INHERITANCE OF COTTON FIBER LENGTH AND STRENGTH

A Dissertation

by

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ABSTRACT

The U.S. cotton industry has become predominantly an export market which requires a higher standard of fiber quality than does the domestic market. To remain competitive, U.S. cotton must meet the quality standards demanded by the consumers of raw cotton whether domestic or abroad. Diallel and generation means analyses (GMA) were conducted on fiber quality data of nine and five parental genotypes, respectively, to gain a better understanding of the genetic control of cotton fiber length and strength as well as to ascertain the value of the reported genotypes toward the improvement of fiber quality. Parental genotypes included extra-long staple uplands (*Gossypium hirsutum,* L.), EMS mutated uplands, high strength uplands, and interspecific hybrids.

General combining ability (GCA) and specific combining ability (SCA) were estimated according to Griffing's diallel Model I, Method 4 for lint percent, high volume instrument (HVI) upper half mean length (UHML), fiber bundle strength (Str), uniformity index, elongation, micronaire, advanced fiber information system (AFIS) upper quartile length on a weight basis, mean length on a number basis, short fiber content on a number basis, immature fiber content, maturity ratio, and standard fineness. Estimates of GCA were significant across environments for all traits. SCA effects were significant for most traits but accounted for a smaller proportion of the variability in comparison to GCA effects. TAM B182-33 ELS would be the parent of choice to simultaneously improve fiber length and Str.

The GMA was conducted on the parental, F_1, F_2, and backcross generations.

Low levels of transgressive segregation for both UHML and Str were observed for some populations. Broad sense heritability ranged from 0.00 to 0.67 for UHML and from 0.22 to 0.82 for Str. Additive gene action was significant for all but three parental combinations for UHML and for all parental combinations for Str. Generally, the significance and magnitude of additive genetic effects were more consistent among parental combinations and years than were non-additive genetic effects for both UHML and Str. Dominance and epistatic genetic effects often were of a greater magnitude than additive genetic effects but in an inconsistent manner, and in both positive and negative directions.

DEDICATION

To Lindsey. This would not have been possible without your love, support, encouragement, and, very often, undeserved patience. You made many sacrifices in order for me to accomplish my dreams for which I am deeply grateful. You truly are one-of-a-kind.

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NOMENCLATURE

AFIS	Advanced fiber information system
Elon	Elongation
ELS	Extra long staple
GCA	General combining ability
GMA	Generation means analysis
Hs	Standard fineness
HVI	High volume instrument
IFC	Immature fiber content
Ln	Mean length on a number basis
LP	Lint percent
Mic	Micronaire
MR	Maturity ratio
SCA	Specific combining ability
SFCn	Short fiber content on a number basis
Str	Fiber bundle strength
UHML	Upper half mean length
UI	Uniformity index
UQLw	Upper quartile length on a weight basis
USDA	United States Department of Agriculture

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1. INTRODUCTION

Cotton (*Gossypium sp.*) is grown in 17 states with two main economic products, fiber and seeds, which generated a combined value of $8.3 billion in 2010 (USDA, 2010). Close to 85%, $7.3 billion in 2010, of that value is attributable to the fiber, which serves as a raw material for the manufacturing of textiles. Texas is the largest producer of upland cotton in the U.S., generating $3.1 billion in 2010 (USDA, 2010). The buyers of U.S. cotton have changed over the past decade. From 2000 to 2010, U.S. domestic textile consumption of raw cotton dropped from 8.9 million to 3.9 million bales, while exports increased from 6.7 million to 14.4 million bales (USDA, 2010).

The shift from a domestic market to primarily an export market requires reexamination of the dominant spinning platforms within each of those markets. The domestic textile industry is dominated by open-end spinning which exhibits high processing speeds leading to lower labor costs and more efficient yarn production. However, the international market primarily employs a slower yet more versatile technology, ring spinning. Ring frames can spin yarns ranging from 147.6 tex to 2.5 tex (one tex = number of grams of cotton fiber required to produce one kilometer of yarn), while open-end spinning effectively can produce yarn sizes from 118.1 tex to 16.9 tex (El Mogahzy, 1998). In 2009, 246.8 million ring spindles were installed worldwide as compared to 7.8 million open-end rotors (ITMF, 2011). On average, one rotor can produce ten times more yarn than one ring spindle, which, on an individual basis, varies greatly depending on quality of yarn being produced, spinner's expertise, and age of equipment, among other factors. Despite the dramatic difference in production speed,

ring spinning still consumes roughly three times the amount of raw cotton as rotor spinning.

Unfortunately, direct selection for yarn performance is unfeasible for cotton breeders. To conserve time, space, and money, breeders desire to begin testing for traits of interest in the earliest segregating generation possible. However, early generation yarn performance testing virtually is impossible due to limited lint production and cost. Even in later generations when enough seeds are available to plant plots large enough to obtain sufficient lint, available financial resources still limit the number of lines that can be tested. Thus, breeders rely upon fiber quality parameters to indirectly select for yarn performance (May and Taylor, 1998; Meredith, 1991). The two spinning platforms require different types and levels of fiber quality in order to produce an optimal yarn (both in terms of yarn productivity and quality). For ring spinning, the most important fiber traits in descending order are fiber length, fiber bundle strength, fiber fineness, and fiber-to-fiber friction. For open-end spinning, fiber strength, fiber fineness, fiber length, and cleanliness are most important (Deussen, 1993). Quality parameters such as yarn tensile strength, elongation of yarn before breakage, hairiness, and yarn evenness are correlated strongly with average fiber length (El Mogahzy, 1999; El Mogahzy and Chewning, 2001; Perkins et al., 1984). Length of cotton fibers, measured a number of ways on High Volume Instrument (HVI) and Advanced Fiber Information System (AFIS) technology today, is critical to manufacturing yarn of specific sizes on draft, i.e. ring, spinning systems (Rusca and Reeves, 1968). Spinners require upper-half mean length (UHML) information provided by HVI testing to set the drafting rollers at the

proper distance to avoid yarn unevenness, floating fibers, and yarn breakage (Behery, 1993; El Mogahzy and Chewning, 2001; Perkins et al., 1984). In ring spinning, long fibers provide more inter-fiber contact, producing more friction forces that enhance yarn tensile strength (Balasubramanian, 1995; El Mogahzy and Chewning, 2001).

Base fiber quality standards in the U.S. differ from those accepted in international markets. Upland cotton with an UHML of 26.7 mm, fiber bundle strength (Str) of 250 kN m kg^{-1}, and micronaire (Mic) between 3.5 and 4.9 is considered nondiscount quality in the U.S., whereas 28.2 mm UHML, 265 kN m kg^{-1} Str, and 3.8 to 4.6 Mic are the minimum requirements on world markets (Hequet et al., 2006). In order for U.S. cotton to remain competitive, it must meet the quality standards demanded by the consumers of raw cotton whether they are domestic or abroad. This demand for higher quality further deepens the need for breeding objectives to improve fiber quality.

Objectives

- Determine combining abilities of HVI and AFIS fiber length and HVI fiber bundle strength among selected parents.
- Estimate gene effects and heritability of HVI fiber length and fiber bundle strength among selected parents.
- Determine the amount of transgressive segregation in the F_2 and BC_1F_1 generations within populations created from selected parents.

2. LITERATURE REVIEW

Fiber Length Measurements

Accurate and precise fiber length and fiber length uniformity measurements are crucial to efficiently produce high quality yarn on ring spinning systems. The distance between drafting rollers is determined by fiber length. If the distance is too small, fibers will be stretched and broken, leading to increased short fibers in the yarn and subsequent yarn hairiness. If the rollers are placed too far apart, then floating fibers and yarn unevenness will occur. Several failed attempts in the early 1900s were made to develop cost-effective testing equipment to objectively measure fiber quality. Prior to the 1980s, commercial U.S. cotton was evaluated for trash, color, and estimated length by subjective human "classers." The High Volume Instrument (HVI) has revolutionized cotton fiber testing and provided the first commercially viable means to objectively measure fiber length as UHML, Str, elongation at break (Elon), Mic, and length uniformity index (UI). Since 1991, all cotton sold in the United States has mandatorily been subjected to HVI testing. The Advanced Fiber Information System (AFIS) (Uster Technologies; Knoxville, TN) is capable of sampling individual fibers in an automated fashion. With AFIS, the length-bias introduced by HVI weight based methodology is eliminated. Bragg and Shofner (1993) reported a 1-2 mm reduction in UHML and a 7% increase in SFC, and the authors concluded that fibers were broken during the fiber individualization process. This may emulate similar conditions encountered during pre-spinning processes. Unfortunately, due to slow processing speeds and costs, AFIS is still relatively unavailable to breeders as a tool to evaluate large numbers of individual

plants. In addition, AFIS does not provide a measurement of fiber strength forcing breeders to overlook strength or test on multiple systems. Length parameters provided by AFIS include upper-quartile length on a weight basis (UQLw), mean length on a weight basis (Lw), length on a number basis (Ln), short fiber content on a weight basis (SFCw), and short fiber content on a number basis (SFCn).

UHML is defined as the mean length by number of the longer one half of the fibers by weight (ASTM, 2013). El Mogahzy and Chewning (2001) found it to be slightly less than 2.5% span length and thus approximates classer staple length. Short fiber content (SFC) is the proportion of fibers measuring 12.7 mm or less on either a weight or number basis. SFC leads to increased waste during carding, combing, and other processes. SFC also decreases the quality of fabric due to weaker, hairier, and less uniform yarn (Backe, 1986; El Mogahzy, 1999; Hequet and Ethridge, 2000).

Fiber Strength Measurements

Fiber strength ranks second for ring spinning and first for rotor spinning in predicting yarn performance. Fiber strength has a direct relationship with yarn strength (May and Taylor, 1998; Meredith et al., 1991). Stronger fibers are necessary to tolerate ever increasing processing speeds (Faerber, 1995). When compared to ring spinning, rotor spinning preserves less of the fiber strength in yarn strength. Thus, rotor spinning requires the strongest fibers to produce quality yarns.

