

TRANSGRESSIVE SEGREGATION FOR FIBER PROPERTIES OF THREE
POPULATIONS IN COTTON

A Thesis

by

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ABSTRACT

Improved fiber quality adds value to U.S. upland cotton and makes U.S. cotton more competitive in global markets. Improving characteristics like fiber length, strength, uniformity and elongation will allow American cotton to be used for a wider range of end products. The issue currently, however, is that breeders must develop more efficient methodology to improve selection of these characteristics.

This study was developed to observe two equivalent generations of a breeding scheme in order to monitor selection opportunities for these desirable fiber traits via comparison of transgressive segregation. A simple pedigree and then pedigree plus backcross system was used that allowed us to look at the F_3 and BC_1F_2 generations following the cross of Tamcot 22/TAM B 182-33 ELSU, 06 WE 62-4/Tamcot 22, and Tamcot 22/04 SID 84-2. Tamcot 22 is a high yielding, average quality cultivar, TAM B 182-33 ELSU is an extra-long staple germplasm release, 06 WE 62-4 is a breeding line with exceptional fiber strength, and 04 SID 84-2 is a breeding line with exceptional length and strength derived from an interspecific cross.

High volume instrument analysis (HVI) of fiber produced from these families and generations in 2011 and 2012 did not suggest any pattern associated with transgressive segregation by family. The majority of the positive transgressive segregates were found in the BC_1F_2 generation that was backcrossed to the high quality parent (TAM B 182-33 ELSU, 06 WE 62-4, 04 SID 84-2), and our observations did not

resemble previous findings by other groups. When averaged over both years, the family derived from the interspecific cross contained the most transgressive segregates.

DEDICATION

This work is dedicated to my parents and family who have supported me in this endeavor. For all of the support and encouragement they have given me along the way, I could not have done it without them. Also to my grandmother (Sue Weger) who was recently lost and never saw this completed. She was always supportive and excited to hear about what was going on even if it wasn't always positive. She was also a true storybook come-to-life, and the best grandmother a grandson could ask for.

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NOMENCLATURE

AFIS	Advance Fiber Information System
ASTM	American Society of Testing Materials
CCC	Commodity Credit Corporation
CCI	Cotton Council International
CI	Cotton Incorporated
ELS	Extra- Long Staple
ELSU	Extra- Long Staple Upland
ERS	Economic Research Service
FAS	Foreign Agricultural Service
FBRI	The Fiber and Bio-Polymer Research Institute
FL _n	Mean fiber length by number (AFIS)
FL _w	Mean fiber length by weight (AFIS)
GxE	Genotype x environment interaction
HPV	High- Parent Value
HVI	High Volume Instrumentation
LPV	Low- Parent Value
MPV	Mid- Parent Value
NASS	National Agricultural Statistics Service
NCC	National Cotton Council of America
NOAA	National Oceanic and Atmospheric Administration

OGTR	Office of the Gene Technology Regulator (Australian Govt.)
SAS	Statistical Analysis Software
SFC	Short fiber content
SFCn	Short fiber content by number (AFIS)
SFCw	Short fiber content by weight (AFIS)
TDA	Texas Department of Agriculture
UHML	Upper- half mean fiber length (HVI)
UQL	Upper- quartile length
UQLw	Upper- quartile length by weight (AFIS)
USDA	United States Department of Agriculture
WAOB	World Agricultural Outlook Board

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INTRODUCTION

Cotton is one of the most important textile crops in the world. In 2011, cotton fiber made up approximately 35 % of total world fiber use (USDA-ERS, 2012). It also was grown on 33.45 million hectares worldwide spanning 80 countries, with China and India being the top two producers (USDA-FAS, 2011). The United States (U.S.) currently ranks third as a producer of cotton fiber, but it is the number one exporter of cotton (The National Cotton Council, 2012; USDA-WAOB, 2013). This presents many challenges, however. Growing conditions are unique to each region coupled with diverse demands for fiber quality desired by a range of mills, spinners, and consumers. Both of these factors along with many others have helped to shape the evolution of cotton, both in the U.S. and worldwide, since its domestication.

In the U.S., cotton is concentrated in the southern regions of the country and grown in 17 states (Cotton Incorporated, 2013f). From the development of the cotton gin in 1793 to becoming “King Cotton” in the mid-1800s, many developments have accompanied the growth of this crop to the large scale, technical production that it is today (Vernon and Bonnin, 1997). The southern regions of the U.S. offer long, warm, and often-times arid growing conditions which are optimum for the growth of this textile crop. These regions, however, also have highly variable weather from year-to-year.

Texas is the largest producing state of cotton in the United States. Cotton is grown in both irrigated and non-irrigated (dryland) conditions in the state, requiring

farmers to properly manage all agronomic aspects of growing the crop to achieve maximum yields (National Cotton Council, 2013; USDA-NASS, 2012). Water limitations, seasonal conditions, and achieving the optimal yield are not the only issues producers have to worry about. The current U.S. domestic use-consumption of cotton is declining. As more and more cotton is shipped overseas, fiber quality is becoming a forefront issue for both growers and processors.

The textile market has become increasingly globalized within the last 15 years (Joy et al., 2010). Within the last decade, U.S. domestic use of cotton has decreased from 10.4 to 3.7 million bales, increasing U.S. exports to over 12.5 million bales. This number is up from 7.5 million bales reported for export ten years ago (Cotton Inc., 2009; USDA, 2008). The broad international textile market produces a variety of high quality end-products causing a shift in the demand of fiber quality (Hequet et al., 2006). Cultivars of upland cotton have been developed over the past 70 years to achieve increasing yields and shorter growing seasons/maturation periods to avoid pests and extreme seasonal conditions (May, 2000; Bridge and Meredith, 1983). More recently, the U.S. textile market has been primarily driven by the use of coarse fibers woven by rotor spinning technology. This system allows for both higher processing speed and efficiency, but the yarns produced are lower in quality than most international customers prefer. The rotor spinning system has caused a shift in the majority of U.S. grown cotton towards shorter fiber length and higher fiber strength cultivars in order to withstand these higher processing speeds. This occurs often at the detriment of other important fiber characteristics (Green and Culp, 1990; Bayles et al., 2005; Bridge et al., 1971; May and

Jividen, 1999). The processing system used and accepted by a majority of the rest of the world is ring spinning (Gregory et al., 2012; Felker, 2001). This system focuses on producing finer and higher quality yarns which allow production of a wider variety of quality end products. Cultivars more beneficial to this system are prone toward longer fiber lengths and increased length uniformity. Competition and marketability at the international level and now the production of synthetic fibers, which can predictably achieve both high fiber length and strength, (Schwartz and Smith, 2008; Joy et al., 2010) are going to be the most important factors driving the breeding of improved cultivars and the production of high quality cotton fiber by U.S. growers in order to keep pace in the future textile market.

The answer to this problem has been the focus of the Texas A&M AgriLife Research Cotton Improvement Lab and its breeders over the last 10-15 years. They have already begun to simultaneously address these issues in many sets of recent germplasm releases that have improved fiber quality, including length and strength (Hague et al., 2011; Smith et al., 2009b; Smith, 2003). Work continues in order to improve the agronomic (and market) value for these type releases and studies similar to this one are monitoring how gene action and selection efficiency in these new releases can be improved.

RESEARCH OBJECTIVES

The distinct pedigrees and HVI fiber properties of the parents used in this study provided an opportunity to observe and verify instances of transgressive segregation.

The objectives of this study were to:

1. Determine the HVI measured fiber properties in segregating generations following the cross of a high yielding, upland cultivar when crossed with an upland ELSU parent, a high strength parent, and an interspecific-derived parent.
2. Determine the impact of environment on HVI measured fiber properties in such derived families and generations.
3. Determine transgressive segregation for HVI measured fiber properties within these three families.
4. Determine the impact of a single backcross as a breeding method to enhance the frequency of transgressive segregates.

LITERATURE REVIEW

Cotton and Cotton Fiber

Cotton is a member of the genus *Gossypium*. Although four species of *Gossypium* have historically been cultivated for fiber, two currently dominate the commercial market (Brubaker et al., 1999). *Gossypium hirsutum* and *G. barbadense* are tetraploid cotton species that are unique in both agronomic traits and fiber characteristics. *Gossypium hirsutum*, upland cotton, is grown on over 90 % of the world's cotton hectareage and is known for its higher yield potential and broad environmental adaptability (Percy et al., 2006). It is known also for its poorer fiber quality and average fiber lengths relative to *G. barbadense*. Despite its high yield and recent improvements in quality, market demand continues to push for improvement of upland cotton (McCreight, 1992; Felkner, 2001). The species grown for the majority of the rest of commercial cultivation is *G. barbadense*. This species of cotton is known for its higher fiber quality and longer fiber lengths but also for its lower yield potential, increased environmental sensitivity, and longer growing period (Kohel et al., 2001). Constant efforts have been made to transfer advantageous traits from one species to the other to include both high yield potential and improved fiber quality within a single plant, but those efforts have largely been of limited success (Stephens, 1949; Rhyne, 1958; Reinisch, 1994; Patterson and Smith, 1999; Smith et al., 1999; Lacape et al., 2005; Wang et al., 2012). Nonetheless, improvement for these areas in cotton continues. May (2000), Percival (1987), and Percy et al. (2006) claim that intensive selection imposed to

maximize yield and adaptation along with selection for maturity has eliminated large amounts of variation from *hirsutum*. They also reported that although portions of *G. barbadense* germplasm do exist with highly desirable fiber characteristics, negative agronomic performance currently linked with these traits in a majority of this material makes their use in a typical breeding program economically unfavorable.

Cotton fibers can be spun and made into an array of end products, and although cotton seeds and their oil can be very useful, this natural fiber has remained the focus of improvement efforts (Braden, 2005). Shirts and almost all types of clothing, plastics, paper, nets, rugs, and a variety of other products all contain processed cotton (Smith, 2001; Cotton Incorporated, 2013e). However, the constant development of alternative textile sources continues to push the global market. Man-made fibers, like polyester, threaten to draw market-share away from cotton and so the improvement of this crop is paramount to its continued success (Joy et al., 2010).

A single cotton fiber consists almost entirely (94 %) of cellulose (Cotton Incorporated, 2013b). It originates from the epidermal cells of the cotton seed and grows in a loose spiral manner alongside other originating fibers, giving it strength and frictional support. Each individual fiber's length, strength, and maturity level work to cumulatively add to a fiber product's overall quality. Processed cotton fibers can be spun or woven individually or as a bundle into different quality and style yarns according to production specifications of various end products. So the characteristics of each

individual fiber, although very small in comparison to the whole, contribute to the quality of the product produced.

Cotton Fiber Characteristics

A variety of fiber characteristics contribute to the “overall” quality of a single cotton fiber. When looking at a number of fibers and their interaction with one another when spun into yarn, even more complexity is introduced. Length, strength, yield (number of fibers), elongation, uniformity, and micronaire (maturity and fineness) are just a number of characteristics breeders and producers commonly monitor. These are also the primary fiber characteristics (excluding yield) reported by a High Volume Instrument (HVI) as it measures cotton quality during processing. The HVI is important to cotton growers, breeders, and processors because it is the fastest and most cost effective way to measure large numbers of cotton fiber samples. Every bale sold on the commercial market in the U.S. is tested by HVI instrumentation. This type of testing method, despite reports claiming disadvantages in certain areas of effectiveness, is currently the standard to measure gains in breeding each year for cotton fiber quality. Green and Culp (1990) stated that HVI testing did not detect any significant differences for fiber properties measured within their study for either general combining ability or specific combining ability. They performed a secondary method of testing (standard laboratory instrumentation) which did detect significant differences for 2.5 % and 50 % fiber span length, uniformity, yarn strength, yield, and lint percent (yield and lint percent not measured by HVI). They concluded that HVI was not effective in detecting small genetic differences. May and Jividen (1999), Latimer et al. (1996) and Kelly et al.

(2012) provide evidence to, the contrary, noting that it is possible to improve fiber quality with HVI just as effectively as single instrument testing methods used by Green and Culp. These groups report equal significance and heritability of values received via HVI on populations for micronaire, fiber strength, and fiber length when compared with other instrumentation.

HVI measures upper-half mean length (UHML), fiber bundle strength, uniformity of fiber lengths, elongation at break, and micronaire based on bundles (or groups) of cotton fibers representing a larger source of harvested cotton fibers such as a bale or module . Multiple biases can occur when using a fiber bundle to represent a larger, non-uniform sample of cotton fiber (lint). The small fiber bundle could not be a true representation of the greater fiber sample and its true fiber quality, and bias will always be present in traits that are standardized and then measured on a bundle. The only way to eliminate this second bias would be to test every single fiber individually in the bundle, which is the case for Advanced Fiber Information System (AFIS) fiber testing. AFIS is available to breeders for evaluating an array of characteristics based on individual fibers rather than bundles of fibers. Shofner et al. (1988, 1990) and Hequet et al. (2007) reported its measurements contained fewer biases compared to HVI, but it is still a much less popular form of fiber testing due to slower speeds of processing and increased cost per sample.

Fiber Length (Upper Half Mean Length)

Fiber length is an important factor when considering overall fiber quality. Fiber length can be measured a number of ways. HVI reports fiber length using the term upper- half mean length (UHML) and measures it in a bundle type system. A bundle of fibers is collected and combed to produce individually positioned parallel fibers known as a “beard.” This beard is then photoelectrically scanned from the base to the tip and measurements of each length are taken. The number of fibers at each length are estimated, due to the nature of differing fiber fineness which is assumed equal throughout the sample (introducing bias as previously mentioned), and then the mean length of the longer half of the fibers is exhibited as the UHML. Mean length, i.e., the average length of all fibers in the beard, also is reported but rarely used by breeders. There are many classifications of fiber length based on UHML and those classifications are often applied to an individual cultivar or to individual species or biotypes. Short staple upland cotton has an UHML that is 25.1 mm or below; medium staple upland is typified by an UHML between 25.6 and 27.9 mm; long staple upland fiber length is between 28.1 and 32.0 mm; and USDA upland extra-long (EL) staple upland is a bundle of fibers with an UHML above 32.0 mm. *G. hirsutum* (upland cotton) has its divisions in fiber length; however *G. barbadense* or Pima is considered traditional extra-long staple (ELS) UHML material and must have UHML equal to or exceeding of 34.9 mm or longer as a non-discount market class (Braden and Smith, 2004b). ELSU in this document will refer to UHML equal to or greater than 34.9 mm. (Figure 1)

Fiber Designation	Fiber Length
1. <i>Pima</i> (traditional ELS)	> 1.375 in. (34.92 mm)
2. ELSU Upland, CIL Standard	> 1.375 in. (34.92 mm)
3. Extra Long (upland EL)	> 1.26 in. (32.00 mm)
4. Long	1.11 – 1.26 in. (28.19 – 32.00 mm)
5. Medium	1.00 – 1.10 in. (25.40 – 27.94 mm)
6. Short	< 1.00 in. (25.4 mm)

Source: Joy et al. (2012)



Figure 1. The fiber length measurement scale.

The U.S. standard base cotton length in 2005 for non-discount market was 26.9 mm. In Texas, the average UHML ranges 25.9 to 27.9 mm over years. The minimum requirement for worldwide markets on fiber length with no deductions in 2005 was 27.9 mm. Most years, this puts both Texas and American grown cotton below the international market standard and places a competitive disadvantage on exported U.S. cotton (Joy et al., 2010).

Research efforts often have concentrated on increasing fiber length, among other traits. However, fiber length has not always been the focus of American grown cultivars. Bayles et al. (2005), with the Oklahoma Agricultural Experiment Station, noted that during particular time periods certain areas of fiber quality or plant physiology became desirable due to changing market demands. With the increase in interest (and selection pressure) of certain fiber properties others often suffered and generally decreased in qualitative and economic value for that time. Bayles et al. (2005) reported on various fiber quality relationships by re-evaluating 12 cultivars, in multiple environments, that were released by the experiment station between 1918 and 1982 and monitoring trends. Fiber strength declined between 1918 and 1940 but then, starting in 1940 showed signs of steady increase. During this same time frame, lint percent increased from 1918 through 1940 before becoming static. Fiber length displayed a linear, positive slope through the duration of the trial period.

Fiber strength became an emphasis for American cotton breeders beginning in the 1970s and 1980s due to technological advancement in processing, but Green and

Culp (1990), Culp and Harrell (1977), and Culp et al. (1979) were quick to note the negative relationship between fiber strength and other properties like fiber length and yield. Bridge et al. (1971) pointed out that for many of these time periods, traits that were not the focus of breeding efforts, were merely kept on par with industry standards or simply ignored. Schwartz and Smith (2008), Smith et al. (2008), and Bridge et al. (1971) all note that for multiple fiber properties like length and strength, previous obsolete material actually exhibited values in ranges equal to or above what was being achieved at that time through concentrated breeding efforts. Thus, it is probable that improvement in fiber length can be achieved despite known relationships and historical trends.

Fiber Strength

Improving fiber strength could add both quality and value to upland cotton. Increased fiber bundle strength allows faster processing speeds during spinning and weaving with fewer problems and less yarn breakage. Zhang et al. (2002) directly noted that, “Since fiber strength translates directly into the strength of rotor yarns, it must possess a higher average level of strength and, most importantly, a lower variability of strength to cope with ever-increasing processing speeds in spinning, weaving and knitting.” Benedict et al. (1999) and Deussen (1992) agreed. Other groups began to focus on fiber strength during the 1970s and 1980s as rotor spinning’s faster processing speeds and higher productivity became desirable by processors in the U.S. (Vaughn and Rhodes, 1977; Pospisil, 1976; Shcherbakova et al., 1983; Pillay, 1975).

The standard of measure for fiber strength is in terms of a bundle of fibers (HVI system). The bundle is clamped 3.17 mm apart between two sets of holding jaws and the force required to break the fibers is measured (Cotton Incorporated, 2013a). The value reported from this measurement is in terms of g tex^{-1} . A “tex” is a unit equal to the weight in g of 1,000 m of spun yarn. Therefore, the value reported is an indirect measurement of fiber strength by reporting the force in grams required to break the bundle of fibers of one tex unit in size, if it were a spun yarn. May et al. (1995) also indirectly related fiber (bundle) strength to fiber maturity and yarn hairiness re-stating its importance to overall economic value. He reported values that as fiber maturity increased, yarn hairiness tended to increase and concluded that the increased friction amongst more mature fibers within the yarn translated to higher fiber (bundle) strength.

Cotton Incorporated partnered with The United States Department of Agriculture- Agricultural Research Service (USDA-ARS) to have set divisions in cotton fiber strength. The U.S. Cotton Fiber Chart (2011, 2012) classifies anything 20 g tex^{-1} and below “very weak.” Any fiber bundle requiring 21-25 g tex^{-1} to break categorized as “weak” and any bundle requiring 26-29 g tex^{-1} is considered the “base” level fiber bundle strength. The range to be considered a “strong” fiber bundle is between 30-32 g tex^{-1} . Any cotton fiber bundle with a strength measurement above 32 g tex^{-1} is considered “very strong.” The no-discount requirement for cotton sold in the U.S. was a minimum of 24 g tex^{-1} for the year 2012 (Cotton Council International, cottonusa.org, 2012).

Fiber Elongation

Fiber elongation has been largely under-utilized as a measurable cotton fiber property (Riley, 1997; Hequet, 2007). It is measured as a percentage of stretch of the fiber bundle at breakage during the HVI measurement process. Cotton Incorporated and the USDA (The U.S. Cotton Fiber Chart, 2011, 2012) consider a cotton sample to have “very low” elongation if its fiber elongation percentage measures below 5 % and “low” if the bundle measures below 5.8 %. A fiber bundle with an elongation of 5.9-6.7 % is considered “average,” while anything above 6.8 % is considered “high.”

Fiber elongation has been related to a number of other major and minor fiber traits. Many of these traits have various roles in fiber quality as they correlate to improving cotton fiber processing. Fiber work-to-break and yarn tenacity are just two traits that Hequet (2007) described in relation to fiber elongation. Fiber work-to-break describes the force required to break a bundle of fibers multiplied by the distance the fiber bundle stretches (elongates) before fiber breakage occurs, and tenacity describes the force exhibited immediately before the complete breakage of a yarn or bundle of fibers occurs. Hequet concluded that concentrated selection for improvement in areas of fiber elongation and fiber tenacity, together, could improve a cotton fiber’s work-to-break value. The growing importance of improvement in work-to-break is visible in today’s mills as they continue to increase rates of fiber processing. Increased processing speeds require cotton fiber that can withstand added pulling, and fibers with added work-to-break value could aid to reduce mechanical stoppage due to fiber breakage, which in turn maintains mill efficiency.

Fiori and Brown (1951) found that fiber fineness (related to maturity, now measured by micronaire) did not significantly affect yarn elongation. Orr, Weiss, and Grant (1955) concluded that both fiber (bundle) elongation and fiber (bundle) tenacity could be directly related to values for elongation and tenacity performed on a single cotton fiber by a stelometer. Fiori and Sands (1956), Hertel and Craven (1956), and Virgin and Wakeman (1956) also related fiber elongation and fiber tenacity to characteristics of spun yarn and concluded that fiber elongation was the primary factor that directly correlated to both yarn elongation and yarn tenacity. Fiori et al. (1956) support that yarn strength and elongation were found to be directly related for commercially grown short and medium staple cottons (staple refers to the length of a textile fiber or bundle of fibers), but the long staple and experimental strong-fibered cottons produced yarns whose strength was disproportionate to their elongation-at-break. Elongation is also often reported to have a negative correlation with extreme fiber length in upland cotton (Smith, personal communication, 2012). Though elongation may not have a direct role in the decision process for selection of varieties grown in the U.S., it nonetheless plays a vital role in the resulting quality of yarn that is produced by growers.

