a large diameter roller to pull the fiber under a stationary knife that will not let the seed pass which effectively separates the fiber from the seed (Anthony, 1999; Mayfield et al., 1999). Roller ginning may require an extra seedcotton cleaning and drying stage prior to ginning. Roller ginning is easier on the fibers, which in turn produces fewer broken fibers and entanglements and maintains high fiber quality.

Fiber Length

Fiber length was the first parameter to be measured for cotton quality determination (May, 1999). It has long been known as a contributor to yarn strength and processing performance (Brown, 1938; May, 1999; Perkins et al., 1984). Moreover, knowing fiber length is important knowledge for spinning yarns of a certain size on ring spinning frames (May, 1999; Rusca and Reaves, 1968). In terms of yarn strength, longer fibers require less twist whereas a shorter staple cotton would require more twist to produce yarn with equivalent

strength if all other fiber quality parameters were held constant (May, 1999).

Because there is a limit to the amount of twist of fibers drawn into yarn, longer

fibers would mean reduced input costs (May, 1999; Perkins et al., 1984) and

would allow finer yarns worth more income to be produced (Landstreet, 1954;

May, 1999).

Suter-Webb

The Suter-Webb array system was used to determine fiber length via the

staple length system (Behery, 1993; May, 1999). The Suter-Webb array method

uses a comb-sorting technique which separates the fibers into different length

groups that are then weighed by each group. This method requires too much

time to test each sample and is thus impractical for breeding programs and is

rarely used (Thibodeaux et al., 2008).

Staple length, which is a subjective estimate of the longest five percent of

fibers is measured in 32nd of an inch increments and was the original method

used by the USDA to classify cotton fiber length (USDA, 1965; Woo, 1967).

However, this method is subjective and does not provide any fiber length

distribution data, and has been replaced by more objective measurements.

 Upper Half Mean Length (UHML)

The HVI upper half mean length (UHML) is the average length of the

longest 50% of fibers in a sample or bale (ASTM, 1994b). This measurement is

used to place cotton into the five upland staple classes which are short (<21.0

mm), medium (22.0 mm – 25.0 mm), medium-long (26.0 mm. -28.0 mm), long

(29.0 mm. – 34.0 mm), and extra long staple (ELS) (>34.0 mm) (Bradow and Davidonis, 2000). The HVI UHML measurement also is what is traditionally used to market fiber length in the United States and the world (Smith et al., 2009) and the data is needed in order to set drafting rollers at the proper distance for spinning (Rusca and Reeves, 1968; Behery, 1993; El Mogahzy and Chewing, 2001; Braden, 2005).

High Volume Instrument

High Volume Instrument (HVI) technology is rapid and measures fiber length using a small beard of paralleled fibers passing through a sensing point of the system (Anthony, 1999). High Volume Instrument can be programmed to provide fiber length measurements in 32^{nd}s, i.e., staple, or in continuous length measurements occurring in 100th of an inch increments.

The basis of the HVI method for measuring fiber length is based on the Hertel (1940) fibrogram methods (Ramey, 1999; Cui et al., 2009). The process begins by clamping a beard of fibers at a random point along their length (Ramey, 1999). The beard is then combed in order to remove loose fibers and to straighten fibers in the clamp. The beard is then scanned to determine the fiber length distribution. The values are calculated based on the scan and averages taken to determine the fiber length properties (Ramey, 1999). The beard sampling procedure presents a fundamental issue as it introduces a bias into the measurement of the fiber parameters (Cai et al., 2010). The original theory was that the probability of a fiber being selected was in proportion

to its length (Hertel and Zervigon, 1936; Hertel, 1940, Cai et al., 2010). This theory is the length-biased assumption and was proven by Zeidman et al. (1991a). However, Chu and Riley (1997) later disproved the theory and proposed that each fiber has an equal chance of being sampled but there were still discrepancies specifically related to fibers less than 12.7 mm in length (Cui et al., 2007; Cai et al., 2010).

Advanced Fiber Information System

The Advanced Fiber Information System (AFIS) is another tool to determine fiber quality parameters. A small sliver of cotton, approximately 0.5 g and containing 3,000 to 10,000 fibers, is prepared manually for analysis by the AFIS (Calhoun et al., 1997). The fibers are individualized and pass through electo-optical sensors via air flow (Bragg and Shofner, 1993: Calhoun et al., 1997). Algorithms based on the duration and speed of a fiber passing through the sensor are used to calculate fiber length (Calhoun et al., 1997). However, the AFIS system can produce biased measurements since the fiber individualizer results in fiber breakage (Bragg and Shofner, 1993). This breakage can reduce the UHML by one to two millimeters and increase Short Fiber Content (SFC) (Bragg and Shofner, 1993).

The AFIS software can be programmed to provide length data in both English or metric units and is calculated on both a number and weight basis (Calhoun et al., 1997). A graphic distribution of fiber length categories can be obtained. The number values are based on actual count data whereas the

weight data is calculated (Calhoun et al., 1997) based on the average fiber

fineness, thereby biasing the measurement (Krifa, 2006). Types of length data

reported include mean length, upper quartile length by weight (UQLw), which is

the average length of the longest 25% of fibers by weight, and short fiber content

(Calhoun et al., 1997). Calhoun et al. (1997) and Smith and Williams (1995)

have shown high correlation between HVI UMHL and AFIS UQLw. Short fiber

content can be reported both by number and by weight.

<u>Mean Length</u>

The average or mean length of fibers (ML) can be calculated in both a

weight and number basis with the later being important in yarn spinning

(Braden, 2005; ASTM, 1994a). However, with the measurements being weight

and number based, the two measurements are not the same. For example, the

fiber length by number (FLn) includes and averages short fibers in the sample

whereas the fiber length by weight (FLw) excludes or discounts them in the

calculated values. Since cotton fibers vary in their diameter, fibers that are

more mature and thicker have an increased mass that biases the results.

Furthermore, a study by Cui et al. (1998) showed that number-based and

weight-based measurements of fiber length can result in different ranks of cotton

fiber lengths both theoretically and experimentally.

<u>Uniformity Index</u>

The uniformity index (UI) of cotton is the ratio of the mean length to the

UHML expressed as a percentage (Behery, 1993). If the fibers in the bale were

the same length, then the uniformity index would be 100 (Cotton Inc., 2011).

However, because cotton fiber lengths vary naturally and because processing

causes fiber breakage, the UI is less than 100.

The classifications for uniformity index are very high (>85), high (83-85),

intermediate (80-82), low (77-79), and very low (<77) (Cotton Inc., 2011).

Uniformity index affects the evenness and strength of yarn and is related to yarn

processing ability. Cottons with a low UI will produce inferior yarns.

Short Fiber Content

Short fiber content (SFC) is defined as the percentage of fibers that are

12.7 mm or shorter (Bragg and Shofner, 1993). Short fibers have a big impact

upon the quality of yarn produced and the performance during spinning (Backe,

1986). Backe (1986) found that SFC had the biggest impact on the number of

thick and thin places in yarn and the adjusted break factor of a yarn This was

observed when the difference in SFC was as little as three percent.

Furthermore, it was shown that SFC had a greater impact than fiber length,

micronaire, and the number of bales used in the laydown procedure.

Anthony (1992) reported on the origin of SFC within cotton bales and

samples. The changes were primarily attributed to different fiber moisture, fiber

strength, and machines used in processing during ginning (Anthony 1985;

Anthony, 1992). The author found that as moisture levels decreased, the

amount of SFC increased in samples. The SFC also increased with more lint

cleaners being used. The SFC of samples increased from 6.8% with no lint

cleaners to 9.8%, 11.1%, and 12.7% as one, two, or three lint cleaners were used, respectively (Anthony, 1992).

The best way to accurately measure SFC is through the Sutter-Webb array method (Thibodeaux et al., 2008). However, this method is too tedious and time consuming to perform on every bale or fiber sample. An advantage of AFIS is that it provides direct measurement of SFC on both a number and weight basis (Bragg and Shofner, 1993; Calhoun et al., 1997).

Determination of SFC must be done using other length parameters as direct determination has been shown to be difficult and unreliable (Zeidman et al., 1991b). This is a sharp contrast to measuring other fiber length properties which are easy to accurately measure. As such, multiple studies have published different methods in which to quantify different fiber property measurements as indicators of SFC in a sample or bale (Ramey and Beaton, 1989; Zeidman, 1991b; Anthony, 1992; Thibodeaux et al., 2008; Cai et al., 2011).

Ramey and Beaton (1989) found a high negative (-0.955) correlation between SFC and UI. However, when the authors broke their data down by year, the correlations between SFC and UI were -0.635 and -0.744 for their samples in 1984 and 1985, respectively. Thibodeaux et al. (2008) looked at Suter-Webb array data and HVI and AFIS fiber properties. The authors stated that SFC similar to what would be found using the Suter-Webb array method could be accurately predicted using AFIS or HVI data.

Zeidman et al. (1991b) tried using ML, UHML, and UI parameters

correlated to estimate SFC using USDA Annual Quality Surveys from 1985, 1986, and 1987. Based on the 1985 data, the authors found coefficient of correlation values of 0.75 and 0.80 between UI and SFCn or SFCw, , respectively. When UI was combined with other length parameters, the coefficient of multiple determination was highest for the 1985 crop year but did not perform as well in the other years. Furthermore, their data was only relevant for the 1985-1987 crop years and is not valid for future samples (Anthony, 1992).

Anthony (1992) also looked at the relationship between UI and SFC. The author found that prediction of SFC from UI could produce an error as large as 47%. Based on 20 different genotypes, only four showed a significant relationship between SFC and UI. The overall relationship between SFC and UI produced an R-square of 0.23 when the genotypes were included (Anthony, 1992).

Lower Half Mean Length

A new statistical parameter to characterize cotton fibers shorter than 12.7 mm is known at the Lower Half Mean Length (Cui et al., 2009). This parameter was developed using algebraic conversion and can be calculated using the UHML and UI measurements (Cai et al., 2011). It is meant to provide more information than current short fiber measurements primarily due to lower coefficient of variation (CV) than AFIS SFCw. Furthermore, current data

suggests that LHML is a better parameter for predicting spinning performance than AFIS SFCw.

<u>Fiber Length Distribution</u>

The length and number of each length within a given sample of a cotton genotype can be displayed as a fiber length distribution. Robert et al. (2000) hand pulled fibers from seedcotton of Pima *(G. barbadense)* cultivar S-6. When the fiber distribution was analyzed, it resembled a normal unimodal curve. However, since lint is rarely hand pulled from seedcotton, fiber length distributions of mature and strong upland cottons machine harvested and saw ginned are typically bimodal (Krifa, 2006). The first peak in the distribution typically occurs around the 3.2mm point. This peak is attributed to fiber breakage during processing and handling. The second peak in the fiber length distribution is associated with the UHML of sample. Unimodal distributions can be seen also in upland cotton. However, they are typically immature and weak cottons that have excessive fiber breakage from processing and handling. Unimodal distributions are possible with mature and strong cotton, but are only seen if excessive forces in cleaning and processing were used (Krifa, 2006). Ultimately, fiber length distribution in upland cotton is based on the inherit genotype and genotype X environment factors and the processes used during ginning, cleaning, and carding (Krifa, 2007).

Textile Industry

The majority of the lint produced is used directly in the production of yarns

to manufacture textiles. The end product for a bale of cotton is ultimately decided by the fiber properties and the type of spinning technology being used to transform the fibers into yarn (Krifa and Etheridge, 2003). The innovations in spinning technology have arisen from changes in processing practices, end products, and various mixes of fiber properties being used.

<u>Ring Spinning</u>

Invention of the ring spinning frame is credited to John Thorpe and dates to 1828 (Fraser, 1993). The modern ring spinning frame involves vertically mounted spindles with several drafting rollers above each of them. Roving is above each spindle where it passes through the drafting rollers in order to reduce it to the desired fineness prior to spinning. As yarn exits the drafting rollers, it passes through a guide eye located above each spindle. Past the guide eye is a traveler, which is free to rotate around a ring as the yarn is fed onto a bobbin.

During this process the yarn is twisted to impart tensile strength (Fraser, 1993). Fiber strength is the most important factor affecting yarn tenacity (Üreyen and Kadoğlu, 2006). However, it should be noted that fiber length and length uniformity are the most important fiber properties that affect ring spun yarn tenacity (Deussen, 1993). Fiber properties that are also important include fiber elongation and fiber fineness (Üreyen and Kadoğlu, 2006). The previous stated fiber properties along with yarn count, yarn twist, roving count, and unevenness

of roving are all factors that impact upon the tenacity of yarn. Roving count is especially important since it is used to set the draft on the ring spinning machine.