Fiber strength is measured either on an individual fiber basis or as a bundle of fibers. Single fiber strength serves as a component of fiber bundle strength. The lack of automation to measure single fiber strength results in labor-intensive testing which limits

its use to only small-scale research. The HVI, Stelometer (Hertel, 1953), or Pressley (Pressley, 1942) instruments all measure fiber bundle strength. The Pressley instrument and the Stelometer are known as single instruments since they measure only one or a few related fiber properties. The Pressley instrument measures only fiber bundle strength, and the Stelometer measures both fiber bundle strength and fiber elongation. Both single instruments require manual sample preparation and thus are time consuming and expensive. The HVI is preferred over the single instruments because it employs mechanized sample preparation and consequently is faster and cheaper. Some believe that the single instruments are more precise than the HVI (Cooper et al., 1988). The two measurements were reported to have a correlation of about 0.7 ($P < 0.05$) in two different populations (May and Jividen, 1999). Heritability of fiber bundle strength was reported to be higher when measured on HVI as opposed to the Pressley (Latimer et al., 1996). May and Jividen (1999) reported much higher heritability for fiber bundle strength when measured by the Stelometer than when measured by the HVI, but response to selection was not different.

Neither fiber bundle strength nor individual fiber strength are independent of other fiber quality parameters. The stronger the individual fibers are, the less likely they are to break during processing, thus affecting fiber length parameters. Both individual fiber and fiber bundle strength are impacted by fiber maturity; more mature fibers tend to be stronger and consequently so are the bundles they make. Finer fibers allow for a greater number of fibers in a bundle at a given weight increasing the strength of the bundle. This highlights the need for a breeder to evaluate the entire fiber quality package

rather than focus on one fiber quality parameter in order to obtain a net gain in fiber quality.

Sources of Genetic Improvement

Cotton breeders have different sources of genetic variability that potentially can be exploited to develop cultivars with improved fiber quality. Breeders can make interspecific crosses in hopes of capturing fiber quality from one species and yield potential from another. The dominant species of cotton grown across the world is *G. hirsutum*, commonly known as upland, which is valued for its wide adaptability and high yields. Pima cotton, *G. barbedense*, is the second most important species prized for its superior quality but criticized for lower yields and longer growing season requirement. Other species of cotton, both diploid and tetraploid, contain potential variation for fiber quality but have less than desirable agronomic properties. Some believe the genetic base within current upland germplasm is too narrow for further improvement (Van Esbroeck et al., 1998). However, others have shown that sufficient variability still exists within upland germplasm to obtain improved quality with intraspecific crossing (Bowman et al., 1996; May et al., 1995; Smith et al., 2008), while avoiding the difficulties associated with interspecific crossing. Mutating a base population is also a method of producing novel variation for traits of interest. This study will explore parents derived through intraspecific crossing of upland by upland, interspecific crossing of upland by Pima, and mutation of upland. A greater understanding of the genetic effects and heritability of fiber length and fiber bundle strength will aid breeders in effectively selecting parents to

develop segregating populations as well as determine appropriate breeding methods for selecting fiber quality in each respective genetic background.

A survey of the Germplasm Resources Information Network (USDA, 2012) revealed the large majority of cotton accessions available for improvement of cotton cultivars exhibit fiber quality below international base standards (Figures 1 and 2). Over 700 accessions met or exceeded the international base standard for UHML of 28.2 mm, but only 48 met or exceeded the standard for Str of 265 kN m kg^{-1} or greater. Of the 2155 accessions with fiber quality data, only 28 exhibited both UHML and Stelometer fiber bundle strength values meeting the international base standards. Only five of those were *G. hirsutum,* four of which were exotic germplasm accessions obtained during collection trips in the 1980s and likely are not adapted to modern production in the United States. The only *G. hirsutum* accession meeting the international base standards was PI 529112, an obsolete Acala variety with a lint percentage of 32.6%.

Tools for Genetic Improvement

Different mating designs and statistical analysis tools exist to study genetic inheritance of quantitative traits. Among them are the diallel and the generation means analysis (GMA).

Diallel

A diallel mating design is one where all possible combinations among a set of parents are made and evaluated in order to estimate general combining ability (GCA)

Figure 1. Breakdown of Upper Half Mean Length (UHML) of cotton accessions available in Germplasm Resource Information Network.

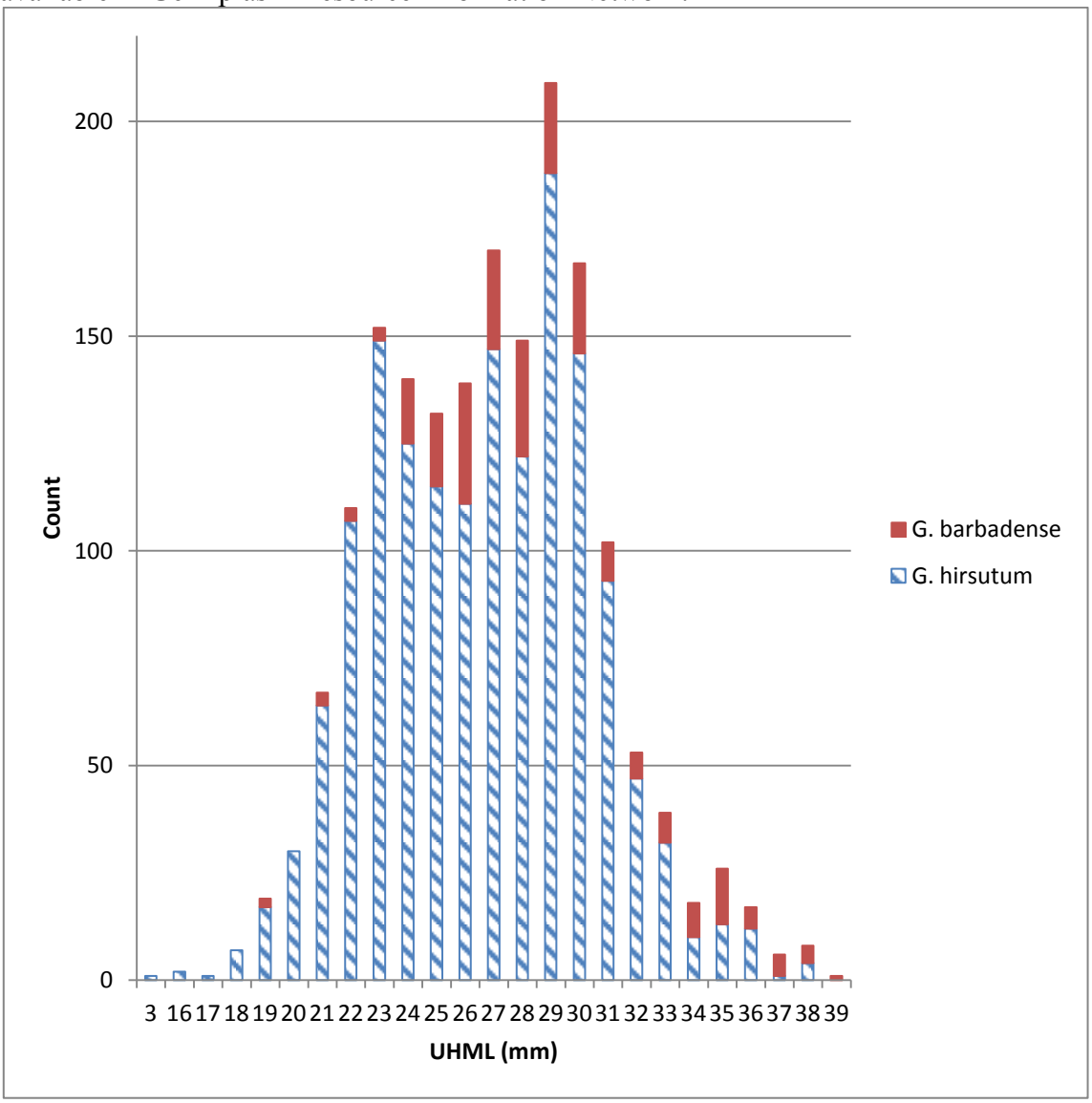
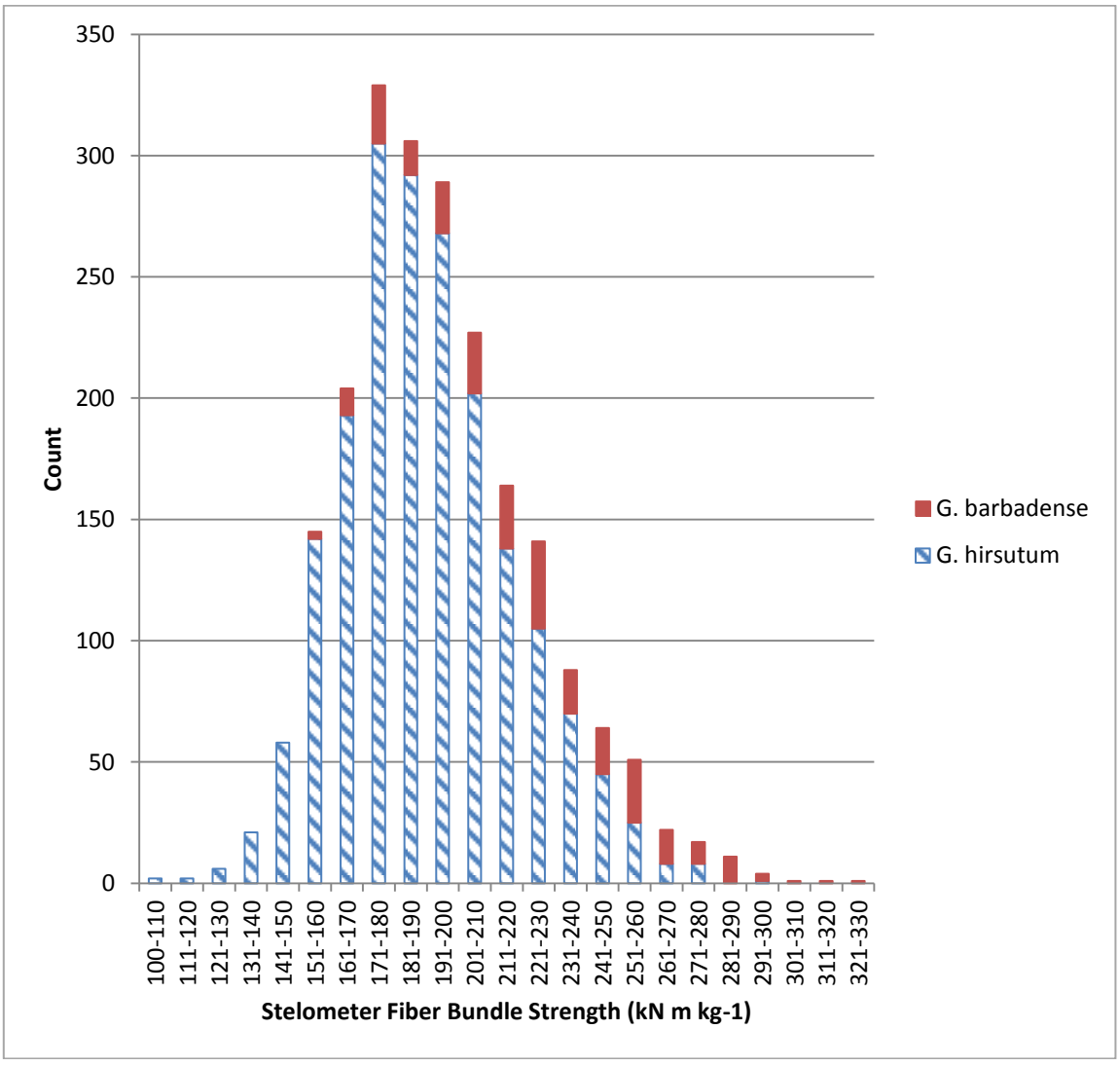