Fiber Micronaire (Maturity and Fineness)

Fiber micronaire is an indirect measurement of both fiber maturity and fiber fineness (Cotton Incorporated, 2013a). Relative to maturity and fineness, micronaire is defined via a complex equation which involves the division of fiber wall area (or thickness) by cross-sectional perimeter and is reported in arbitrary units of micronaire (Montalvo, 2005). It is measured with an instrument that forces air through a specified

mass of cotton fibers compressed to a specified volume, thus recording the air-flow permeability of the sample. This air flow is related to the cross sectional diameter of the sample fibers. The diameter and circularity of a cotton fiber has been confirmed as it relates to maturity (Wartelle et al., 1995; Matic-Leigh and Cauthen, 1994). Cross-sectional analysis performed on individual cotton fibers by Wartelle, Matic-Leigh, and Cauthen have shown to correlate with micronaire values reported by HVI, and confirmed this result.

Many factors can affect the maturity (and fineness) of cotton. Environmental conditions such as moisture, temperature, and amount of sunlight during fiber growth can affect fiber maturity. An immature fiber has a larger cross-sectional diameter (Matic-Leigh and Cauthen, 1994; Heap, 2000). These immature fibers lack secondary wall, i.e., cellulose deposition, development that results in a flat, ribbon shaped structure. Thus, a sample of immature fibers will compress in such a manner as to not allow as much forced air through its mass, resulting in a lower micronaire value (suggesting either finer fibers or immature fibers). A mature fiber sample will produce the opposite result. The majority of mature fibers will have reduced cross-sectional values because of their characteristic kidney bean shape rather than a flattened ribbon shape found in immature fibers. These fibers will not compress to form a “matted” structure and will allow more air through its compressed mass, thus resulting in a higher micronaire value (meaning coarser or more mature fibers). Micronaire values can be misleading as the difference in maturity between “coarse” and mature fibers could be significant, but the micronaire value reported does not present any more information and reflect this difference. The

same holds true for the difference between immature and “fine” fibers, thus making this a source of concern for error in the industry (Paudel et al., 2012; May, 1999; Gordon, 2007). Though micronaire (as measured by HVI) has the ability to be misleading, its value as an efficient high-throughput system of measurement for cotton fiber maturity and fineness cannot be matched at this time by alternative methods. Breeding for the optimum maturity level is also a complex process and cotton growers can be penalized at their local market for being both below the premium micronaire range and above the premium micronaire range. This range is seen as being the optimum micronaire values that allow for both the highest quality yarn and optimum cotton processing efficiency. The premium range (added selling value to cotton) set by the USDA-AMS (Cotton Incorporated, 2012) is between 3.7 and 4.2 units. A base (non-discount) range extends a little further being between 3.5 and 4.9 units, while anything reported below a micronaire value of 3.4 (very immature) and above 5.0 (very mature) is considered in the discount range. Fibers below a 3.4 micronaire value are known for poor spinning performance and poor dye uptake which is important for manufacturers, while samples typically reported above 5.0 are known for being too coarse and can only be used for larger yarns. Cotton with a 5.0 or above micronaire may slow processing due to increased friction. In a typical year, the micronaire range for upland cotton grown in the U.S. is between 3.0 and 5.5 (Cotton Incorporated, 2013c).

Fiber (Length) Uniformity

Fiber length uniformity is the ratio between mean length and UHML of fibers in a sample (Cotton Incorporated, 2013d), expressed as a percentage (mean length /

UHML) * 100. If the mean length and the upper half mean length of the sample were the same (meaning all the fibers in the sample were the same length) the uniformity index would be 100. However, there exists a natural variation in fiber length of all cotton fibers, which cause this value to always be less than 100.

Fiber length uniformity is known to be related to many yarn properties (Lacape et al., 2005). High length uniformity can contribute to increased processing speeds and efficiency. Lower values are known to be related to increased short fiber content (fibers shorter than 12.7 mm) and poor yarn quality due to lack of fiber evenness and low yarn strength (Hequet, personal communication, 2010; Hequet and Ethridge, 2000).

Lint Percent

Lint percent, although not measured by HVI, is a very important trait when observing genotypes and making germplasm selections. It is calculated as the value of the weight of lint (fibers) as a percentage of the total seed cotton weight (lint + seed) of a sample. For this study it was measured on a single plant basis. The goal for cotton breeders is to continue to select and breed for higher lint percent which potentially translates to increased yield of lint for growers.

The typical commercial cultivar in Texas ranges in lint percent from 35-45 %. These upland cultivars are known for high yields, but only produce average fiber quality. Lint yield potential is negatively associated with improved fiber properties (Smith and Coyle, 1997). Extra-long staple upland cotton cultivars usually have *G. barbadense* in their pedigree and are products of this same predicament. Although extra-long staple

cotton cultivars have added fiber quality and desirable traits like increased fiber length and strength, they are known to have substantially lower lint percent (Feaster and Turcotte, 1976; Hewolde et al., 1994). Percy et al. in 2006 continued to show that lint percent had an inverse relationship with both fiber length and strength when attempting to introgress fiber characteristics (like length and strength) from a population with a *G. barbadense* background into a standard *G. hirsutum* population. It has only been until recently that groups have made progress in breaking the antagonistic relationships within these two species of cotton hoping to incorporate them into commercial viability (Culp and Harrell, 1975; Smith et al., 2008).

Progress in improving lint percent in ELSU germplasm has been reported recently at Texas A&M AgriLife Research (Smith, 2003; Smith et al., 2008). Whereas most comparable material before the releases were in the range of 27.8- 29.4 %, the latest releases have reported lint percentages ranging anywhere from 32.1- 37.0 % (Culp and Harrell, 1977; Calhoun et al., 1997; Smith et al., 2009a). The ELSU material developed and released by Smith et al. (2008, 2009b) was developed from intraspecific crosses, i.e., upland X upland, whereas those reported by Culp and Harrell (1977) and Calhoun et al. (1997) resulted from interspecific crosses.

Increased yield and quality is necessary if the U.S. is to remain competitive in a global market. The complicated manipulation of genetics and gene interaction along with the antagonistic nature of many fiber traits are what have been making the

simultaneous improvement of multiple fiber properties so difficult (Culp et al., 1979; Culp, 1992; May et al., 1995).

Tools for Crop Improvement

Improvement

Crop improvement requires the ability to select higher-performing individuals from a population. Selection must be effective in improving crops, able to be completed quickly, and be able to cover large numbers of plants (Longenberger, 2005; Johnson, 1980). Plant breeders constantly improve and develop methods that allow them a greater number and more efficient opportunities to select desired plant phenotypes. These opportunities can range from a particular screening method to an entire breeding scheme. Time and resources are constant limiting factors to these processes. Nonetheless, enhancement to selection must persist as crop improvement continues to move forward.

Breeding schemes are important when dealing with both issues of time and resources. The correct breeding scheme can increase both selection opportunity and efficiency of resource use. Over time, breeders have developed a number of advanced breeding techniques to achieve this. The use of limited backcross breeding may increase the probability of accumulating positive (beneficial) alleles from selected parents while maintaining a level of heterozygosity for variability or selection potential for traits that may be under recessive gene action. For the purposes of this study, we hypothesized that selection opportunity was increased through one backcross to a desirable parent while at the same time maintaining levels of heterozygosity relative to a normal pedigree method

which is beneficial in keeping wanted variation within a segregating population. Meredith et al. (1977), Chee et al. (2005), Liu et al. (2000), and Lacape et al. (2005) have all used backcross breeding methods to make crop improvements in cotton. They have implemented improved fiber quality traits including fiber length and strength, while noting the benefits to using this method in increasing selection opportunity as well as transferring beneficial alleles to desired material.

Gene Action

There are many key factors that add difficulty to crop improvement in cotton. The ability to select higher performing individuals within the impact of environment and agronomic practices adds complexity (as their relationship can mask plant performance) to the absolute and many genetic factors. The fact that most cotton fiber quality traits are quantitative adds a level of complexity to cotton fiber quality improvement. These traits can have a number of beneficial alleles, unlikely contained in one individual, requiring careful selection of parentage and large progeny populations. Linkage also complicates things as they can be difficult to break, preventing simultaneous selection for multiple traits. Epistasis also exists with cotton germplasm. Epistasis can be present in the expression of one gene that is affected or manipulated by the allelic sequence at another locus within germplasm. And finally, pleiotropy, where one gene affects the expression of more than one trait, may complicate the selection process. Each of these genetic factors can contribute to less efficient crop improvement (Green and Culp, 1990; Miller and Rawlings, 1967; Liu et al., 2000; Shen et al., 2006b).

Heritability

The likelihood of improvement is determined by the amount and type of genetic control of a trait (Braden, 2005). Broad-sense heritability is the ratio of genetic variance to phenotypic variance while narrow-sense heritability is the relationship of additive genetic variance to total phenotypic variance (Fehr, 1991). These values directly reflect the difficulty in improving a trait, as highly-heritable traits are easier to improve in comparison to lowly-heritable traits. Heritability values are reported between values of 0.00-1.00, where the closer to a value of 1.00 reflects the ease of genetic transfer from one set of material to another. Values being significantly different between broad and narrow-sense heritability estimates can also reflect the best method in which a breeder should seek to arrive at their desired phenotype (result). A large narrow-sense heritability value suggests additive variance has a considerable affect upon potential genetic gain and that breeders should be able to quickly improve the trait in question via selection through pedigree-type methods. High values of broad-sense heritability estimates coupled with low narrow-sense values reflect high amounts of non-additive genetic variance which suggest that crop improvement would be better improved via alternate methods of breeding. These values can be an important factor for breeders looking to improve cotton quality in one specific area or another.

Most fiber traits in cotton, although quantitative, are highly heritable with large amounts of additive variance. This allows breeders to continually make progress in fiber quality, within the limits of parental variation, through standard pedigree selection. Fiber

quality traits are primarily transferred into desired material relatively quickly and trait performance can be passed on through multiple generations.

Narrow-sense heritability estimates from eight experiments for 2.5 % span length (a variant of UHML) ranged from 0.10 to 1.00, with an average of 0.52. Broad-sense heritability estimates from four experiments for 2.5 % span length ranged from 0.54 to 0.91, averaging 0.77 (May, 1999). From these results May (1999) stated that selection for various length characteristics in cotton should be effective. Herring in 2005 reported a narrow-sense heritability range from 0.29 to 0.46 for UHML of a Paymaster parental background population, thus agreeing with May (1999). Kohel et al. (2001) and Bayles et al. (2005) also monitored heritability values of multiple traits through several generations and found improvement could be achieved through selection. Other results indicated that mating excellent fiber quality parents with lesser quality parents, also reported similar heritability estimates for traits suggesting that improvement could be achieved through back-cross and pedigree-type breeding methods in cotton (May and Jividen, 1999).

Genetics

As mentioned earlier, most current cultivars of cotton grown around the world today are tetraploid ($4x= 52$) species (Brubaker et al., 1999). The most common two species in cultivation, *G. hirsutum* and *G. barbadense*, are allotetraploid species. Diploid species in cotton were not known for their excessive amounts of lint production or high seed set. They are adapted to their region of origin, and known for hardiness in a range

of conditions. *G. herbaceum* is a diploid ($2n= 26$) species of cotton native to Africa and Asia. It is considered an “old world” species of cotton consisting of the “A” genomic group (genome) of the *Gossypium* genus. *G. raimondii* is another diploid ($2n= 26$) species of cotton and is considered a “new world” species native to Central and South America. It comprises the “D” genomic group (genome) of *Gossypium*. With the hybridization of these two species approximately 6000 years ago (Wendel and Cronn, 2003; Fryxell, 1979a; Smith, 1995; Moulherat et al., 2002), resulted in a new, improved, and highly stable species of cotton consisting of four complete sets of genetic material (genomes). This species combined both the “new” and “old” world genomes of *herbaceum* and *raimondii*, being known as an allotetraploid, and consisted of 52 chromosomes ($2n= 52$) (Office of Gene Technology of Australia, 2008).

Beasley was one of the first to report on another successful tetraploid hybridization in 1940, and since then many have continued to explore this unique area in hopes of unlocking additional useful variation (Zhang et al., 2002). Recent technological advancement has produced a new generation of breeding and selection techniques that takes place within a lab setting accompanying traditional field-based techniques. Genetic markers are being used to monitor gene movement through populations and generations. Patterson et al. in 1993 developed a quick and consistent method for extracting genomic data in cotton aided with PCR or RFLP analysis. Other groups have conducted similar work in this area and continue to improve marker systems making genetic work more reliable and useful for breeding (Han et al., 2006; Rungis et al., 2005). Shen et al. (2004) and Jiang et al. (1998) supported that continued genetic study and improving

biotechnology promise to provide powerful tools for enhanced genetic improvement in the future of cotton breeding.

The current issue for upland cotton, however, is its lack of a wide genetic base. Meredith in 1991 believed that many current, successful cultivars of cotton were closely related in parentage and continued in 1997 to state that a push for an expanded genetic base was needed. Closed gene pools and frequent market domination by a few cultivars further promotes a narrow base. Genetic base has been a constant issue for other crops as well and has been exacerbated by GMO's. Tanksley and McCouch (1997) report instances where this issue has caused problems in large sets of uniform material spread over large expanses of land-area. This homogenous material has the potential to cause problems through exposed weaknesses in the material itself and thus to the industry relying on that material. Variation would not only work to prevent scenarios like those, but variation is what also allows progress to be made through selection. The USDA (1994) contains multiple landrace accessions with widely unique genetic backgrounds for use in any breeding program. Stores like these can aide to combat this issue, and can help in continuing to unlock improved yield and fiber quality in cotton.

Transgressive Segregation

Although seen as a form of gene action, transgressive segregation plays an important role for plant breeders and for the purposes of this study. The art of plant breeding since its beginning has been due to the ability to select those individual plants that can outperform their peers. Transgressive segregation is defined by deVicente and

Tanksley (1993) as the appearance of individuals in a segregating population that fall beyond their parental phenotypes. Others consider just a deviation from the mid-parent average value of the two parents enough for transgressive segregation (Braden and Smith, 2004a). Progeny capable of outperforming parental lines has been essential to improving agricultural productivity. Transgressive segregation has been important in its improvement for multiple fiber traits and increasing overall yield and quality. Traits for resistance to parasitic nematode by Wang, Uloa, and Roberts in 2007; resistance to root-knot nematode by Goodell and Montez in 1994; verticillium wilt resistance by Bolek et al. in 2005; and fusarium wilt resistance by Wang and Roberts in 2006 have all resulted from transgressive segregation. Interspecific crosses and populations have been reported for cotton and other crops as a source for higher rates of this phenomenon (Kohel et al., 2001; deVicente and Tanksley, 1993). Evidence exists to support that transgressive segregation in cotton could be used to improve both fiber quality and yield of *hirsutum* by *hirsutum* and *hirsutum* by *barbadense* populations in the U.S. (El-Aid and Miller, 1970; Kohel et al., 2001).

Transgressive segregation can be caused by any number of factors. It is thought of many times as appearing in generations beyond the scope of normal heterotic behavior by progeny which are found in the F₁ and F₂ generations (Smith, 1952; Williams, 1959). Groups have speculated and reported that this phenomenon has been due to multiple genetic factors involving recombination of additive alleles, complementary genes, previously masked alleles, epistatic interactions, overdominance caused by heterozygosity at specific loci, and even mutation (Bell and Travis, 2005;

Rieseberg et al., 1999). A novel combination of alleles in progeny due to the result of parental crossing always carries endless opportunity for beneficial results. This unpredictable part of breeding is what continues to prompt plant breeders and scientists to continue to try new combinations of parents in the hopes of a new and improved result. Transgressive segregation rates for the families contained herein could indicate possible selection pressure for extra-long fiber length could be applied even when one parent is not of that type, being short or medium staple in length.

Previous Work by Braden and Smith

Development of Extra-Long Staple Upland Material

The development of improved extra-long staple upland (ELSU) cotton types has more recently played a larger role toward the approach of improving fiber quality. It has also played a major role in a number of studies, including the outline of this study, at Texas A&M University. Extra-long upland cotton types are any predominantly upland cotton variety that consistently reaches into a fiber length of 1.26 inches (32mm) or above (Cotton Incorporated, 2007). These improved upland types are a major positive breakthrough for U.S. breeders and have the potential to be a primary possibility for incorporating cotton fiber length and quality improvement.

Since efforts were first reported in the 1860s, attempts to achieve improved fiber quality coupled with high levels of yield potential were made, largely unsuccessfully, through the hybridization of *G. hirsutum* with *G. barbadense* (Smith et al., 1999). However, there were a few successful *G. hirsutum* and *G. hirsutum* by *G. barbadense*

accessions that do exist in the USDA-ARS (2008) National Plant Germplasm Collection and reported in GRIN (Germplasm Resources Information Network). “Ewing Long Staple x Tidewater” (PI 528726) and “Sealand” (PI 528727) are listed as *G. hirsutum* (meaning a majority of the ancestry of this material is of *G. hirsutum* decent) with lengths reported of 35.8 and 36 mm, respectively. “Spears Upland Early Long Staple” (PI 529043) also is reported to have UHML over 35 mm (Smith et al., 2008). Accessions containing larger amounts of *G. barbadense* lineage (enough to be listed as such) are “Bleak Hall” and “Coker Wilds” with fiber lengths reported at the 51-64 mm and 38 mm levels, respectively (Calhoun et al., 1997). Other programs have also been successful in introgressing *G. barbadense*'s characteristics within that of *G. hirsutum* (Culp and Harrell, 1977).

A major drawback to early high fiber quality materials that hindered their development was poor lint percent, which in turn correlated to poor yield. This relationship between low lint percent and poor yield limited the above cultivars' desirability due to the fact that, although they contained desirable fiber traits and properties, they also caused a significant decline in yield. In order to produce progeny that contained positive trait expression from both parents (*G. hirsutum* and *G. barbadense*), more extensive breeding had to be done, equaling more time and resources for the breeder.

A milestone was achieved when Smith et al. (2009b) released ELSU lines that were much higher in lint percent and yield potential than previously available. This

achievement allowed cotton breeders to utilize the positive genetics of fiber quality that the ELSU lines could potentially add to other germplasm, as well as not sacrifice so much in yield potential. The new lines had the potential to be used directly as viable sources of parentage for programs looking to improve fiber quality (specifically fiber length and strength).

The key difference between Smith et al. (2009b) and previous releases was in the ancestry of the material. Smith accomplished the increased levels of lint percent and yield potential by making multiple inter-mating crosses and using only upland parentage. This strategy allowed his releases to achieve 8-11 % higher lint percent than previously reported in earlier ELSU releases. These early ELSU materials reported values ranging in lint percent between 27.8 % and 29.4 % . Smith's group in 2008 reported values of lint percent in their material releases of consistently 34.0 and above (as high as 37.0 %). This significant increase puts them on par to being similar to many short and medium staple, high yielding cultivars that are commercially in production and in use today.

The improved ELSU germplasm lines were released by Texas A&M in 2009. These eight ELSU germplasm lines were all developed using a common parent, TAM 94L-25 (Smith, 2003), which is a near-long staple germplasm release also by Smith. This parent was seen as containing proper potential to increase fiber quality traits for Texas A&M's Cotton Improvement Program. This common parent was coupled with other germplasm releases (TAM 94WE-37s, TAM 95BB-54s, PD 6992, GA 161, TAM 92Z-32-1, TAM 88F-28, TAM 90M-8, TAM 89E-51) from Texas A&M and other

programs that were seen to have similar potential to produce progeny with properties that would merit ELSU line nomenclature. Smith attributes the increase in fiber length of his ELSU lines to TAM 94L-25's superb general combining ability. The germplasm can be characterized as having increased fiber length and fiber bundle strength although yield potential is not equal to lower quality commercial cultivars at the time. Fiber length for the eight released lines all reached levels higher than 1.26 inches (32 mm) while a few even reached into levels of 1.375 inches (34.8 mm) and higher. Fiber UHML of 1.375 inches (34.8 mm) or higher constitutes a level equal to pima or ELSU designation. Fiber bundle strength was also improved for these releases, generally above 320 kN m kg⁻¹, 15 % higher than commercial cultivars at the time, which averaged a strength of 278 kN m kg⁻¹. These ELSU lines maintained normal ranges within upland cotton for all other fiber traits (measurable by HVI). This fiber length increase and 15 % strength increase improves not only fiber and yarn quality, but they also improve processing speed and efficiency (Smith et al., 2008). Joy et al. confirmed this conclusion by reporting in a study published in 2010 that these ELSU lines produced stronger carded 11.8 tex, ring-spun yarns than a leading commercial check. They also showed better yarn elongation and hairiness. These germplasm lines have the potential to be a donor for improved fiber quality and Smith suggested that they should provide public and private breeders with the potential to produce ELSU upland cultivars (Smith et al., 2009b).

Smith and Braden (2004a) investigated the length of time, or boll maturation period, of TAM 94L-25, having longer UHML than other upland cultivars, compared with short or medium UHML cultivars in an attempt to explain how this unique

germplasm arrived at its extended fiber length. The investigators reported that ELSU germplasm lines were comparable to commercial uplands in most aspects of growth rate and rate of maturity for both boll and fiber development. The ELSU lines produce fruit (bolls) very similarly to other upland cotton types, achieving averages of approximately three days in vertical boll appearance dates and approximately six days between horizontal boll appearance dates. Smith's lines also were not significantly different in date or rate of fruit (boll) appearance in comparison to other upland material.