Ring spun yarn elongation before breaking is highly dependent upon yarn count, twist, and the roving count (Üreyen and Kadoğlu, 2006). Üreyen and Kadoğlu (2006) also found elongation of the yarn increased with more twists or in coarser yarns but decreased when a finer roving was used. Fiber elongation and fineness highly influence yarn elongation and have a positive effect on it. Other fiber parameters influencing yarn elongation were reflectance, fiber strength, SFC, and length but had a lower effect.

Yarn evenness and hairiness are other characteristics were influenced by fiber properties (Üreyen and Kadoğlu, 2006). Yarn evenness is affected primarily by the yarn count and unevenness of the roving. This characteristic is highly dependent upon fiber strength and prevention of fiber breakage leads to better yarn evenness.   Yarn hariness, which are fibers that are protruding from the spun yarn, was affected mostly by twist with strength, elongation, and length also affecting this yarn appearance measurement. Fiber length was shown to have the biggest impact on skein break factor, an important yarn quality parameter that is determined based upon the load applied and the yarn number (El Mogahzy et al., 1990). As such, increasing fiber strength, UHML, UI, yarn twist, and yarn count will reduce the hairiness of yarn when ring spun.

Ring spinning is considered the best platform for spinning short staple upland cotton (Özgüney et al., 2007) and is the standard by which other spinning

forms are judged (Fraser, 1993). It continues to undergo further improvement despite the need for high energy inputs and low production rates (Chang et al., 2003).

<u>Compact Spinning</u>

Compact spun yarns are a relatively novel type of spinning technology (Artzt, 2000). Compact spinning offers yarn spinners the possibility of producing high quality yarns from shorter staple upland cotton rather than using more expensive long or extra long staple cultivars (Krifa et al., 2002). Krifa and Etheridge (2003) were able to produce a 50 Ne carded yarn that was comparable to a combed yarn produce on a conventional ring spun frame with significantly reduced hairiness.

Compact spun yarns do not pass through a traditional spinning triangle as conventional ring spun yarns, but uses a much smaller triangle designed to minimize its width and height (Krifa et al., 2002). The advantage of this system is that the fibers are put into a more organized structure than ring spun yarns (Artzt, 2000; Krifa et al., 2002). The yarns produced represent a superior ring spun yarn which is attributed to the uniform integration of fibers into the yarn cross section (Artzt, 2000). This is accomplished by compacting the fibers into a narrow sliver in a process devoid of tension and then twisting them as a compact sliver. The process also has the distinct advantage of being able to utilize shorter staple cotton fibers than ring spun yarns.

The advantages of compact spinning is not only in the ability to use shorter fibers (Krifa et al., 2002), but other yarn structure qualities can be achieved (Artzt, 2000). Artzt (2000) analyzed the structure of a compact spun yarn using Scanning Electron Microscopy (SEM) and found that there was a better arrangement of fibers, a distinct twist, and a relatively small number of both short (1-2 mm) and long (6-8 mm) protruding hairs. Furthermore, Krifa et al. (2002) showed there was also improved elongation and yarn strength and Yilmaz et al. (2007) showed 30% higher packing density in compact versus ring spun yarns.

The advantages of compact spun yarn in terms of reduced hairiness and improvement in yarn parameters such as elongation and strength has been well documented in the literature (Krifa et al., 2002; Cheng and Yu, 2003; Krifa and Ethridge, 2003; Göktepe et al., 2006; Krifa and Ethridge, 2006; Kretzschmar et al., 2007; Omeroglu and Ulku, 2007; Yilmaz et al., 2007; Özgüney et al., 2008; Wang et al., 2009). Omeroglu and Ulku (2007) showed fabrics woven from compact spun yarns also had higher resistance to pilling, or the breaking of fibers and subsequent formation of fiber entanglements. Fabrics made with compact spun yarns also showed better dying and printing properties when compared to ring spun yarns by Kretzschmar et al. (2007) and Özgüney et al. (2008).

As with any new technology, it becomes critical to match quality with profitability (Krifa and Ethridge, 2003). If the fiber properties are not correct,

compact spinning may not be an economically viable option for spinners since the value added to the yarn will not match the increased production costs (Krifa and Etheridge, 2006). The primary benefit of compact spinning appears to be the potential for reducing the combed yarn process (Krifa and Etheridge, 2003). The primary criteria for dealing with combed cotton is the SFC. Krifa and Etheridge (2003) found the ability of compact yarns to compensate for any benefit from fiber combing decreased as SFC increased. Thus if fiber distributions are not taken into account, compact spinning may not counteract any fiber impurities that would otherwise be removed by combing. If the impurities are not removed, compact yarns will be significantly lower in quality than traditional ring spun yarns.

Open-End/Rotor Spinning

Rotor or open-end (OE) spinning produces yarn with a different structure than ring and compact spinning frames and does not use a spindle (Lord, 1971). It begins by drafting individual or small groups of fibers rather than using a sliver. This is such that no torque is created to be transmitted upstream and an open-end is created. Thus, fibers or small groups of fibers are attached at the end and wrapped into the yarn. The economic implication of this is that the speed is no longer limited to the size and shape of the yarn, which can be made to any size and shape desired.

Compared to ring spun yarn, OE yarn is 10-30% weaker, fuller, and has better elongation (Lord and Nichols, 1974; Mohamed and Lord, 1973). This has

been attributed to the unsystematic method of fiber integration into the yarn.

This results in decreased fiber migration and an increase in the number of fiber

tanglements in the yarn. In OE yarns, most of the fibers are in the fiber core

(Mohamed and Lord, 1973). The fiber core is then wrapped by fibers that vary in

twist level. This differential structure results in an uneven distribution of

stresses, thus resulting in the reduced strength but increased elongation

properties. However, the strength of OE yarn may be improved by increasing

the twist level.

Similar to other studies, El Mogahzy et al. (1990) determined that fiber

strength had an impact upon the skein break factor of OE spun yarn, although

fiber fineness had the biggest impact on skein break factor. As with other yarns,

fiber length and length uniformity also had a significant impact upon yarn quality.

<u>Air Jet Spinning</u>

Air-jet spinning has advantages over the other spinning methods in both

speed and cost (Basu and Oxenham, 1999). The air jet spinning system was

first commercialized by the DuPont Company in 1963 (Grosberg et al., 1987).

The system involves a false-twisting zone that is made up of a set of drafting

rollers, the air-jet, and take-up rollers. Yarn is twisted in one direction by the

rollers is then twisted in the opposite direction by the air-jet. The air-jet nozzle

produces axial velocity and tangential velocity (Zeng and Yu, 2003). The axial

velocity pulls fibers or strands of fibers from the front roller into the nozzle and

then transfers them out onto the take-up roller. The tangential velocity is

responsible for the twisting of the yarn. The three biggest factors affecting yarn quality in air-jet spinning are the nozzle pressure, the jet orifice angle, and the jet orifice position.

Modern air-jet spinning systems use two air-jets to introduce false twist into the yarn (El Mogahzy, 1998). In this set up, the second jet orifice operates at the opposite direction and at a higher velocity to the first jet orifice. Important fiber properties for air-jet spinning are fiber length, length uniformity, SFC, fiber bending resistant, fine trash content, and fiber/fiber friction (El Mogahzy, 1998).

The structure of air-jet spun yarn varies along its length (Grosberg et al., 1987). Class 1 structure has a thick yarn core that is wrapped by a thin yarn strand of wrapping fibers and has a corkscrew appearance. This structure represents 80% of the yarn structure in air-jet spun yarns. The class 2 structure has looser wrapping fibers and sometimes no wrapping fibers which makes it appear like twisted yarns and weaker. It is further divided into subclasses (Grosberg et al., 1987). Some sections will have a regular helix wrap angle with sections that have fiber wraps similar to open-end spun yarns (Lawrence and Baqui, 1991). There are also regions that are unwrapped and these can either have some twist or no twist at all.

The tenacity of air-jet spun yarns is different than other spinning methods (Grosberg, 1987). Coarse yarns have reduced tenacity compared to fine yarns. When fine yarns are spun using an air-jet system, a smaller number of fibers enter the front roller, which causes them to become individualized. This in turn

allows fibers on the edges to move away from the primary bundle and to become wrapping fibers. However, this can also negatively impact the evenness of the yarn during spinning.

A new adaptation of air-jet spinning is the Murata Vortex Spinning (MVS) system (Soe et al., 2004). This system differs from air-jet spinning by drafting fibers into a spindle orifice using an air vortex. The fiber property critical in MVS is SFC and dust content (El Mogahzy, 1998). The system tends to remove short fibers thereby allowing 100% cotton yarn to be spun with more variation for fiber length (Soe et al., 2004), while also giving the yarn a combed-like structure (El Mogahzy, 1998). Thus, fine yarns such as those produced by ring spinning can be spun on the MVS system. Another advantage of the system is that yarn can be spun at 400 m min^{-1} (Soe et al., 2004). Between the speed and quality of yarn produced, air-jet and MVS spinning was expected to become the predominant system (El Mogahzy, 1998).

Improvement for Fiber Length in Upland Cotton

Tetraploid cotton is thought to have arisen one to two million years ago through a chance hybridization of a *Gossypium* diploid A-genome and a D-genome (Iqbal et al., 2001). The resulting F_1 hybrid then doubled its chromosome number to create an allotetraploid. The polyploidization of the A and D-genomes has led to five different AD allotetraploid species. Two AD species, *G. hirsutum* and *G. barbadense*, comprise the majority of cotton planted in the world (Iqbal et al., 2001).

Eventually, tetraploid *Gossypium* species would be domesticated (Brubaker et al., 1999; Iqbal et al., 2001); however, there still exists one wild *G. hirsutum* genotype known as 'yucantanense' (Iqbal et al., 2001). Over time the phenotypes of *G. hirsutum* would be further domesticated from photoperiodic perennials that produced very short and coarse fiber to a non-photoperiodic annual that produces longer and finer fiber suitable for the manufacturing of various textiles (Brubaker et al., 1999; Iqbal et al., 2001). This drastic change has caused several bottlenecks and the subsequent reduction in genetic diversity of upland cotton (Iqbal et al., 2001).

<u>Genetic Diversity</u>

A variety of studies have looked at genetic variation for fiber properties within germplasm resources (May and Green, 1994; Zhang et al., 2005) and genetic variability among cotton cultivars (May et al., 1995; Bowman et al., 1996; Van Esbroeck et al., 1998; Bowman et al., 2003). In terms of fiber length and other fiber properties, significant genetic variation existed within populations of elite Pee Dee germplasm released by the Pee Dee Cotton Germplasm program and Acala type cottons from the New Mexico Cotton Breeding program (May and Green, 1994; Zhang et al., 2005). However, overall the gene pool of cotton in the U.S. contains very little genetic diversity (May et al., 1995; Bowman et al., 1996; Van Esbroeck et al., 1998; Bowman et al., 2003; Paterson et al., 2004). The reduction in genetic diversity has resulted in increased genetic vulnerability (Paterson et al., 2004). This has resulted from commercial breeding programs

utilizing a small number of elite genetic backgrounds to develop new cultivars. Furthermore, the dominance of planting transgenic cultivars has resulted in even more genetic uniformity and subsequent lack of genetic variation within U.S. cotton cultivars (Paterson et al., 2004).

A study to examine the genetic gain for fiber length among cultivars adapted to Central Texas was performed by Schwartz and Smith (2008). The authors planted nine different cotton cultivars released from 1905-2002 in different plant densities. The densities were four individual plant densities and a commercial density. Based on the commercial plant density data, 'Lone Star' (PI 528636) a variety released in 1905, had an UHML equivalent to Stoneville 213 (PI 529229) and Deltapine 55 (PI 529282), which were cultivars released in 1962 and 1974, respectively. Four cultivars in the study 'Half and Half' (PI 528511), 'Deltatype Webber' (PI 528717), 'Rowden 41B' (PI 528818), and 'Deltapine 14' (PI 528970) were released in 1910, 1922, 1930, and 1941, respectively, and all had lower UHML. This was attributed to an increase in selection solely for yield since no fiber objective quality testing was available until the 1960s. The authors found genetic gain rate of 0.048 mm/year in the commercial density and smaller slopes in the individual plant densities. This implied that genetic gain for increased interplant competition has occurred and that less genetic gain for UHML has occurred over the period of 1905-2002.

Sources for Fiber Length Improvement

Kohel (1999) suggested that wild species and accessions are likely

sources of new alleles for fiber length improvement. These sources include both the A-genome diploid species *G. arboretum* and *G. herbaceum* and the AD-genome tetraploid species *G. barbadense* and *G. hirsutum.* The major drawback in determining the potential of a wild parent for enhancing fiber length however is that not all of the germplasm lines produce spinnable fibers (Kohel, 1999).