Figure 2. Breakdown of the strength of a bundle of fibers measured on a Stelometer with the jaws separated by a 1/8 inch spacer of cotton accessions available in Germplasm Resource Information Network.



and specific combining ability (SCA). Griffing describes two models and four methods (1956). Model 1 considers genotypes, years, and blocks to be fixed effects, and thus, results are applied only to genotypes included in the study whereas model 2 is applicable to the universe of genotypes. When parents are selected at random from a population, model 2 is appropriate. Each model is further divided into four methods. Method 1 contains parents and all possible hybrids including reciprocals. In method 2, parents and hybrids are retained but reciprocals are dropped from the analysis. Hybrids and their reciprocals but not parents are analyzed for method 3 and no reciprocals for method 4. Since reciprocal effects have not been observed for fiber quality (Al-Rawi and Kohel, 1970), method 4 was utilized.

When the number of parental lines is fewer than 10, or selection was applied to the parents prior to diallel mating, both of which are the case in the present study, a fixed effects model is appropriate. In a fixed effects model, inferences can be applied only to the genotypes included in the study. Additionally, a fixed effects model does not allow estimation of variance due to genetic sources. While genetic control of a quantitative trait cannot be determined directly in a fixed effects model, it is often approximated using the relative magnitude of GCA and SCA effects. GCA is the difference of the average performance of hybrids for a given parent and the average performance of all hybrids included in a study. SCA is the deviation of a specific hybrid's performance from what would be expected given the GCA of each of its parents. GCA and SCA are most commonly used to determine the best parents to be used in the production of commercial hybrids for species grown as hybrids. They also have utility in inbred crops

by approximating additive and dominance effects for traits of interest. GCA reflects additive genetic effects, and SCA relates to dominance effects (Wu et al., 2010).

Braden et al. (2009) conducted a diallel of five parents which included TAM 94L-25 (Smith, 2003; PI 631440), a common parent to five of the parental lines included in the present study, and 'FiberMax 832' (FM832) (Constable et al., 2001; PI 603955) which is included in the present study. TAM 94L-25 followed by FM832 exhibited the highest GCA for fiber length. Cheatham (2003) also evaluated FM832 which had the highest GCA for 2.5% span length and second highest GCA for Str among the parental lines included, both of which were significantly different than zero.

Heterosis occurs when a hybrid outperforms its parents. Mid-parent heterosis compares the performance of the hybrid to the average performance of the two parents, and high-parent heterosis compares hybrid performance to performance of the better parent. Like GCA and SCA, heterosis is most useful in crops such as maize and sorghum where hybrids are commercialized. While the majority of cotton planted worldwide is inbred cultivars, the identification of heterosis still serves valuable functions for cotton breeders. First, it sheds light on the genetics controlling traits of interest. Al-Rawi and Kohel (1970) concluded that 50% span length, 2.5% span length, Str, and Elon are primarily under additive gene action because very low levels of mid-parent heterosis and no inbreeding depression were observed. Second, almost all cotton production in India is actually from commercial hybrids, thus the analysis will serve its traditional purpose for readers in that region.

Generation Means Analysis

Understanding the genetic control of a trait will aid in the development of an effective strategy for genetic improvement. Additive gene action (a) is the effect each additional allele has on a given trait and is known as the breeding value. The deviation of the heterozygote from the mid-point of the two homozygotes is due to dominant gene action (d), also known as the dominance deviation. The single locus model of Fisher (1919) sets the midpoint of the two homozygotes equal to zero. Using the ratio of the genotypic value of the heterozygote to the genotypic value of the better homozygote $\left(\frac{d}{a}\right)$ determines the degree of dominance. A trait is under complete additive gene action when this ratio is equal to zero, i.e., no dominance gene action. When the degree of dominance is equal to one, complete dominant gene action is indicated. Overdominance results when $\frac{d}{a}$ is greater than one. Incomplete dominance results when the ratio is between negative one and zero or zero and one. When the model is expanded to include multiple loci, the interaction between genes can occur which is known as epistasis or non-allelic interaction. For two loci, epistasis can be broken into additive by additive, additive by dominance, and dominance by dominance epistasis which is dependent on the degree of dominance and average effects of the trait at each locus.

The generation means analysis employs six generations to estimate the mean of the inbred population, additive, dominance, additive by additive, additive by dominance, and dominance by dominance gene effects. The generations included are parent 1 (P_1), parent 2 (P_2), the cross of P_1 and P_2 (F_1), the self of F_1 (F_2), and the backcross of the F_1 to each of the parents (BC_1P_1 and BC_1P_2). Several authors have reported genetic models

to calculate genetic effects from generation means (Anderson and Kempthorne, 1954; Eberhart and Gardner, 1966; Gamble, 1962; Hayman, 1958; Hayman, 1960; Mather and Jinks, 1971). Generation means analysis is most effective when the parents involved are completely divergent for the trait of interest, that is to say all the favorable alleles are found in one parent and all the negative alleles are found in the other parent (Bernardo, 2002). For a quantitative trait, estimates of genetic effects as determined by a generation means analysis are a summation of all loci contributing to the phenotype of the trait of interest. Thus, negative effects will cancel out positive effects limiting the effectiveness of the generation means analysis for parental combinations in which both parents are contributing favorable alleles. However, for practical outcomes, it is usually preferable to conduct crossing between elite parents both superior for a trait of interest. The generation means analyses reported herein include parental combinations of both types, and thus should be interpreted within the previously mentioned limitations.

Additive variance has been found to outweigh non-additive variance for fiber length in numerous studies (Al-Rawi and Kohel, 1969; Al-Rawi and Kohel, 1970; Green and Culp, 1990; Lee et al., 1967; Meredith and Bridge, 1972; Miller and Marani, 1963; Tang, 1993). Results from several other studies reported that non-additive variance was more important for fiber length (Baker and Verhalen, 1973; Cheatham et al., 2003; Verhalen, 1969). Smith et al. (2009a) reported significant additive, dominant, and epistatic interactions for different fiber length measurements depending on the population under discussion. Cheatham et al. (2003) reported that additive effects were

predominant with only negligible dominance effects, which agreed with Verhalen and Murray (1967) and Verhalen (1969).

Heritability

A phenotype is impacted by genetic and environmental, i.e., non-genetic, factors. The degree to which a quantitative trait is controlled by genetic factors is known as heritability and is one of the most helpful statistics used by plant breeders to determine which method of selection should be employed in improving such a trait of interest. Single-plant selection will likely be successful for highly-heritable traits while lowly-heritable traits will require more extensive replication. Heritability calculations fall into two main categories. Broad-sense heritability is the ratio of genotypic variance to phenotypic variance, and narrow-sense heritability is the ratio of additive genetic variance to phenotypic variance (Fehr, 1991). Heritability is influenced by several factors and thus is not constant across all circumstances for a given trait. For example, a population developed by the cross of two closely related parents will tend to have a much lower genetic variance and heritability estimate than a population developed using several diverse parents. Therefore, estimates of heritability should be used in the context of the conditions in which they were acquired.

3. DIALLEL

Materials and Methods

Experimental Material

Parents were selected based upon their HVI UHML and Str as well as genetic background (Table 1). Genetic backgrounds included extra-long staple uplands, mutated uplands, high strength uplands, and interspecific hybrids. Extra-long staple uplands included TAMB 182-33 ELS (ELS33) and TAMB139-17 ELS (ELS17) (Smith et al., 2009b; PI 654362 and PI 659699 respectively). The EMS mutated upland parents were TAM 94L-25-M24 (M24) (Brown et al., 2012; PI 664553) and 94 L-25 (M4)-05-9651 (M9651) (unreleased). The high strength uplands were 06 WE 62-4 (HS624) (unreleased) and MD 9ne (HSMD9) (Meredith and Nokes, 2011; PI 659507). The interspecific hybrids included were 04 SID 84-2 (SID84) (unreleased) and 04 SIG 83-1 (SIG83) (unreleased). FM832 and 'Tamcot 22' (TAM22) (Thaxton et al., 2005; PI 635877) are high and medium quality, respectively, commercial cultivars. Due to poor seed set during the summer of 2008 for the cross SID84 x SIG83, no test plots could be established thus SIG83 and all of its combinations were dropped from the analysis.

Generation Development

In the summer of 2008, approximately 25 plants of each of the nine parents were planted approximately 0.5 m apart at the Texas A&M Agrilife Research Farm near College Station, TX. These plants were used simultaneously to verify parental phenotypes and to produce F_1 seeds. Open-pollinated bolls were harvested from each plant, ginned on a laboratory 10-saw gin without lint cleaner, and HVI fiber properties

Table 1. Pedigrees, preliminary upper half mean length (UHML), and preliminary fiber bundle strength (Str) of genotypes used in diallel as measured in College Station 2008.