There were, however, a few key differences. The first major difference is the average daily growth rate of cotton fiber for the new ELSU germplasm. For the extra-long staple upland germplasm the average daily growth rate is higher than for short and medium staple upland material. This allows the ELSU material to grow longer fiber lengths in essentially the same amount of time as other upland material achieves their shorter fiber lengths. Even with this occurrence, however, the boll maturation period of TAM 94L-25 was greater than for medium UHML cultivars included in the study, suggesting that the extra length required extra time to develop. Braden and Smith (2004) reported that TAM 94L-25 required 3-6 extra days for boll maturation than their comparison cultivars. Smith also reported later (Smith et al., 2008) that ELSU upland material required two extra weeks to fully mature in comparison with commercially viable upland material currently.

With such few differences separating the two sets of germplasm, there are not a large number of factors deterring the successful use of ELSU upland material to achieve

added fiber quality (specifically through increased length and strength) for any breeding program. Genetic contributions by this material to progeny will be closely monitored as the ELSU upland trait plays a large role in the study held within this thesis. Added fiber quality is a key to keeping a competitive edge in the global textile market, and increasing Texas and American cotton fiber length and strength through the use or selection of extra-long staple upland cotton lines is one possible way to do it.

Braden and Smith and leading up to this Study

The previous sections on transgressive segregation and the development of the ELSU upland material are the basis for the study reported herein. Much of the focus on this study is due to what has previously been found by Dr. Wayne Smith and multiple graduate students in the past (Chris Braden and Kolbyn Joy). Braden (2005) performed a study with similar populations for near-long staple fiber length (near-long x near-long parentage vs. near-long x short parentage) and reported similar rates of transgressive segregation for longer fiber in each population. Braden et al. concluded that for long fiber length, two near-long fiber parents were not needed in order to produce a population in which selection for transgressive progeny with long fiber expression appeared. Other groups, one in cooperation with Texas A&M University, have also observed similar transgressive segregation rates in differing populations of cotton and other crops (deVicente and Tanksley, 1993; Fabrizius et al., 1998).

Developing methods in order to more easily produce and identify these positive outliers (transgressive segregates) could alter the emphasis of a cotton improvement

(breeding) program. Hopefully this will give an indication of where more time and resources for Texas and U.S. cotton improvement should be placed in the future.

MATERIALS AND METHODS

Population Development and Background

Parents for this study were selected based on agronomic performance, HVI fiber properties, especially UHML and fiber bundle strength, and pedigree. Upland genotypes selected for use in this study were Tamcot 22 (Thaxton and Smith, 2004) (PI 635877), TAM B 182-33 ELSU (Smith et al., 2009b) (PI 654362), 06 WE 62-4 HS (high strength), and 04 SID 84-2 ISH (interspecific hybrid).

Multiple parental combinations and generations of these genotypes were created using a generation means analysis breeding scheme by Kolbyn Joy (2010), former graduate student of Dr. Wayne Smith. Generations used in this study were the BC₁F₂ and F₃ generations of the following parental combinations.

Family 1: Tamcot 22 / 06 WE 62-4 HS (Upland x Upland High Strength)

F₃: Tamcot 22 / 06 WE 62-4 HS

BC₁P₁F₂: Tamcot 22 / 06 WE 62-4 HS // 06 WE 62-4 HS

BC₁P₂F₂: Tamcot 22 / 06 WE 62-4 HS // Tamcot 22

Family 2: Tamcot 22 / 04 SID 84-2 ISH (Upland x *G. barbadense* Biotype Sea Island)

F₃: Tamcot 22 / 04 SID 84-2 ISH

BC₁P₁F₂: Tamcot 22 / 04 SID 84-2 ISH // 04 SID 84-2 ISH

BC₁P₂F₂: Tamcot 22 / 04 SID 84-2 ISH // Tamcot 22

Family 3: Tamcot 22 / TAM B 182-33 ELSU (Upland x Upland Extra-Long Staple)

F₃: Tamcot 22 / TAM B 182-33 ELSU

BC₁P₁F₂: Tamcot 22 / TAM B 182-33 ELSU // TAM B 182-33 ELSU

BC₁P₂F₂: Tamcot 22 / TAM B 182-33 ELSU // Tamcot 22

Abbreviated Pedigree and Description of Parental Genotypes

Tamcot 22: Developed by the Texas A&M AgriLife Research Cotton Improvement Program and released in 2004. Both parents were experimental breeding lines developed by Texas A&M AgriLife Research. It was developed for production in central and south Texas and is most similar to ‘Deltapine 50’ (PVP 8400154) when grown under irrigated conditions. Tamcot 22 can be characterized as having average fiber quality with medium staple fiber length. It has a reported lint percent value of 40 and high yield potential, outperforming both ‘Sure-Grow 125’ (Calhoun et al., 1994; PVP 9400063) and ‘FiberMax 832’ (Constable et al., 2001; PVP 200500137) in a number of trials reported in its release (Thaxton and Smith, 2004; PI 635877). Its use in this study is to try and capture increased yield potential in progeny resulting from its cross.

06 WE 62-4 HS: An experimental breeding line developed by Texas A&M Cotton Improvement Program. It was developed from a double cross involving four parents, Deltapine 491/TAM 96 WD-18 (PI 635879; Thaxton and Smith, 2005)//TAM

91C-95Ls (PI 614952; Smith, 2001)/ 'Deltapine Acala 90' (PVP 8100143). This breeding line has improved fiber bundle strength, thus producing improved yarn quality. Smith et al. (2009a) reported that 06 WE 62-4 HS was ring spun into 30Ne count yarns with 30 % higher yarn tenacity than either FiberMax 832 or Deltapine 491. It also averaged 22 % greater fiber bundle strength and required 33 % more energy to break yarn spun using the line over these two commercial checks. In Weslaco, Texas in 2009, 06 WE 62-4 HS exhibited a fiber bundle strength of 38.2 g tex⁻¹ under irrigated conditions. This line has slightly longer upper-half mean fiber length and slightly finer fibers than Deltapine 491 and FiberMax 832.

04 SID 84-2 ISH: Developed by the Texas A&M University Cotton

Improvement Program as an experimental line to contribute novel, unique combinations of alleles to germplasm within the program. It is the result of a cross between TAM 94L-25 and New Mexico Sea Island 1331 (Roberts et al., 1997). This sea island biotype exhibits cotton fiber quality characteristic of genotypes within the species *G. barbadense*. 04 SID 84-2 ISH was developed in an effort to capture both improved fiber quality, especially UHML and fiber bundle strength from the *G. barbadense* parent, and the yield characteristics and yield stability of the *G. hirsutum* parent. This line was a successful interspecific cross, and is reported by Joy et al. (2011) as possessing the extra-long staple fiber length trait as well as improved fiber strength. Its use in this study is to capture these traits in progeny resulting from this cross as well as to influence transgressive segregation rates, known to be increased as the result of interspecific crossing (de Viscente and Tanksley, 1993; Kohel et al., 2001).

TAM B 182-33 ELSU: Developed by the Texas A&M University Cotton Improvement Program and released in 2009. It was the product of a cross between TAM 94L-25 (Smith, 2003) and GA 161 (PI 612959; PVP 200000149). TAM 94L-25 has a complex ancestry, but contains possible genotypic and phenotypic influence from distant *G. barbadense* lineage. TAM B 182-33 ELSU achieves extra-long staple fiber length and improved yarn quality relative to current upland cotton cultivars with the potential for production in Texas (Smith et al., 2009b). Joy et al. (2010) reported that TAM B 182-33 ELSU exhibited the highest quality cotton fiber and produced the highest quality yarn based on HVI, AFIS, and spinning data, compared with FiberMax 832. It yields consistently higher among similar germplasm lines released at the same time in 2009 and commonly above the lowest commercial check, ‘Deltapine 491’ (PVP 200100159). Smith et al. designated this germplasm line, and similar quality lines, as ELSU because it produces fiber with UHML equal to the minimum classing requirements of pima cotton.

Experimental Design

The three upland cotton families and generations included in this study were propagated in College Station, Texas in the summer of 2011 and 2012.

The experimental design was a randomized complete block design with four replications. Rows within plots were 1 m x 12.8 m. There were ten rows of each segregating generation ($BC_1P_1F_2$, $BC_1P_2F_2$, and F_3) and two rows of each parental generation in each replication. Replications contained all three families, which were randomized, and generations within families were also randomized. Entries were planted

28 April 2011 and 09 May 2012 and normal cultural practices for south-central Texas were performed throughout the growing season, including regular spraying for weed and insect pests, and furrow irrigation. The soil type was a Weswood silt loam, a fine-silty, mixed thermic Fluventic Ustochrept, integrated with a Ships clay that is a very fine, mixed, thermic Udic Chromustert.

Plants within each plot were thinned after establishment to a spacing of 35-45 cm to minimize interplant competition. At maturity, individual plants were selected at random and hand harvested. Populations' numbers were established large enough to ensure random selection. However, visual preference was imposed to guarantee selecting plants that produced enough cotton lint for HVI testing. Fiber collected from a single plant was stored in individual paper sacks until processing. Twenty-five plants were selected in each replication of each segregating generation ($BC_1P_1F_2$, $BC_1P_2F_2$, and F_3) of the three families, while three plants were selected for each parent of the three families in each replication.

After hand harvest, each plant was ginned separately on a 10-saw laboratory gin without a lint cleaner. Care was taken to maintain each individual sample's purity during the process, and all fiber samples were sent to the Fiber and Bio-Polymer Research Institute (FBRI) in Lubbock, Texas for fiber testing. HVI analysis was performed on each sample, and statistical analysis was conducted with SAS 9.3 (SAS Institute; Cary, NC, 2012).

Analysis of variance for phenological means among generations, families, and years was run to determine significant relationships. Repetitions were combined and two-way analysis of variance was run to determine significant differences among generations and families for number of transgressive segregates and was constructed using year as replication and error control. A t-test statistic was used to separate mean number of transgressive segregates across generations within families and years for discussion purposes but otherwise the following discussion will focus on absolute numbers regarding transgressive segregates.

Detailed Growing Conditions Each Year

The 2011 growing season consisted of a number of complications. Beginning at planting, poor seed quality coupled with harsh planting conditions led to extremely low plant population numbers. Seedling vigor was below the projected level, and dry seed beds at planting led to the need for irrigation immediately after planting. This action, however, produced a hardened crust on the surface of the soil (as the applied moisture evaporated) and prevented many successfully germinated seeds from breaking through the soil surface. Three subsequent re-plants (and individual seedling moisture application) by hand were performed in order to achieve sufficient plant populations for the desired level of selection in all generations. This setback at planting was the source of future spray application issues due to the later maturity date of my study compared to the neighboring cotton crops. Late season issues common to South- Central Texas also came into play, possibly affecting cotton fiber quality.

The summer of 2011 was also characterized by extremely high temperature levels and very low levels of moisture that persisted through the duration of the cotton growing season (Table 1). From 1 May- 31 August, only one significant rain event, i.e., equal to or greater than 1.27 cm, occurred on 22 June when just over 5 cm of precipitation occurred. June, July, and August are consistently the three hottest months at College Station, TX and in 2011,- high temperature consistently was above 35 C in June and July, while in August only two days were below the 38.8 C (noaa.gov and climatexas.tamu.edu, 2013).

Table 1. Weather data for College Station, Texas in July of 2011.

Jul-11

Day	Daily Temperature			Total	Daily Precipitation Monthly Temperature Summary		
	Maximum	Minimum	*Departure		Mean	Value	*Departure
1	37°C	25°C	+2°C		Maximum	38°C	+2°C
2	37°C	24°C	+2°C		Minimum	25°C	+2°C
3	37°C	24°C	+2°C		Average	31°C	+2°C
4	37°C	24°C	+2°C		Degree Days	Total	*Departure
5	37°C	24°C	+1°C		Heating	0	0
6	37°C	23°C	+1°C		Cooling	737	130
7	37°C	23°C	+1°C		Number of Days:	Total	*Departure
8	38°C	24°C	+2°C		Maximum $\geq 32^\circ\text{C}$	31	4
9	37°C	26°C	+3°C		Maximum $\leq 0^\circ\text{C}$	0	0
10	38°C	24°C	+2°C		Minimum $\leq 0^\circ\text{C}$	0	0
11	38°C	25°C	+3°C		Monthly Precipitation Summary		
12	38°C	26°C	+3°C		Precipitation	Value	*Departure
13	38°C	26°C	+2°C		Monthly Total	0.30 cm	-4.62 cm
14	38°C	25°C	+2°C		Year-to-date Total	27.05 cm	-30.10 cm
15	39°C	26°C	+3°C	0.18 cm	Days ≥ 0.03 cm		2-3
16	35°C	26°C	+1°C	0.08 cm	Monthly Extremes		
17	38°C	25°C	+2°C		Extreme	Value	Date(s)
18	37°C	27°C	+2°C		Highest Temperature	39°C	9 times
19	33°C	26°C	0°C		Lowest Temperature	23°C	7th
20	37°C	25°C	+2°C		Max. 24-hour Precip.	0.25 cm	15th-16th
21	38°C	25°C	+2°C		Maximum Wind Gust	60 kph	2nd
22	38°C	26°C	+2°C				
23	39°C	25°C	+3°C				
24	39°C	24°C	+2°C				
25	39°C	26°C	+3°C				
26	39°C	26°C	+3°C				
27	39°C	26°C	+3°C				
28	39°C	27°C	+3°C				
29	37°C	26°C	+2°C				
30	39°C	26°C	+3°C				
31	39°C	23°C	+2°C				

Source: noaa.gov (2013)

Much of the effects of these harsh conditions in 2011 were offset with supplemental irrigation on a regular basis, but it was still visually apparent that the cotton crop was under high levels of stress during this time. During periods when the supplemental irrigation (shared with other research programs with experiments at the Texas A&M AgriLife Research Farm) was in high demand, these cotton plots were forced to go extended periods without sufficient moisture, thus affecting its growth and production potential. In summary, environmental stress levels were significant for this year.

The 2012 growing season (Table 2) was much more mild and, in many ways, opposite of the conditions in 2011. It can be characterized as “mild” in both temperature and stress level for the cotton crop of this year. Seedling vigor proved to be much higher and plant populations were established with the initial planting. Rain events were steady and often throughout the summer months of 2012, with nine significant rain events occurring in June, July, and August alone (and many smaller events occurring throughout). Higher levels of moisture are known to correlate with higher levels of disease and insect pressure, but such stress levels for this crop never appeared to achieve a significant level. Temperatures were noticeably lower as well this year as June and July contained multiple days where temperatures were within a range of 26.6-31.6 C and only reached temperatures higher than 34.4 C less than 50 % of the time. August, the hottest month of 2012, had high temperatures above 37.7 C 12 times, but never above the 38.8 C exhibited in 2011.

Table 2. Weather data for College Station, Texas in July of 2012.

Jul-12

Day	Daily Temperature			Daily Precipitation Total	Monthly Temperature Summary		
	Maximum	Minimum	*Departure		Mean	Value	*Departure
1	32°C	23°C	-1°C	0.64 cm	Maximum	35°C	-0.2°C
2	35°C	24°C	+1°C		Minimum	24°C	+0.3°C
3	34°C	24°C	0°C		Average	29°C	+0.1°C
4	36°C	24°C	+1°C		Degree Days	Total	*Departure
5	36°C	23°C	+1°C		Heating	0	0
6	37°C	23°C	+1°C		Cooling	622	11
7	36°C	24°C	+1°C		Number of Days:	Total	*Departure
8	33°C	25°C	0°C	0.13 cm	Maximum ≥ 32°C	27	-1
9	35°C	22°C	0°C	1.68 cm	Maximum ≤ 0°C	0	0
10	30°C	23°C	-2°C	2.29 cm	Minimum ≤ 0°C	0	0
11	28°C	23°C	-4°C	0.08 cm	Monthly Precipitation Summary		
12	31°C	24°C	-2°C	0.08 cm	Precipitation	Value	*Departure
13	33°C	23°C	-2°C	4.67 cm	Monthly Total	11.58 cm	+6.15 cm
14	34°C	24°C	0°C		Year-to-date Total	75.79 cm	+17.78 cm
15	33°C	23°C	-2°C	0.33 cm	Days ≥ 0.03 cm	11	5
16	34°C	22°C	-1°C		Monthly Extremes		
17	33°C	24°C	-1°C	0.81 cm	Extreme	Value	Date(s)
18	34°C	23°C	-1°C	0.20 cm	Highest Temperature	38°C	29th
19	36°C	24°C	+1°C		Lowest Temperature	22°C	9th, 16th
20	36°C	26°C	+1°C		Max. 24-hour Precip.	4.67 cm	12th-13th
21	37°C	25°C	+2°C		Maximum Wind Gust	71 kph	13th
22	34°C	26°C	+1°C				
23	34°C	24°C	0°C				
24	36°C	24°C	+1°C	0.69 cm			
25	36°C	25°C	+1°C				
26	36°C	25°C	+1°C				
27	36°C	24°C	+1°C				
28	37°C	24°C	+1°C				
29	38°C	24°C	+2°C				
30	37°C	24°C	+1°C				
31	38°C	25°C	+2°C				

Source: noaa.gov (2013)

Rationale for Transgressive Segregation and Selection Methodology

The three families in this study included a common medium staple upland parent, Tamcot 22, crossed to three distinct genotypes. As noted above, TAM B 182-33 ELSU is reported (Smith et al., 2009b) to produce UHML equal to pima cotton, 06 WE 62-4 HS produces fibers with exceptional fiber bundle strength (Gregory et al., 2012), and 04 SID 84-2 ISH is descended from a *G. hirsutum* / *G. barbadense* cross and exhibits UHML equal to or approaching pima cotton plus improved fiber bundle strength (Smith, personal communication, 2013). The distinct pedigrees and HVI fiber properties of these parents provided an opportunity to determine transgressive segregation and determine the impact of a single backcross on HVI fiber properties and recovery of transgressive segregates for fiber quality, especially length and strength. Opportunities for improvement (through identification and selection of transgressive phenotypes) between and within families could dictate possible breeding emphasis for the future of cotton breeding.

Mendelian genetics suggests that the BC₁F₂ and F₃ generations should still be segregating populations. If a trait such as fiber length is treated like a simply inherited, diploid trait, then segregation rates within these generations should be predictable. Within both the BC₁F₂ and F₃ generations, the level of heterozygosity should be equal for both generations. However, the average fiber length of the back-crossed populations should be closer to the mean of the trait in the recurrent parent. The BC₁F₂ and F₃ generations theoretically have the same frequency of heterozygosity for an individual gene, assuming normal diploid segregation, no linkage, and no epistasis. The BC₁F₂,

however, should have a higher frequency of the allelic condition of the recurrent parent. Thus, for a generalized gene, A, the frequencies in the F₃ following the cross of AA and aa would be 0.375 AA : 0.25 Aa : 0.375 aa while the BC₁F₂(parent AA) would be 0.625 AA : 0.25 Aa : 0.125 aa.

Smith and Braden (2008) reported essentially equal rates of transgressive segregates for long fiber length in two diverse crosses (long staple upland / long staple upland versus a long staple upland / short staple upland). Their finding has potentially significant implications as transgressive segregation rates for these populations could indicate that selection pressure for fiber length could be applied for extra-long staple fiber length even when one parent is a high yielding, short or medium staple type.

Special emphasis on selection will also take place for those genotypes which produce exceptional progeny in the areas of fiber length and fiber strength. Specifically for fiber length, progeny reaching UHML designation of ELSU (32.00 mm) or higher will be specifically monitored for selection with potential to contribute to increased fiber length. Fiber strength will also be closely monitored for progeny produced that exhibit strength values above 30 g tex⁻¹. Progeny that exhibit both exceptional fiber length and fiber strength will be further analyzed for possible selection and breeding value potential.

RESULTS AND DISCUSSION

This study was conducted to observe fiber trait performance and instances of transgressive segregation for improved fiber strength and ELSU fiber length in three families of upland cotton developed by the Texas A&M AgriLife Research Cotton Improvement Lab. The ANOVA indicated that with the exception of uniformity and strength, all other HVI fiber properties varied significantly across Years, Families, and/or Generations (Table 3). Many of the interaction terms in the ANOVA also were significant; significant Family x Year interactions occurred for micronaire, uniformity and strength; Generation x year interactions were observed for micronaire and elongation; and Generations x Family interactions were present for all HVI fiber properties except uniformity. The finding that Family x Year and Generations x Year sources of variation were not significant for all fiber properties suggest that irrigation was a successful management practice to mediate the drought and heat environment of 2011 and/or that fiber properties are stable across environments.

Trends of significance also appeared in Table 4 which contained the mean squares for lint yield and lint percent. ANOVA for these two characteristics also indicated significant variation across Years, Families, and Generations. Interaction terms for Families indicated that they responded differently to Years for lint yield but not for lint percent. Generations exhibited significance for all interaction terms for both lint yield and lint percent including Generations x Year, Generations x Family, and Generations x Year x Family.

Table 3. Mean squares for HVI† fiber properties across three upland cotton families and five generations (P₁, P₂, F₃, BC₁P₁F₂, and BC₁P₂F₂) when grown at College Station, TX in 2011 and 2012.

Source of Variation	df	Mic.‡	UHML	Unif.	Strength	Elong.
Year (Y)	1	23.72 **	350.97 **	4.6	341.2 **	6.61 *
Error A	6	1.14	30.32	2.4	2.0	1.07
Family (F)	2	9.49 **	295.48 **	39.1 **	5.7	31.39 **
F x Y	2	3.60 **	0.65	27.9 **	73.5 **	1.28
Error B	12	0.78	3.23	3.3	5.2	0.39
Generation (G)	4	13.32 **	614.84 **	273.4 **	1431.9 **	22.07 **
G x Y	4	7.84 **	11.61	2.6	18.8	2.72 **
G x F	8	4.81 **	68.39 **	9.3	49.7 **	7.24 **
G x Y x F	8	2.62 **	1.94	3.2	21.6	1.56 **
Error C	71	0.52	5.16	5.4	12.2	0.39

† HVI= High Volume Instrument.