Kebede et al. (2007) used microsatellite markers to determine the amount of genetic variation for fiber length in 20 *G. herbaceum* (A1-genome) and 21 *G. arboretum* (A2-genome) germplasm lines. The authors included three D-genome diploid species and upland and Pima type cultivars in the study. Genetic variation within *G. herbaceum* and *G. arboreum* both had an average polymorphic information content (PIC) value of 0.89. The PIC when *G. hirsutum* was 0.69 when included with *G. herbaceum* and 0.52 when included with *G. arboreum*. The three D-genome species used in the study, *G. raidondii*, *G. gossypioides*, and *G. thurberi* had PIC values of 0.61, 0.60, and 0.54, respectively, when compared with *G. hirsutum*. These data suggest thatthe wild *Gossypium* diploids used in the study could be used to increase genetic diversity within upland cotton (Kebede et al., 2007). Nevertheless, utilizing a diploid germplasm source requires more time and resources to breed out any undesirable agronomic traits and to derive a useful genotype, thus making it infeasible for any short term gains (Ragsdale and Smith, 2007).

Another wild species source is the primitive allotetraploid cotton accessions found in the USDA-ARS Cotton Collection (McCarty et al., 2004). In order to make these accessions more fully accessible to cotton breeders outside the tropics, they must first be used in a backcross breeding program to derive day-neutral germplasm lines. While time and resources are required to remove undesirable agronomic traits, this type of germplasm source can be used to enhance current germplasm in less time than diploid species.

Mutation breeding is a system that has been used to enhance cultivars of other crops and has been used in cotton (Fehr, 1987; Auld et al., 2000; Herring et al., 2004). Mutation breeding is only useful when genetic variation for the trait of interest does not exist (Fehr, 1987). Moreover, it also requires a large population to discover individuals that possess the desired trait change while minimizing undesirable agronomic traits.

Another method to enhance fiber length and other fiber properties has been through interspecific hybridization of *G. hirsutum* with improved *G. barbadense* cultivars (Smith et al., 2008). Efforts to improve upland cotton fiber quality via interspecifc hybridization with Pima date to the 1860s with little success reported. The primary deterrents to the adoption of improved upland cottons derived through interspecific hybridization has been low gin turnout and low lint yield (Smith et al., 2008).

The preferred source of germplasm for fiber length enhancement is through using natural genetic variation within upland cotton. This method

requires the least amount of time to overcome any reproductive obstacles and undesirable agronomic traits associated with interspecifc hybridization with both diploids and closely related tetraploids. Sources for alleles can be found in obsolete and improved cultivars and germplasm.

Inheritance

The number of alleles that affect fiber length in cotton is not known. Fiber length is most likely controlled by a few major genes and numerous genes that have smaller direct and indirect effects (Want et al., 2006; Zhang et al., 2009; Liu et al., 2011; Wang et al., 2011). Knowledge of how a trait is inherited is important when determining the best methods for improvement (Braden, 2005).

May (1999) looked at various fiber length studies and found a strong genetic base regardless of the type of system used to measure it. He concluded that the amount of variation observed was due to genetic factors more than nongenetic effects. Genotype X Enviroment and other interactions were found in populations but the effect was small when compared to genetic variation. Thus, selection for fiber length can be made without the need to maximize testing locations such as is used for yield potential. Meredith and Bridge (1972), using an array of material that included genotypes that were phenotypically upland cottons but derived from interspecific hybridization not only with *G. barbadense* but also *G. thurberi* and *G. arboreum,* went as far as to state that selection for fiber properties could be made in a single environment.

Genetic studies for fiber length have identified additive variance as the primary source of genetic variation (Al-Rawi and Kohel, 1969; Al-Rawi and Kohel, 1970; Campbell et al., 2008; Lee et al., 1967; May and Green, 1994; Meredith, 1970; Meredith and Bridge, 1972; Meredith et al., 1970; Miller and Lee, 1964; Miller and Marani, 1963; Miller et al., 1959; Miller et al., 1962; Percy et al., 2006; Quisenberry, 1975; Tang et al., 1993; Braden and Smith?????? (or Smith and Braden)). This was found among parental material used in crosses that included elite cultivars from different regions of the cotton belt, obsolete varieties, double haploids, and germplasm lines developed using interspecific hybridization. Furthermore, studies by Meredith et al. (1970) and Meredith and Bridge (1972) did not find that lines developed from interspecific hybridation were specifically superior in fiber length to *G. hirsutum* lines developed solely by intraspecific hybridization. Dominance variance was a source of genetic variation for fiber length, however it did not have as large of an effect as additive variance (Al-Rawi and Kohel, 1969; Al-Rawi and Kohel, 1970; Campbell et al., 2008; Lee et al., 1967; May and Green, 1994; Meredith, 1970; Meredith and Bridge, 1972; Meredith et al., 1970; Miller and Lee, 1964; Miller and Marani, 1963; Miller et al., 1959; Miller et al., 1962; Percy et al., 2006; Quisenberry, 1975; Tang et al., 1993). Significant deviations from expected heterosis in F_2, F_3, and F_4 populations (May and Green, 1994; Meredith et al., 1970; Meredith and Bridge, 1972; Meredith, 1990; Quisenberry, 1975; Tang et al., 1993) and transgressive segregation in a $F_{5:6}$ Recombinant Inbred Line population (Percy

et al., 2006) support the conclusion that additive variance is the primary source of genetic variation for fiber length.

Testcross of *per se* Performance

The testcross is a mating scheme in which a set of individuals are crossed to a set of genotypes that are meant to act as genetic standards (Hallauer et al., 2010). The use of the testcross allows evaluation of breeding value of potential parents for improvement. In order to do this, a tester that reflects breeding goals and allows discrimination of potential among genotypes must be chosen. Therefore, genetic diversity among lines and testers is crucial to determine *per se* performance. The three traits that all testers must possess are simplicity in use, correctly classify usefulness of lines, and provide maximum genetic gainIt is important to evaluate a potential parent based on its performance averaged across all testers Hallauer et al., 2010).

Analysis of testcross *per se* performance will give estimates of general combining ability (GCA), which is the average performance of line in a hybrid combination and theoretically estimates the additive gene action, and specific combining ability (SCA), which is the average performance of a specific hybrid combination over the combined performance of the hybrid mean, line GCA, and tester GCA and theoretically estimates dominant and epistatic gene action (Hallauer et al., 2010). Broad sense heritability (H^2) estimates may also be obtained from testcross *per se* performance (Meeks et al., 2011).

The testcross method of genotype evaluation has been used primarily in maize improvement (Narro et al., 2003; Nelson and Goodman, 2008; Bolduan et al., 2010; Badu-Apraku et al., 2011). However, it also has been used for the improvement of summer squash (*Cucurbita pepo* L.) (Ahmed et al., 2003), grain sorghum (*Sorghum bicolor* L. Moench) (Kishan and Borikar, 1988), and soybean (*Glycine max* L. Merr.) (Feng et al., 2004). The testcross method has been used for determining improvement for fiber length in cotton using both intraspecific hybrid crosses (Miller and Lee, 1964) and in testcrosses involving lines derived through interspecific hybridization with *G. barbadense* (Jenkins et al., 2007).

Diallel

A diallel is a mating scheme in which parents, preferably chosen at random, are hybridized in all possible combinations (Griffing, 1956; Falconer and Mackay, 1996). There are four primary methods in the diallel mating scheme. Method 1 involves taking data on all possible crosses between parents and their reciprocal combinations for a total of p^2 entries when p parents are used. Method 2 is the same as method 1 with the exception of the reciprocal cross combinations. Thus in method 2, data for p parents and $p((p-1)/2)$ F_1's are collected. Method 3 is the same as method 1 except parents are not included and thus $p(p-1)$ F_1s are analyzed. Method 4 is the same as method 3 except reciprocal crosses are not included and thus $p((p-1)/2)$ F_1s are analyzed.

Each of the four methods are analyzed differently and are used to provide different estimates of genetic parameters (Griffing, 1956). Furthermore, each can be analyzed as a different model. Model one is when the parents evaluated are chosen based on their performance and are therefore fixed. Model two is when parents are chosen at random from a universe of possibilities. A summary by Baker (1978) stated that a fixed model can be used to make inferences on combining ability of the set of parents chosen from the population. However, for a random model, inferences may be made on the universe because individuals are selected at random. Because plant breeders are typically interested in the genetic parameters for a set of parents, model one is typically used (Eberhart and Gardner, 1966; Baker, 1978).

Diallel analysis provides information on genetic control for quantitative traits of the parental lines. However, in a fixed effect model, the GCA and SCA are estimated values rather than true parameters that are available with the random models (Griffing, 1956). Nevertheless, plant breeders often use the relative magnitude of GCA and SCA estimates to determine which parents and combination might be best for improvement of the trait in question (Braden, 2005).

Recombinant Inbred Line

A recombinant inbred line (RIL) population is derived by crossing two unrelated parents and then deriving lines that have been inbred through several generations, typically through the single seed decent method. Recombinant

inbred line populations typically are used for tagging molecular markers for

quantitative trait loci in cotton (Wang et al., 2006; Zhang et al., 2009; Liu et al.,

2011; Wang et al., 2011). However, it is possible to use a RIL population to

analyze fiber traits (Percy et al., 2006).

In RIL populations, it is possible to perform analysis on $F_{2:3}$ lines (Wang et

al., 2011); however RIL populations are typically inbred further while still being

derived from individual F_2 plants (Zhang et al., 2009) or selected from inbred

individual plants at a later generation such as the F_5 (Percy et al., 2006; Wang et

al., 2006; Liu et al., 2011). The advantage of RIL populations is that they allow

the analysis of the amount of genetic variation in a population from two parents,

providing information on agronomic and fiber quality traits, heritability of traits,

and utility of a line for improvement (Percy et al., 2006). Their disadvantage,

however, is that they take a long time to establish if using generations later than

the F_2 as is commonly practiced. Furthermore, RIL populations also limit the

number of parents that can be studied because of demand for field plot space

relative to limited time and monetary resources.

The method and fiber quality bred into each experimental strain in route

to becoming a cultivar ultimately depends upon the type of spinning system that

is used (Meredith et al., 1991; May, 2003). Thus, as spinning technology

evolves, new fiber quality requirements will arise (May, 2002). While direct

knowledge of a specific genotype's spinning ability will not be known in early

generations, breeders must make selection based on the fiber properties known

to affect yarn quality (Meredith et al., 1991; May and Taylor, 1998; May, 2002; May, 2003). In order to obtain the desired fiber package, new sources of germplasm containing alleles for enhanced fiber quality must be studied (Paterson et al., 2004).

CHAPTER III

MATERIALS AND METHODS

Population Development

Testcross

Twenty-nine upland cotton cultivar accessions in the USDA-ARS
Germplasm System that were collected from foreign countries were obtained
from Dr. Richard Percy. Twelve of the cultivars were from China: China 632 (PI
451750), Chung Mein-Jue #7 (PI 529467), Duck Shelter (PI 452101), Jiangsu #3
(PI 452103), Kang Bin Chang Mienne (PI 433732), Lintsing Sze Tze 4B (PI
528889), Lishan Big Boll (PI 452105), Nanging #12 (PI 529483), Pengze (PI
529486), Shan 5245 (SA-3202), Small Leaf (PI 438958), and Zhopng Mian Suo
9 Hao (SA-3207). Seven were from West Africa and are Allen 333 (PI 392289),
Allen 333-61 CB 4027 (PI 529302), BJA 592 (PI 529492), F 280 (PI 529383),
Funtua FT-5 (PI 607222), PAN 575 (PI 529385), and Reba W296 (PI 529387).
Lastly, 10 from South Africa included A 7215 (PI 529054), A-637-33 (PI 408999),
ALA 70-11 (PI 529332), Albacala 7 (PI 529319), BPA 68 CB 4030 (PI 529305),
Komati (PI 607192), Limpopo (PI 607199), Marico (Smooth) (PI 607197), Sabie
(PI 607193), and UK 64 (PI 407455). Additionally, seven upland cotton cultivars
representing different regions of the U.S. Cotton Belt were included: Acala 1517-
99 (PVP 200000181, PI 612326), Deltapine 491 (DP491) (PVP 200100159, PI
618609), Phytogen 72 (PHY 72) (PVP 200100115, PI 617043), Stoneville 474
(ST 474) (PVP 9400152, PI 578877), Tamcot 22 (PVP 200500006, PI 635877),

and Paymaster Tejas (PM Tejas) (PVP 9500252, PI 591047). The seventh U.S.

genotype was Del Cerro (PI 529358), a high fiber quality upland type cotton

derived through introgression of *G. hirsutum* with *G. tuberi* Tod., *G. aroboreum*

L., *G. barbadense*, and *G. hirsutum* var. *puntartum* (Meredith and Bridge, 1972).