Genotype	Pedigree	Genetic background	UHML	Str	Plant inventory
			mm	kN m kg^{-1}	
TAM B182-33 ELS	TAM 94L-25 x PSC 161	ELS upland	35.8	369.7	PI 654362
TAM B139-17 ELS	TAM 94L-25 x (PD 6992 x TAM 94L-25)	ELS upland	35.1	355.0	PI 659699
TAM 94L-25-M24	M_4 (TAM 94L-25)	Mutant upland	35.6	361.9	PI 664553
94 L-25 (M4)-05-9651	M_4 (TAM 94L-25)	Mutated upland	35.1	347.2	Unreleased
06 WE 62-4	(DPL 491 x 96WD-18) x (91C-95Ls x DPL90)	High-strength upland	30.7	396.2	Unreleased
MD 9ne	MD 15 x MD 9-1-1-2	High-strength upland	29.5	376.6	PI 659507
04 SIG 83-1	NMSI 1331 x (90M-8 x 89E-51)	Interspecific hybrid	34.3	415.8	Unreleased
04 SID 84-2	TAM 94L-25 x NMSI 1331	Interspecific hybrid	37.3	334.4	Unreleased
Fibermax 832	Sicala V-1 x Siokra 1-4	High-quality commercial cultivar	31.2	344.2	PI 603955
Tamcot 22	TAM $87G^3$-27 x (90M-8 x 89E-5)	Moderate-quality commercial cultivar	28.2	271.7	PI 635877

determined at the Fiber and Biopolymer Research Institute in order to verify the phenotype of each parental plant. Standard deviations were calculated across plants for each genotype for UHML and Str. To ensure high fiber length, phenotypes of TAM B182-33 ELS (ELS33), TAM B139-17 ELS (ELS17), FM 832, 94 L-25 (M_4)-05-9651 (M9651), TAM 94L-25-M24 (M24), and 04 SID 84-2 (SID84), any parent plant having UHML two standard deviations below the parent plant with the highest UHML within each genotype was discarded. For the same genotypes, any plant with Str two standard deviations above or below the mean Str for each genotype was also discarded. To ensure high Str phenotypes of 06 WE 62-4, MD 9ne, and 04 SIG 83-1, any parent plant having Str two standard deviations below the parent plant with the highest Str within each genotype was discarded. For these genotypes, any plant with UHML two standard deviations above or below the mean UHML for each genotype was also discarded.

The parents were crossed in a diallel without reciprocals. The day prior to anthesis, unopened flower buds were emasculated. Paper straws with the top pinched shut were placed over stigmas after emasculation and after pollination to prevent outcrossing. Selfed seeds of each parental plant were obtained by clipping the corolla tips closed with metal clips the afternoon prior to the day of anthesis. Since parental phenotypes of each plant were yet to be verified, the specific male and female plant used in each individual cross was recorded on the tag identifying the cross, ensuring that any F_1 or selfed seeds obtained on undesirable plants were discarded. Selfed parental seeds and F_1 seeds from verified parental plants were planted during the 2009 growing season to increase F_1 seeds. Since all parents were selected specifically rather than at random

from all upland, mutated upland, and interspecific genotypes, inferences made will apply solely to genotypes included in the study.

Field Study

All parents and F_1s were planted in a randomized complete block design with four replications on 5 May 2009 and 27 April 2010 at the Texas A&M Agrilife Research Farm near College Station, TX on a Weswood silt loam, a fine-silty, mixed, superactive, thermic Udifluventic Haplustepts integrated with Ships silty clay, a very-fine, mixed, active, thermic Chromic Hapluderts. Plots were 4.6 m x 1.0 m. Cultural practices, such as furrow irrigation, weed control, and insect control, including boll weevil, *Anthronomus grandis*, eradication, were normal for cotton production in central Texas. Twenty-five bolls were harvested from each plot on 17-18 October 2009 and 27-28 September 2010. First-position and second-position bolls from the middle fruiting zone were harvested preferentially to minimize the variation due to environment. Samples were ginned on a laboratory saw-gin without lint cleaner and sent for HVI and AFIS analyses at Cotton Incorporated in Cary, NC.

Statistical Analysis

Highly influential observations were identified by Cook's D influence statistic (JMP, Version 9.0.0. SAS Institute Inc., Cary, NC, 1989-2012). The most influential observations were deleted with a maximum of six observations (representing less than two percent of the total observations) removed per trait and no more than one deleted observation per genotype per year. Since diallel analysis requires a balanced data set (Ragsdale and Smith, 2007), deleted observations were replaced with predicted values

obtained from the OUTPUT statement in the General Linear Models procedure (PROC GLM) of SAS (SAS, Version 9.2, SAS Institute Inc., Cary, NC, 2002-2008).

Model assumptions of normality of errors and homogeneity of error variance were verified using JMP. SFCn failed the Shapiro-Wilk test for normality (Shapiro and Wilk, 1965). Numerous transformations were attempted to normalize errors with no success. Therefore, further statistical analysis for SFCn was conducted on untransformed data. The Brown-Forsythe F-test revealed heterogeneity of variances between years for UI, Str, and MR and between genotypes for LP, Mic, and UI, however this presents little concern since sample sizes were equal (Ott and Longnecker, 2001).

Analyses of variance were conducted across years and per year using PROC GLM in SAS. Years and replications nested within years were considered random, and genotypes considered fixed. Parents and F_1s were partitioned out of G, and the parent x year interaction (PxY) and the F_1 x year interaction (F_1xY) out of the genotype x year interaction (GxY). Genotypes tested over GxY, GxY over genotype x replication nested within year interaction (GxR(Y)), F_1 over F_1xY, F_1xY over F_1 x replication nested within year interaction (F_1xR(Y)), parents over PxY, and PxY with parents x replication nested within year (PxR(Y)). Means of genotypes, including both parents and F_1s, were separated using Fisher's LSD.

To further dissect significant GxY interactions, interaction elements were calculated and separated using a Fisher LSD (Smith, 1978). Interaction elements were calculated by subtracting the mean performance of a genotype in year one from its mean performance in year two. Since each comparison included four means rather than the

usual two, the standard error used in calculating the LSD was calculated as [(Error Mean Square*4)/r]$^{1/2}$(Smith, 1978). In this manner, genotypes with interaction elements different from zero, a value indicating the genotype responded the same to years, were identified in addition to those genotypes which responded differently to years than did the control cultivars. General combining ability (GCA) and specific combining ability (SCA) were determined using DIALLEL SAS05 as described by Zhang et al. (2005) utilizing Model I, Method 4 of Griffing (1956).

Results and Discussion

Tables 2 and 3 indicate that significant variation was observed for most sources of variation. In cases where significant interactions occurred, the discussion below will be based on appropriate separation of means within years and a discussion of interaction elements to determine if any particular parent or combination of parents resulted in F_1s that responded differently to years.

Parent Analysis

Genotypes were significant for all traits reported allowing for the partitioning of variability into parents and F_1s (Tables 2 and 3). Significant GxY interactions were observed for LP, Mic, UHML, UI, Str, Elon, and UQLw necessitating mean separation by year and interaction analyses performed which are discussed later. Parents differed ($p<0.05$) for all traits except Ln which was significant at $p=0.066$. Parents performed similarly to preliminary studies for UHML and Str, the traits used in selecting parents (Tables 1, 3, and 4).

Table 2. Combined analyses of variance of diallel crosses among nine cotton genotypes upper half mean length (UHML), length by number, percentage of fiber by number shorter than 12.7 mm (SFCn), and uniformity index (UI) when grown near College Station, TX, in 2009 and 2010.

Source	df	Mean squares				
		UHML	UQLw	Ln	SFCn	UI
Year (Y)	1	32.56**	0.6	15.9	59.1	114.84***
Reps(Y)	6	1.68	8.1	27.7	245.6	1.08
Genotypes (G)	44	27.75***	32.9***	7.8***	78.6***	6.05***
Parents (P)	8	52.96***	63.4***	11.5†	143.9*	11.23*
F_1	35	21.91***	25.8***	6.4***	64.5***	4.52***
GCA‡	8	92.24***	108.0***	16.6***	171.1***	15.36***
SCA§	27	1.07***	1.4***	3.4*	32.9*	1.30*
G x Y	44	0.74***	1.3***	1.7	17.6	1.52***
P x Y	8	0.67	1.7**	3.7	37.2	1.94*
F1 x Y	35	0.68**	1.2***	1.3	13.5	1.20*
GCA x Y	8	0.93**	2.2***	1.7	12.3	1.37
SCA x Y	27	0.60*	0.9*	1.2	13.8	1.15*
Error	260	0.38	0.5	1.9	20.5	0.76

*Significant at the 0.05 probability level.
** Significant at the 0.01 probability level.
***Significant at the 0.001 probability level.
†Significant at p=0.066
‡ GCA, general combining ability.
§ SCA, specific combining ability.

Table 3. Combined analyses of variance of diallel crosses among nine cotton genotypes for fiber bundle strength (Str), fiber elongation at break (Elon), micronaire (Mic), immature fiber content (IFC), maturity ratio (MR), standard fineness (Hs), and lint percentage (LP) when grown near College Station, TX, in 2009 and 2010.

Source	df	Mean squares						
		Str	Elon	Mic	IFC	MR	Hs	LP
Year (Y)	1	570**	84.09***	5.06**	317.75***	221.46**	9.63**	30.2*
Reps(Y)	6	22	1.88	0.16	8.14	7.69	0.35	3.6
Genotypes (G)	44	243***	10.10***	15.87***	2.82***	4.73***	6.56***	72.3***
Parents (P)	8	557**	12.89***	37.76***	6.06***	11.64***	15.53***	192.6***
F1	35	178***	9.72***	11.17***	2.15***	3.26***	4.67***	40.9***
GCA†	8	695***	35.96***	46.69***	7.29***	10.00***	19.33***	163.2***
SCA‡	27	25**	1.95***	0.64***	0.63	1.07**	0.33***	4.7***
G x Y	44	27***	0.85**	0.35***	0.37	0.49	0.13	2.3***
P x Y	8	54**	0.81	0.35	0.40	0.30	0.16	3.9**
F1 x Y	35	21*	0.84***	0.36***	0.37	0.55	0.12	1.9***
GCA x Y	8	46***	1.40***	0.62***	0.43	0.70	0.15	2.8***
SCA x Y	27	13	0.68*	0.28**	0.36	0.50	0.11	1.6***
Error	261	13	0.50	0.15	0.54	0.56	0.10	0.7

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

Table 4. Average upper-half mean length (UHML), upper quartile length by weight (UQLw), fiber length by number (Ln), and uniformity index (UI) of 36 F_1 combinations and nine parents from a diallel without reciprocals when grown near College Station, TX, in 2009 and 2010.