* , ** Significant at p< 0.05 and 0.01, respectively.

‡ Mic.= Micronaire; UHML= Upper- Half Mean Length; Unif.= Uniformity; Elong.= Elongation.

Table 4. Mean squares for lint yield and lint percent across three upland cotton families and five generations (P₁, P₂, F₃, BC₁P₁F₂, and BC₁P₂F₂) when grown at College Station, TX in 2011 and 2012.

Source of Variation	df	Lint Yield	Lint Percent
Year (Y)	1	14516.97 **	103.36 **
Error A	6	1139.41	42.29
Family (F)	2	8591.15 **	1584.99 **
F x Y	2	5583.01 **	33.43
Error B	12	728.4	10.02
Generation (G)	4	6081.72 **	1086.99 **
G x Y	4	920.52 **	227.81 **
G x F	8	2751.37 **	308.41 **
G x Y x F	8	1035.04 **	100.71 **
Error C	71	611.98	27.57

*, ** Significant at the $p < 0.05$ and 0.01 , respectively.

Agronomic and HVI Fiber Properties

The goal of this study was to determine and identify transgressive segregation for fiber properties, particularly improved fiber bundle strength and length and to evaluate the backcross breeding scheme as a tool in increasing the frequency of transgressive segregates. However, the general fiber attributes of these families and generations are of interest as breeding populations and thus discussed below. The many significant interactions shown in Tables 3 and 4 mandates presenting the data in multiple tables in order to properly discuss through statistics. Higher, or lower in the case of micronaire, means may be indicative of parental combinations or generations that would be of interest to a breeder for developing new and improved material, as would positive transgressive segregates discussed subsequently. Exceptional progeny could be entered into the basic breeding program and eventually released as improved germplasm lines or cultivars.

Although 2011 appeared to be a more stressful year based on environmental conditions, means for all fiber traits did not necessarily reflect such stress because of the supplemental irrigation during boll maturation (Table 5). Fiber length, elongation, and lint percent appeared to be the only fiber and agronomic characteristics that benefitted positively from 2012s growing conditions as micronaire, fiber strength, and lint yield were lower than those reported in 2011.

Table 5. Means for micronaire, UHML, uniformity, fiber strength, elongation, lint yield, and lint percent for all (three) families grown in College Station, Texas in 2011 and 2012.

Fiber Trait	Year	
	2011	2012
Micronaire, units	3.8 a *	3.4 b
UHML, mm	29.5 b	31.0 a
Uniformity, %	83.0 a	83.3 a
Fiber Strength, g tex ⁻¹	32.1 a	30.5 b
Elongation, %	6.8 b	7.0 a
Lint Yield †, g	49.3 a	40.5 b
Lint Percent, %	34.8 b	35.6 a

* Means for fiber traits compared across years using Fisher LSD ($\alpha = 0.05$).

† Lint yield interpreted as a per plant average. Single plants selected were harvested entirely, ginned, and lint weighed in g.

Overall seed quality and performance, based on germination rate and early stand count evaluation, was numerically higher in 2012. Although 2012 was seen as a less stressful growing season (based on moisture level and fewer number of extreme temperature days), this environment could also introduce multiple factors that could have contributed detrimental effects not previously affecting cotton fiber growth in 2011. Cotton favors long, hot, dry growing conditions (Quisenberry and Kohel, 1975; Franca et al., 2000; Draye et al., 2005). Lower temperatures and increased moisture at a constant level are known to slow the rate of cotton fiber growth (National Cotton Council of America and The Cotton Foundation, 2007; Heap, 2000). Increased amounts of rainfall and moisture levels are also known to contribute to higher levels of insect stress, weed competition, and disease/fungal stress (Hake, Hake, and Kerby, 1996b).

Although not quantitatively measured in each year of this study, elevated levels of biotic stress were observed in 2012 compared to 2011. In 2011, biotic stress levels were almost non-existent due to extremely low moisture levels. This could possibly contribute to higher means observed in 2011 for certain traits.

Due to the presence of G x E interactions in several traits, it was only valid to do across year means and means tests for length, elongation, and lint percent (Table 6). Family means for length are as expected during the planning of this research with TAM B 182-33 ELSU / Tamcot 22 family having the longest UHML and the 06 WE 62-4 / Tamcot 22 family exhibiting significantly shorter length. While the family with 06 WE 62-4 parent had numerically the highest strength exhibited for a number of individual

plants selected, when averaged across generations and years in Table 6, it was not significantly higher than the other parental combinations. The family with 04 SID 84-2 averaged the highest fiber strength across years while also exhibiting the lowest lint yield per plant and the lowest lint percent.

Table 6. Means for micronaire, UHML, uniformity, fiber strength, elongation, lint yield, and lint percent for three families and five generations grown over two years (2011 and 2012) in College Station, Texas.

Source	Family Parents	Mic., units	UHML, mm	Unif., %	Fiber Strength, g tex ⁻¹	Elong., %	Lint Yield, g	Lint Percent, %
Fam. 1 †	06 WE 62-4 / Tamcot 22	3.77 a	28.96 c	82.78 b	31.27 b	6.86 b	47.50 a	37.29 a
Fam. 2	04 SID 84-2 / Tamcot 22	3.37 c	30.48 b	83.29 a	31.68 a	7.39 a	37.20 b	32.59 c
Fam. 3	TAM B 182-33 / Tamcot 22	†3.71 b	30.99 a	83.28 a	30.88 c	6.51 c	49.00 a	35.46 b

† Means within columns followed by the same letter are not different at $p < 0.05$ according to Fisher LSD.

‡ Mic. = Micronaire (measured in arbitrary units); Fam.= Family; Gen.= Generation; Unif.= Uniformity; Elong.= Elongation.

Fiber Length (UHML)

Early stages of fiber development are known to require high levels of moisture, which is often times the primary limiting factor for fiber length development (Walhood, 1960; Kerby et al., 1992; Matic- Leigh and Cauthen, 1994). These high levels of moisture can lead to longer growing seasons which permit increased time for fiber length development (Hake, Hake, and Kerby, 1996c; Braden and Smith, 2004a).

As previously stated, fiber length as an average of all families and generations was significantly higher in 2012 compared to 2011 (Table 5). The BC₁P₁F₂ generation (BC to the high quality parent- 06 WE 62-4, 04 SID 84-2, and TAM B 182-33) for each family also reported the highest fiber length mean values across both years of the study in comparison to the other generations (F₃ and BC₁P₂F₂) as expected; however, they did not surpass the parental generations for this trait (Table 7). The F₃ generation produced the numerically second highest fiber length mean values for each family, among generations, followed by the BC₁P₂F₂ (Tamcot 22 parent) across both years.

The numerically highest mean fiber lengths for progeny generations were found in the BC₁P₁F₂ generations of Family 2 and Family 3 averaged over both years with UHMLs above 32mm (1.30 inches). The fiber length mean of Tamcot 22/06 WE 62-4//06 WE 62-4 was statistically not different ($p < 0.05$) than the longer parent, 06 WE 62-4 for this trait averaged over both years. In the Tamcot 22/06 WE 62-4 parental combination, which was chosen for fiber strength and not fiber length considerations, the F₃ generation length mean in both years also was not different than the longer parent, 06 WE 62-4, suggesting elevated numbers of transgressive segregation could be possible (to be confirmed later in this section) and possibility for improvement for fiber length in this family, as two progeny generations exhibit means not statistically different from the higher parent generation for this trait.

Table 7. Genotypic means for UHML[‡] of P₁, P₂, F₃, BC₁P₁F₂, and BC₁P₂F₂ generations of three families grown in College Station, Texas combined over the years 2011 and 2012.

Fam.	Gen.	Pedigree	UHML, mm
1	P ₁	06 WE 62-4	29.59 ef
1	P ₂	Tamcot 22	†27.31 h
1	F ₃	Tamcot 22/ 06 WE 62-4	29.16 f
1	BC ₁ P ₁ F ₂	Tamcot 22/ 06 WE 62-4 // 06 WE 62-4	29.81 e
1	BC ₁ P ₂ F ₂	Tamcot 22/ 06 WE 62-4 // Tamcot 22	28.64 g
2	P ₁	04 SID 84-2	33.84 b
2	P ₂	Tamcot 22	27.68 h
2	F ₃	Tamcot 22/ 04 SID 84-2	29.69 e
2	BC ₁ P ₁ F ₂	Tamcot 22/ 04 SID 84-2 // 04 SID 84-2	32.50 c
2	BC ₁ P ₂ F ₂	Tamcot 22/ 04 SID 84-2 // Tamcot 22	29.40 ef
3	P ₁	TAM B 182-33	34.43 a
3	P ₂	Tamcot 22	27.44 h
3	F ₃	Tamcot 22/ TAM B 182-33	31.27 d
3	BC ₁ P ₁ F ₂	Tamcot 22/ TAM B 182-33 // TAM B 182-33	32.21 c
3	BC ₁ P ₂ F ₂	Tamcot 22/ TAM B 182-33 // Tamcot 22	29.62 ef
		Test Mean	30.23
		LSD (0.05)	0.49
		% CV	4.79

† Mean values followed by the same letter are not different at $p < 0.05$ according to Fisher LSD.

‡ UHML= Upper-Half Mean Fiber Length; Fam.= Family; Gen.= Generation.

Fiber Strength

Fiber length and strength values have been shown to be inversely related, possibly contributing to higher strength levels seen in 2011 results (Culp and Harrell, 1977; Culp et al., 1979; Green and Culp, 1990). All families and generations within families exhibited strength means higher for 2011 compared to 2012. Looking within families, the BC₁P₁F₂ generation consistently exhibited the highest fiber strength means among progeny generations across years, followed by the F₃ generation and the BC₁P₂F₂ generation. The family derived from the parent selected for high strength (Family 1), when combined over generations and years (Table 6), did not average the highest mean. However this family did contain the highest numerical fiber strength mean value recorded amongst progeny generations over both years which occurred in the BC₁P₁F₂ generation with a value of 33.15 g tex⁻¹ (Table 8). This, however, was lower than the exhibited high parental mean for this family (06 WE 62-4 which recorded a fiber strength of 36.89 g tex⁻¹ that year). Families 2 and 3 did exhibit strength values above 30 g tex⁻¹ for both BC₁P₁F₂ and F₃ generations in each family, which is regarded as “strong” cotton fiber. Their mean results, however, also did not surpass the high quality parental strength value exhibited in their subsequent families across years.

Table 8. Genotypic means for fiber strength of P₁, P₂, F₃, BC₁P₁F₂, and BC₁P₂F₂ generations of three families grown in College Station, Texas combined over the years of 2011 and 2012.

Fam.	‡Gen.	Pedigree	Strength, g tex ⁻¹
1	P ₁	06 WE 62-4	36.89 a
1	P ₂	Tamcot 22	26.04 h
1	F ₃	Tamcot 22/ 06 WE 62-4	†31.61 e
1	BC ₁ P ₁ F ₂	Tamcot 22/ 06 WE 62-4 // 06 WE 62-4	33.15 c
1	BC ₁ P ₂ F ₂	Tamcot 22/ 06 WE 62-4 // Tamcot 22	28.98 g
2	P ₁	04 SID 84-2	32.84 cd
2	P ₂	Tamcot 22	26.97 h
2	F ₃	Tamcot 22/ 04 SID 84- 2	32.32 de
2	BC ₁ P ₁ F ₂	Tamcot 22/ 04 SID 84- 2// 04 SID 84-2	32.92 cd
2	BC ₁ P ₂ F ₂	Tamcot 22/ 04 SID 84- 2// Tamcot 22	30.29 f
3	P ₁	TAM B 182-33	35.37 b
3	P ₂	Tamcot 22	27.37 h
3	F ₃	Tamcot 22/ TAM B 182-33	30.75 f
3	BC ₁ P ₁ F ₂	Tamcot 22/ TAM B 182-33// TAM B 182- 33	32.53 cd
3	BC ₁ P ₂ F ₂	Tamcot 22/ TAM B 182-33// Tamcot 22	29.25 g
		Test Mean	31.27
		LSD (0.05)	0.81
		% CV	7.64

† Mean values followed by the same letter are not different at $p < 0.05$ according to Fisher LSD.
‡ Fam.= Family; Gen.= Generation.

Other Fiber Traits

Other fiber and yield traits are of interest, although not involved in the primary purpose of this research.

The genotypes and populations in this study exhibited micronaire values generally within the premium range of 3.5 to 4.9 in 2011 but only half of the generations produced comparable micronaire values in 2012 (Table 9). Family 1 averaged a slightly higher micronaire value numerically than Family 3 for 2011, while over both years the average micronaire of Family 2 was reduced by the use of the interspecific parent, 04 SID 84-2, which exhibited an exceptionally low micronaire value. Family 2 averaged the lowest statistical means across both years and the 04 SID 84-2 parent exhibited the lowest absolute micronaire value across generations in 2011 and 2012 followed by the BC₁P₁F₂ generation in each year.

Analysis of variance indicated that uniformity exhibited consistent results for the material within this study (Table 3). Years were not a significant determining factor for this characteristic, as displayed by ANOVA and confirmed in Table 5, possibly indicating that the plant material within this study could be stable across multiple environments for this trait. Families did perform significantly different across years and Family 1 exhibited a statistically lower uniformity value than both Family 2 and Family 3 (which did not perform statistically different) in Table 6.

Elongation values reported in Table 10 for the segregating generations developed from 04 SID 84-2/Tamcot 22, Family 2, suggest the possibility of transgressive

segregation since both of the BC generation means numerically exceeds the parental means in 2011 and 2012. Only minor variation in mean values are observed for the families developed with TAM B 182-33 ELSU and 06 WE 62-4, and no progeny generation mean exhibits a value outside of the parental range for this trait over both years to suggest transgressive segregation for either of these families. These assumptions must be confirmed with transgressive segregation data, which will be discussed later in this section. Tamcot 22 consistently reported elongation means above the high quality parent in each family in both years.

Table 9. Genotypic means for micronaire of P₁, P₂, F₃, BC₁P₁F₂, and BC₁P₂F₂ generations of three families grown in College Station, Texas in 2011 and 2012.

Fam.	Gen.	Pedigree	2011	2012
			Micronaire, units ‡	Micronaire, units
1	P ₁	06 WE 62-4	4.22 ab †	3.37 cde
1	P ₂	Tamcot 22	4.04 b	3.41 cd
1	F ₃	Tamcot 22/ 06 WE 62-4	4.02 bcd	3.71 ab
1	BC ₁ P ₁ F ₂	Tamcot 22/ 06 WE 62-4 // 06 WE 62-4	3.77 cde	3.55 abc
1	BC ₁ P ₂ F ₂	Tamcot 22/ 06 WE 62-4 // Tamcot 22	4.32 a	3.22 e
2	P ₁	04 SID 84-2	2.24 g	2.87 f
2	P ₂	Tamcot 22	4.41 a	3.79 a
2	F ₃	Tamcot 22/ 04 SID 84-2	4.05 b	3.23 e
2	BC ₁ P ₁ F ₂	Tamcot 22/ 04 SID 84- 2// 04 SID 84-2	2.95 f	2.86 f
2	BC ₁ P ₂ F ₂	Tamcot 22/ 04 SID 84- 2// Tamcot 22	3.76 de	3.32 de
3	P ₁	TAM B 182-33	3.52 e	3.48 bcd
3	P ₂	Tamcot 22	4.07 b	3.92 a
3	F ₃	Tamcot 22/ TAM B 182-33	3.78 cde	3.71 a
3	BC ₁ P ₁ F ₂	Tamcot 22/ TAM B 182-33// TAM B 182-33	3.57 e	3.69 ab
3	BC ₁ P ₂ F ₂	Tamcot 22/ TAM B 182-33// Tamcot 22	4.04 bc	3.44 cd
		Test Mean	3.78	3.44
		LSD (0.05)	0.27	0.21
		% CV	12.46	12.50

† Mean values followed by the same letter are not different at $p < 0.05$ according to Fisher LSD.

‡ Micronaire (measured in arbitrary units); Fam.= Family; Gen.= Generation.

Table 10. Genotypic means for fiber elongation of P₁, P₂, F₃, BC₁P₁F₂, and BC₁P₂F₂ generations of three families grown in College Station, Texas in 2011 and 2012.

Fam.	Gen. ‡	Pedigree	2011	2012
			Elongation, %	Elongation, %
1	P ₁	06 WE 62-4	6.64 d †	6.93 c
1	P ₂	Tamcot 22	7.06 bc	7.24 b
1	F ₃	Tamcot 22/ 06 WE 62-4	6.83 cd	7.05 c
1	BC ₁ P ₁	Tamcot 22/ 06 WE 62-4	6.20 e	6.87 c
	F ₂	// 06 WE 62-4		
1	BC ₁ P ₂	Tamcot 22/ 06 WE 62-4	7.08 bc	7.06 bc
	F ₂	// Tamcot 22		
2	P ₁	04 SID 84-2	6.98 ab	6.98 c
2	P ₂	Tamcot 22	7.01 bc	7.18 b
2	F ₃	Tamcot 22/ 04 SID 84-2	6.94 cd	7.34 ab
2	BC ₁ P ₁	Tamcot 22/ 04 SID 84-	7.47 a	7.46 a
	F ₂	2// 04 SID 84-2		
2	BC ₁ P ₂	Tamcot 22/ 04 SID 84-	7.60 a	7.62 a
	F ₂	2// Tamcot 22		
3	P ₁	TAM B 182-33	6.02 e	5.95 e
3	P ₂	Tamcot 22	6.93 cd	7.69 a
3	F ₃	Tamcot 22/ TAM B 182-33	6.21 e	6.55 d
3	BC ₁ P ₁	Tamcot 22/ TAM B	5.97 e	6.35 d
	F ₂	182-33// TAM B 182-33		
3	BC ₁ P ₂	Tamcot 22/ TAM B	6.90 cd	7.00 c
	F ₂	182-33// Tamcot 22		
		Test Mean	6.79	7.02
		LSD (0.05)	1.32	0.29
		% CV	8.25	7.69

† Mean values followed by the same letter are not different at $p < 0.05$ according to Fisher LSD.

‡ Fam.= Family; Gen.= Generation.

Lint Yield and Lint Percent

Lint yield and lint percent, although not directly reported by HVI were calculated for this study to gain a more complete idea of how plant material used in this study responded to the environment. Changes seen in means or numbers of transgressive segregates for certain fiber traits may not positively impact this aspect of cotton production, and although emphasis on minor fiber traits has been greatly increased in recent years, farmers' primary concern still lies in achieving the highest yields.

There are many influential factors when reviewing overall yield of upland cotton. For this study, seed cotton weight and lint weight (lint yield) were measured prior to and after ginning. These two measurements also impact the reported lint percent value, which breeders take into account when selecting plant material for use in their program. Seed cotton weight, as measured in this study, was the weight of the raw cotton as picked from a plant in the field. This weight value includes both cotton lint weight plus cotton seed weight (as extracted from the boll) prior to ginning the sample. Lint weight (lint yield) alone was also taken for each sample (selected plant) in the study, and its value is calculated using just the weight of the same sample's lint after it has been ginned and separated from the seed. These two weights can be drastically different. If a plant variety produces large or a high number of seeds the final lint weight (which is the only weight farmers get paid for at the gin) can end up being much lower than expected if a high seed cotton weight had been previously reported. The ratio of lint produced in comparison to the overall seed cotton weight is expressed in the lint percent value. This value can quickly convey how much lint a breeder or farmer can expect from plant

material grown in the field. Lint percent can also be another factor that breeders consider when evaluating how alterations to cotton fiber traits resulting from a planned cross affect the overall value of the material for use. Correlation values for lint percent to other fiber traits reported in this study were not calculated, however, it might be useful to consider this for future studies. Lint yield alone and lint percent (lint weights relationship to original seed cotton weight) were the only values reported for this study.

Yield means for both lint yield and lint percent were higher in 2011 than 2012 for all generations in all three families (Table 11). Tamcot 22 outperformed the high quality parent, as expected, in both of these areas consistently for all three families across both years. It also exhibited the highest lint yield mean over both years with a value of 63.54 g in 2011. The parent 04 SID 84-2 for Family 2 had the lowest mean value for lint yield observed over both years with a value of 13.29 g in 2011. This was expected of this genotype as it has a pedigree with a background involving a “Sea Island” or *G. barbadense* parent. The means for other generations of Family 2 involving the 04 SID 84-2 parent also indicate poor performance in relation to yield for all families both years of the study. The Tamcot 22 parent had the highest means for lint yield for Family 2 in 2011 and 2012.

Table 11. Genotypic means for lint yield of P₁, P₂, F₃, BC₁P₁F₂, and BC₁P₂F₂ generations of three families grown in College Station, Texas in 2011 and 2012.