Flowers of the 36 lines from China, West Africa, South Africa, and the

U.S. were emasculated and hand pollinated with either Tamcot CAMD-E (PI

529633; Bird, 1979) or TAM B182-33 ELS (PI 654362; Smith, et al., 2009). The

two testers, Tamcot CAMD-E and TAM B182-33 ELS were chosen based on

their UHML. Tamcot CAMD-E is an early maturing, short staple cultivar

released in 1979 by the Texas AgriLife Reserach. TAM B182-33 ELS is a high

fiber quality upland cotton derived through intraspecific hybridization of a long

staple upland and a short staple upland and capable of producing an UHML

greater than 35 mm

Diallel Development

Fifteen upland cotton germplasm lines that had reported UHML of 33 mm

or greater were obtained from the national germplasm collection. Seed of the

germplasm lines were sown into pots and thinned to obtain two plants per pot in

a greenhouse in the winter of 2008-2009. Seed of TAM B182-33 ELS (PI

654362) was also sown into pots and thinned to one plant per pot. Bolls were

harvested at maturity from individual plants, ginned on a laboratory style saw

gin, and fiber samples sent to Cotton Inc., Cary, NC, for HVI analysis.

Germplasm lines that did not meet the selected criteria of an UHML of 33 mm or

greater were discarded. Of the 15 genotypes, only three met this criteria.

Among the selected germplasm lines, TAM B182-33 ELS, and TAM 94L-25, a

long staple upland, a standard error for UHML was calculated and any plant that

exhibited an UHML more than two times the standard error of the longest parent

were discarded. Two of the three germplasm lines selected for the experiment

were 'Ewings Long Staple X Tidewater' (PI 528726) and Sealand 1 (PI 528871).

Both of these parents were developed using interspecific hybridization with *G.

barbadense*. The third selected line was D & PL 45-867 (PI 528771). The

parentage and development of this germplasm line is unknown.

The three confirmed germplasm lines, TAM B182-33 ELS, and TAM 94L-

25 were then sown in a crossing block during the summer of 2009 at College

Station, TX. The parents were crossed by hand emasculation and pollination in

a half diallel mating scheme, i.e., no reciprocal crosses. Parents were crossed

again in the greenhouse during the winter of 2009-10 and again in a crossing

block in 2010 at College Station, TX.

Recombinant Inbred Line Population

To determine inheritance and to test published regression equations to

estimate SFC from HVI parameters, an F_2 population derived from the cross of

TAM B182-39 ELS/DP 491. TAM B128-39 ELS is an unreleased sister line to

TAM B182-33 ELS and expresses the ELS trait. Twenty-seven individual F_2

plants were selected at Weslaco, TX, in 2008, ginned on a laboratory saw gin

and the fibers sent to FBRI, Lubbock, TX, for HVI analysis. The fiber samples

were returned and sent to Cotton Inc., Cary, NC for AFIS analysis. Progeny

rows from the twenty-seven individual plants were established at the Texas A&M

Research Farm in College Station, TX, during the summer of 2009 along with

Tamcot 22 and FM 832 as checks. Fourteen rows were selected based 2008

HVI UHML data and 10 individual plants within each row were taken at random.

The individual plants were ginned and progeny rows planted in 2010 to increase

seed supply and establish 140 $F_{3:5}$ RIL's for planting replicated trails.

Experimental Design

<u>Testcross</u>

Parents and their F_1 progenies were planted at the Cotton Winter Nursery

at Tecoman, Colima, Mexico, on November 20th, 2009 (MX2010) and at College

Station, TX, on April 27th, 2010 (CS 2010), and April 18th, 2011 (CS 2011). Plots

were planted in a randomized complete block design (RCBD) with three

replications at Mexico and four replications for both of the College Station

environments. At all three locations, plots were randomized by the female

parent and subsequently by generation (i.e., female parent, female

parent/Tamcot CAMD-E, and female parent/TAM B182-ELS). The two testers

were used as checks and appeared three times in each block at MX2010 and

four times in each block at CS 2010 and CS 2011. At MX2010, three hills of

each entry in each block were planted by hand and thinned to one to two plants

per hill with 1.02 m between rows and approximately 0.4 m between hills. At CS

2010 and CS 2011, parents and progenies were planted with a cone type

research planter with 1.02 m between rows and were 5.5 m long. After

emergence, the plots were thinned to 0.4 m between plants. The West Africa

cultivar BJA 592 did not produce enough fiber to obtain UHML at CS 2010 to

bring the total number of observations to 1268 for parents and progenies.

Standard cultural practices including furrow irrigation were used at the three

locations. The soil at Tecoman, Colima, Mexico, is a sandy loam and the soil

type at the Texas A&M Univeristy Research Farm located outside College

Station, TX, is a Westwood silt loam.

At harvest, 30 boll samples were hand harvested from each plot. Bolls at

CS 2010 and CS 2011 were preferentially taken from the first position of the

middle fruiting branches. The boll samples were then ginned on a laboratory

style saw gin and the fibers sent to the Fiber and Biopolymer Research Institute

(FBRI), Lubbock, TX, for HVI analysis.

Diallel

Parents and their 10 F_1 progenies were established at MX2010, CS 2010,

and CS 2011 environments for diallel analysis. Three replications were used at

Mexico and four at each of the College Station, TX, plantings. The planting

dates were November 20th, 2009 for MX2010, April 27th, 2010 for CS 2010, and

April 18th, 2011 for CS 2011. Plots at MX2010 were hand planted into three hills

and thinned to obtain one to two plants per hill. Row spacing was approximately

1.02 m and approximately 0.4 m between hills. Plots planted at College Station,

TX, in 2010 and 2011 were planted with a cone type research plot planter with

1.02 m row spacing and 5.5 m long. Plots were thinned to 0.4 m between plants. Standard cultural practices including furrow irrigation were used in the three environments.

At harvest, 30 boll samples were hand harvested from each plot. Bolls at CS 2010 and CS 2011 were preferentially taken from the first position of the middle fruiting branches. The boll samples were then ginned on a laboratory style saw gin and the fibers sent to the Fiber and Biopolymer Research Institute (FBRI), Lubbock, TX, for HVI analysis.

Recombinant Inbred Line Population

One hundred and forty $F_{3:5}$ RIL's with parents were planted at the Texas A&M University Research Farm outside of College Station, TX, on April 18th, 2011. A randomized complete block design with two replications was used. A research cone type planter was used with 1.02 m row spacing. Plots were 5.5 m long. Standard cultural practices including furrow irrigation were used in the test.

At harvest, a 30 boll sample were hand harvested from each plot. Bolls were preferentially harvested from the first position of the middle fruiting branches. The boll samples were then ginned on a laboratory style saw gin and the fiber samples were sent to FBRI, Lubbock, TX, for HVI analysis. The fiber samples were returned and then sent to Cotton Inc., Cary, NC, for AFIS analysis.

Statistical Analysis

<u>Testcross Statistical Analysis</u>

Analysis of variance for UHML among the parents and progenies was performed using SAS 9.2 (Cary, NC) Proc GLM with Environments, Reps(Environments), and Genotypes X Environments as random effects. Sums of squares for Parents (P), Crosses, Parents Vs. Crosses (Pvs.C), Line (L), Tester (T), Line X Tester (LxT), Parents X Environments, Crosses X Environments, (Parents Vs. Crosses) X Environments, Line X Environment, Tester X Environment, and Line X Tester X Environment were also obtained.

Calculation of GCA and SCA was performed using methods described in Falconer and Mackay (1996). General combining abilities of the female lines were calculated as:

$$GCA_i = \mu_{i.} - \mu_{..}$$

where GCA_i is the general combining ability of line i, $\mu_{i.}$ is the mean of all hybrids with line I, and $\mu_{..}$ is the mean of all hybrids. General combining abilities of the male testers were calculated as:

$$GCA_j = \mu_{.j} - \mu_{..}$$

where GCA_j is the general combining ability of tester j, $\mu_{.j}$ is the mean of all hybrids with tester j, and $\mu_{..}$ is the mean of all hybrids. Specific combining ability was calculated as:

$$SCA_{ij} = \mu_{ij} - GCA_i - GCA_j - u_{..}$$

where SCA_{ij} is the specific combining ability of line I with tester j and μ_{ij} is the

mean UHML between line i with tester j, GCA_i is the calculated GCA of line i,

GCA_j is the GCA of tester j, and $\mu_{..}$ is the mean of all hybrids.

Significance of GCA and SCA estimates were determined by calculating

the standard error for GCA of lines, GCA of testers, and SCA. A 95% and 99%

confidence interval was then calculated by multiplying the standard error by 2

and 3, respectively.   Standard errors were calculated according to Singh and

Chaudhary (1985). Standard error for GCA of lines were calculated as:

$$\text{S.E. } (GCA_i) = \sqrt{MSE/(r \cdot t)}$$

where MSE is the mean square of error, r is the number of replications and t is

the number of testers. Standard error for GCA of testers were calculated as:

$$\text{S.E.}(GCA_j) = \sqrt{MSE/(r \bullet l)}$$

where MSE is the mean square of error, r is the number of replications and l is

the number of lines. Standard error for SCA of lines X testers was calculated as:

$$\text{S.E.}(SCA_{ij}) = \sqrt{MSE/r}$$

where MSE is the mean square of error and r is the number of replications. For

example, the 95% confidence interval of a line was calculated as:

$$GCA_i \pm 2 \bullet \text{S.E.}(GCA_i)$$

where GCA_i is the calculated GCA value for line i and $\text{S.E.}(GCA_i)$ is the

calculated standard error for lines.

Heritability

Broad sense heritability (H^2) estimates was calculated was calculated on the testcross population using the equation:

$$H^2 = \sigma_G{}^2/(\sigma_G{}^2 + (\sigma_{GxE}{}^2/E) + (\sigma_{error}{}^2/ER))$$

where E is the number of environments and ER is the total number of replications among the three environments. The variances were obtained using the expected mean squares calculated by SAS 9.2 (Cary, NC) and the values in the Type III sums of squares.

Diallel Analysis

Statistical analysis of the diallel was performed according to Griffing's (1956) Model 1, Method 2. In Model 1, the genotype effects are fixed because they were selected specifically for this study and inferences can only be made among the parents used. Method 2 states that parents and one set of F_1 progenies (i.e., no reciprocals) are used to determine GCA and SCA. Analysis of variance, calculation of GCA and SCA, and significance of GCA and SCA was determined using Diallel SAS-05 as described by Zhang et al. (2005) using SAS 9.2 (Cary, NC). Means of parents and hybrids were separated using the Duncan-Waller means separation test.

Heritability

Broad sense heritability (H^2) estimates was calculated was calculated on the testcross population using the equation:

$$H^2 = \sigma_G{}^2/(\sigma_G{}^2 + (\sigma_{GxE}{}^2/E) + (\sigma_{error}{}^2/ER))$$

where E is the number of environments and ER is the total number of replications among the three environments. The variances were obtained using the expected mean squares calculated by the general linear model given in Diallel SAS-05 (Zhang et al., 2005) and the values in the Type III sums of squares.

<u>Recombinant Inbred Line Analysis</u>

Values for Mean Length (ML) among the 140 $F_{3:5}$ RILs, TAM B182-39 ELS, and DP491 and their $F_{2:3}$ parents were calculated using the equation:

$$ML=(UI/100)\bullet UHML$$

Lower half mean length values were calculated according to Cai et al. (2011):

$$LHML = (UHML\bullet(UI/100))/(9.38 - 14.86(UI/100) + 6.5(UI/100)^2)$$

Ziedman et al. (1991) have previously reported regression equations to determine SFCw from HVI fiber properties. These equations were adjusted for metric length units from standard English length units and included in this study for both the $F_{2:3}$ and $F_{3:5}$ generations to make comparisons with previous work completed related to this topic. The equations used were:

$$SFCw_1 = 126.21 - (15.81/25.4)\bullet UHML - 1.23\bullet UI$$

$$SFCw_2 = -(0.249/25.4)\bullet UHML - 0.533\bullet UI$$

Analysis of variance for AFIS SFCw and HVI fiber properties UHML, ML, LHML, Micronaire, Uniformity Index, Strength, and Elongation on the 140 $F_{3:5}$ RILs and parents TAM B182-39 ELS and DP 491 were performed using SAS 9.2 (Cary,

NC) using Proc GLM with blocks (reps) considered as a random effect. Homoscedasity of error variance among genotypes for AFIS SFCw was tested using the hovtest=Bartlett option in the Means statement of Proc GLM. Regression equations to determine SFCw from HVI properties were developed using data from the 140 $F_{3:5}$ RILs and parents TAM B182-39 ELS and DP 491 grown at College Station, 2011 using SAS 9.2 Proc Reg with and without an intercept. Tests for collinearity among HVI fiber parameters were performed using the collin, tol, and vif options in the Means statement of Proc Reg. Selection of the regression equation used was based on Mallow's C(p) statistic and the adjusted coefficient of determination (R^2) values. Pearson's correlation coefficients (r) among HVI fiber properties and regression equations to determine SFCw from HVI fiber properties ($SFCw_x$) and AFIS SFCw in both the $F_{2:3}$ and $F_{3:5}$ generations were calculated using SAS 9.2Proc Corr.