Genotype	UHML		UQLw		Ln	SFCn	UI	
	2009	2010	2009	2010			2009	2010
	mm		mm		mm	%	%	
ELS17 x FM832	32.8 h-j[†]	32.5 g-l	34.9 h-k	34.7 f-j	22.8 c-k	23.2 d-m	84.4 a-d	84.1 a-c
ELS17 x HSMD9	32.6 i-k	31.5 n-p	34.8 h-l	34 i-l	23.2 a-g	20.9 i-o	84.8 a-b	85.1 a
ELS17 x M24	34.6 c-e	33.8 a-c	37.1 a-d	37.3 a	23.5 a-g	23.6 d-l	83.2 h-m	82 g-l
ELS17 x M9651	33.3 f-i	33.1 c-h	35.8 e-h	36.2 b-e	22.5 c-l	25.5 b-h	83 j-n	83 b-j
ELS17 x SID84	35.4 a-c	34.3 a-b	37.8 a	36.9 a-c	22.9 c-j	26 b-f	84.4 a-d	83.3 b-g
ELS33 x ELS17	35 a-d	33.7 b-d	36.5 c-e	36.1 c-e	22.4 e-l	27 b-d	84.8 a-b	83.2 b-h
ELS33 x FM832	32.7 h-j	33.1 c-h	34.4 i-n	36.1 c-e	24.4 a	18.2 n-o	84 b-j	83.8 a-d
ELS33 x HSMD9	32.1 j-l	31.2 o-q	34.2 j-n	33.6 l-m	23 c-i	20.9 i-o	84.3 a-f	83.3 b-g
ELS33 x M9651	34.5 d-e	34.3 a-b	37.2 a-c	36.7 a-c	23.6 a-e	22.7 d-m	83.9 b-k	83.1 b-i
ELS33 x SID84	35.6 a-b	34.5 a	37.6 a-b	36.7 a-c	22.1 g-l	28 b-c	84.4 a-f	83.2 b-h
HS624 x ELS17	32.9 h-j	32.4 h-m	35.2 g-j	34.9 f-i	22.8 c-k	23.4 d-l	84.2 a-g	83.9 a-d
HS624 x ELS33	33.3 f-i	31.6 m-p	35.4 f-i	34.2 h-l	23.6 a-f	19.8 l-o	85.1 a	82.3 e-l
HS624 x FM832	31.4 l-m	30.4 q-s	33.5 n-q	33 m-n	22.7 c-k	20.6 i-o	84.4 a-d	83.3 b-g
HS624 x TAM22	29.8 n	29.5 t	31.7 r-s	32.1 n-p	21.7 i-n	21.8 f-n	82.8 l-n	81.8 i-l
HSMD9 x HS624	29.4 n-p	29.7 s-t	31.2 s	32.1 n-p	22.9 c-j	17.2 o	83.9 b-k	83.4 b-f
HSMD9 x M24	31.8 k-m	31.8 k-p	34.1 k-o	34.5 h-l	23.7 a-d	19 m-o	84.5 a-d	83.5 b-e
HSMD9 x TAM22	28.8 p-q	29.5 s-t	30 t	31.2 p-r	20.3 o	25.4 b-h	82.3 m-n	82.9 b-j
M24 x ELS33	34.2 d-f	33.5 b-f	37.2 a-c	36.7 a-c	24.3 a-b	20.7 i-o	83.4 f-l	82.9 b-j
M24 x HS624	33.3 g-i	32.5 g-l	35.2 g-j	34.6 g-k	22.5 c-l	23.8 c-l	84.2 a-g	83.2 b-i
M24 x M9651	33.8 e-g	33.7 a-d	36.1 d-g	37 a-c	23.6 a-f	22.9 d-m	83.3 f-m	82.3 e-l
M24 x SID84	35.6 a	34.4 a-b	37.8 a	37.1 a-b	23.2 a-g	24.9 b-i	84.2 a-g	82.1 f-l
M24 x TAM22	32.2 j-l	31.5 n-p	33.7 m-q	34.5 g-k	21.8 h-m	25.5 b-g	83.1 i-m	81.6 j-m
M9651 x FM832	31.5 l-m	32 j-o	33 p-q	34.8 f-j	22.5 d-l	22 f-n	83.9 b-k	82.8 c-k

Table 4. Continued

Genotype	UHML		UQLw		Ln	SFCn	UI	
	2009	2010	2009	2010			2009	2010
	mm		mm		mm	%	%	
M9651 x HS624	33.2 g-i	32.5 g-l	36.1 d-g	34.9 f-i	23.9 a-c	20 k-o	84.5 a-c	83.4 b-f
M9651 x HSMD9	31.8 l-m	31 p-r	33.5 n-q	33.7 k-m	22.7 c-l	21.1 h-o	84.2 a-h	81.9 h-l
M9651 x SID84	35 a-d	34.2 a-b	37.3 a-c	37.3 a	23.1 a-g	24.6 b-i	83.7 c-l	81.9 h-l
M9651 x TAM22	31.1 m	31.1 p-q	33.5 n-q	34.1 h-l	22.3 e-l	22.8 d-m	83 i-n	81.3 l-m
SID84 x FM832	33.5 f-i	32.7 f-j	35.8 e-h	35.4 e-g	23.1 b-h	22.9 d-m	84.3 a-g	84.2 a-b
SID84 x HS624	32.8 h-j	33 d-i	34.4 i-n	34.5 g-k	21.7 i-n	26.7 b-e	84.8 a-b	84 a-c
SID84 x HSMD9	33.5 f-h	32.8 e-j	35.8 e-h	34.9 f-i	23.4 a-g	21.9 f-n	85.1 a	84.2 a-b
FM832 x HSMD9	29.7 n	29.3 t-u	31.8 r-s	31.9 o-q	23 b-i	17 o	84.9 a-b	83.7 a-d
FM832 x M24	32.8 h-j	32.4 g-m	34.6 i-m	35.6 d-f	23 b-i	22.6 d-m	83.5 d-l	83.1 b-i
TAM22 x ELS17	31.1 m	31.2 o-p	33.1 o-q	33.9 j-l	20.5 m-o	28.6 b	83 i-m	82.2 e-l
TAM22 x ELS33	31.6 l-m	30.2 r-t	33.8 l-p	33.7 k-m	22.9 c-j	20.1 j-o	83.2 g-m	80.4 m
TAM22 x FM832	29.7 n-o	29.5 s-t	31.9 r-s	31.9 o-q	21.5 k-o	22.4 e-n	83 i-n	82.9 b-j
TAM22 x SID84	32.1 j-l	31.7 l-p	33.7 m-q	34.5 h-l	22.3 f-l	23.1 d-m	82.9 k-n	82.7 d-l
SID84	34.5 d-e	33.3 c-g	36.1 d-g	36.4 a-d	20.4 n-o	33.6 a	84 b-i	83.2 b-h
HS624	30 n	29.4 t-u	31.2 s	31.8 o-q	21.6 j-o	21.4 g-o	84.5 a-d	83.5 b-e
M24	34.7 b-d	33.8 a-d	36.9 a-d	36.6 a-c	23.3 a-g	24.3 b-k	84.4 a-d	82.6 d-l
M9651	34.4 d-e	32.3 i-n	36.6 b-e	35 f-h	22.7 c-l	24.5 b-j	83.6 c-l	81.9 h-l
ELS17	34.2 d-f	32.6 g-k	35.7 e-h	35.6 d-f	22.9 c-j	23.5 d-l	83.7 c-l	81.5 k-m
ELS33	34.2 d-f	33.6 b-e	36.3 c-f	36.5 a-d	23.4 a-g	23 d-m	83.9 b-k	82.7 d-l
FM832	30 n	29.4 t-u	32.7 q-r	32.6 n-o	22.9 c-j	18.8 m-o	83.7 c-l	81.8 i-l
HSMD9	28.8 o-q	28.6 u	29.3 t	31.1 q-r	21.3 l-o	19.9 k-o	83.9 b-k	82.8 c-k
TAM22	28.4 q	27.4 v	29.5 t	30.4 r	20.4 n-o	23.5 d-l	82 n	77.9 n
Test Mean	32.5	31.9	34.5	34.6	22.6	22.9	83.9	82.7
CV	1.8	2	2.2	1.9	6	19.7	0.9	1.2

† Means within a column followed by the same letter are not different 0.05 probability level according to Fisher LSD.

The two commercial cultivars and the two high-strength lines ranked the highest for LP in both years. TAM22 produced the largest LP in 2009 at 38.6% while not different from HSMD9 and HS624 in 2010. SID84 had the lowest LP at 22.2% and 22.5% in 2009 and 2010, respectively. Among these parents, higher-length genotypes exhibited lower LP, which may limit the ability to simultaneously improve these traits.

The five high-length lines were not different ($p<0.05$) for UHML in 2009 and separated into two groups in 2010 with M24, SID84 and ELS33 being better than ELS17 and M9651. UHML among the parents ranged from 28.4 to 34.7 mm in 2009 and 27.4 to 33.8 mm in 2010. As expected, TAM22 was the shortest parent in both years. A similar trend is observed with UQLw measurements. The five high-length lines were longer in UHML and UQLw than TAM22 and HSMD9 (Table 4).

The high-length lines were again among the longest ($p<0.05$) in Ln except for SID84 which was not different than TAM22 having a length of 20.4 mm (Table 4). This parameter, i.e., Ln, is the average length of all fibers as measured by AFIS while UHML is the average length of only the longest 50% of the fibers as measured by HVI. Line SID84 had a low Ln because it contained a large amount of fibers less than 12.7 mm, i.e., SFCn. Such a high amount of short fiber content is undesirable to spinners as it leads to waste, production inefficiency, and lower quality yarns. This large amount of SFCn may be due in part to the breakage of immature fibers during harvest and ginning since SID84 had the lowest ($p<0.05$) MR and lower Hs, i.e., fibers with the smallest fiber diameter. Pima-type cottons are typically roller ginned as it is less strenuous on the fibers, thus preserving its elite fiber quality. It is possible that had these samples been

roller ginned as opposed to saw ginned that SID84 may have exhibited a more desirable length distribution. Several of the parents used in this study exhibited similar UI with TAM 22, lower ($p<0.05$) than all other parents in both 2008 and 2009 (Tables 2 and 4). High Str line HS624, while not different than several other parents in either year, exhibited the numerically best UI in both years. Although AFIS indicated a large amount of SFCn for SID84, UI as measured by HVI failed to identify any length uniformity issues in this line. This trait may take on added importance in the selection process in cotton breeding programs if the marketing system ever rewards producers for a raw cotton product that produces better yarn.