Fam.	‡Gen.	Pedigree	2011	2012
			Lint Yield, g	Lint Yield, g
1	P ₁	06 WE 62-4	54.92 abc	30.79 efgh
1	P ₂	Tamcot 22	63.54 a †	42.96 bc
1	F ₃	Tamcot 22/ 06 WE 62-4	53.86 bc	42.97 bc
1	BC ₁ P ₁ F ₂	Tamcot 22/ 06 WE 62-4 // 06 WE 62-4	60.14 ab	38.42 cd
1	BC ₁ P ₂ F ₂	Tamcot 22/ 06 WE 62-4 // Tamcot 22	54.20 bc	35.06 defg
2	P ₁	04 SID 84-2	13.29 f	27.67 h
2	P ₂	Tamcot 22	55.25 abc	64.08 a
2	F ₃	Tamcot 22/ 04 SID 84-2	41.94 de	30.17 fgh
2	BC ₁ P ₁ F ₂	Tamcot 22/ 04 SID 84-2// 04 SID 84-2	33.53 e	28.98 gh
2	BC ₁ P ₂ F ₂	Tamcot 22/ 04 SID 84-2// Tamcot 22	50.67 cd	36.93 cdef
3	P ₁	TAM B 182-33	37.42 e	37.42 cde
3	P ₂	Tamcot 22	61.17 ab	57.58 a
3	F ₃	Tamcot 22/ TAM B 182- 33	54.30 bc	47.46 b
3	BC ₁ P ₁ F ₂	Tamcot 22/ TAM B 182- 33// TAM B 182-33	50.29 cd	44.01 bc
3	BC ₁ P ₂ F ₂	Tamcot 22/ TAM B 182- 33// Tamcot 22	54.33 bc	43.91 bc
		Test Mean	49.25	40.53
		LSD (0.05)	8.94	7.18
		% CV	31.69	33.98

† Mean values followed by the same letter are not different at $p < 0.05$ according to Fisher LSD.

‡ Fam.= Family; Gen.= Generation.

Lint yield is a per plant average for each genotype. Based on lint weight, post ginning, of entire single plant selection.

Although lint yield exhibited higher means in 2011, to gain a complete perspective as to which year allowed for the optimum (most efficient) lint production, lint percent values must also be considered. Even if overall lint yield values appear to be higher for one year over the other, a cotton plant's rate of fiber production in comparison to overall seed cotton weight may be different. This is, in fact, the case for this study as the mean for lint percent is significantly higher for 2012 as opposed to 2011 (Table 5). Significant interaction terms for this trait (Table 4) prevent further general main effect conclusions. However, conclusions can be drawn when data are analyzed at the $G \times Y \times F$ level (Table 12). The Tamcot 22 parent reported the highest numerical lint percent means across the three families in both years (mean, ~ 39 %). The BC_1F_2 Tamcot 22 backcross progeny, with one exception in Family 1, were the highest performing progeny generations in all families in both years of the study. Again excluding Family 1 (where the 06 WE 62-4 and Tamcot 22 parents did not perform significantly differently for lint percent), the F_3 generations of each family ranked second in performance of this trait regarding progeny (segregating) generations; followed by the backcross generation to the high fiber quality parent. Means for Tamcot 22 and the BC_1F_2 generations to Tamcot 22 for all three families indicate equivalent or better performance for lint percent in 2011 despite the negative trend observed in this year (Table 5). This could possibly indicate that Tamcot 22 (the high yielding parent) responds better to harsh growing conditions as was seen in 2011 for College Station, Texas, or that cotton plants resulting from the genetic contribution from this parent produce cotton fiber more efficiently

under hotter, drier conditions. Means following this trend do perhaps correspond to the fact that lint yield means were also higher on average for 2011.

As was previously stated, poor stand counts which allowed for full plant development with little competition for resources in mid-to-late season conditions, and possible visual selection toward plants that would provide sufficient fiber for HVI testing may have contributed to the result of lint yield being higher in 2011 (despite what growing conditions would suggest) while lint percent means were higher for 2012. This impact, although not measured in this study could be significant in affecting how results were reported. However more study in these areas is required to make further conclusions.

Table 12. Genotypic means for lint percent of P₁, P₂, F₃, BC₁P₁F₂, and BC₁P₂F₂ generations of three families grown in College Station, Texas in 2011 and 2012.

Fam.	‡Gen.	Pedigree	2011	2012
			Lint Percent, %	Lint Percent, %
1	P ₁	06 WE 62-4	38.25 bc †	37.08 abc
1	P ₂	Tamcot 22	37.65 bc	38.87 a
1	F ₃	Tamcot 22/ 06 WE 62-4	37.38 bcd	37.17 abc
1	BC ₁ P ₁	Tamcot 22/ 06 WE 62-4 //	35.84 def	38.21 ab
	F ₂	06 WE 62-4		
1	BC ₁ P ₂	Tamcot 22/ 06 WE 62-4 //	38.71 ab	36.08 bcd
	F ₂	Tamcot 22		
2	P ₁	04 SID 84-2	21.99 j	29.02 g
2	P ₂	Tamcot 22	40.21 a	38.80 a
2	F ₃	Tamcot 22/ 04 SID 84-2	31.81 hi	32.73 e
2	BC ₁ P ₁	Tamcot 22/ 04 SID 84-2//	30.14 i	30.34 f
	F ₂	04 SID 84-2		
2	BC ₁ P ₂	Tamcot 22/ 04 SID 84-2//	35.46 ef	35.15 cd
	F ₂	Tamcot 22		
3	P ₁	TAM B 182-33	30.79 i	32.32 ef
3	P ₂	Tamcot 22	40.23 a	39.08 a
3	F ₃	Tamcot 22/ TAM B 182-33	34.30 fg	38.49 a
3	BC ₁ P ₁	Tamcot 22/ TAM B 182-33//	32.77 gh	34.46 de
	F ₂	TAM B 182-33		
3	BC ₁ P ₂	Tamcot 22/ TAM B 182-33//	36.91 cde	35.78 cd
	F ₂	Tamcot 22		
Test Mean			34.83	35.56
LSD (0.05)			1.78	2.21
% CV			7.71	9.61

† Mean values followed by the same letter are not different at $p < 0.05$ according to Fisher LSD.

‡ Fam.= Family; Gen.= Generation.

Lint percent is calculated as a per plant average for each genotype using the pre- and post-ginning lint weight.

Transgressive Segregation

Transgressive segregation is important for any progress in plant breeding, and for this study it is a focal point of discussion. Transgressive segregates can be described as any progeny with characteristics exceeding the mid-parent value (MPV), or as any progeny above the highest single parental plant value (HPV) or below the lowest single parental plant value (LPV) for any plant characteristic. Transgressive segregation above either the MPV or the HPV is a positive occurrence for a breeder to observe for many fiber characteristics in cotton. Both can be an indication of potential for improvement within the selected plant material. This study distinguishes between transgressive segregates appearing above or below the MPV and/or above the HPV or below the LPV. Obviously, higher numbers often appear when observing transgressive segregates above the MPV, while it is rarer to exceed the HPV and LPV for most traits in upland cotton. In this study, positive transgressive segregates above the MPV appeared for all traits observed in all three families, while there were multiple instances of no transgressive segregation beyond parental means for traits within the three families. When transgressive segregation above the HPV or below the LPV did occur, however, it occurred predominantly in the direction above the highest parental value for most characteristics, a positive result for this study for fiber length and strength, which are primary selection goals of the Cotton Improvement Lab. This could indicate that there is a possibility for continued improvement within the material used, and that chances are higher for a positive resulting transgressive segregate for these traits. The only instances

of large numbers of negative transgressive segregates were for fiber elongation and for micronaire.

In order to base conclusion on a relative large sampling, the reps described above were combined to provide a sample of 100 plants each of the generations evaluated, F_3 , $BC_1P_1F_2$, and $BC_1P_2F_2$, in each of the three families. Thus, an analysis of variance to determine significant differences among generations and families for number of transgressive segregates was constructed using year as replication and error control. A t-test statistic was used to separate mean number of transgressive segregates across generations within families and within years for discussion purposes but otherwise the following discussion will focus on absolute numbers.

Main effects (Family and Generation) were significant when observing transgressive segregation rates according to the ANOVA for most traits (Tables 13 and 14). There were, however, instances where fiber traits did not exhibit significance in regards to main effects and their interactions; micronaire, lint yield, and lint percent did not exhibit statistical significance in regards to Family, Generation, and F x G. Thus, from looking at these numbers alone it cannot be inferred as to which year (or environment) was more conducive to higher rates of positive transgressive segregation, or which year might indicate the best crop performance. Means of data must be coupled with transgressive segregation numbers to make the final conclusion.

Table 13. Two-way ANOVA for transgressive segregation rates on micronaire, UHML, uniformity, fiber strength and elongation appearing in the F₃, BC₁P₁F₂, and BC₁P₂F₂ generations of three families grown at College Station, Texas in 2011 and 2012.

Source	df	Micronaire			UHML			Uniformity			Fiber Strength			Elongation		
		above MPV	below LPV	above HPV	above MPV	below LPV	above HPV	above MPV	below LPV	above HPV	above MPV	below LPV	above HPV	above MPV	below LPV	above HPV
Family (F)	2	43.7	114.0	132.7	816.2 *	10.9 **	213.7 **	597.2 **	6.2	6.2 **	1118.7 **	2.0	223.2 *	1486.2 **	272.4	366.9 **
Error A	3	422.3	22.4	49.4	109.1	5.6	4.1	274.5	13.0	1.8	192.3	1.9	114.8	2.1	326.7	77.1
Gen. (G) [‡]	2	1287.7	16.2	62.7	4452.7 **	2.7 **	50.9 *	2041.2 **	14.0	8.2 **	3720.2 **	1.2	66.2	1539.5 **	145.7	57.1 *
G x F	4	230.0	12.2	9.2	376.5 *	2.2 **	28.9	54.6	7.9	4.2 **	209.5 *	0.9	52.1	605.9 *	51.3	26.5 *
Error B	6	476.1	59.9	43.7	78.1	0.1	6.9	45.7	3.5	0.4	31.3	1.4	39.1	125.1	65.8	5.6

* , ** Significant at p< 0.05 and 0.01, respectively.

[‡] Gen., Generation; Mic., Micronaire; UHML, Upper- Half Mean Length; Unif., Uniformity; Elong., Elongation; Above MPV, above the mid-parent value; Below LPV, below the low-parent value; Above HPV, above the high-parent value.

Table 14. Two-way ANOVA for transgressive segregation rates on lint yield and lint percent appearing in the F₃, BC₁P₁F₂, and BC₁P₂F₂ generations of three families grown at College Station, Texas in 2011 and 2012.

Source	df	Lint Yield			Lint Percent		
		above MPV	below LPV	above HPV	above MPV	below LPV	above HPV
Family (F)	2	87.5	23.7	17.2	99.5	39.1	17.4
Error A	3	1706.3	45.0	24.8	374.8	24.6	38.9
Gen. (G) [‡]	2	66.5	11.1	4.7	1380.7	31.7	14.2
G x F	4	261.5	3.1	9.8	272.7	8.1	13.4
Error B	6	113.2	5.5	8.1	304.8	8.7	17.4

* , ** Significant at p< 0.05 and 0.01, respectively.

[‡] Gen., Generation; Above MPV, above the mid-parent value; Below LPV, below the low-parent value; Above HPV, above the high-parent value.

Transgressive Segregation for UHML

Determining transgressive segregation in the F_3 and BC_1F_2 , two equivalent segregating generations relative to a single gene, in three families of unique and appropriate parental origin was the primary goal of this study. The fiber quality breeding program of the Cotton Improvement Lab has concentrated on length and strength, so the possibility of observing positive transgressive segregation for these characteristics was a source of encouragement for continued improvement in upland cotton from this program.

Combined over years and the segregating generations under study, 402 of 600 single plants from Family 1, 268 of 600 plants from Family 2, and 300 of 600 plants tested from Family 3 exhibited fiber length values above the MPV (Tables 15 and 16). Forty-two more MPV transgressive segregates were documented in 2012 than in 2011 but the difference in total number represents only a 9 % change in 2012 relative to 2011 so it probably is not biologically important, although it could suggest that one could find MPV transgressive segregates in some years and not others and may specifically, in this case, be indicative of better seasonal moisture in 2012 since fiber length is environmentally related to turgor pressure and the ability of cotton fiber cells to uptake nutrients and elongate during their developmental period. Fiber length means for all genotypes and numbers of EL and ELSU designated progeny performance across years also support this conclusion. Fiber length means for all genotypes used in this study were higher in 2012 as opposed to 2011, which supports the long held axiom that the environment must allow for genetic expression to maximize selection potential.

Table 15. Transgressive segregation for micronaire, fiber length, uniformity, fiber strength, and elongation appearing in the F₃, BC₁P₁F₂, and BC₁P₂F₂ generations for three families grown in College Station, Texas in 2011.

2011		Micronaire			UHML †			Uniformity			Fiber Strength			Elongation		
Family		above MPV	below LPV	above HPV	above MPV	below LPV	above HPV	above MPV	below LPV	above HPV	above MPV	below LPV	above HPV	above MPV	below LPV	above HPV
1 ‡	Total	145	3	21	196	3	29	156	14	2	124	0	3	115	82	19
1	F ₃	49 b	1 a	6 b	70 b	1 a	5 b	52 b	4 b	1 a	44 b	0 a	0 b	49 a	22 b	9 a
1	BC ₁ P ₁ F ₂	26 c	2 a	1 c	84 a	0 a	21 a	73 a	0 c	1 a	74 a	0 a	3 a	7 b	49 a	0 b
1	BC ₁ P ₂ F ₂	70 a	0 a	14 a	42 c	2 a	3 b	31 c	10 a	0 a	6 c	0 a	0 b	59 a	11 c	10 a
2	Total	183	1	17	113	3	1	167	3	4	204	2	57	187	9	30
2	F ₃	82 a	0 a	14 a	15 b	3 a	0 a	51 b	2 a	0 b	73 b	0 a	34 a	40 b	7 a	7 b
2	BC ₁ P ₁ F ₂	20 b	0 a	0 c	87 a	0 b	1 a	81 a	1 a	4 a	85 a	0 a	21 b	76 a	2 b	8 ab
2	BC ₁ P ₂ F ₂	81 a	1 a	3 b	11 b	0 b	0 a	35 c	0 a	0 b	46 c	2 a	2 c	71 a	0 b	15 a
3	Total	156	27	1	155	0	0	140	12	0	153	1	11	103	18	4
3	F ₃	55 b	10 a	0 a	61 b	0 a	0 a	44 b	2 b	0 a	45 b	0 a	1 b	24 b	5 b	1 ab
3	BC ₁ P ₁ F ₂	27 c	14 a	0 a	81 a	0 a	0 a	69 a	3 ab	0 a	80 a	0 a	9 a	6 c	13 a	0 b
3	BC ₁ P ₂ F ₂	74 a	3 b	1 a	13 c	0 a	0 a	27 c	7 a	0 a	28 c	1 a	1 b	73 a	0 c	3 a

† UHML, Upper- half mean length; Above MPV, above the mid-parent value; Below LPV, below the low-parent value; Above HPV, above the high-parent value. Values for each generation (F₃, BC₁P₁F₂, and BC₁P₂F₂) taken from 100 selections / family / year.

‡ Family 1, 06 WE 62-4 X Tamcot 22; Family 2, 04 SID 84-2 X Tamcot 22; Family 3, TAM B 182-33 X Tamcot 22.

§ Values followed by the same letter are not different based on independent T-test ($p \leq 0.05$). Values are compared vertically within a single family, between generations for a trait.

Table 16. Transgressive segregation for micronaire, fiber length, uniformity, fiber strength, and elongation appearing in the F₃, BC₁P₁F₂, and BC₁P₂F₂ generations for three families grown in College Station, Texas in 2012.

2012		Micronaire			UHML †			Uniformity			Fiber Strength			Elongation		
Family		above MPV	below LPV	above HPV	above MPV	below LPV	above HPV	above MPV	below LPV	above HPV	above MPV	below LPV	above HPV	above MPV	below LPV	above HPV
1 ‡	Total	170	17	45	206	3	37	217	1	6	155	1	0	112	7	16
1	F ₃	78 a	3 b	25 a	62 b	1 a	13 ab	83 a	0 a	3 a	64 b	0 a	0 a	45 a	1 a	5 a
1	BC ₁ P ₁ F ₂	60 b	1 b	15 b	83 a	0 a	17 a	86 a	0 a	3 a	79 a	0 a	0 a	28 b	4 a	1 b
1	BC ₁ P ₂ F ₂	32 c	13 a	5 c	61 b	2 a	7 b	48 b	1 a	0 b	12 c	1 a	0 a	39 a	2 a	10 a
2	Total	103	13	4	155	13	4	199	11	8	204	5	13	189	9	67
2	F ₃	38 a	4 ab	4 a	43 b	6 a	0 b	60 b	5 a	2 ab	67 b	3 a	5 a	55 b	3 ab	14 b
2	BC ₁ P ₁ F ₂	16 b	8 a	0 b	85 a	3 a	4 a	80 a	3 a	6 a	80 a	2 ab	6 a	61 b	5 a	25 a
2	BC ₁ P ₂ F ₂	49 a	1 b	0 b	27 c	4 a	0 b	59 b	3 a	0 b	57 b	0 b	2 a	73 a	1 b	28 a
3	Total	132	35	13	145	0	3	126	13	0	103	6	0	98	2	1
3	F ₃	50 a	6 b	7 a	52 b	0 a	2 a	38 b	3 a	0 a	34 b	1 a	0 a	27 b	2 a	0 a
3	BC ₁ P ₁ F ₂	46 ab	4 b	5 ab	76 a	0 a	1 a	60 a	3 a	0 a	59 a	1 a	0 a	11 c	0 a	0 a
3	BC ₁ P ₂ F ₂	36 b	25 a	1 b	17 c	0 a	0 a	28 b	7 a	0 a	10 c	4 a	0 a	60 a	0 a	1 a

† UHML, Upper- half mean length; Above MPV, above the mid-parent value; Below LPV, below the low-parent value; Above HPV, above the high-parent value. Values for each generation (F₃, BC₁P₁F₂, and BC₁P₂F₂) taken from 100 selections / family / year.

‡ Family 1, 06 WE 62-4 X Tamcot 22; Family 2, 04 SID 84-2 X Tamcot 22; Family 3, TAM B 182-33 X Tamcot 22.

§ Values followed by the same letter are not different based on independent T-test ($p \leq 0.05$). Values are compared vertically within a single family, between generations for a trait.

The greatest number of transgressive segregates for UHML, summed over both years of the study, were found in Family 1, although neither parent exhibited EL or ELSU length and only 20 transgressive segregates exhibited EL fiber length (Table 17). Of the 72 progeny exhibiting UHML below LPV or above HPV, 66 were above the HPV in Family 1. Twenty-nine of the 66 positive transgressive segregates were found in 2011 and 37 were found in 2012, suggesting a consistent segregation pattern. Although not reflective of actual fiber length means across families, these high numbers were unexpected for Family 1, which contains the standard common upland parent, Tamcot 22, and the high strength parent, 06 WE 62-4, which has better length than Tamcot 22 but not similar to the ELSU length found in the other two family pedigrees. Parental means for fiber length were lower for this family and the most extreme parental value was significantly lower than the extreme parental values for Family 2 or Family 3. Besides indicating the possibility that parental means were lower and more achievable, these values also indicate the possibility for further improvement for fiber length in this plant material (Family 1) and the possibility that genes for fiber length consistently combined favorably from this cross.

Table 17. Number of individual plants sampled from the F₃, BC₁P₁F₂, and BC₁P₂F₂ generations exhibiting upland extra long (EL) or extra long staple upland (ELSU) length classification from three families grown in College Station, Texas in 2011 and 2012.

Year	Family	Generation	Genotype	Number of each genotype reaching designation	
				† EL	ELSU
2011	1	F ₃	Tamcot 22/ 06 WE 62-4	0	0
		BC ₁ P ₁ F ₂	Tamcot 22/ 06 WE 62-4 // 06 WE 62-4	0	0
		BC ₁ P ₂ F ₂	Tamcot 22/ 06 WE 62-4 // Tamcot 22	1	0
	2	F ₃	Tamcot 22/ 04 SID 84-2	2	0
		BC ₁ P ₁ F ₂	Tamcot 22/ 04 SID 84-2// 04 SID 84-2	48	1
		BC ₁ P ₂ F ₂	Tamcot 22/ 04 SID 84-2// Tamcot 22	0	0
	3	F ₃	Tamcot 22/ TAM B 182-33	12	0
		BC ₁ P ₁ F ₂	Tamcot 22/ TAM B 182-33// TAM B 182-33	39	0
		BC ₁ P ₂ F ₂	Tamcot 22/ TAM B 182-33// Tamcot 22	2	0
				Total	104
2012	1	F ₃	Tamcot 22/ 06 WE 62-4	7	0
		BC ₁ P ₁ F ₂	Tamcot 22/ 06 WE 62-4 // 06 WE 62-4	8	0
		BC ₁ P ₂ F ₂	Tamcot 22/ 06 WE 62-4 // Tamcot 22	4	0
	2	F ₃	Tamcot 22/ 04 SID 84-2	16	1
		BC ₁ P ₁ F ₂	Tamcot 22/ 04 SID 84-2// 04 SID 84-2	71	11
		BC ₁ P ₂ F ₂	Tamcot 22/ 04 SID 84-2// Tamcot 22	9	2
	3	F ₃	Tamcot 22/ TAM B 182-33	49	5
		BC ₁ P ₁ F ₂	Tamcot 22/ TAM B 182-33// TAM B 182-33	72	9
		BC ₁ P ₂ F ₂	Tamcot 22/ TAM B 182-33// Tamcot 22	13	0
				Total	249

†EL designation, > 32.00 mm fiber length; ELSU designation, > 34.92 mm fiber length.

The greatest number of transgressive segregates above the HPV in Family 1 appeared in the BC₁P₁F₂ generation (backcross to 06 WE 62-4) (Tables 15 and 16). This generation included 21 (of the 29 positive) transgressive progeny in 2011 and 17 (of 37) transgressive progeny in 2012 above the HPV for fiber length. The F₃ generation of this family exhibited only five transgressive progeny above the HPV in 2011 and 13 in 2012. The back-cross (BC₁F₂) generation to Tamcot 22 (the low quality parent) produced the fewest positive transgressive progeny for UHML with three transgressive progeny appearing in 2011 and seven appearing in 2012.