<u>Heritability</u>

Parent-offspring regression was used to determine the narrow sense (h^2) heritability of SFCw and LHML among the 140 $F_{3:5}$ RILs as described by Holland et al., (2003). Both the values for AFIS SFCw and LHML in the $F_{2:3}$ generation and the mid-parent values obtained from TAM B182-39 ELS and DP491 at College Station in 2011 were used. The mid-parent values of TAM B182-39 ELS and DP491 were calculated on a per block basis. SAS 9.2 (Cary, NC) Proc Reg was used to derive the regression coefficient. The heritability estimate

obtained when the $F_{3:5}$ AFIS SFCw and LHML were regressed on the respective

individual $F_{2:3}$ plants were adjusted using:

$$h^2 = b_{OP} / (1 + F_t(1 - b_{OP}))$$

where F_t is the inbreeding coefficient of generation t as described by Holland et

al., (2003).

CHAPTER IV

RESULTS AND DISCUSSION

Testcross *per se* Performance for UHML

Table 1 presents analysis of variance results for UHML among a cohort of upland cotton cultivars and seven U.S. cotton cultivars when crossed to TAM CAMD-E and TAM B182-33 ELS. Calculated mean square values were highly significant for all of the estimated parameters with the exception of (Parents Vs. Crosses) x Environment and Tester X Environment, which were not significant. Variation due to tester and environment represented 29.7% and 24.1% of the total variation, respectively.

Broad sense heritability (H^2) was 0.785 for UHML among these lines and testers, indicating that the primary source of variation for UHML is due to genotypes and is most likely due to the extremes of the testers used in the study. Because of highly significant Line X Environment and (Line X Tester) X Environment effects, calculated GCA and SCA estimates are presented independently for each environment.

One environment for this study was conducted at the Cotton Winter Nursery in Tecoman, Colima, Mexico, during the winter of 2009-10. The remaining two environments were in College Station during the summers of 2010 and 2011. Upper half mean lengths of parents and hybrids were numerically higher at MX2010 than either of the two College Station

Table 1. Analysis of variance for and broad sense heritability (H^2) estimate for Upper Half Mean Length (UHML, mm) among upland cotton parents and F1 progenies evaluated at Tecoman, Mexico 2009-10 and College Station in 2010 and 2011.

Source	DF	Mean Square
Environment (E)	2	1059.984***
Reps within (E) (Error A)	8	5.007
Genotypes (G)	109	39.637***
Parents (P)	37	43.835***
Crosses (C)	71	31.901***
P Vs. C	1	433.505***
Line (L)	35	14.375***
Tester (T)	1	1719.036***
LxT (Error B)	35	1.224
GxE	218	1.078***
PxE	74	0.948***
CxE	142	1.162***
(PxC)*E	2	0.000
LxE	70	1.585**
TxE	2	0.793
LxTxE (Error C)	70	0.749
Error D	930	0.461
H^2 = 0.785		

*Significant at the 0.05 probability level.
**Significant at the 0.01 probability level.
***Significant at the 0.001 probability level.

environments. Thus MX2010 might allow expression of true genetic potential of parents and progeny for UHML.

General Combining Ability

Parental UHML for the 36 lines and two testers and their associated GCA estimates can be found in Table 2. Parent UHML ranged from 25.40 mm for Lintzing SZE TZE 4B at CS2010 to 36.24 mm for TAM B182-33 ELS at MX2010. The calculated GCA estimates ranged from -2.07 for Lintsing SZE TZE 4B at CS 2010 to 2.57 for Del Cerro at MX2010.

Parental UHML for cultivars from China ranged from 26.25 mm to 27.89 mm when averaged over the three environments. Overall the Chinese cultivars were poor general combiners for UHML indicating that alleles which would contribute to further UHML improvement were not present.

Parental UHML for cultivars from West Africa ranged from 27.98 mm to 30.02 mm when averaged over the three environments. Of the West African cultivars, Allen 333 was a poor general combiner at MX2010 and CS2010. Allen 333 had a negative GCA estimate at CS2011, but it was not significantly different from zero. The cultivars F 280, UK 64, and Reba W 296 were good general combiners for UHML at CS2010 producing estimates of 1.20 ($P<0.01$), 0.83 ($P<0.01$), and 0.69 ($P<0.05$), respectively. Allen 333-61 CB 4027, A-637-33, and Pan 575 had GCA estimates that were not different from zero at MX2010, but were positive and significantly different from zero at CS2010 and CS2011.

Table 2. Parental UHML (mm) and calculated General Combining Ability (GCA) estimates (mm) for fiber length among 12 lines from China, 7 lines from West Africa, 10 lines from South Africa, and 7 lines from the U.S. of upland cotton (*G. hirsutum*) and testers TAM B182-33 ELS and TAM CAMD-E planted at Tecoman, Mexico in 2009-10 (MX2010), College Station in 2010 (CS2010), and College Station 2011 (CS2011).

Line	Country of Origin	MX2010		CS2010		CS2011		Average
		UHML	GCA	UHML	GCA	UHML	GCA	UHML
Jiangsu #3	China	29.30	-0.31	27.31	-0.10	27.43	-0.56*	27.89
Lishan Big Boll	China	29.21	-0.65*	27.50	-0.20	26.73	-0.62*	27.69
Small Leaf	China	29.72	-0.35	26.73	-1.34**	26.86	-0.59*	27.59
Nanging #12	China	28.96	-1.37**	26.86	-0.80**	26.92	-0.50*	27.46
Duck Shelter	China	29.04	-0.90 *	26.61	-1.34**	26.48	-0.85**	27.22
Zhopng Mian Suo 9 Hao	China	29.21	-0.18	26.42	-0.61*	26.16	-0.37	27.08
Pengze	China	29.04	-1.20**	26.48	-0.67*	26.16	-1.07**	27.06
Shan 5245	China	28.87	-0.31	26.48	-0.93**	26.23	-0.37	27.04
China 632	China	29.13	-1.33**	26.48	-1.09**	25.97	-0.46*	27.02
Chung Mien-Jue #7	China	28.96	-0.01	26.16	-1.05**	25.97	-0.88**	26.85
Lintsing SZE TZE 4B	China	28.28	-0.35	25.40	-2.07**	26.16	-0.78**	26.46
Kang Bin Chang Mienne	China	28.03	-0.78*	25.40	-0.96**	25.78	-0.75**	26.25
Allen 333-61 CB 4027	W. Africa	32.09	0.11	29.34	0.76**	29.15	0.52*	30.02
F280	W. Africa	31.41	0.28	29.08	1.20**	28.96	0.90	29.67
Pan 575	W. Africa	30.90	0.16	29.02	1.14**	28.96	0.65*	29.51
Allen 333	W. Africa	30.57	-1.62**	27.62	-2.01**	27.94	-0.31	28.54
Reba W 296	W. Africa	31.41	-0.14	27.88	0.69*	26.67	0.23	28.40
UK 64	W. Africa	28.96	-0.01	28.45	0.88**	26.80	0.17	27.99
A-637-33	W. Africa	29.55	-0.48	27.75	0.60*	27.05	0.46*	27.98
BPA 68 CB 4030	S. Africa	32.77	2.15**	29.85	1.58**	28.83	0.68**	30.27
A 7215	S. Africa	32.26	1.17**	28.64	0.63*	27.56	-0.08	29.23
Funtua FT-5	S. Africa	31.33	0.71*	28.83	0.82**	27.62	0.74**	29.07
Marico (Smooth)	S. Africa	31.16	0.45	28.51	1.39**	28.00	0.62*	29.05

Table 2 continued

Line	Country of Origin	MX2010 UHML	MX2010 GCA	CS2010 UHML	CS2010 GCA	CS2011 UHML	CS2011 GCA	Average UHML
Limpopo	S. Africa	31.41	0.16	28.51	1.14**	27.81	0.74**	29.05
Albacala 7	S. Africa	31.24	0.50	28.58	0.63*	27.69	0.52	28.98
Ala 70-11	S. Africa	30.14	0.50	28.19	-0.07	27.24	-0.37	28.38
BJA 592	S. Africa	30.57	0.79*	28.32	0.57*	26.29	0.33	28.17
Sabie	S. Africa	29.55	0.07	36.23	0.18	26.61	-0.02	27.27
Komati	S. Africa	29.21	0.20	26.67	-1.34**	26.35	-0.12	27.24
Del Cerro	U.S.	33.61	2.57**	30.35	1.96**	30.67	1.63**	31.36
Acala 1517-99	U.S.	32.51	0.20	29.08	0.85	29.34	0.93**	30.11
Phytogen 72	U.S.	30.48	1.22**	28.39	0.53*	28.64	0.68**	29.05
Deltapine 491	U.S.	31.16	1.05**	27.75	1.20**	27.62	-0.02	28.63
Tamcot 22	U.S.	29.38	-0.18	27.12	-0.20	27.56	0.08	27.89
Stoneville 474	U.S.	26.36	-0.44	27.62	-0.71*	26.61	-0.12	27.45
PM Tejas	U.S.	28.53	-1.45**	25.40	-1.28**	25.53	-1.07**	26.67
S.E. (GCA$_i$)		0.306		0.245		0.221		

Tester		MX2010 UHML	MX2010 GCA	CS2010 UHML	CS2010 GCA	CS2011 UHML	CS2011 GCA	Overall UHML
TAM B182-33 ELS	U.S.	36.24	1.55**	33.04	1.47**	32.24	1.44**	33.43
TAM CAMD-E	U.S.	30.37	-1.55**	27.45	-1.47**	27.40	-1.44**	28.07
S.E. (GCA$_i$)		0.072		0.058		0.052		

*Significant at the 0.05 probability level.
**Significant at the 0.01 probability level.

Parental UHML for the South African cultivars ranged from 27.24 mm to 30.27 mm when average across the three environments. The South African cultivar BPA 68 CB 4030 was a good general combiner for UHML in all three environments. The calculated GCA estimates were 2.15 (P<0.01), 1.58 (P<0.01), and 0.68 (P<0.01) for MX2010, CS2010, and CS2011, respectively. Additionally, Funtua FT-5 combined well for UHML in all three environments. Marico (Smooth) and Limpopo were good general combiners at CS2010 and CS2011 but not MX2010.

Parental UHML for the U.S. cultivars ranged from 26.67 mm to 31.36 when averaged across the three environments. Of the seven cultivars, Paymaster Tejas was the worst general combiner and produced statistically significant (P<0.05) negative GCA estimates in all three environments. Del Cerro and Phytogen 72 combined well for UHML in all three environments, while Acala 1517-99 was the second longest parent of the U.S. cultivars and had highly significant (P<0.01) positive GCA estimates for enhancing UHML at CS2010 and CS2011. Deltapine 491 was a good general combiner for UHML at MX2010 and CS2010, but not at CS2011.

Two lines used in this study, Phytogen 72 and Acala 1517-99, are known high fiber quality cultivars adapted to the western cotton producing states. A third line, Del Cerro, has a *G. hirsutum* phenotype but is known to contain alleles for enhanced fiber length from interspecific hybridization. As such it is expected that these lines would serve as superior parents for enhancing fiber length. A

previous study by Lee et al. (1967) found Acala 1517, a parent of Acala 1517-99, showed positive GCA effects for enhanced fiber length. A study by Meredith and Bridge (1972) showed significant heterosis for fiber length in a cross made between Deltapine 16 and Del Cerro.

The UHML of the testers Tamcot CAMD-E and TAM B182-33 ELS were 28.07 mm to 33.43 mm, respectively, when averaged over the three environments. As expected, TAM B182-33 ELS was a better general combiner for UHML than the short staple TAM CAMD-E. In all three environments, GCA estimates were highly significantly different from zero.