Line HS624 expressed the strongest fibers in both years, 380.3 and 359.4 kN m kg^{-1}, respectively, although not significantly stronger than SID84 and ELS33 in 2010 (Tables 3 and 5). Again as expected, TAM22 exhibited the weakest ($p<0.05$) fibers among the parents at 273.1 and 275.1 kN m kg^{-1} in 2009 and 2010, respectively.

Although significant differences were found among these parents for Mic, all parents except SID84 were within the nondiscount range for Mic (Tables 3 and 5) according to the 2013 CCC Loan Premium and Discount Schedule for upland cotton (National Cotton Council, 2013). However, Mic is of little value to a breeder as it is a combination of fiber fineness and fiber maturity. Thus, it is not possible to separate a fine, mature fiber (desirable) from a coarse, immature fiber (undesirable). For example, HS624 exhibited a significantly finer fiber at a Hs of 174 mtex and a more mature fiber with a MR of 1.02 than TAM22, which averaged a Hs of 183 mtex and MR of 0.94. Yet, HS624 averaged higher Mic in both years at 4.8 and 4.7 units compared with 4.4 and 4.2

Table 5. Average fiber bundle strength (Str), fiber elongation at break (Elon), micronaire (Mic), immature fiber content (IFC), maturity ratio (MR), standard fineness (Hs), and lint percentage (LP) of 36 F_1 combinations and nine parents from a diallel without reciprocals when grown near College Station, TX, in 2009 and 2010.

Genotype	Str		Elon		Mic		IFC	MR	Hs	LP	
	2009	2010	2009	2010	2009	2010				2009	2010
	kN m kg^{-1}		-- % --				%		mtex	-- % --	
ELS17 x FM832	340.5 h-m[†]	337.9 b-k	3.5 p	4 p-q	4.4 e-h	4.4 c-d	4.6 d-n	0.96 h-p	174 e-f	35.5 h-k	35.6 i-k
ELS17 x HSMD9	333.2 j-o	332 e-l	3.8 k-p	4.5 g-m	4.1 l-q	4.1 f-i	4.4 g-p	0.97 f-n	176 d-e	34.2 l-p	36.4 e-j
ELS17 x M24	336.6 i-n	340.3 b-k	3.7 l-p	4.1 o-q	3.8 t-v	3.8 o-r	4.7 c-m	0.96 k-q	167 j-l	32.6 q-r	33.0 o-q
ELS17 x M9651	323.4 n-q	325.6 k-o	3.6 o-p	4.1 o-q	4.0 o-r	4 i-n	4.6 e-o	0.97 e-l	168 i-j	35.2 h-l	34.1 n-o
ELS17 x SID84	341.3 g-m	335.6 c-k	4.4 c-d	4.8 c-g	3.4 y-z	3.3 u-w	5.4 a-b	0.93 r-s	156 p-q	30.4 s-t	31.1 t-u
ELS33 x ELS17	345 e-l	343.7 b-h	3.7 l-p	4.2 m-q	4.1 m-r	3.9 j-o	4.8 b-k	0.96 i-p	168 i-k	33.2 o-q	34.3 m-n
ELS33 x FM832	354.8 b-h	346.9 a-e	3.8 k-p	3.9 q	4.1 l-p	4.1 f-i	4.1 k-s	0.99 b-g	169 i-j	34.7 j-n	35.3 j-m
ELS33 x HSMD9	365.3 a-c	337.3 b-k	3.8 k-p	4.2 l-q	4.2 i-m	4.1 f-j	4 m-t	0.98 d-l	170 h-i	34.5 k-o	37 c-g
ELS33 x M9651	348.6 c-j	334.2 d-k	3.6 m-p	4.1 n-q	3.8 t-v	3.6 s-t	5.0 a-g	0.95 m-r	160 n-o	30.7 s-t	31.7 r-t
ELS33 x SID84	357.5 b-g	331.7 f-l	4.2 d-i	4.5 f-l	3.3 z	3.2 w	5.4 a-c	0.93 r-s	152 r	30.7 s-t	30.7 t-u
HS624 x ELS17	361.9 b-d	350.8 a-b	4.1 d-j	4.7 d-i	4.4 e-g	4.3 c-e	4.7 b-l	0.97 f-m	174 e-g	35.8 g-j	36.2 f-j
HS624 x ELS33	359.9 b-f	341.8 b-h	4.2 d-i	4.5 g-m	4.4 e-g	4.2 c-f	3.8 p-u	1 a-d	168 i-l	35.1 i-m	36.2 f-j
HS624 x FM832	349.6 c-j	346.2 a-f	4.1 d-j	4.3 k-q	4.7 b-c	4.6 a	3.9 o-u	0.99 b-g	176 c-e	38.1 a-d	38.4 a-b
HS624 x TAM22	322.2 n-q	308.7 p-q	4.7 b	4.7 d-i	4.6 c	4.4 b-c	4.2 j-r	0.98 b-j	179 c	39.1 a	38.7 a
HSMD9 x HS624	345 e-l	347.2 a-d	4.6 b-c	4.6 e-j	4.9 a	4.7 a	3.4 s-u	1.0 a-c	179 b-c	38.3 a-c	38.4 a-b
HSMD9 x M24	349.3 c-j	343 b-h	3.9 j-o	4.2 l-q	4.1 k-o	4.2 e-i	4 n-u	1.0 a-e	172 f-h	36.2 f-i	37 c-h
HSMD9 x TAM22	304.5 r-s	314.8 n-p	4.4 c-d	4.8 c-f	4.5 d-e	3.9 k-p	4.7 d-n	0.96 l-q	178 c-d	38.4 a-c	37.2 c-f
M24 x ELS33	346.9 d-k	342.8 b-h	4 g-l	4.2 m-q	3.8 s-u	3.6 r-t	4.4 f-p	0.97 f-n	162 m-n	31.5 r-s	30.7 t-u
M24 x HS624	361.4 b-e	336.6 b-k	4.1 d-j	4.3 j-o	4.2 g-k	4.1 f-j	4.3 g-q	0.97 f-m	168 i-j	35 i-m	35.7 i-k
M24 x M9651	328.3 l-q	326.3 i-o	3.9 j-o	4.1 m-q	3.7 u-w	3.6 r-t	5 a-g	0.94 p-s	165 k-m	33.8 m-q	32.5 q-s
M24 x SID84	346.7 d-k	329.3 h-n	4.3 d-f	4.8 c-f	3.3 z	3.4 u-v	5.4 a-d	0.93 s	155 q-r	31.4 r-s	32.8 p-r
M24 x TAM22	317 o-r	304 p-q	4.3 d-f	4.6 e-j	4 n-r	3.9 l-p	4.9 b-i	0.95 o-s	174 e-f	35.9 g-j	35.6 j-k
M9651 x FM832	334.7 i-n	325.8 j-o	4.0 f-k	4.0 q	4.1 k-o	4.1 f-l	4.2 i-q	0.99 b-i	172 f-h	36.0 g-j	35.5 j-l

Table 5. Continued

Genotypes	Str		Elon		Mic		IFC	MR	Hs	LP	
	2009	2010	2009	2010	2009	2010				2009	2010
	kN m kg^{-1}		-- % --				%		mtex	-- % --	
M9651 x HS624	346.4 d-k	338.8 b-k	3.8 k-p	4.1 n-q	4.4 e-g	4.2 d-h	4.0 l-t	0.99 b-h	168 i-k	35.2 h-l	35.8 i-k
M9651 x HSMD9	333.4 j-o	330.3 g-m	3.9 i-n	4.2 m-q	4.3 f-j	4 g-m	3.9 o-u	0.98 c-k	170 h-j	36.9 d-g	38.1 a-c
M9651 x SID84	341.3 g-m	337.4 b-k	4.2 d-g	4.5 g-m	3.4 z	3.2 v-w	5.0 b-i	0.94 p-s	153 r	29.7 t	32.4 q-s
M9651 x TAM22	314.1 q-s	317 l-p	4.3 d-f	4.4 i-o	4.2 j-n	4.1 f-l	5.0 b-h	0.94 p-s	173 e-g	36.4 f-h	35.8 i-k
SID84 x FM832	350.6 b-i	337.1 b-k	4.6 b-c	5 a-d	3.7 u-x	3.7 q-s	4.5 e-p	0.96 j-q	163 m-n	33.4 o-q	33.7 n-p
SID84 x HS624	367.3 a-b	335.2 d-k	4.2 d-h	4.7 d-h	3.9 r-t	3.9 m-q	4.9 b-j	0.96 l-q	165 k-m	35.0 i-m	35.7 i-k
SID84 x HSMD9	357.7 b-g	337.6 b-k	4.6 b-c	5.2 a-b	3.6 v-x	3.7 p-s	4.3 h-q	0.96 h-p	163 m	33.0 p-q	34.4 l-n
FM832 x HSMD9	325.3 m-q	333.7 d-k	3.9 i-m	4.2 k-q	4.5 c-d	4.6 a-b	3.4 t-u	1.01 a-b	179 c	37.3 c-f	37.9 a-c
FM832 x M24	342.5 g-l	341.3 b-i	3.8 k-p	4.3 k-q	4 p-s	4 i-n	4.5 e-p	0.97 g-o	171 g-i	34.8 j-n	35.9 g-j
TAM22 x ELS17	314.1 q-s	310.4 p-q	3.9 h-l	4.7 d-h	4.2 g-k	4.2 d-g	5.1 a-f	0.95 n-s	182 a-b	36.5 f-h	35.9 h-j
TAM22 x ELS33	312.6 q-s	315.5 m-p	4.0 g-l	4.5 f-k	4.2 h-l	4 h-n	4.3 h-q	0.97 f-m	173 e-g	35.6 g-k	35.7 i-k
TAM22 x FM832	297.6 s	297.4 q	4.3 c-e	4.4 h-n	4.3 e-i	4.4 b-c	4.3 g-q	0.97 f-m	178 c-d	37.7 b-e	38 a-c
TAM22 x SID84	316.3 p-r	316 m-p	5.4 a	5.3 a	3.6 v-x	3.8 n-q	4.7 d-n	0.96 l-q	168 i-j	34.4 k-o	35.4 j-m
SID84	354.5 b-h	350.4 a-c	4.8 b	5.1 a-c	2.6 a	2.5 x	5.7 a	0.89 t	138 s	22.2 u	22.5 v
HS624	380.3 a	359.4 a	4.7 b	4.9 b-e	4.8 a-b	4.7 a	3.2 u	1.02 a	174 e-f	35.3 h-l	37.8 a-d
M24	354.3 b-h	340.8 b-j	4.1 e-j	4.2 k-q	3.6 x-y	3.4 t-u	5.2 a-e	0.95 o-s	165 l-m	30 t	31.5 s-t
M9651	345.7 d-k	308.7 p-q	3.6 n-p	4.1 o-q	3.6 w-x	3.6 r-t	4.9 b-i	0.95 m-r	163 m-n	30.9 s-t	34.7 k-n
ELS17	331.5 k-p	339.3 b-k	3.8 k-p	4.3 j-p	3.9 q-t	4.1 f-k	4.9 b-j	0.96 h-p	172 f-h	33.7 n-q	33.8 n-p
ELS33	342 g-m	345.2 a-g	3.8 k-p	4.1 n-q	3.7 u-x	3.6 r-t	4.4 f-p	0.97 g-o	158 o-p	30.4 s-t	30.3 u
FM832	344.5 f-l	311.4 o-q	4 g-l	4.1 o-q	4.7 b-c	4.6 a-b	3.5 r-u	1 a-c	179 c-d	35.4 h-l	36.7 d-i
HSMD9	334.2 i-n	334.2 d-k	4.3 d-f	4.6 e-j	4.5 d-e	4.2 d-h	3.6 q-u	0.99 b-f	180 b-c	36.8 e-g	37.5 b-e
TAM22	273.1 t	275.1 r	4.6 b-c	4.4 h-m	4.4 d-f	4.2 d-h	5 a-g	0.94 q-s	183 a	38.6 a-b	38 a-c
Test Mean	339.0	331.0	4.1	4.4	4.0	4.0	4.5	0.97	169	34.3	34.9
CV	3.6	3.2	5.1	5.3	2.7	3.4	16.4	2.4	1.9	2.8	2.3