Trends for MPV transgressive segregation numbers for Family 1 were similar to the HPV transgressive segregation trends with the backcross F₂ to 06 WE 62-4 containing the most transgressive segregates (84 in 2011 and 83 in 2012), followed by the F₃ generation (70 in 2011 and 62 in 2012), and lastly the backcross F₂ to Tamcot 22 (42 in 2011 and 61 in 2012) (Table 15 and Table 16).

High and low individual plant performance values for UHML also reflect better results for 2012 (Table 18). The highest parental fiber length achieved was 30.2 mm in 2011 for Family 1 and 31.5 mm in 2012. The highest individual plant within a segregating generation in 2011 was 32.5 mm while in 2012 it was 33.5 mm.

Table 18. High and low values reported for UHML[‡] in each generation for three families grown in College Station, Texas in 2011 and 2012.

Family	Generation	Genotype	2011		2012	
			low value	high value	low value	high value
					(mm)	
1	P ₁	06 WE 62-4	-	30.2	-	31.5
1	P ₂	Tamcot 22	25.9	-	25.9	-
1	F ₃	Tamcot 22/ 06 WE 62-4	25.1	31.5	25.4	33.5
1	BC ₁ P ₁ F ₂	Tamcot 22/ 06 WE 62-4 // 06 WE 62-4	27.4	31.5	26.7	33.5
1	BC ₁ P ₂ F ₂	Tamcot 22/ 06 WE 62-4 // Tamcot 22	25.4	32.5	25.4	33.5
2	P ₁	04 SID 84-2	-	35.1	-	35.8
2	P ₂	Tamcot 22	25.1	-	27.4	-
2	F ₃	Tamcot 22/ 04 SID 84-2	24.4	33.0	25.7	35.1
2	BC ₁ P ₁ F ₂	Tamcot 22/ 04 SID 84-2// 04 SID 84-2	28.9	35.3	27.2	37.1
2	BC ₁ P ₂ F ₂	Tamcot 22/ 04 SID 84-2// Tamcot 22	25.1	31.5	26.4	35.8
3	P ₁	TAM B 182-33	-	34.3	-	35.8
3	P ₂	Tamcot 22	24.6	-	26.9	-
3	F ₃	Tamcot 22/ TAM B 182- 33	27.2	33.8	28.4	36.1
3	BC ₁ P ₁ F ₂	Tamcot 22/ TAM B 182- 33// TAM B 182-33	29.2	34.0	27.9	36.6
3	BC ₁ P ₂ F ₂	Tamcot 22/ TAM B 182- 33// Tamcot 22	24.9	33.3	28.2	34.3

[‡] UHML, Upper- half mean fiber length.

Family 2, with the Sea Island introgressed parentage actually exhibited fewer UHML transgressive segregates above the HPV than it did for those below the LPV in both 2011 and 2012 (Tables 15 and 16). Only one UHML transgressive segregate above the HPV appeared in 2011, while three plants produced UHML values below the LPV. The only generation that produced positive transgressive segregates above the HPV for fiber length in Family 2 in both years was the BC₁F₂ generation to the interspecific parent, 04 SID 84-2. This generation also included 87 transgressive segregates in 2011 and 85 transgressive segregates in 2012 which exhibited UHML above the MPV. The F₃ generation of Family 2 produced no transgressive segregates above the HPV for either year in the study, but did produce the highest number of transgressive segregates performing below the LPV, with three progeny in 2011 and six progeny in 2012. Despite containing the most transgressive segregates below the LPV, the F₃ generation contained the second most transgressive segregates above the MPV for fiber length with 15 transgressive progeny in 2011 and 43 transgressive progeny in 2012. No transgressive segregation beyond the HPV or LPV appeared in BC₁F₂ to Tamcot 22 in 2011, while four progeny performed below the LPV in 2012. The mid-parent transgressive segregation numbers were 11 in 2011 and 27 in 2012 for this generation.

Despite fewer positive transgressive segregates, Family 2 exhibited more individual plants with EL or ELSU UHML (fiber length) values than did Family 1 (Table 17). Individual parental performance for length was also higher for this family with the highest single plant UHML of 35.1 mm in 2011 and 35.8 mm in 2012 versus 30.2 and 31.5 mm for the best performing parental plants in Family 1 in 2011 and 2012,

respectively (Table 18). Progeny in the BC₁P₁F₂ generation exhibited UHMLs of 35.3 mm in 2011 and 37.1 mm in 2012, both exceeding the ELSU minimum of 34.9 mm. These data suggest the potential of epistatic interactions of alleles for fiber length from *G. barbadense* when combined with Tamcot 22, a *G. hirsutum* parent of average quality. One plant exhibiting ELSU fiber length was identified in the BC₁F₂ (BC to 04 SID 84-2) in 2011 but 11 such plants were identified in 2012, again indicating that environment can obscure or impact genotype (Table 17). Interestingly, one F₃ plant and two BC₁F₂ (BC to Tamcot 22) exhibited ELSU fiber length, supporting the premise that recovery of ELSU fiber length phenotypes can be enhanced by a single backcross to the high quality parent.

Family 3 contained no transgressive segregates above the HPV or below the LPV in 2011 (Table 15); however, above the MPV, segregate numbers for each generation followed a pattern similar to those seen in Families 1 and 2. The BC₁F₂ to TAM B 182-33 ELSU contained 81 transgressive progeny above the MPV, the F₃ generation contained 61 transgressive progeny, and the BC₁F₂ to Tamcot 22 produced 13 transgressive progeny relative the MPV. Mid-parent values for transgressive segregation for UHML were similar in 2012 with the BC₁F₂ to TAM B 182-33 ELSU containing the most transgressive progeny (Table 16). Three transgressive progeny were identified above the HPV, 35.8 mm, for this family in 2012, two in the F₃ generation, both at 36.1 mm, and one in the BC₁F₂ to TAM B 182-33 ELSU that exhibited 36.6 mm UHML (Table 18). Similar to Family 2 in 2012, 14 individual plants exhibited ELSU fiber length, five in the F₃ generation, and nine in the BC₁F₂ to the high length parent (Table 17).

Fiber Length Classification

As fiber length is of primary importance for this study, special attention was given to identifying progeny that achieved exceptional UHML (Table 17). Progeny for each family were recorded that met or exceeded the UHML range for upland EL designation as well as for ELSU designation. This was monitored for both years of the study. Length values were recorded for 300 plants per family each year (100 plants observed in the three segregating generations of each family; F_3 , $BC_1P_1F_2$, and $BC_1P_2F_2$). Family 1 exhibited the fewest progeny reaching either EL or ELSU designation for both years. In 2011 this family only exhibited one progeny reaching EL designation. In 2012, 19 progeny in this family reached the EL designation, while still none reached ELSU length. The majority of the progeny occurring in the exceptional length range for Family 1 appeared in the F_3 or $BC_1P_1F_2$ (to the high quality parent 06 WE 62-4). This is perhaps not a surprising result as Family 1 contains a pedigree which focuses on fiber strength and yield, not fiber length. As expected, no parental values for Family 1 reached either fiber length designation; however, progeny resulting from this cross did exhibit exceptional fiber length (EL fiber length), indicating the possibility for improvement in this area. Years appeared to have an impact on these data. Across years, for all families, more progeny reached either EL or ELSU fiber length designations in the 2012 growing year as opposed to 2011, providing further evidence that environment impacts gene expression.

Family 2 exhibited 51 progeny in either designation for 2011. The $BC_1P_1F_2$ generation produced 96 % of the exceptional length progeny for this family. It was also

the generation that produced the only ELSU length progeny in 2011. The only other generation for this family which produced exceptional length progeny in 2011 occurred in the F₃ generation, where two plants exhibited EL length status. Results, for 2012 for Family 2 indicated a total of 110 exceptional progeny. Exceptional progeny appeared for both designations in all generations in this year for Family 2, with 71 EL progeny and 11 ELSU progeny identified in the BC₁P₁F₂. The F₃ generation contained 16 EL and one ELSU designated progeny, and the BC₁P₂F₂ produced nine EL and two ELSU designated progeny. With numbers again appearing higher for 2012, this suggests that the environment was more favorable for achieving increased fiber length.

Family 3 exhibited the highest number of exceptional fiber length progeny over both years of the study. In 2011, 53 progeny reached EL fiber designation (none reached ELSU) with 39 of the 53 reaching this distinction coming from the BC₁P₁F₂ generation (BC₁F₂ to TAM B 182-33 ELSU) and 12 such progeny from the F₃ generation. The BC₁P₂F₂ generation only exhibited two EL progeny. In 2012, a total of 148 Family 3 progeny exhibited these two designations for fiber length. The BC₁P₁F₂ generation contained 72 EL progeny and nine ELSU progeny. The F₃ generation exhibited progeny within both designations as it contained 49 EL progeny and five ELSU progeny. The BC₁P₂F₂ generation of Family 3 produced the lowest number of exceptional fiber length progeny in 2012 with 13 ELSU designated progeny.

Family 3 contains one parent that is designated ELSU and, thus, should contribute positively toward longer fiber length. Results for this study (when looking at

the number of progeny for each family which displayed exceptional fiber length) support the hypothesis that including a parent of this distinction increases the probability of longer fiber length in progeny resulting from the cross.

Transgressive Segregation for Fiber Strength

Fiber strength was also a major point of emphasis for this study, as the main objective was to produce and observe transgressive progeny with exceptional fiber length and improved fiber strength. Simultaneous improvement in these areas could add to the marketability and competitiveness (based on fiber quality) of U.S. cotton.

Family 1 exhibited only three positive transgressive segregates with values above the HPV for fiber strength in 2011 and none in 2012 (Tables 15 and 16). These segregates all occurred in the $BC_1P_1F_2$ generation (BC_1F_2 to 06 WE 62-4) where the highest single plant exhibited a value of 41.8 g tex^{-1} (also the highest strength recorded in the study) (Table 19). The only other extreme transgressive segregate appearing in this family (other than those exceeding the MPV), was a LPV segregate in 2012 in the $BC_1P_2F_2$ generation (BC_1F_2 to Tamcot 22). This family contained a parent that had been selected for increased fiber strength, so the lack of appearance of transgressive segregates for this family was unexpected. Means and individual plant performance continued to indicate, however, that the parental background with added fiber strength contributed to progeny exhibiting good strength. Forty- one percent of the Family 1 single plants evaluated in the segregating generations (F_3 , $BC_1P_1F_2$, and $BC_1P_2F_2$) in 2011 and 52 % evaluated in 2012 exhibited strength above the MPV (Tables 15 and 16).

Table 19. High and low values reported for fiber strength in each generation for three families grown in College Station, Texas in 2011 and 2012.

Family	Generation	Genotype	2011		2012	
			low value	high value	low value	high value
					(g tex ⁻¹)	
1	P ₁	06 WE 62-4	-	39.7	-	38.8
1	P ₂	Tamcot 22	24.6	-	21.7	-
1	F ₃	Tamcot 22/ 06 WE 62-4	25.4	38.6	25.8	35.5
1	BC ₁ P ₁ F ₂	Tamcot 22/ 06 WE 62-4 // 06 WE 62-4	28.4	41.8	26.9	36.2
1	BC ₁ P ₂ F ₂	Tamcot 22/ 06 WE 62-4 // Tamcot 22	25.1	37.4	24.6	34.0
2	P ₁	04 SID 84-2	-	35.7	-	35.9
2	P ₂	Tamcot 22	24.9	-	24.9	-
2	F ₃	Tamcot 22/ 04 SID 84-2	25.2	40.6	23.6	39.8
2	BC ₁ P ₁ F ₂	Tamcot 22/ 04 SID 84-2 2// 04 SID 84-2	26.4	39.9	25.3	37.6
2	BC ₁ P ₂ F ₂	Tamcot 22/ 04 SID 84-2 2// Tamcot 22	23.4	35.5	25.5	37.1
3	P ₁	TAM B 182-33	-	36.9	-	38.1
3	P ₂	Tamcot 22	24.8	-	25.6	-
3	F ₃	Tamcot 22/ TAM B 182-33	25.7	37.0	24.3	35.4
3	BC ₁ P ₁ F ₂	Tamcot 22/ TAM B 182-33// TAM B 182-33	27.3	38.8	24.5	36.5
3	BC ₁ P ₂ F ₂	Tamcot 22/ TAM B 182-33// Tamcot 22	23.9	37.1	24.7	32.9

Family 2, involving an interspecific parent, exhibited the most positive transgressive segregates performing above the HPV for fiber strength in both 2011 and 2012 (Tables 15 and 16). Fifty- seven total positive segregates were observed for this family in 2011 with the highest number, 34, occurring in the F₃ generation of this family, followed by 21 in the BC₁P₁F₂ generation (which contained the highest single plant value for this family of 40.6 g tex⁻¹ (Table 19)). Only two negative segregates were recorded for this year, and they appeared in the BC₁P₂F₂ generation. In 2012, 13 total transgressive segregates with strength values above the HPV occurred in Family 2. All three generations exhibited HPV segregates, with the BC₁P₁F₂ having the most with six, the F₃ generation with five, and the BC₁P₂F₂ with two. The large number of transgressive segregates exceeding the HPV in this family was not unexpected given that it was developed with an interspecific parent with fiber strength well above the norm for upland cotton, e.g., Tamcot 22. Positive segregates exceeding the HPV appeared in all generations each year for Family 2 and could be an indication of the contribution of positive alleles for fiber strength by both parents in the cross combination. Transgressive numbers for the 2011 growing season coupled with mean data also indicate that this environment could be better for producing progeny that exceed its parents for fiber strength. While this experiment was not designed to study this phenomenon, one speculation is that higher temperature is a driver of increased strength while consistent moisture availability is more important in reaching genetic potential in fiber length.

In 2011, 11 total positive transgressive segregates above the HPV were recorded for Family 3 (Table 15). Nine of these segregates occurred in the BC₁P₁F₂ generation

with values above 36.9 g tex^{-1} (Table 19). One positive transgressive segregate appeared in each of the F_3 and $BC_1P_2F_2$ generations. The only negative transgressive segregate for this year also appeared in the $BC_1P_2F_2$ generation. The 2012 year exhibited no positive transgressive segregates for Family 3, but six negative transgressive segregates with strength values below the LPV of 25.6 g tex^{-1} .

All plants within segregating generations exhibited strength values above the discount range of 24 g tex^{-1} for 2012 (Cotton Council International, cottonusa.org, 2012), despite parental contribution that indicated performance below this level. All families and generations also exhibited values above the “very strong” distinction level. This indicates that improving fiber strength should not be an issue.

Special Progeny

Individual plant progeny were identified during the conduct of this research that showed transgressive behavior for both fiber length and fiber strength. A total of nine progeny exhibited values that were transgressive for both fiber length and fiber strength across both years of this study. Although this number might not be large, this value demonstrates that it is indeed possible to achieve added fiber length and strength within this plant material simultaneously. Five of the nine transgressive progeny appeared in Family 2 and the remaining four appeared in Family 1. Parental values should be considered again when reviewing these results. Parental values set the upper and lower values that a progeny must overcome in order to be considered transgressive. There are also a number of progeny that, although not transgressive, exhibited exceptional fiber

length and strength. Progeny within this category exhibited both EL or ELSU fiber length and strong or very strong fiber strength simultaneously. Three- hundred and fifty progeny achieved both of these fiber distinctions. All three families were represented within these 350, which constituted 19 % of all plants evaluated. Slightly more than half were reported from Family 3, which has TAM B 182-33 ELSU as one parent, while the remaining half came primarily from Family 2, which has 04 SID 84-2 interspecific as one parent. Family 1 represented only 8 % of the exceptional progeny.

These findings suggest that breeding for improved length and strength in U.S. upland material is possible. This also indicates that breeding for germplasm with added fiber length and strength may be achieved through selection in plant material that contains parentage that does not necessarily exhibit those characteristics (in this case parentage being short or medium staple length, average strength types). Although it was observed in this study that parentage that more closely resembled the desired result did, in fact, increase probability for achieving the result.

Overall, for length and strength the interspecific cross contained the highest number of both positive and negative transgressive segregates. DeVicente and Tanksley (1993) and Kohel et al. (2001) also reported that interspecific crosses have been known to contain the highest chance for transgressive segregation. Results also indicate that the majority of transgressive segregates across families appear in the BC₁F₂ generation back to the high quality parent (06 WE 62-4, 04 SID84-2, or TAM B 182-33 ELSU), although numbers appear in both the BC₁F₂ generation back to Tamcot 22 and F₃ generation as

well. Similar trends are found for other fiber and agronomic properties (micronaire, elongation, uniformity, and lint percent). This result would seem reasonable as the high quality parent would be most likely to contribute positive or beneficial alleles to a cross resulting in a higher chance for a transgressive progeny. But this result also indicates that there is still opportunity for further positive improvement in these fiber property areas. This plant material and methodology of breeding and selection may be of interest to upland cotton breeders looking to improve these fiber quality characteristics in Texas and the United States.

Transgressive Segregation for Other Fiber Traits

Micronaire, uniformity, elongation, and lint percent are also important selection criteria. These traits can be important when looking for potential within plant material and their trends can be valuable in improvement in upland cotton material.

The families and generations included in this study averaged 148 transgressive progeny (300 possible per family) above the MPV for micronaire across the two years of the study (Tables 15 and 16). Family 1 averaged the most transgressive progeny above the HPV with 21 in 2011 and 45 in 2012. It is hard to gauge which generation exhibited the highest probability for this occurrence, as the BC₁P₂F₂ generation was responsible in 2011 for the highest transgressive behavior and the BC₁P₁F₂ and F₃ generations made up the majority of this occurrence in 2012. Family 2 and 3 also displayed large occurrences for positive transgressive behavior for this trait as well but were not consistent. Family 2 displayed large amounts of transgressive progeny in the F₃ generation in 2011 with 14

progeny and Family 3 displayed a similar amount split between its BC₁P₁F₂ and F₃ generations in 2012. Large numbers of negative transgressive segregates also exist for this trait across years. In 2011, Family 1 displayed large amounts of negative occurrences with 14 negative transgressive segregates in the BC₁P₁F₂ generation and 10 in the F₃ generation. In 2012, all three families displayed a large amount of negative transgressive segregation. Little significance can be placed on these data since most values (data not shown) were within the non-discount market range and micronaire is a measure of fiber fineness that is confounded or influenced by fiber maturity.

Uniformity of fiber length is important in spinning since equipment must be set to account for specified fiber lengths and thus short fibers may be lost in processing. As with other fiber traits, a relatively large number of plants representing the three generations and families of this study exhibited transgressive segregation above the MPV, with fewer than 15 (5 %) plants in any given family in either year being transgressive above HPV or below the LPV (Tables 15 and 16). There were numbers that did appear on the negative side for this trait, but those numbers were almost equally matched by the number of positive transgressive segregates that were reported. Families 1 and 2 exhibited at least two positive transgressive segregates for this trait, but none were found in Family 3 in either year of this study. While numbers were not overwhelming for the transgressive segregates relative to the high and low parental plant value, the data suggest that, with these parents, improving uniformity of fiber length may be more difficult for breeders than improving some other HVI traits.

Segregating generations contained large numbers of transgressive progeny on both extremes of the parental range in this study for fiber elongation (Tables 15 and 16). Family 1 exhibited 19 and Family 2 contained 30 positive transgressive segregates above the HPV in 2011, both with the majority of these segregates appearing in the BC₁P₂F₂ generations, which would be the opposite of the preferred selection populations for fiber length and strength (Tables 15 and 16). These two families again in 2012 contained large numbers of positive transgressive segregates with Family 1 containing 16 total, 10 originating in the BC₁P₂F₂ generation. Family 2 exhibited large amounts of positive transgressive behavior in all generations in 2012 with a total of 67 transgressive progeny. Twenty-five of those progeny appeared in the BC₁P₁F₂ generation and 28 in the BC₁P₂F₂, and 14 in the F₃ generation. The 2011 growing season also contained two instances of large numbers of negative transgressive segregates for elongation in Family 1 and Family 3, again suggesting that in these families that the higher temperature environment of 2011 impacted the development of elongation. Transgressive segregation above the MPV averaged 134 for each family across years and generations. The families with large numbers of individuals exhibiting transgressive values below the LPV also contained lower numbers of transgressive segregates relative to the MPV. Family 2, that exhibited the most positive transgressive segregates over both years above the HPV had the highest number of transgressive segregates above the MPV each year. In cases where large amounts of positive and negative transgressive segregates are exhibited for this trait, these trends are also reflected in the means data for elongation for the families where these numbers occur.

Transgressive Segregation for Agronomic Traits

Lint percent can be an important selection criterion when selecting for agronomic or yield potential. Although this study was designed to evaluate transgressive potential for fiber length and strength based on individual plant data, the opportunity existed to evaluate the material for yield per plant and lint percent, both important components of economic and agronomic value. Improved cultivars obviously have a large basis in yield and yield- associated characteristics.

Family 1 had parents with the most favorable agronomic phenotypes, with Tamcot 22 which was developed and released as an adapted cultivar by Thaxton and Smith (2005) and 06 WE 62-4, which is an adapted breeding strain developed by the Texas A&M AgriLife Research Cotton Improvement Lab (C.W. Smith, pers. comm.). Unsurprisingly, the segregating generations within this family exhibited the most desirable lint percent values and equal or better lint yield values (Tables 6 and 12). In 2011, Family 1 exhibited 22 negative transgressive segregates below the LPV and 21 positive transgressive segregates above the HPV for lint percent (Table 20). The majority of these transgressive progeny on the negative side appeared in the BC₁P₁F₂ generation (lower lint percent parent) and the majority of the transgressive progeny appearing on the positive side were exhibited in the BC₁P₂F₂ generation (BC to the Tamcot 22 parent). The only other instance of large numbers of transgressive segregation appeared in Family 3 in 2012. This family exhibited 15 transgressive segregates below the LPV and 19 above the HPV. Nine of the 15 negative transgressive segregates originated in the BC₁P₁F₂ generation (BC to the lower lint percent parent),

while 14 of the 19 positive transgressive segregates were exhibited from the F₃ generation.