Specific Combining Ability

Specific combining ability is a measurement of deviation from expected hybrid performance based on the GCA of the two parents. It represents effects due to dominance or favorable epistatic allele interactions. While SCA is typically more important in hybrid crops, eight ELSU lines were derived from combinations of long staple upland (LSU) and SSU cottons by Smith et al. (2008, 2009). While some of these lines may have alleles from *G. barbadense*, others were derived using only alleles from the *G. hirsutum* genome (Smith and Hague, 2008). The crosses made among the LSU and SSU genotypes resulted in favorable epistatic allelic combinations and produced stable transgressive segregates that could be selected among (Braden, 2005; Smith et al. 2008; Smith et al., 2009).

Upper half mean lengths and SCA estimates for the 72 hybrids can be found in Table 3. The UHML ranged from 27.02 mm for Allen 333/TAM CAMD-E to 33.64 mm for Del Cerro/TAM B182-33 ELS when averaged over the three environments. Among the 72 hybrids planted at MX2010 and CS2010, there were 10 SCA estimates that were significantly different from zero. At College Station in 2011, no SCA estimates were significantly different from zero .

Among the 12 Chinese cultivars, there were no hybrids with TAM CAMD-E and TAM B182-33 ELS that produced SCA estimates for UHML that were significantly different from zero in any of the three environments. Data on some of the SCA of the 36 lines with the two testers do agree with the GCA data. While no SCA estimates in 2011 were significantly different from zero, the South African lines Limpopo and Funtua FT-5 were both good general and specific combiners for improved UHML. Limpopo and had positive GCA estimates at both CS2010 and CS2011 and specifically combined well with Tamcot CAMD-E at CS2010 for improved UHML. Additionally, Funtua FT-5 had positive and significant GCA estimates at CS2010 and CS2011 and had a positive SCA that was significant when crossed with TAM B182-33 ELS at CS2010. Del Cerro was the best general combiner for UHML among the U.S. lines, but it did not specifically combine with Tamcot CAMD-E nor TAM B182-33 ELS in any of the three environments.

Hybrids of the West African cultivar UK 64 had SCA estimates of 1.00 and -1.00 (P<0.05) at MX2010 when crossed to TAM CAMD-E and TAM B182-

Table 3. Hybrid UHML (mm) and calculated Specific Combining Ability (SCA) estimates of 12 Chinese, 7 West African, 10 South African, and 7 U.S. upland cotton (*G. hirsutum*) cultivars when crossed to TAM CAMD-E and TAM B182-33 ELS and planted at Tecoman, Mexico in 2009-10 (MX2010), College Station in 2010 (CS2010), and College Station in 2011 (CS2011).

TAM CAMD-E Hybrids	Country of Origin	MX2010 UHML	MX2010 SCA	CS2010 UHML	CS2010 SCA	CS2011 UHML	CS2011 SCA	Average UHML
Jiangsu #3	China	30.31	0.11	27.50	-0.18	26.80	-0.02	28.01
Zhopng Mian Suo 9 Hao	China	30.31	-0.02	27.24	0.07	27.05	0.04	28.01
Lishan Big Boll	China	29.80	-0.06	27.62	0.04	26.99	0.23	27.98
Chung Mein-Jue #7	China	30.82	0.32	26.61	-0.12	26.80	0.30	27.82
Shan 5245	China	30.14	-0.06	26.92	0.07	26.80	-0.21	27.76
Kang Bin Chang Mienne	China	29.63	-0.10	27.24	0.42	26.54	-0.08	27.64
Nanging #12	China	29.46	0.32	26.92	-0.05	26.80	-0.08	27.57
China 632	China	29.29	0.11	26.48	-0.21	26.67	-0.24	27.32
Lintsing SZE TZE 4B	China	30.14	-0.02	25.97	0.26	26.48	-0.12	27.29
Small Leaf	China	29.72	-0.23	26.10	-0.34	26.54	-0.24	27.25
Pengze	China	28.53	-0.78	26.80	-0.31	26.67	0.36	27.23
Duck Shelter	China	29.46	-0.14	26.29	-0.15	26.04	-0.50	27.06
F 280	W. Africa	30.82	0.03	28.96	-0.02	28.00	-0.27	29.12
UK 64	W. Africa	31.50	1.00*	28.64	-0.02	27.11	-0.43	28.86
A-637-33	W. Africa	30.23	0.20	28.89	0.52	27.37	-0.47	28.70
Pan 575	W. Africa	30.48	-0.19	28.38	-0.53	27.37	-0.47	28.70
Reba W 296	W. Africa	30.31	-0.06	28.51	0.04	27.69	0.08	28.70
Allen 333-61 CB 4027	W. Africa	30.23	-0.40	28.19	-0.34	27.94	0.04	28.66
Allen 333	W. Africa	28.19	-0.69	25.59	-0.18	27.56	0.49	27.02
Limpopo	S. Africa	31.33	0.66	29.97	1.06**	28.70	0.58	29.88
BPA 68 CB 4030	S. Africa	32.60	-0.06	29.53	0.17	27.88	-0.18	29.76
Marico(Smooth)	S. Africa	30.99	0.03	29.65	0.49	27.94	-0.05	29.40
Funtua FT-5	S. Africa	31.41	0.20	27.81	-0.78*	28.19	0.08	28.93

Table 3 continued

TAM CAMD-E Hybrids	Country of Origin	MX2010		CS2010		CS2011		Average
		UHML	SCA	UHML	SCA	UHML	SCA	UHML
Albacala 7	S. Africa	30.48	-0.52	28.77	0.36	27.88	-0.02	28.91
A 7215	S. Africa	31.75	0.07	28.26	-0.15	27.37	0.07	28.89
BJA 592	S. Africa	30.90	-0.40	28.19	-0.15	30.80	0.21	28.68
Ala 70-11	S. Africa	31.50	0.49	27.62	-0.09	27.31	0.30	28.56
Sabie	S. Africa	30.48	-0.10	28.26	0.30	27.18	-0.18	28.47
Komati	S. Africa	30.90	0.20	27.37	0.93*	27.50	0.23	28.38
Del Cerro	U.S.	32.68	-0.40	29.59	-0.15	28.64	-0.37	30.09
Deltapine 491	U.S.	32.09	0.54	29.40	0.42	27.94	0.58	29.60
Phytogen 72	U.S.	31.75	0.03	28.07	-0.24	28.32	0.27	29.16
Acala 1517-99	U.S.	30.82	0.11	28.19	-0.44	28.32	0.01	28.96
Tamcot 22	U.S.	30.65	0.32	27.50	-0.09	27.50	0.04	28.36
Stoneville 474	U.S.	29.38	-0.69	26.35	-0.72*	27.62	0.36	27.64
Paymaster Tejas	U.S.	29.21	0.15	26.61	0.10	26.29	-0.02	27.20

TAM B182-33 ELS Hybrids	Country of Origin	MX2010		CS2010		CS2011		Average
		UHML	SCA	UHML	SCA	UHML	SCA	UHML
Jiangsu #3	China	33.19	-0.11	30.80	0.18	29.72	0.02	31.06
Zhopng Mian Suo 9 Hao	China	33.44	0.02	30.04	-0.07	29.85	-0.04	30.90
Shan 5245	China	33.36	0.06	29.72	-0.07	30.10	0.21	30.85
Lishan Big Boll	China	33.02	0.06	30.48	-0.04	29.40	-0.23	30.78
Small Leaf	China	33.27	0.23	29.72	0.34	29.91	0.24	30.76
Duck Shelter	China	32.85	0.14	29.53	0.15	29.91	0.50	30.57
Pengze	China	33.19	0.78	30.35	0.31	28.83	-0.36	30.57
China 632	China	32.17	-0.11	28.95	0.21	30.04	0.24	30.55
Chung Mein-Jue #7	China	33.27	-0.32	29.78	0.12	29.08	-0.30	30.48

Table 3 continued

TAM B182-33 ELS Hybrids	Country of Origin	MX2010		CS2010		CS2011		Average
		UHML	SCA	UHML	SCA	UHML	SCA	UHML
Nanging #12	China	31.92	-0.32	29.97	0.05	29.85	0.09	30.46
Kang Bin Chang Mienne	China	32.94	0.10	29.34	-0.42	29.85	0.09	30.41
Lintsing ZSE TZE 4B	China	33.27	0.02	28.38	-0.26	29.59	0.12	30.16
Pan 575	W. Africa	33.95	0.18	32.39	0.53	31.24	0.34	32.40
F 280	W. Africa	33.87	-0.03	31.94	0.02	31.43	0.28	32.28
Allen 333-61 CB 4027	W. Africa	34.12	0.40	31.81	0.34	30.73	-0.04	32.05
Reba W 296	W. Africa	33.53	0.06	31.37	-0.04	30.42	-0.07	31.61
UK 64	W. Africa	32.60	-1.00*	31.62	0.02	30.86	0.43	31.61
A-637-33	W. Africa	32.94	-0.20	30.80	-0.52	31.18	0.47	31.52
Allen 333	W. Africa	32.68	0.69	28.89	0.18	29.46	-0.49	30.13
BPA 68 CB 4030	S. Africa	35.81	0.06	32.13	-0.17	31.12	0.18	32.77
Funtua FT-5	S. Africa	34.12	-0.20	32.32	0.79*	30.92	-0.07	32.30
BJA 592	S. Africa	34.80	0.40	31.43	0.15	30.80	0.21	32.12
Marico (Smooth)	S. Africa	34.04	-0.03	31.62	-0.49	30.92	0.05	32.03
Albacala 7	S. Africa	34.63	0.52	30.99	-0.36	30.80	0.02	31.91
A 7215	S. Africa	34.71	-0.07	31.50	0.15	30.10	-0.07	31.87
Sabie	S. Africa	33.78	0.10	30.61	-0.30	30.42	0.18	31.40
Limpopo	S. Africa	33.10	-0.66	30.80	-1.06**	30.42	-0.58	31.29
Ala 70-11	S. Africa	33.61	-0.49	30.73	0.09	29.59	-0.30	31.10
Komati	S. Africa	33.61	-0.20	28.45	-0.93*	29.91	-0.23	30.39
Del Cerro	U.S.	36.58	0.40	32.83	0.19	32.26	0.37	33.64
Acala 1517-99	U.S.	33.70	-0.11	32.00	0.44	31.18	-0.01	32.17
Phytogen 72	U.S.	34.80	-0.03	31.50	0.25	30.67	-0.27	32.10
Deltapine 491	U.S.	34.12	-0.54	31.50	-0.42	29.65	-0.58	31.54
Stoneville 474	U.S.	33.87	0.69	30.73	0.72*	29.78	-0.36	31.24
Tamcot 22	U.S.	33.10	-0.32	30.61	0.09	30.29	-0.04	31.17

Table 3 continued

TAM B182-33 ELS Hybrids	Country of Origin	MX2010		CS2010		CS2011		Average
		UHML	SCA	UHML	SCA	UHML	SCA	UHML
Paymaster Tejas	U.S.	32.00	-0.15	29.34	-0.11	29.21	0.02	30.02
S.E.(SCA)		0.425		0.347		0.313		

*Significant at the 0.05 probability level.
**Significant at the 0.01 probability level.

.

33 ELS, respectively. The South African cultivars Limpopo and Komati were good specific combiners with TAM CAMD-E at College Station in 2010 and produced significant estimates. The U.S. cultivar Stoneville 474 was a good specific combiner with TAM B182-33 ELS at College Station in 2010. This indicates obsolete short staple upland cotton cultivars might possess alleles for UHML improvement in modern ESLU.

Based on the observed values for both GCA and SCA estimates, the majority of the variation among this set of parents is due to additive effects. This would agree with previous reports for inheritance of fiber length in cotton (Al-Rawi and Kohel, 1969; Al-Rawi and Kohel, 1970; Campbell et al., 2008; Lee et al., 1967; May and Green, 1994; Meredith, 1970; Meredith and Bridge, 1972; Meredith et al., 1970; Miller and Lee, 1964; Miller and Marani, 1963; Miller et al., 1959; Miller et al., 1962; Percy et al., 2006; Quisenberry, 1975; Tang et al., 1993).

Based on the parents used in the study, it appears that cultivars used in China likely do not contain any additional alleles for further UHML improvement. In order to enhance UHML in upland cotton, it appears that germplasm lines developed through interspecific hybridization would produce the largest gains. However, yield drag and other factors such as reduced turnout would hinder efforts to improve UHML.

In order to meet short term goals for UHML improvement, upland cotton cultivars from West and South Africa could be used in crosses with current elite

lines. Because yield was not taken, it is not known if yield drag or reduced

turnout at ginning could be adverse effects in lines derived from these cultivars.