† Means within a column followed by the same letter are not different 0.05 probability level according to Fisher LSD.

units for TAM22 in 2008 and 2009, respectively. Thus, based on Mic alone, one might select TAM22 under the impression that a lower Mic indicated a finer and more desirable fiber.

Since Mic is a combination of fiber diameter and fiber maturity, it should be more beneficial to breeders to look at diameter and maturity individually using AFIS IFC, MR, and Hs. While these parents differed significantly for all of these AFIS traits, comparison of HS624 and FM832 will serve to support the value of using IFC, MR, and Hs rather than Mic for breeders during selection. FM832 and HS624 averaged the same ($p<0.05$) IFC and MR (Table 5). However, HS624 averaged a finer Hs than FM832 at 174 and 179 mtex, respectively. In this study, HS624, however, averaged a significantly higher Mic in both 2008 and 2009. Gregory et al. (2012) reported that HS624 (designated TAM 06WE62-4 in their report) produced 50 Ne cotton yarn that was significantly stronger than that produced by FM832, required more work to break, had fewer yarn variations, and was more stable across years. SID84 and TAM22 had the greatest amount of immature fibers at 5.7 and 5.0%, respectively, and SID84 averaged the lowest MR of 0.89 and finest fibers with an Hs of only 138 mtex. TAM22 exhibited the coarsest fibers at 183 mtex Hs, followed by HSMD9 at 180 mtex and FM832 at 179 mtex, which was not different ($p<0.05$) than HSMD9.

Elon ranged from 3.6% to 4.8% in 2009 and 4.1% to 5.1% in 2010. All of these values except for the 5.1% exhibited by SID84 in 2010 are in the “very low” category (2012), thus the parents included in this study would not be useful for improving Elon.

SID84 ranked first in both years but was not different than HS624 in 2009 and 2010 and TAM22 in 2009.

General Combining Ability

F_1s were significant for every trait allowing for the partitioning of variability into GCA and SCA effects (Tables 2 and 3). GCA effects were observed ($P \leq 0.05$) for all fiber quality parameters. Significant GCA x Y interactions were detected for UHML, UQLw, Mic, and LP. Thus, GCA effects for these traits are reported by year. Most of the combining ability of these parents was explained by the GCA component, suggesting additive gene effects for the fiber properties reported plus LP. Variance due to GCA for UHML was 86 times greater than the variance due to SCA, while GCA for UQLw, Ln SFCn, UI, Str, Elon, Mic, IFC, MR, Hs and LP were 77, 5, 5, 12, 28, 18, 73, 12, 9, 59, and 35 times greater, respectively. Ln, SFCn, UI, IFC, and MR were the only fiber properties reported that had GCA to SCA ratios remotely suggesting any meaningful dominance gene effects. Ln, SFC, and UI are all related values that reflect length distribution and all can be influenced by human handling, e.g., ginning, but these distributions of variance due to GCA and SCA suggest that additional investigation could be worthwhile. MR and IFC also may need additional evaluation as to the impact of dominance gene action.

All GCA effects for UHML and UQLw were significantly different than zero (Table 6). GCA effects for UHML ranged from -2.12 to 1.79 mm in 2009 and -1.82 to 1.51 mm in 2010. Similarly, GCA effects for UQLw ranged from -2.35 to 1.79 mm in 2009 and -1.73 to 1.32 mm in 2010. All five parents selected based on their high UHML,

Table 6. Estimates of general combining ability (GCA) for upper-half mean length (UHML), upper quartile length by weight (UQLw), fiber length by number (Ln), percentage of fibers by number shorter than 12.7 mm (SFCn), and uniformity index (UI) of nine parents when grown near College Station, TX, in 2009 and 2010.

Genotype	UHML				UQLw				Ln		SFCn		UI			
	2009		2010		2009		2010						2009		2010	
	mm										%		%			
ELS17	0.97	***	0.81	***	1.07	***	0.86	***	-0.21		2.37	***	0.07		0.47	**
ELS33	1.13	***	0.74	***	1.24	***	0.82	***	0.60	**	-0.58		0.27	*	-0.19	
M24	1.05	***	0.97	***	1.16	***	1.31	***	0.51	**	0.22		-0.25		-0.42	*
M9651	0.45	***	0.70	***	0.68	***	0.93	***	0.31		0.01		-0.25		-0.55	**
SID84	1.79	***	1.51	***	1.79	***	1.32	***	-0.05		2.38	***	0.36	**	0.30	
HS624	-0.68	***	-0.77	***	-0.72	***	-1.12	***	-0.04		-1.20		0.38	**	0.26	
HSMD9	-1.61	***	-1.44	***	-1.75	***	-1.73	***	0.02		-2.59	***	0.38	**	0.62	***
FM832	-0.98	***	-0.70	***	-1.12	***	-0.66	***	0.13		-1.80	**	0.15		0.62	***
TAM22	-2.12	***	-1.82	***	-2.35	***	-1.73	***	-1.26	***	1.18		-1.13	***	-1.10	***
$LSD_{0.05}$ g_i-g_j[†]	0.31		0.31		0.41		0.36		0.57		1.53		0.39		0.51	

*Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

***Significant at the 0.001 probability level.

[†] $LSD_{0.05}$ g_i-g_j, least significant difference of GCA for genotype *i* and GCA for genotype *j* at the 0.05 probability level.

i.e., ELS17, ELS33, M24, M9651, and SID84, exhibited positive GCA effects for both UHML and UQLw, with the interspecific, SID84, exhibiting the largest numerical GCA values for the traits. Cultivars, TAM22 and FM832, and both high strength parents, HS624 and HSMD9, exhibited negative GCA effects for UHML and UQLw. These results using this set of parents were not unexpected, because the GCA effects followed the relative mean values of the parents. However, this expectation did not hold true for SID84 and ELS17 for AFIS Ln and SFCn as will be pointed out below. As expected, TAM22 was the worst or not different than the worst general combiner for UHML and UQLw.

SID84 was the best ($p<0.05$) general combiner for UHML improving length on the average by 1.79 mm and 1.51 mm in 2009 and 2010, respectively (Table 6). Additionally, it was the best general combiner for UQLw in 2009 but not different than M24 in 2010. This parent exhibited a positive and significant GCA for UI in 2009 and a positive GCA value in 2010 for UI, although not significantly different from zero. However, a potential weakness of SID84 as a parent to improve fiber length was indicated by a significant and positive GCA for SFCn and significant and positive GCA estimate for IFC combined with significant and negative GCA estimate for MR (Table 7). These data suggest that using SID82 as a parent to produce segregating progeny from which to select for longer UHML or UQLw could result in such progeny having shorter average fiber length, more immature fibers, and more fibers less than 12.7 mm in length. This line's low Hs might be desirable if it could be combined with improved MR and reduced SFC. The other parental genotypes selected based on their known UHML all

Table 7. Estimates of general combining ability (GCA) for fiber bundle strength (Str), fiber elongation at break (Elon), micronaire (Mic), immature fiber content (IFC), maturity ratio (MR), standard fineness (Hs), and lint percentage (LP) of nine parents when grown near College Station, TX, in 2009 and 2010.