Family 2 was developed using the interspecific strain 04 SID 84-2 that exhibits a low lint percent relative to the Tamcot 22 parent (Tables 6 and 12). Thus, although Family 2 had a comparable number of transgressive segregates above the MPV relative to Family 1 and Family 2, only four plants in the segregating generations of this family exhibited transgressive segregation above the HPV, those being in the BC₁P₂F₂ generation (Table 20). While this could be discouraging from a breeding and selection perspective, these four plants would contain as much heterozygosity for other traits as the F₃ generation and could be of considerable value in a breeding program.

Also encouraging is the large number of transgressive segregates above the MPV (Table 20). This suggests that breeders could select for improved lint percent relative to the low lint percent parent in any segregating population.

Table 20. Transgressive segregation for lint yield and lint percent appearing in the F₃, BC₁P₁F₂, and BC₁P₂F₂ generations for three families grown in College Station, Texas in 2011 and 2012.

2011		Lint Yield			Lint Percent		
Family		above MPV	below LPV	above HPV	above MPV	below LPV	above HPV
1	Total	108	1	6	140	22	21
1	F ₃	31 b	0 a	4 a	45 b	5 b	6 b
1	BC ₁ P ₁ F ₂	51 a	1 a	2 ab	30 c	15 a	1 c
1	BC ₁ P ₂ F ₂	26 b	0 a	0 b	65 a	2 b	14 a
2	Total	198	0	21	186	0	0
2	F ₃	67 b	0 a	8 a	57 b	0 a	0 a
2	BC ₁ P ₁ F ₂	43 c	0 a	0 b	38 c	0 a	0 a
2	BC ₁ P ₂ F ₂	88 a	0 a	13 a	91 a	0 a	0 a
3	Total	161	4	1	112	14	1
3	F ₃	57 ab	1 ab	0 a	28 b	3 b	0 a
3	BC ₁ P ₁ F ₂	46 b	3 a	0 a	14 c	9 a	0 a
3	BC ₁ P ₂ F ₂	58 a	0 b	1 a	70 a	2 b	1 a
2012		Lint Yield			Lint Percent		
1	Total	155	26	8	119	1	2
1	F ₃	65 a	3 b	2 a	40 b	0 a	1 a
1	BC ₁ P ₁ F ₂	49 b	11 a	4 a	52 a	0 a	1 a
1	BC ₁ P ₂ F ₂	41 b	12 a	2 a	27 c	1 a	0 a
2	Total	35	4	0	118	0	4
2	F ₃	8 b	1 a	0 a	39 b	0 a	0 b
2	BC ₁ P ₁ F ₂	8 b	2 a	0 a	18 c	0 a	0 b
2	BC ₁ P ₂ F ₂	19 a	1 a	0 a	61 a	0 a	4 a
3	Total	117	17	0	153	15	19
3	F ₃	43 a	3 a	0 a	69 a	4 ab	14 a
3	BC ₁ P ₁ F ₂	38 a	6 a	0 a	32 c	9 a	3 b
3	BC ₁ P ₂ F ₂	36 a	8 a	0 a	52 b	2 b	2 b

† Above MPV, above the mid-parent value; Below LPV, below the low-parent value; Above HPV, above the high-parent value. Values for each generation (F₃, BC₁P₁F₂, and BC₁P₂F₂) taken from 100 selections / family / year.

‡ Family 1, 06 WE 62-4 X Tamcot 22; Family 2, 04 SID 84-2 X Tamcot 22; Family 3, TAM B 182-33 X Tamcot 22.

§ Values followed by the same letter are not different based on independent T-test ($p \leq 0.05$). Values are compared vertically within a single family, between generations for a trait.

Numbers appearing as transgressive segregates for lint yield displayed drastic differences for all three families over both years of the study (Table 20). In 2011, Family 1 contained a total of 108 progeny above the MPV, while in 2012, 155 progeny exceeded the MPV. Family 2 contained 198 progeny with values above the MPV for lint yield, but in 2012 this number dropped sharply to only 35. Family 3 displayed similar, although not so drastic, results as it contained 161 progeny above the MPV in 2011 but only 117 progeny above the MPV for lint yield in 2012. Transgressive segregation above the HPV or below the LPV numbers follow a similar pattern across years as 28 total progeny exhibit lint yields above the HPV across the three families in 2011, with 21 of the 28 found in Family 2. Only five progeny exhibit values below the LPV across all three families in 2011. This trend is reversed for 2012, as larger numbers of progeny were found below the LPV for all three families than above the HPV for this trait. These results may be a consequence of the difficult growing season in 2011 where the higher yield parents did not reach their yield potential essentially leveling individual plant yields. Forty-seven transgressive segregates appeared below the LPV in 2012, and only eight appeared above the HPV, again reflecting the better growing conditions. Twenty-six of the 47 (55 %) progeny below the LPV and all eight of the transgressive segregates above the HPV in 2012 were found in Family 1.

CONCLUSIONS

- Environment had a significant effect on fiber property performance, and abiotic stress levels for the plants appeared more visible in the 2011 growing season.
- Fiber length, uniformity, elongation and lint percent measured by HVI performed better in 2012 than in 2011; fiber strength, micronaire, and lint yield performed better in 2011 as opposed to 2012.
- The backcross generations toward the high and low quality parents did produce progeny that more closely resembled the phenotype of the recurrent parent in each population, and the backcross generation toward the high quality parents also provided a higher rate of transgressive segregation for these populations in the study suggesting its use would give the highest probability of achieving transgressive progeny.
- Although progeny were identified exhibiting EL fiber length in all families in this study, the families containing parentage with a background of extended fiber length, however, produced more progeny within both the EL and ELSU designated fiber length range.
- Parents with a specific fiber quality characteristic contributed, as expected, and produced progeny with higher means in those characteristics; although this result was not necessarily reflected in numbers of transgressive segregation observed in that population for that trait.

Data observed for means and transgressive segregation rates for plant material in this study indicated that both improved fiber length and strength could be achieved even when one parent used is not of that type. Although similar rates were not observed or confirmed as seen by Braden and Smith (2004a), selection of progeny with exceptional fiber quality was possible in the populations under study. This germplasm could be useful for other breeders looking to add value to their program's germplasm in these areas. This breeding and selection system could also be of value if applied to other plant material, but further study in these areas needs to be performed. This study confirmed, however, that for ELSU fiber length and improved fiber strength a cross designed with a parent more closely resembling the desired result would increase the probability for progeny resulting from the cross to achieve or exceed the desired result.

REFERENCES

- Al- Rawi, K.M., and R.J. Kohel. 1970. Gene action in the inheritance of fiber properties in intervarietal diallel crosses of Upland cotton, *Gossypium hirsutum* L. *Crop Sci.* 10:82- 85.
- American Society for Testing Materials (ASTM). 1994. Standard test methods for measurement of cotton fiber by high volume instruments (HVI) (D 4605- 86). p. 486- 494. *In Annual Book of ASTM Standards*. Vol. 07.02. ASTM, Philadelphia, PA.
- Australian Government Office of the Gene Technology Regulator. 2008. The biology of *Gossypium hirsutum* L. and *Gossypium barbadense* L. (cotton). February 2008. Version 2. OGTR, Barton ACT, Australia.
- Bayles, M.B., L.M. Verhalen, W.M. Johnson, and B.R. Barnes. 2005. Trends over time among cotton cultivars released by the Oklahoma Agricultural Experiment Station. *Crop Sci.* 45:966-980.
- Bell, M.A., and M.P. Travis. 2005. Hybridization, transgressive segregation, genetic covariation, and adaptive radiation. *Trends Ecol. Evol.* 20:358-361.
- Benedict, C.R., R.J. Kohel, and H.L. Lewis. 1999. Cotton Fiber Quality. p. 269-288. *In:* C. W. Smith and J. T. Cothren (ed.). *Cotton: Origin, history, technology, and production*. John Wiley & Sons Inc., New York, NY.

- Benzina, H., E. Hequet, N. Abidi, J-Y. Drean, and O. Harzallah. 2007. Using Fiber elongation to improve genetic screening in cotton breeding programs. *Textile Res. J.* 77(10): 770-778.
- Berger, G., S.S. Hague, C.W. Smith, P.S. Thaxton, and D.C. Jones. 2011. Development of Sea Island/Upland (SIUP) germplasm with unique fiber properties. *J. Cotton Sci.* 15:260–264.
- Bolek, Y., K.M. El-Zik, A.E. Pepper, A.A. Bell, C.W. Magill, P.M. Thaxton, and O.U. Reddy. 2005. Mapping of *verticillium* wilt resistance genes in cotton. *Plant Sci.* 168:1581-1590.
- Bowman, D.T., O.L. May, and D.S. Calhoun. 1996. Genetic base of upland cotton cultivars released between 1970 and 1990. *Crop Sci.* 36:577–581.
- Braden, C.A. 2001. Boll and fiber development in long staple upland cotton. MS Thesis. Texas A&M University, College Station, TX.
- Braden, C.A. 2005. Inheritance of cotton fiber length and distribution. Ph.D. Diss. Texas A&M University, College Station, TX.
- Braden, C.A., and C.W. Smith. 2004a. Fiber length development in near-long staple upland cotton. *Crop Sci.* 44:1553– 1559.
- Braden, C.A., and C.W. Smith. 2004b. Phenology measurements and fiber associations of near- long staple upland cotton. *Crop Sci.* 44:2032– 2037.

- Bridge, R.R., and W.R. Meredith, Jr. 1983. Comparative performance of obsolete and current cotton cultivars. *Crop Sci.* 23:949-952.
- Bridge, R.R., W.R. Meredith, Jr., and J.F. Chism. 1971. Comparative performance of obsolete varieties and current varieties of upland cotton. *Crop Sci.* 11:29-32.
- Brubaker, C.L., F.M. Bourland, and J.F. Wendell. 1999. The origin and domestication of cotton. p. 3-31. *In* C.W. Smith and J.T. Cothren (ed.). *Cotton –Origin, history, technology, and production.* John Wiley & Sons, New York, NY.
- Calhoun, D.S. , D.T. Bowman, and O.L. May. 1997. Pedigrees of upland and pima cotton cultivars released between 1970 and 1995. *Mississippi Agric. For. Exp. Stn. Bull.* 1069.
- Calhoun, D.S., J.E. Jones, W.D. Caldwell, E. Burris, B.R. Leonard, S.H. Moore, and W. Aguillard. 1994. Registration of La. 850082FN and La. 850075FHG, two cotton germplasm lines resistant to multiple insect pests. *Crop Sci.* 34:316-317.
- Chee, P., X. Draye, C.X. Jiang, L. Decanini, T. Delmonte, R. Bredhauer, C.W. Smith, A.H. Paterson 2005. Molecular dissection of interspecific variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcross-self approach: III. Fiber length. *Theor. Appl. Genet.* 111:772–781.
- Constable, G.A., P.E. Ried, and N.J. Thomson. 2001. Approaches utilized in breeding and development of cotton cultivars in Australia. p. 1–16. *In* J.N. Jenkins and S.

Saha (ed.). Genetic improvement of cotton: Emerging technologies. Science Publ. Inc., Enfield, NH.

Cotton Council International. 2012. Economic and Market data. Available at <http://www.cottonusa.org/economicdata/index.cfm?ItemNumber=820&navItemNumber=2540>. CCI, Washington, DC.

Cotton Incorporated and The United States Department of Agriculture. 2011. The U.S. cotton fiber chart. Available at <http://www.cottoninc.com/fiber/quality/US-Fiber-Chart/> (verified Dec. 2012). Cotton Inc., Cary, NC. USDA, Washington, DC.

Cotton Incorporated and The United States Department of Agriculture. 2012. The U.S. cotton fiber chart. Available at <http://www.cottoninc.com/fiber/quality/US-Fiber-Chart/> (verified Dec. 2012). Cotton Inc., Cary, NC. USDA, Washington, DC.

Cotton Incorporated and The United States Department of Agriculture- Agricultural Management Service. 2012. Quality summary of 2012 U.S. Upland cotton- by classing office. Available at <http://www.cottoninc.com/fiber/quality/Crop-Quality-Reports/Final-Cotton-Crop-Quality-Summary/> (verified Dec. 2012). Cotton Inc., Cary NC. USDA- AMS, Washington, DC.

Cotton Incorporated. 2009. Monthly Economic Newsletter, Mar. 2009. Cotton Inc., Cary, NC.

Cotton Incorporated. 2011. U.S. cotton fiber chart 2009/2010. Available at <http://www.cottoninc.com/2010-US-Cotton-Fiber-Chart/> (verified 26 August 2012). Cotton Inc., Cary, NC.

Cotton Incorporated. 2013a. Classification of upland cotton. Available at <http://www.cottoninc.com/fiber/quality/Classification-Of-Cotton/> (verified 18 Feb. 2013). Cotton Inc., Cary, NC.

Cotton Incorporated. 2013b. Classification of upland cotton. Available at <http://www.cottoninc.com/fiber/quality/Classification-Of-Cotton/Classification-Upland-Cotton/> (verified 18 Feb. 2013). Cotton Inc., Cary, NC.

Cotton Incorporated. 2013c. Cotton crop quality. Available at <http://www.cottoninc.com/fiber/quality/Crop-Quality-Reports/>. Cotton Incorporated, Cary, NC.

Cotton Incorporated. 2013d. Cotton standards. Available at <http://www.cottoninc.com/fiber/quality/Standards/> (verified 19 Feb. 2013). Cotton Inc., Cary NC.

Cotton Incorporated. 2013e. Fiber processing information. Available at <http://www.cottoninc.com/product/Textile-Research/Fiber-Processing/> (verified 26 August 2013). Cotton Inc., Cary, NC.

Cotton Incorporated. 2013f. U.S. Cotton Fiber Chart.

<http://www.cottoninc.com/fiber/quality/US-Fiber-Chart/> (accessed 4 April 2013). Cotton Incorporated, Cary, NC.

Culp, T. W., D. C. Harrell and T. Kerr. 1979. Some genetic implications in the transfer of high fiber strength genes to upland cotton. *Crop Sci.* 19: 481–484.

Culp, T.W. 1979. Notice to plant breeders and geneticists relative to release of five Noncommercial breeding stocks of extra-long staple Upland cotton, Sealand 542, Earlistaple 7, Line F (Hybrid 330), FJA, and FTA. *S.C. Agric. Exp. Stn Bull.*

Culp, T.W. 1992. Simultaneous improvement of lint yield and fiber quality in upland cotton. p. 301. *In* Jia, S. (ed.). *Transgenic cotton*. Elsevier Sci., New York, NY.

Culp, T.W., and C.C. Green. 1992. Performance of obsolete and current cultivars and Pee Dee germplasm lines of cotton. *Crop Sci.* 32:35-41.

Culp, T.W., and D.C. Harrell. 1973. Breeding methods for improving yield and fiber quality of upland cotton (*Gossypium hirsutum* L.). *Crop Sci.* 3:686- 689.

Culp, T.W., and D.C. Harrell. 1974. Breeding quality cotton at the Pee Dee experiment station, Florence, S.C. USDA ARS-S-30, New Orleans, LA.

Culp, T.W., and D.C. Harrell. 1975. Influence of lint percentage, boll size, and seed size on lint yield of upland cotton with high fiber strength. *Crop Sci.* 15:741-746.

- Culp, T.W., and D.C. Harrell. 1977. Yield and fiber quality improvements in upland cotton (*Gossypium hirsutum* L.). S.C. Agric. Exp. Stn. Tech. Bull. No.1061.
- Deussen, H. 1992. Improved cotton fiber properties: the textile industry's key to success in global competition. p. 43-64. *In*: Proc Cotton Fiber Cellulose: Structure, Function and Utilization Conference. National Cotton Council of America, Memphis, TN.
- deVicente, M.C., S.D. Tanksley. 1993. QTL analysis of transgressive segregation in an interspecific tomato cross. *Genetics*. 134:585-96.
- Draye, X., P. Chee, C.X. Jiang, L. Decanini, T.A. Delmonte, R. Bredhauer, C.W. Smith, and A.H. Patterson. 2005. Molecular dissection of interspecific variation between *Gossypium hirsutum* and *G. barbadense* (cotton) by a backcross-self approach: II Fiber fineness. *Theor. Appl. Genet.* 111:764-771.
- Feaster, C.V., and E.L. Turcotte. 1976. Registration of Pima S-2 cotton. *Crop Sci.* 16: 603.
- Fehr, W.R. 1991. Principles of cultivar development. Vol. I. Theory and Technique. Macmillan Publishing, New York, NY.
- Felker, S.G. 2001. Fiber quality and new spinning technologies. p. 5-7. *In* Proc. Beltwide Cotton Conf., 9-13 Jan. 2001, Anaheim, CA. Natl. Cotton Council, Memphis, TN.

Fiori, L.A., and J.E. Sands. 1956. Some observations of maximum yarn strength and its relation to processing efficiency. *Textile Quality Control Papers* 3: 218-225.

Fiori, L.A., and J.J. Brown. 1951. Effects of cotton fiber fineness on the physical properties of single yarns. *Textile Research J.* 21: 750-757.

Fiori, L.A., J.J. Brown, and J.E. Sands. 1956. The effect of cotton fiber strength on the properties of 2-ply carded yarns. *Textile Research J.* 26: 296-302.

Fiori, L.A., J.J. Brown, N.A. Howell, J.E. Sands, and H.W. Little. 1957. Evaluation of the yarn properties of a high-strength interspecies cotton. *Textile Research J.* 27: 332-339.

Franca, M.G.C., A.T.P. Thi, C. Pimental, R.O.P. Rossiello, Y.Z.Fodil and D. Laffary. 2000. Differences in growth and water relations among *Phaseolus vulgaris* cultivars in response to induced drought stress. *Environ. Exp. Bot.* 43:227-237.

Fryxell, P.A. 1979a. The origin and spread of the tribe. Chapter 4. p. 131-145. *In* The natural history of the cotton tribe (*Malvaceae*, tribe *Gossypieae*). Texas A & M University Press, College Station, TX, USA.

Fryxell, P.A. 1979b. The influence of man. Chapter 6. p. 159-177. *In* The natural history of the cotton tribe (*Malvaceae*, tribe *Gossypieae*). Texas A & M University Press, College Station, TX, USA.

- Goodell, P.B., and G.H. Montez. 1994. Acala cotton tolerance to southern root-knot nematode, *Meloidogyne incognita*. p. 265-267. Proc. of Beltwide Cotton Prod. Conf., Natl. Cotton Council of America, Memphis, TN.
- Gordon, S. 2007. Cotton fibre quality. p. 68-100. *In* Gordon, S., & Y-L. Hsieh (ed.). Cotton: Science and technology. Woodhead Publishing Limited, Boca Raton, Florida.
- Green, C.C., and T.W. Culp. 1990. Simultaneous improvement of yield, fiber quality, and yarn strength in upland cotton. *Crop Sci.* 30:66- 69.
- Gregory, K., E.H. Ng, C.W. Smith, E. Hequet, and S. Hague. 2012. Fiber and yarn performance of upland cotton with improved fiber bundle strength. *Crop Sci.* 52:1-7.
- Hague, S.S., C.W. Smith, G. Berger, J. Clement, and D.C. Jones. 2011. Variation in an extra- long staple upland X medium staple upland cotton F2 population. *J. of Cotton Sci.* 15:265-270.
- Hake, S.J., K.D. Hake, and T.A. Kerby. 1996a. Cotton and the environment. p. 324-325. *In* S.J. Hake, T.A. Kerby, and K.D. Hake (ed.). Cotton production manual. University of California-Division of Agriculture and Natural Resources Publication. No. 3352. Communication Services, University of California, Oakland, CA.

Hake, S.J., K.D. Hake, and T.A. Kerby. 1996b. Cotton and the environment. p. 326-328.

In S.J. Hake, T.A. Kerby, and K.D. Hake (ed.). Cotton production manual.

University of California-Division of Agriculture and Natural Resources

Publication. No. 3352. Communication Services, University of California,

Oakland, CA.

Hake, S.J., K.D. Hake, and T.A. Kerby. 1996c. Preharvest/harvest decisions. p. 143-144.

In S.J. Hake, T.A. Kerby, and K.D. Hake (ed.). Cotton production manual.

University of California-Division of Agriculture and Natural Resources

Publication. No. 3352. Communication Services, University of California,

Oakland, CA.

Han, Z.G., C.B. Wang, X.L. Song, et al. 2006. Characteristics, development and

mapping of *Gossypium hirsutum* derived EST-SSRs in allotetraploid cotton.

Theor. Appl. Genet. 112:430-439.

Heap, S.A. 2000. The meaning of micronaire. p. 97-113. *In* Proc. Int. Cotton Conf.

Bremen, Bremen, Germany, 1-4 Mar. 2000. Faserinstitut, Bremen, Germany.

Hequet, E. Personal Communication. 2010.

Hequet, E., B. Wyatt, N. Abidi, and D.P. Thibodeaux. 2006. Creation of a set of

reference material for cotton fiber maturity measurements. Textile Res. J. 76:

576-586.

Hequet, E., N. Abidi, and J. Gannaway. 2007. Relationships between HVI, AFIS, and yarn textile properties. International Cotton Research Conference 10-14 Sept. 2007, Lubbock, TX.