Furthermore based on the data reported it would appear using U.S. upland elite

cultivars with good UHML measurements could be used for improvement. This

is evident as Acala 1517-99, Deltapine 491, and Phytogen 72 had GCA

estimates that were positive and significantly different from zero in the three

environments. Furthermore, based on a positive SCA estimate, ST474 and

other obsolete short staple upland US cultivars might possess alleles or

beneficial epistatic combinations for improvement of UHML in ELSU cottons.

Diallel Analyis of UHML Among Three Confirmed Extra Long Staple Upland

Accessions from USDA-ARS

Analysis of variance revealed significant variation due to Environments,

Reps within Environments, and Genotypes (Table 4). Broad sense heritability

 (H^2) was 0.927. This indicated that the majority of the variation within study was

due to genotypes. The general combining ability (GCA) and specific combining

ability (SCA) effects were significant but the GCAxEnvironment and

SCAxEnvironment interaction effects were not significant, thus data were

combined across the three environments.

The five parents and 10 hybrids differed for UHML when averaged over

the three environments (Table 5). The three longest parents were TAM B182-33

ELS (Smith et al, 2009), EwingsLongStapleXTidewater, and Sealand 1. Their

mean UHML ranged from 34.06 mm to 33.92 mm and were different (P≤0.05)

Table 4. Analysis of variance and broad sense (H^2) estimate for UHML (mm) among three confirmed ELS upland cotton lines, TAM B182-33 ELS, and TAM 94L-25 and their 10 F_1 progeny lines derived from a half diallel mating scheme.

Source†	df	Mean square
Environment (E)	2	114.6105***
Reps within E	8	1.8882
Genotypes (G)	14	10.0956***
GCA	4	26.1007***
SCA	10	3.4482***
GxE	28	0.5502
GCAxE	8	0.8342
SCAxE	20	0.4366
Error	112	0.4606

$$H^2 = 0.927$$

*Significant at the 0.05 probability level.
**Significant at the 0.01 probability level.
***Significant at the 0.001 probability level.
†GCA = general combining ability; SCA = specific combining ability.

from TAM 94L-25 but not D&PL 45-867. The mean of D&PL 45-867, was 33.41 mm, numerically the shortest of the three accessions. The long staple upland TAM 94L-25 was significantly shorter than the four other parents, as expected, and the 10 F_1 hybrids tested. The average UHML of hybrids TAM B182-33 ELS/EwingsLongStapleXTidewater and TAM B182-33 ELS/Sealand 1 were significantly longer than the five parents or any of the other hybrid combinations but were not different from each other. The hybrid of EwingsLongStapleX-Tidewater/Sealand 1 produced a mean UHML of 34.10 mm but was significantly shorter (P<0.05) than the hybrids made with TAM B182-33 ELS and not significantly different than TAM B182-33 ELS, EwingsLongStapleXTidewater, and Sealand 1. The hybrid of TAM B182-33 ELS/TAM 94L-25 was shorter

Table 5. Means and standard deviations for UHML of three confirmed ELS Upland Cotton lines from GRIN, TAM B182-33 ELS, and TAM 94L-25 crossed in a half diallel mating scheme grown at Tecoman, Mexico 2009-10, College Station 2010, and College Station 2011.

Genotype	UHML (mm)	s
TAM B182-33 ELS	34.06bc†	1.79
EwingsLongStapleXTidewater	33.94bc	1.86
Sealand 1	33.92bc	1.32
D&PL 45-867	33.41cd	0.96
TAM 94L-25	30.80f	1.07
TAM B182-33 ELS/EwingsLongStapleXTidewater	34.87a	1.63
TAM B182-33 ELS/Sealand 1	34.75a	1.46
EwingsLongStapleXTidewater/Sealand 1	34.10b	1.60
TAM B182-33 ELS/D&PL 45-867	34.06bc	1.62
EwingsLongStapleXTidewater/D&PL 45-867	33.94bc	1.14
D&PL 45-867/Sealand 1	33.78bcd	1.43
EwingsLongStapleXTidewater/TAM 94L-25	33.71bcd	1.59
D&PL 45-867/TAM 94L-25	33.57bcd	1.13
Sealand 1/TAM 94L-25	33.23de	1.37
TAM B182-33 ELS/TAM 94L-25	32.77e	1.31

†Mean values followed by the same letter were not different at P≤0.05.

(P<0.05) than the four ELS parents and all of the hybrid combinations with the exception of Sealand 1/TAM 94L-25. However, the hybrid combination was significantly longer than TAM 94L-25. This was expected as TAM 94L-25 is a parent of TAM B182-33 ELS. Based on this data, it appears the three longest parents would be ideal for improvement of UHML in both ELS upland and LSU cottons. However, it also suggests that TAM B182-33 ELS, which Smith et al. (2008, 2009) suggested was an ELS upland developed without introgression from *G. barbadense*, has the same or essentially the same alleles for fiber length as the accessions from the USDA Cotton Collection, which are considered to be introgressed lines (Smith and Hague; 2008).

General combining ability represents that average performance of parents in a hybrid combination. The analysis of variance (Table 4) did not reveal a significant GCAxE interaction and therefore the data were pooled. The calculated estimates for GCA effects (Table 6) revealed that TAM B182-33 ELS (Smith et al., 2008) and EwingsLongStapleXTidewater were good general combiners. TAM B182-33 ELS and EwingsLongStapleXTidewater produced significant GCA estimates of 0.370 and 0.364, respectively. Sealand 1 had a GCA estimate of 0.248, not significantly different from zero. The shortest parent, TAM 94L-25 had a GCA estimate of -1.012 that was highly significantly different from zero, as expected when grouped with this set of ELS upland phenotypes. These data agree with conclusions from the mean and standard deviation for UHML among the parents and hybrids in this study as discussed above. Based on the available data, TAM B182-33 ELS and EwingsLongStapleXTidewater would be the most desirable parents to use for UHML improvement among these parents.

Specific combining ability represents the deviation from expected performance of a hybrid combination based on the mean of all hybrids and the GCA of the parents. Good SCA deviations can be due to dominance effects or favorable epistatic gene interactions and suggest that the trait in question can be improved through selection of specific parental combinations. However, superior specific combiners can and might still have poorer performance than elite lines. When averaged over the three environments, only D&PL 45-

Table 6. Estimates of specific combining ability (SCA) effects, general combining ability (GCA) effects, and the overall mean for UHML among three confirmed Extra Long Staple upland cottons, TAM B182-33 ELS, and TAM 94L-25 crossed in a half diallel mating scheme grown at Tecoman, Mexico 2009-10, College Station 2010, and College Station 2011.

Parent	Parent 1	2	3	4	GCA
	SCA				
1. TAM B182-33 ELS					0.370*
2. EwingsLongStaplexTidewater	0.473				0.364*
3. Sealand 1	0.472	-0.169			0.248
4. D&PL 45-867	-0.004	-0.112	-0.158		0.030
5. TAM 94L-25	-0.254	0.699	0.330	0.893*	-1.012***

*Significant at the 0.05 probability level.
***Significant at the 0.001 probability level.

867/TAM 94L-25 produced a SCA estimate that was significantly different from zero. Because neither parent exhibited a good GCA estimate, this particular combination might possess different alleles contributing to UHML via dominance effects or a favorable epistatic gene interaction. The hybrid produced a mean UHML of 33. 57 mm when averaged over the three environments and was not significantly different than the mean UHML of TAM B182-33 ELS, EwingsLongStapleXTidewater, or Sealand 1.

Heritability of Lower Half Mean Length and Short Fiber Content by Weight

in an Extra Long Staple X Medium Staple Upland Cotton Cross

Short fiber content adversely affects yarn spinning and spinning

performance (Backe, 1986). Lowering short fiber content is important to

spinners because it represents waste and increases the number of thick and thin

places in yarn. Currently breeders must use AFIS to determine short fiber

content in a sample of cotton lint as HVI does not have a short fiber content

measurement. Recently Cai et al. (2001) found that lower half mean length was

a better indicator of yarn spinning performance. Currently there are no narrow

sense (h^2) estimates for SFCw or LHML for ELSU X MSU crosses.

Narrow sense (h^2) heritability estimates were obtained for both LHML and

AFIS SFCw using parent-offspring regression.. Estimates were obtained using

both individual $F_{2:3}$ data from College Station in 2009 and mid-parent data from

TAM B182-39 ELS and DP491 planted with the 140 $F_{3:5}$ RIL's at College Station

in 2011. The h^2 estimates estimates obtained when the RILs were regressed on

their respective individual parent plant in the $F_{2:3}$ generation were adjusted using

the correction factor from Holland et al. (2003) and $F_t = 1/2$. The mid-parent

values were calculated on a per block basis. Any negative regression

coefficients were interpreted as a heritability estimate of zero.

Estimates of h^2 ranged from 0 to 0.48 (Table 7). Estimates of h^2 for AFIS

SFCw and LHML were 0.27 and 0.00, respectively, when based on mid-parent

Table 7. Narrow sense heritability (h^2) estimates and their standard error for LHML and AFIS SFCw in a F$_{3:5}$ RIL population using both F$_{2:3}$ individual plant data from College Station 2009 and parents grown in a RCBD with 2 replications at College Station, TX in 2011.

Fiber Parameter	Generation	Narrow sense heritability (h^2) estimate	Standard Error
AFIS SFCw	Mid-Parent	0.27	0.69
	F$_{2:3}$	0.15***	0.04
LHML	Mid-Parent	0.00	0.42
	F$_{2:3}$	0.48***	0.06

***Significant at the 0.001 probability level.

values obtained at College Station in 2011. Furthermore, the heritability estimate obtained for SFCw was not significantly different from zero.

Narrow sense heritability (h^2) estimates obtained when 2011 F$_{3:5}$ plot values were regressed on F$_{2:3}$ individual plant values from 2009 were 0.15 and 0.48 for AFIS SFCw and LHML, respectively. Based on the standard errors for the regression coefficients, there was a drastic reduction in error when plot values were regressed on individual parental F$_{2:3}$ selections.

Cai et al. (2011) found a high correlation (r = -0.986) between AFIS SFCw and LHML among 28 different cotton samples. The authors also found LHML was a better predictor of yarn performance when spun. Higher coefficients of determination (R^2) were found for spinning performance when LHML replaced AFIS SFCw. While the fiber parameters of the cottons used are not known, evidence in their study suggests that selecting for improved LHML in populations has the potential to aide in the development of cottons with fiber properties that yarn spinners desire at a faster pace versus selecting on AFIS SFCw.

Data collected in the study found a low h^2 of 0.15 in a F$_{3:5}$ RIL population derived from a ELSU X MSU cross for AFIS SFCw when plot values were regressed on F$_{2:3}$ individual plant data. The h^2 of LHML was a moderate 0.48. This indicates a greater amount of genetic variation for LHML than AFIS SFCw. If the conclusions of Cai et al. (2011) hold for cottons developed from ELSU X MSU crosses, cotton breeders would be able to increase genetic gain by selecting cottons with improved yarn spinning properties. However, further data on the spinning performance in relation to AFIS SFCw and LHML using lines derived from ELSU X MSU crosses is needed.

Determining Short Fiber Content by Weight in an Extra Long Staple X Medium Staple Upland Cotton Cross

Analysis of variance of 140 F$_{3:5}$ RILs and their parents, TAM B182-39 ELS and DP 491 indicated that genotypes were the primary source of variation for AFIS SFCw and HVI fiber properties (Table 8). Replications (Reps) were, however, a significant (P<0.01) source of variation for fiber micronaire but not for any other HVI traits reported. This indicates that the fiber properties were mostly affected by genotypes and not by variation from the field. Because of this it can be concluded that fiber properties are stable among the genotypes and it is possible to use HVI fiber properties to determine SFCw using a regression equation.

Coefficients of variation (CV) indicated that there was a lot of variation for SFCw but not for HVI fiber properties. This suggests there are more factors

than the genotype that affect SFCw. The AFIS instrument itself is known to bias

SFCw measurement from fiber breakage caused by the fiber individualizer

(Bragg and Shoffner, 1993). Among the traits reported in Table 8, the CV for

AFIS SFCw was the highest at 20.75, while the HVI fiber properties had much

lower CVs. Lower Half Mean Length had the highest CV of the HVI based fiber

properties at 6.29. These results agree with the findings of Cai et al. (2011).