Hequet, E., and N. Abidi. 2007. Thermogravimetric analysis of cotton fibers and relationships with their physical properties. *Journal of Appl. Poly. Sci.* 103 (6): 3476-3482.

Hequet, E.F., and M.D. Etheridge. 2000. Fiber properties and textile performance of transgenic cotton versus parent varieties. p. 488-494. *In Proceedings of the Beltwide Cotton Conference*. Dugger, P., and D. Richter (ed.). National Cotton Council of America, Memphis, TN.

Herring, R.J. 2005. Miracle seeds, suicide seeds and the poor: GMOs, NGOs, farmers, and the state. *In R. Ray and M.F. Katzenstein (ed.). Social movements in India: Poverty, power, and politics*. New Delhi: Oxford University Press.

Hertel, K.L., and C.J. Craven. 1956. Cotton fiber bundle elongation and tenacity as related to some fiber and yarn properties. *Textile Research J.* 26:479-484.

Jiang, C.X., R.J. Wright, K.M. El-Zik, A.W. Paterson. 1998. Polyploid formation created unique avenues for response to selection in *Gossypium* cotton. *Proc. Natl. Acad. Sci., USA.* 95:4419-4424.

- Johnson, D.R. 1980. Suppression of *Heliothis* spp. on cotton by using *Bacillus thuringiensis*, *Baculovirus heliothis*, and two feeding adjuvants. *J. of Econ. Ento.* 75 (2): 207-210.
- Joy, K., C.W. Smith, E. Hequet, S. Hague, P.S. Thaxton, and C. Souder. 2010. Fiber properties and mini-spun yarn performance of extra long staple upland cotton. *J. Cotton Sci.* 14:82–90.
- Joy, K.S., C.W. Smith, S. Hague, and D.C. Jones. 2011. Diallel analysis of fiber length and fiber bundle strength using extra long staple upland, mutated upland, and interspecific hybrid germplasm [Online]. Available at <http://ncc.confex.com/ncc/2011/flvgateway.cgi/id/3405?recordingid=3405> (accessed Oct. 2012). Beltwide Cotton Conf. Atlanta, GA. 4- 7 Jan. 2011. Natl. Cotton Council, Memphis, TN.
- Joy, K.S., C.W. Smith, S. Hague, and D.C. Jones. 2012. Generation means analysis of fiber length and fiber bundle strength using extra-long staple upland, mutated upland, and interspecific hybrid germplasm. Beltwide Cotton Conf. Orlando, FL. 3- 6 Jan. 2012. Natl. Cotton Council, Memphis, TN.
- Kelly, C.M., E.F. Hequet, and J.K. Dever. 2012. Interpretation of AFIS and HVI fiber property measurements in breeding for cotton fiber quality improvement. *J. of Cotton Sci.* 16:1-16.

- Kennett, R.M. 2009. The evaluation of high tannin cotton lines for resistance to *Rhizoctonia solani* and *Pythium aphanidermatum*. MS Thesis. Texas A&M University, College Station, TX.
- Kerby, T.A., J. Supak, J.C. Banks, and C.E. Snipes. 1992. Timing defoliations using nodes above cracked boll. p. 155-156. *In* D.J. Herber and D.A. Richter (ed.). Proc. Beltwide Cotton Res. Conf. Nashville, TN. 7 – 10 Jan. 1992. National Cotton Council of America, Memphis, TN.
- Kohel, R.J., J. Yu, Y-H. Park and G. R. Lazo. 2001. Molecular mapping and characterization of traits controlling fiber quality in cotton. *Euphytica* 121: 163–172.
- Lacape, J.M., and T.B. Nguyen. 2005. Mapping quantitative trait loci associated with leaf and stem pubescence in cotton. *J. Hered.* 96(4):441–444.
- Lacape, J.M., T.B. Nguyen, S. Thibivilliers, B. Bojinov, B. Courtois, and R.G. Cantrell. 2003. A combined RFLP-SSR-AFLP map of tetraploid cotton based on a *Gossypium hirsutum* · *Gossypium barbadense* backcross population. *Genome* 46:612–626.
- Latimer, S.K., T.P. Wallace, and D.S. Calhoun. 1996. Cotton breeding: High volume instruments versus conventional fiber quality testing. p. 1681. *In* Proc. Belt. Cotton Res. Conf., New Orleans, LA. 9-12 Jan. 1996. Natl. Cotton Council, Memphis, TN.

- Liu, S., R.G. Cantrell, J.C. McCarty, Jr., and J.M. Stewart. 2000. Simple sequence repeat- based assessment of genetic diversity in cotton race stock accessions. *Crop Sci.* 40:1459-1469.
- Longenberger, P.S. 2005. Development of a screening method for drought tolerance in cotton seedlings. MS Thesis. Texas A&M University, College Station, TX.
- Longenberger, P.S. 2008. Evaluation of chlorophyll fluorescence as a tool for the identification of drought tolerance in upland cotton. Ph. D. Diss. Texas A&M University, College Station, TX.
- Longenberger, P.S., C.W. Smith, P.S. Thaxton, and B.L. McMichael. 2006. Development of a screening method for drought tolerance in cotton seedlings. *Crop Sci.* 46:2104- 2110.
- Matic-Leigh, R. and D.A. Cauthen. 1994. Determining cotton fiber maturity by image analysis. Part I. Direct measurement of cotton fiber characteristics. *Text. Res. J.* 64:534–544.
- May, O. L. 2000. Genetic variation in fiber quality. p. 183–229. *In* A.S. Basra (ed.). Cotton fibers, developmental biology, quality improvement, and textile processing. Food Products Press, New York, NY.
- May, O.L. 1999. Genetic variation in fiber quality. Chapter 9. p. 183-229. *In* A.S. Basra (ed.) Cotton fibers, developmental biology, quality improvement, and textile processing. Hawthorne Press, New York, NY.

- May, O.L. 2001. Registration of PD 94045 germplasm line of Upland cotton. *Crop Sci.* 41:279-280.
- May, O.L., and G.M. Jividen. 1999. Genetic modification of cotton fiber properties as measured by single- and high-volume instruments. *Crop Sci.* 39:328-333.
- May, O.L., D.T. Bowman, and D.S. Calhoun. 1995. Genetic diversity of U.S. upland cotton cultivars released between 1980 and 1990. *Crop Sci.* 35:1570–1574.
- McCreight, D.J. 1992. Cotton quality requirements for producing world class textiles. *In: Proc. Beltwide Cotton Conf., Natl. Cotton Council of America, Memphis, TN.*
- McMichael, B.L., and J.E. Quisenberry. 1993. The impact of the soil environment on the growth of root systems. *Environ. Exp. Bot.* 33:53-61.
- Meredith, W.R., Jr. 1977. Backcross breeding to increase fiber strength of cotton. *Crop Sci.* 17:172–175.
- Meredith, W.R., Jr., J.J. Heitholt, W.T. Pettigrew, and S.T. Rayburn, Jr. 1997. Comparison of obsolete and modern cotton cultivars at two nitrogen levels. *Crop Sci.* 37:1453-1457.
- Meredith, W.R., Jr., T.W. Culp, K.Q. Robert, G.F. Ruppenicker, W.S. Anthony, and J.R. Williford. 1991. Determining future cotton variety fiber quality objectives. *Textile Res. J.* 61:715-720.

- Meyer, L., J. Kiawu, and S. MacDonald. 2012. Cotton and wool outlook: December 2012. <http://www.ers.usda.gov/publications/cws-cotton-and-wool-outlook/cws-12i.aspx> (updated 13 Dec. 2012; accessed Jan. 2013). USDA- ERS, Washington, DC.
- Miller, P. A., and J.O. Rawlings. 1967. Selection for increased lint yield and correlated responses in upland cotton, *Gossypium hirsutum* L. *Crop Sci.* 7: 634-640.
- Montalvo, J.G., Jr. 2005. Relationship between micronaire, fineness, and maturity. Part I. Fundamentals. *J. of Cotton Sci.* 9:81-88.
- Montalvo, J.M., Jr., and T. Von Hoven. 2005. Cotton fiber quality. p. 822. In *Near Infrared Spectroscopy in Agriculture*. Roberts, C.A., J. Workman Jr., and J.B. Reeves III (ed.). Crop Science Society of America Pub., Washington, DC.
- Moulherat, C., M. Tengberg, J.F. Haquet, and B. Mille. 2002. First evidence of cotton at neolithic Mehrgarh, Pakistan: Analysis of mineralized fibers from a copper bead. *J. of Archaeological Sci.* 29: 1393-1401.
- National Cotton Council of America and The Cotton Foundation. 2007. The first 40 days, the most critical period in cotton production. Available at www.cottonexperts.com. The Cotton Foundation, Cordova, TN.
- National Cotton Council of America. 2009. 2009 CCC Loan schedule of premiums and discounts for upland and ELS cotton. [Online]. Available at

<http://www.cotton.org/econ/govprograms/cccloan/upload/2009Loan.pdf> (verified 3 March 2013).

National Oceanic and Atmospheric Administration, ClimateTexas, and Texas A&M University. Monthly weather report: July 2011 & 2012. Available at <http://climatexas.tamu.edu/cs-monthly-summaries/july-2012> (visited Sept. 2013). NOAA, Silver Spring, MD. ClimateTexas- Texas A&M, Dickinson, TX.

Orr, R.S., L.C. Weiss, and J.N. Grant. 1955. Relation of single fiber to flat bundle strength and elongation of cotton. *Textile Research J.* 25:939-946.

Paterson, A.H., R. Smith. 1999. Future horizons: Biotechnology for cotton improvement. p. 415-432. *In* Smith, C.W., and J.T. Cothren (ed.). *Cotton: Origin, history, technology and production*. John Wiley & sons, New York, NY.

Paudel, D.R. 2012. Evaluating the potential of new testing methods for cotton (*Gossypium hirsutum* L.) breeding. MS Thesis. Texas Tech University, Lubbock, TX.

Percival, A.E. 1987. The national collection of *Gossypium* germplasm. USDA Southern Cooperation Series Bulletin No. 321. Texas Agricultural Experiment Station, College Station, TX.

Percy, R.G. 2003. Comparison of bulk F2 performance testing and pedigree selection in thirty Pima cotton populations. *J. Cotton Sci.* 7: 170–178.

- Percy, R.G., R.G. Cantrell, and J. Zhang. 2006. Genetic variation for agronomic and fiber properties in an introgressed recombinant inbred population of cotton. *Crop Sci.* 46:1311-1317.
- Pillay, K.P.R. 1975. The structure and properties of open-end yarns, Part I: A study of fiber configuration and migration. *Textile Res. J.* 45: 366-372.
- Quisenberry, J.E., and R.J. Kohel. 1975. Growth and development of fiber and seed in upland cotton. *Crop Sci.* 15:463-467.
- Ragsdale, P.I. 2003. Diallel analysis of within-boll seed yield components and fiber properties in upland cotton (*Gossypium hirsutum* L.) and breeding potential for heat tolerance. Ph. D. Diss. Texas A&M University, College Station, TX.
- Reddy, K.N., I.C. Burke, J.C. Boykin Jr., and J.R. Williford. 2009. Narrow-row cotton production under irrigated and nonirrigated environment: Plant population and lint yield. *J. of Cotton Sci.* 13:48-55.
- Reinisch, A., J.M. Dong, C.L. Brubaker, D.M. Stelly, J.F. Wendel, and A.H. Paterson. 1994. A detailed RFLP map of cotton *Gossypium hirsutum* × *Gossypium barbadense*: chromosome organization and evolution in a disomic polyploid genome. *Genetics* 138:829-847.
- Rhyne, C.L. 1959. Linkage studies in *Gossypium*. I. Altered recombination in allotetraploid *G. hirsutum* L. following linkage group transference from related diploid species. *Genetics* 43 : 822-834.

- Rieseberg, L.H., A. Widmer, A.M. Arntz, and J.M. Burke. 2003. The genetic architecture necessary for transgressive segregation is common in both natural and domesticated populations. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 358:1141–1147.
- Riley Jr., C.R., 1997. Improved high volume instrument elongation measurements. *J. of Cotton Sci.* 1:61-71.
- Roberts, P.M., G.A. Herzog, D.C. Jones, and J.R. Ruberson. 1997. Cotton insects. *Ga. Agric. Exp. Stn. Spec. Publ.* 91:709.
- Rungis, D., D. Llewellyn, E.S. Dennis, and B.R. Lyon. 2005. Simple sequence repeat (SSR) markers reveal low levels of polymorphism between cotton (*Gossypium hirsutum* L.) cultivars. *Aust. J. Agric. Res.* 58: 301-307.
- SAS Institute. 1999. SAS/STAT guide for personal computers, Version 8 ed. SAS Institute, Cary, NC.
- SAS version 9.3. 2013. SAS Institute, Cary, NC.
- Schwartz, B.M., and C.W. Smith. 2008. Genetic gain in yield potential of upland cotton under varying plant densities. *Crop Sci.* 48:601-605.
- Shen, X., G.V. Becelare, P. Kumar, R.F. Davis, O.L. May, and P. Chee. 2006a. QTL mapping for resistance to root-knot nematodes in the M-120 RNR Upland cotton line (*Gossypium hirsutum* L.) of the Auburn 623 RNR source. *Theor. Appl. Genet.* [Online]. Available at <http://dx.doi.org/10.1007/s00122-006-0401-4>.

- Shen, X.L., W.Z. Guo, Q. Lu, X.F. Zhu, Y.L. Yuan, and T.Z. Zhang. 2006b. Genetic mapping of quantitative trait loci for fiber quality and yield trait by RIL approach in Upland cotton. *Euphytica* 155:137-380.
- Shen, X.L., W.Z. Guo, X.F. Zhu, Y.L. Yuan, J.Z. Yu, R.J. Kohel, and T.Z. Zhang. 2004. Molecular mapping of QTL for fiber qualities in three diverse lines in Upland cotton using SSR markers. *Mol. Breed.* 15:169–181.
- Shofner, F.M., G.F. Williams, C.K. Bragg, and P.E. Sasser. 1988. Advanced fiber information system: A new technology for evaluating cotton. Conference of The Textile Institute. 7-8 Dec. 1988. Coventry, UK.
- Shofner, F.M., Y.T. Chu., and D.P. Thibodeaux. 1990. An overview of the advanced fiber information system. p. 173–181. *In Proc. Int. Cotton Conf., Faserinstitut, Bremen, Germany.*
- Smith, C.W. 1995. Cotton (*Gossypium hirsutum* L.). Chapter 6. p. 287-349. *In* C.W. Smith (ed.). *Crop production: Evolution, history, and technology.* John Wiley and Sons Inc., New York, NY.
- Smith, C.W. 2003. Registration of TAM 94L-25 and TAM 94J-3 germplasm lines of upland cotton with improved fiber length. *Crop Sci.* 43:742–743.
- Smith, C.W. Personal communication. 2012.
- Smith, C.W. Personal communication. 2013.

- Smith, C.W., and G.G. Coyle. 1997. Association of fiber quality parameters and within boll yield components in upland cotton. *Crop Sci.* 37:1775-1779.
- Smith, C.W., C.A. Braden, and E.F. Hequet. 2009a. Generation mean analysis of near long staple fiber length in TAM 94L-25 upland cotton. *Crop Sci.* 49:1638–1646.
- Smith, C.W., R.G. Cantrell, H.S. Moser, and S.R. Oakley. 1999. History of cultivar development in the United States. p. 99–171. *In* C.W. Smith and J.T. Cothren (ed.). *Cotton: Origin, history, technology, and production*. John Wiley & Sons, New York, NY.
- Smith, C.W., S. Hague, E. Hequet, P.S. Thaxton, and I.N. Brown. 2008. Development of extra long staple upland cotton. *Crop Sci.* 48:1823–1831.
- Smith, C.W., S. Hague, P.S. Thaxton, E. Hequet, and D. Jones. 2009b. Registration of eight extra long staple upland cotton germplasm lines. *J. Plant Registration* 3:81–85.
- Smith, D.T. 2001. Cotton gin by-product use in beef cattle and dairy cow diets. *Soil & Crop Sci. Dept. Technical Report*. 8 Jan. 2001. Texas A&M University, College Station, TX.
- Smith, H., and R. Zhu. 1999. The spinning process. pp. 729–749. *In* C.W. Smith and J.T. Cothren (ed.). *Cotton: Origin, history, technology, and production*. John Wiley & Sons, Inc., New York, NY.

- Stephens, S.G. 1949. The cytogenetics of speciation in *Gossypium*. I. Selective elimination of the donor parent genotype in interspecific backcrosses. *Genetics* 34:627–637.
- Tanksley, S.D., and S.R. McCouch. 1997. Seed banks and molecular maps: unlocking genetic potential from the wild. *J. of Sci.* 277:1063-1066.
- Texas Department of Agriculture. 1998. Producer Info- Texas Agricultural Statistics Service- Crop Reports- Cotton. Available at <http://www.agr.state.tx.us/> (accessed Nov. 2012). TDA, Austin, TX.
- Thaxton, P., and C.W. Smith. 2005. Registration of Tamcot 22 high yielding upland cotton cultivar. *Crop Sci.* 45:1165.
- Thaxton, P.M., C.W. Smith, and R. Cantrell. 2004 Registration of TAM 96WD-18 Upland cotton germplasm line with improved fiber length and strength. *Crop Sci.* 45(3):1172.
- The National Cotton Council of America. 2012. The economic outlook for U.S. cotton. Available at <https://www.cotton.org/econ/reports/annual-outlook.cfm> (accessed 26 Jan. 2013). NCC, Washington, DC.
- USDA. 1994. Landraces within breeding programs. *Cotton. Exploiting genetic diversity.* p. 26. USDA, Washington, DC.
- USDA- Agricultural Research Service, National Genetic Resources Program. 2009. Germplasm Resources Information Network (GRIN). [Online Database].

Available at <http://www.ars-grin.gov/cgi-bin/npgs/html/taxgenform.pl>. (verified 2 Oct. 2013). National Germplasm Resources Laboratory, Beltsville, MD.

USDA- Economic Research Service. 2012. Cotton and wool- overview [Online].

Available at <http://www.ers.usda.gov/topics/crops/cotton-wool.aspx> (accessed Nov. 2012). USDA- ERS, Washington, DC.

USDA- Foreign Agricultural Service. 2011. Cotton- Circular series report:

December, 2011-2012. USDA- FAS, Washington, DC.

USDA- National Agricultural Statistics Service, Agricultural Statistics Board. 2012.

Crop production report (May 2012). Available at

<http://usda.mannlib.cornell.edu/MannUsda/viewDocumentInfo.do?documentID=1046> (accessed May 2013). USDA- NASS, Washington, DC.

USDA- World Agricultural Outlook Board. 2013. January world agricultural supply and

demand estimates report. Available at

<http://www.usda.gov/oce/commodity/wasde/> (accessed 14 March 2013). USDA- WAOB, Washington, DC.

USDA. 2008. United States Cotton Supply and Distribution. 10 Oct. 2008. United States

Department of Agriculture. 26 Oct. 2008. Available at

<http://www.fas.usda.gov/psdonline/psdreport.aspx?hidReportRetrievalName=BVS&hidReportRetrievalID=857&hidReportRetrievalTemplateID=3> (verified 12 Sept. 2013). USDA, Washington, DC.

- Vaughn, E., and Rhodes, J. 1977. The effects of fiber properties and preparation on trash removal and properties of open-end cotton yarns. *J. Engineer. Ind.* 99(1): 71-76.
- Vernon, B.O., and P.D. Bonnin. 1997. "King Cotton In The Civil War." The American Civil War Home Page. Available at <http://www.civilwarhome.com/> (modified 16 Feb. 2002; accessed 14 Nov. 2012). Macmillan, New York, NY.
- Virgin, W.P., and H. Wakeham. 1956. Cotton quality and fiber properties. Part IV: The relation between single fiber properties and the behavior of bundles, slivers, and yarns. *Textile Research J.* 26: 177-191.
- Walhood, V.T. 1960. Growth in immature bolls after defoliation. p. 14-20. *In Proc. Beltwide Cotton Physiology and Defoliation Conf. Memphis, TN. 14-15 Jan. 1960. National Cotton Council of America, Memphis, TN.*
- Wang, C., and P.A. Roberts. 2006. A Fusarium wilt resistance gene in *Gossypium barbadense* L. and its effect on root-knot nematode-wilt disease complex. *Phytopathology* 96:727-734.
- Wang, C., M. Ulloa, and P.A. Roberts. 2007. Identification and mapping of microsatellite markers linked to the root-knot nematode resistance gene *rkn1* in Acala NemX cotton (*Gossypium hirsutum* L.). *Theor. Appl. Genet.* 112:770-777.
- Wang, K., Z. Wang, F. Li, W. Ye, J. Wang *et al.* 2012. The draft genome of a diploid cotton *Gossypium raimondii*. *Nat. Genet.* 44: 1098-1103.

- Wartelle, L.H., J.M. Bradow, O. Hinojosa, and A.B. Pepperman. 1995. Quantitative cotton fiber maturity measurements by x-ray fluorescence spectroscopy and Advanced Fiber Information System. *J. Agric. Food Chem.* 43: 1219-1223.
- Wendel J.F., and R.C. Cronn. 2003. Polyploidy and the evolutionary history of cotton. *Adv. Agron.* 78:139–186.
- Zhang, M., J.C. McCarty, J.N. Jenkins, and S. Saha. 2002. Assessment of day-neutral backcross populations of cotton using AFLP markers. *J. Cotton Sci.* 6:97-103.
- Zhang, T., Y. Yuan, J. Yu, W. Guo, and R.J. Kohel. 2003. Molecular tagging of a major QTL for fiber strength in Upland cotton and its marker-assisted selection. *Theor. Appl. Genet.* 106:262-268.