Two regression equations from Zeidman et al. (1991) were used in this

study. They are:

$$SFCw_1 = 126.21 - (15.81/25.4) \bullet UHML - 1.23 \bullet UI$$

$$SFCw_2 = -(0.249/25.4) \bullet UHML - 0.533 \bullet UI$$

A third regression equation for this study was developed using SAS 9.2 Proc

Reg setting the SFCw values given from AFIS measurements equal to the $F_{3:5}$

RIL fiber samples to the HVI fiber tests. Selection for the regression equation

used herein was based upon Mallow's C(p) statistic and the associated adjusted

coefficient of determination (R^2) values, the regression equation. The regression

equation developed is:

$$SFCw_3 = 40.825 - 0.320 \bullet UI - 1.129 \bullet Micronaire$$

Pearson correlation coefficients (r) were calculated among AFIS SFCw and two

regression equations to determine SFCw from HVI fiber properties published by

Zeidman et al. (1991) and the regression equation developed in this study

($SFCw_3$) (Table 9). The two regression equations from Zeidman et al. (1991)

$SFCw_1$ and $SFCw_2$ were positively and statistically significantly ($P<0.05$)

Table 8. Mean square values and coefficients of variation among 140 F$_{3:5}$ RILs and their parents, TAM B182-39 ELS and DP 491, for AFIS SFCw and HVI fiber properties grown at College Station in 2011.

Source	SFCw	UHML -mm-	ML -mm-	LHML -mm-	Micronaire	Uniformity	Strength -kN m kg⁻¹-	Elongation
Genotype	1.75***	4.38***	4.08***	3.38***	0.26***	2.45***	840.38***	0.66***
Replications	0.25	1.68	2.07	2.18	0.48**	1.53	60.11	0.26
Error	0.87	0.87	0.95	0.97	0.07	0.97	208.97	0.14
C.V.	20.75	3.19	4.03	6.29	5.56	1.19	4.51	5.71

*Significant at the 0.05 probability level.
**Significant at the 0.01 probability level.
***Significant at the 0.001 probability level.

Table 9. Pearson correlation coefficients (r) among AFIS SFCw and HVI fiber properties LHML, UI, micronaire, and fiber strength and three regression equations to determine AFIS SFCw from HVI properties in individual plant data from the $F_{2:3}$ generation grown at College Station, TX in 2009 and among 140 $F_{3:5}$ RILs and parents TAM B182-39 ELS and DP 491 grown at College Station, TX, in 2011 in a RCBD with 2 replications.

	$F_{2:3}$ Generation							
	SFCw	$SFCw_1$	$SFCw_2$	$SFCw_3$	LHML	UI	Micronaire	Strength
SFCw	1.000	0.366**	0.555**	0.574**	-0.225**	-0.560**	-0.308**	-0.227**
$SFCw_1$		1.000	0.812**	0.578**	-0.960**	-0.803**	0.252**	-0.673**
$SFCw_2$			1.000	0.857**	-0.618**	-0.999**	-0.198*	-0.467**
$SFCw_3$				1.000	-0.367**	-0.863**	-0.556**	-0.496**
	$F_{3:5}$ Generation							
	SFCw	$SFCw_1$	$SFCw_2$	$SFCw_3$	LHML	UI	Micronaire	Strength
SFCw	1.000	0.252**	0.409**	0.613**	-0.177**	-0.415**	-0.241**	-0.433**
$SFCw_1$		1.000	0.939**	0.472**	-0.988**	-0.932**	-0.498**	-0.531**
$SFCw_2$			1.000	0.666**	-0.876**	-0.999**	0.317**	-0.601**
$SFCw_3$				1.000	-0.368**	-0.674**	-0.400**	-0.702**

*Significant at the 0.05 probability level.
**Significant at the 0.01 probability level.

correlated to AFIS SFCw. Between both generations $SFCw_2$ had a higher correlation with r values of 0.555 and 0.409 in the $F_{2:3}$ and $F_{3:5}$ generation respectively. The regression equation derived from the $F_{3:5}$ RIL data in 2011 ($SFCw_3$) was significantly (P<0.05) correlated to AFIS SFCw in both generations as well with r values of 0.574 and 0.613 in the $F_{2:3}$ and $F_{3:5}$ generations, respectively. When the three regression equations were compared to the previous work by Zeidman et al. (1991), $SFCw_2$ and $SFCw_3$ were the highest correlated in both generations with r values of 0.857 in the $F_{2:3}$ generation and 0.666 in the $F_{3:5}$ generation.

Pearson correlation coefficients (r) were calculated among AFIS SFCw and HVI fiber parameters for both the $F_{2:3}$ and the $F_{3:5}$ generations. Between both generations, LHML, UI, micronaire, and fiber strength were significantly correlated with AFIS SFCw (Table 9). In the $F_{2:3}$ generation, UI correlated the highest with AFIS SFCw. However, in the $F_{3:5}$ generation, fiber strength was higher correlated with AFIS SFCw with r=-0.433. Uniformity Index correlated slightly less than fiber strength with r=-0.415. This was to be expected as UI is the ratio of ML to UHML. Therefore, as UI increases, SFCw should theoretically decrease.

Lower half mean length was correlated with AFIS SFCw with r = -0.225 and -0.177 in the $F_{2:3}$ and $F_{3:5}$ generations, respectively. This was a stark contrast to the correlation coefficient of -0.986 reported by Cai et al. (2011).

Thus, basing selection for improved AFIS SFCw via LHML might not be as efficient in ELSU X MSU crosses.

Pearson correlation coefficients (r) were also calculated among the three regression equations and AFIS SFCw (Table 9). In both the $F_{2:3}$ generation grown in 2009 and the replicated $F_{3:5}$ generation grown in 2011, $SFCw_1$ correlated the best to LHML of the three regression equations and AFIS SFCw.

Regression equations derived by Zeidman et al. (1991) were highly correlated to UI. Pearson correlation coefficient values (r) ranged from -0.803 to -0.999. Thus the regression equations developed by Zeidman et al. (1991) places a high emphasis on UI. The regression equation $SFCw_3$ was also highly correlated to UI with r values of -0.863 and -0.674 in the $F_{2:3}$ and $F_{3:5}$ generations, respectively. Therefore $SFCw_3$ appears to also emphasize UI but not to the same degree as $SFCw_1$ and $SFCw_2$.

Pearson correlation coefficients (r) among the HVI fiber micronaire and strength and AFIS SFCw and the regression equations varied between the two generations (Table 9). The r values for $SFCw_1$ changed from 0.252 to -0.498 in the $F_{2:3}$ and $F_{3:5}$ generations, respectively. The regression equation $SFCw_2$ changed from having a positive r value of 0.317 in the $F_{2:3}$ generation to -0.198 in the $F_{3:5}$ generation. The regression equation $SFCw_3$ remained negatively correlated (P<0.01) with HVI fiber micronaire in both generations but r values decreased from -0.556 to -0.400 between the $F_{2:3}$ and $F_{3:5}$ generation, respectively. When pearson correlation coefficients (r) were calculated among

the three regression equations and fiber strength, $SFCw_1$ was the highest

correlated (-0.673) in the $F_{2:3}$ generation and $SFCw_3$ was the highest correlated

(-0.702) in the $F_{3:5}$ generation. This indicates that the regression equations were

not emphasizing selection for higher fiber strength per se or that the two

equations developed by Zeidman et al. (1991) emphasize fiber micronaire.

Cai et al. (2011) found a high correlation (r = -0.986) between AFIS SFCw

and LHML among 28 different cotton samples. The authors also found LHML

was a better predictor of yarn performance when spun. Higher coefficients of

determination (R^2) were found for spinning performance when LHML replaced

AFIS SFCw. While the fiber parameters of the cottons used are not known,

evidence in their study and this study suggests that selecting for improved LHML

in populations has the potential to aide in the development of cottons with fiber

properties that yarn spinners desire at a faster pace versus selecting on AFIS

SFCw.

Data collected in the study found a low narrow sense (h^2) heritability of

0.15 in a $F_{3:5}$ RIL population derived from a ELSU X MSU cross for AFIS SFCw

when plot values were regressed on $F_{2:3}$ individual plant data. The narrow

sense heritability (h^2) of LHML was a moderate 0.48. This indicates a greater

amount of genetic variation for LHML than AFIS SFCw.   If the conclusions of

Cai et al. (2011) hold for cottons developed from ELSU X MSU crosses, cotton

breeders would be able to increase genetic gain by selecting cottons with

improved yarn spinning properties. However, further data on the spinning

performance in relation to AFIS SFCw and LHML using lines derived from ELSU X MSU crosses is needed.

Based on the data presented herein, the conclusions of Cai et al. (2011) do not apply in ELSU X MSU cotton crosses. This study found significant but lower r values between AFIS SFCw and LHML. The study by Cai et al. (2011) however found a high negative correlation between the two parameters. Therefore, further testing is needed using lint derived from ELSU in mini-spinning performance trials.

Furthermore the variation for Pearson's correlation coefficients suggests that a second year of data is needed in order to determine the stability of AFIS SFCw and HVI fiber micronaire and strength values. Based on the variation seen for r values, the regression equation developed herein ($SFCw_3$) might have advantages over equations developed by Zeidman et al. (1991) by placing emphasis on other fiber properties important in the spinning process. Because there was a significant and negative ρ value, breeders must exercise caution when selecting using $SFCw_3$ as higher micronaire values will be obtained.

In agreement with Cai et al. (2011), this study observed a much higher coefficient of variation for AFIS SFCw than LHML. It is possible that further improvements in spinning performance could be obtained because LHML measurements have a lower coefficient of variation. Because there is less variation in the data, it would be easier for breeders to select cottons with enhanced yarn spinning properties.

There are advantages of using micronaire values in a regression equation. Micronaire is an indirect measurement of fineness and maturity. Thus, adding micronaire into an equation to select for lower AFIS SFCw could prevent selection of cottons that produce immature fibers.

It is important to understand the role that fiber strength plays in determining AFIS SFCw. Strong fibers are less prone to breaking which in turn increases yarn strength making them more desirable. When cotton fibers are less to prone to breakage, less short fibers will form during the harvesting and handling process regardless of machine setting.

Lastly, it is important to determine what is happening in terms of fiber length distributions of ELSU X MSU crosses. Due to the drastic disagreement with the findings of Cai et al. (2011), it appears that predicting spinning performance of ELSU cultivars or cultivars derived in ELSU X MSU crosses deviates from the expectations of commercial type upland cultivars.

CHAPTER V

CONCLUSIONS

Genetic improvement of UHML and LHML and reduction of SFCw are imperative in order for the U.S. to maintain competiveness in a global community. This study answers some fundamental question for continued improvement of both short staple upland and modern ELSU cotton cultivars.

The cultivars developed in China and used in this study apparently do not contain any additional alleles for UHML improvement in ELSU phenotypes developed at Texas AgriLife Research. Upland cotton cultivars from West and South Africa could be used in crosses with current elite lines. Because yield was not taken, it is not known if yield drag or reduced turnout at ginning could be adverse effects in lines derived from these cultivars. Furthermore based on the data reported it would appear using U.S. upland elite cultivars with good UHML measurements could be used for improvement. This is evident as Acala 1517-99, Deltapine 491, and Phytogen 72 had GCA estimates that were positive and significantly different from zero in the three environments. Furthermore, based on a positive SCA estimate, ST474 and other obsolete short staple upland US cultivars might possess alleles or beneficial epistatic combinations for improvement of UHML in ELSU cottons.

Combining ELSU accessions from the USDA Cotton Collection with Texas AgriLife Research ELSU material may provide the opportunity for UHML improvement but such improvement would be incremental relative to the

advancement from LSU UHML to ELSU UHML. However, yield drag and other unknown factors such as reduced gin turnout could hinder efforts to develop upland cultivars exhibiting the ELS UHML.

Lower half mean length had a much higher narrow sense heritability than SFCw among lines derived from TAM B182-39 ELS/DP 491. Additionally, LHML also had a much lower coefficient of variation than SFCw. Thus selection for improved LHML could enhance efforts to develop lines with superior spinning properties. However, LHML and SFCw among lines developed from TAM B182-39 ELS/DP491 were not as strongly correlated as a previous study found. As a result further testing is needed in order to determine how well LHML predicts spinning performance in a ELSU X MSU cross.

A regression equation developed using a $F_{3:5}$ RIL population might possess advantages over previous work to determine SFCw using HVI fiber properties. The equation developed uses the strength and micronaire fiber properties to determine SFCw. This is important as fiber strength plays an important role in preventing fiber breakage during harvesting and processing. Furthermore, micronaire is an indirect measure of fiber fineness and maturity. Using micronaire as a part of a regression equation to determine SFCw should ensure cottons with mature fibers are selected. However, breeders must be careful so that selected cottons have micronaire values in the non-discount range.

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