Genotype	Str				Elon				IFC		MR		Hs		LP			
	2009		2010		2009		2010								2009		2010	
	-------- kN m kg-1 ---------				---------- % ----------				----- % -----		-- ratio --		-- mtex --		---------- % ----------			
ELS17	-1.94		3.60		-0.28	***	-0.07		0.34	*	-0.008		1.8	***	-0.70	***	-0.76	***
ELS33	11.58	***	6.11	**	-0.23	***	-0.20	***	-0.01		0.002		-4.4	***	-1.75	***	-1.47	***
M24	2.75		1.78		-0.13	***	-0.12	**	0.18		-0.008		-2.8	***	-1.01	***	-1.25	***
M9651	-5.61	**	-2.25		-0.22	***	-0.30	***	0.12		-0.004		-3.4	***	-0.62	***	-0.88	***
SID84	9.87	***	1.25		0.44	***	0.48	***	0.51	**	-0.023	***	-11.1	***	-2.90	***	-2.24	***
HS624	14.88	***	7.73	***	0.15	***	0.06		-0.38	*	0.018	***	3.5	***	1.90	***	1.89	***
HSMD9	0.61		3.52		0.01		0.06		-0.57	***	0.017	***	4.9	***	1.49	***	2.06	***
FM832	-1.97		2.16		-0.10	**	-0.20	***	-0.34	*	0.014	**	4.1	***	1.32	***	1.20	***
TAM22	-30.17	***	-23.90	***	0.36	***	0.29	***	0.17		-0.008		7.5	***	2.26	***	1.46	***
$LSD_{0.05}\ g_i\text{-}g_j$ †	6.27		5.55		0.10		0.11		0.29		0.012		1.7		0.43		0.42	

*Significant at the 0.05 probability level.
** Significant at the 0.01 probability level.
***Significant at the 0.001 probability level.
† $LSD_{0.05}\ g_i\text{-}g_{j,}$ least significant difference of GCA for genotype *i* and GCA for genotype *j* at the 0.05 probability level.

performed well in GCA for most if not all fiber length parameters (Tables 6 and 7). Line M24, when combined with the other parents in this study, averaged increasing ($p<0.05$) UHML by 1.05 mm in 2009 and 0.97 mm in 2010; increasing UQLw by 1.16 mm in 2009 and 1.31 mm in 2010; and Ln by 0.51 mm across both years. This parent outperformed ELS17, ELS33, and M9651 only for UQLw GCA in 2010 and outperformed only ELS17 for Ln when averaged across years. ELS17 significantly increased SFCn and Hs when crossed with this set of parents and increased IFC, while ELS33, M24, and M9651 decreased Hs, a desirable occurrence. Finally, ELS33 was a better combiner than M24 in 2009 for UI but not different in 2010. Both ELS 33 and M24 should prove to be valuable parents to improve both HVI and AFIS fiber length traits.

GCA effects for Str ranged from -30.17 to 14.88 kN m kg^{-1} and -23.90 to 7.73 kN m kg^{-1} in 2009 and 2010, respectively (Table 7). HS624 was numerically the best general combiner for Str in both years with ELS33 and SID84 not significantly different than HS624 it in 2009, and ELS33 and HSMD9 not different than HS624 in 2010 and significantly different than zero. M9651 and TAM22 were significant and negative for GCA for Str 2009 and in 2010 for TAM22. Crosses involving TAM22 were, on average, 30.17 and 23.90 kN m kg^{-1} below the average of all progeny in the study. The large negative impact TAM22 had on Str compared to the other parents caused the range of GCA effects to be skewed so unevenly around zero. It is important to note that ELS33 combines very well for Str in addition to being one of the best combiners for length across HVI and AFIS length measurements as noted above. It may prove to be useful in

simultaneously improving length and strength. HS624, on the other hand, may prove very useful parent to improve LP, as discussed above, and Str concurrently.

Numerous significant GCA effects were observed for Elon with values ranging from -0.28 to 0.44% in 2009 and -0.07 to 0.48% in 2010 (Table 7). SID84, which is a poor parent among this set because of its increasing SFCn, IFC, and MR, was numerically the best general combiner in both years performing similarly to TAM22 in 2009 (Tables 6 and 7). Both mutant parents, both ELS parents, and FM832 all exhibited negative GCA effects for Elon.

HSMD9, HS624, and FM832 were the most desirable ($p<0.05$) general combiners for IFC (-0.57, -0.38, and -0.34%, respectively) and for MR (0.018, 0.017, and 0.014, respectively). Here HSMD9 exhibits its value as a parent to improve fiber quality. It is numerically the best combiner for IFC and MR. The improved fiber maturity and lack of immature fiber content in progeny likely led to HSMD9 to be the best combiner for reducing SFCn. As parents, ELS17 and SID84 were the worst combiners increasing IFC by 0.34 and 0.51%, respectively. SID84 was the only parent with a significantly negative GCA effect for MR at -0.023.

All GCA effects for Hs were significantly different from zero ranging from -11.1 to 7.5 mtex (Table 7). SID84 was best combiner for decreasing Hs at -11.1 mtex, which is 2.5 fold better than the next best general combiner, ELS33, which was not different than M24 and M9651.ELS17, and both high strength parents had positive (undesirable) GCA effects. TAM22, which averaged increasing Hs by 7.5 mtex when crossed with this

set of parents. Without question, SID84 is the parent of choice among these nine parents to improve Hs but it would be detrimental to use this line as a parent as noted above.

GCA effects for all parents in both years were significantly different than zero for LP (Table 7). TAM 22 and HS624 were the best general combiners for LP in 2009 with values of 2.26 and 1.90, respectively, while in 2010, HSMD9 added 2.06% to the average LP when crossed with all other parents in this study and HS624 added 1.89 percent. In both years, SID84 was the worst combiner for LP at -2.90 in 2009 and -2.24% in 2010. All of the high length parents exhibited negative GCA effects for LP when combined with the other parents in this study, suggesting that it will be difficult to simultaneously improve LP and fiber length parameters with these parents.

Mic values of 3.5 to 4.9 are considered nondiscount according to the CCC Loan Premium and Discount Schedule for upland cotton (National Cotton Council, 2013). Consequently, breeders select progeny expressing Mic values within this range, i.e., they do not minimize nor maximize Mic. High Mic values usually indicate coarse fiber, and low Mic values indicate immature fibers. However, Mic cannot distinguish between a coarse, immature fiber and a fine, mature fiber as discussed above. Therefore, the concept of combining ability for Mic is of little to no value. Instead, the reader should refer to the combining ability analyses for IFC, MR, and Hs below. Additionally, readers are referred to mean values of Mic for the parents.

Specific Combining Ability and Heterosis

The ANOVA revealed significant SCA effects for all traits except IFC (Tables 2 and 3). SCA x Y was significant for UHML, UQLw, UI, Elon, Mic, and LP. There were

no consistent trends of significant SCA effects for all fiber length traits (Table 8). Only SID84 x HSMD9 exhibited significant and positive SCA effects in both years for UHML, but was significantly shorter than its high-parent, SID84. M24 x SID84 expressed high-parent heterosis in 2009 and was the highest performing hybrid, but this did not occur to 2010. In 2010, ELS33 x SID84, ELS17 x SID84, and M9651 x SID84 possessed high-parent heterosis and were among the top six longest hybrids. No hybrid exhibited significant SCA effects in both years for UQLw. Similar to their performance for UHML, ELS33, ELS17, M9651, and M24 when crossed to SID84 had superior mean performance for UQLw. High-parent heterosis was observed for ELS17 x SID84 and ELS33 x SID84 in 2009 with none expressed in 2010. However, these combinations are not desirable specific combinations when considering Ln and SFCn. They expressed a relatively shorter Ln with increased levels of SFCn. No single F_1 was best across all length measurements. ELS33 x M9651 ranked in the top five numerical values for UHML and UQLw in at least one year and was the fifth best for Ln, but again had more SFCn than was desirable.

Very few SCA effects were significant for Str (Table 9). Only M9651 x TAM22 was significant in both years, increasing Str by 11.2 and 11.8 kN m kg^{-1} for 2009 and 2010, respectively. While its mean performance was significantly better than TAM22, it was significantly weaker in 2009 and not different in 2010 than M9651 (Table 5). No hybrid outperformed HS624 in either year. The only instance of high-parent heterosis was in 2009 for ELS33 x HSMD9 with a mean similar to HS624.

Table 8. Estimates of specific combining ability (SCA) for upper-half mean length (UHML), upper quartile length by weight (UQLw), fiber length by number (Ln), percentage of fibers by number shorter than 12.7 mm (SFCn), and uniformity index (UI) of nine parents when grown near College Station, TX, in 2009 and 2010.

Genotype	UHML				UQLw				Ln		SFCn		UI			
	2009		2010		2009		2010						2009		2010	
	------- mm -------				-------- mm --------				-- mm --		--- % ---		------- % -------			
ELS17 x FM832	0.16		0.29		0.26		-0.23		0.12		-0.08		0.25		0.06	
ELS17 x HSMD9	0.66	*	0.01		0.77	*	0.15		0.68		-1.54		0.45		1.04	*
ELS17 x M24	-0.03		-0.05		0.14		0.34		0.41		-1.71		-0.57		-0.98	*
ELS17 x M9651	-0.70	**	-0.48		-0.71	*	-0.36		-0.31		0.39		-0.77	*	0.10	
ELS17 x SID84	0.05		-0.14		0.28		-0.01		0.37		-1.48		0.05		-0.37	
ELS33 x ELS17	0.27		-0.01		-0.51		-0.32		-0.79		2.49		0.56		-0.03	
ELS33 x FM832	-0.06		0.99	***	-0.42		1.20	**	0.94	*	-2.12		-0.34		0.45	
ELS33 x HSMD9	-0.07		-0.21		0.02		-0.27		-0.42		1.42		-0.23		-0.10	
ELS33 x M9651	0.28		0.70	*	0.58		0.18		-0.04		0.62		-0.04		0.90	*
ELS33 x SID84	0.02		0.18		-0.15		-0.21		-1.18	*	3.55	*	-0.17		0.14	
HS624 x ELS17	-0.01		0.23		0.12		0.42		0.26		-0.42		-0.15		0.25	
HS624 x ELS33	0.27		-0.47		0.13		-0.25		0.27		-1.15		0.53		-0.71	
HS624 x FM832	0.48		-0.29		0.65		-0.03		-0.12		0.86		-0.03		-0.55	
HS624 x TAM22	-0.04		-0.06		0.04		0.21		0.23		-0.90		-0.40		-0.28	
HSMD9 x HS624	-0.93	***	-0.19		-1.00	**	0.15		0.18		-1.75		-0.81	*	-0.40	
HSMD9 x M24	-0.24		0.17		-0.02		0.13		0.46		-1.32		0.47		0.32	
HSMD9 x TAM22	-0.13		0.67	*	-0.64		-0.06		-1.20	*	4.14	**	-0.83	*	0.40	
M24 x ELS33	-0.64	*	-0.30		0.10		-0.20		0.46		-1.66		-0.49		0.56	
M24 x HS624	0.29		0.20		0.02		-0.36		-0.68		2.10		0.20		0.39	
M24 x M9651	-0.34		-0.07		-0.42		0.01		-0.01		0.00		-0.07		0.32	
M24 x SID84	0.16		-0.24		0.19		-0.32		0.00		-0.34		0.23		-0.73	

Table 8. Continued

Genotype	UHML				UQLw				Ln		SFCn		UI			
	2009		2010		2009		2010						2009		2010	
	------- mm -------				--------- mm ---------				-- mm --		------- % -------		------- % -------			
M24 x TAM22	0.64	*	0.23		0.13		0.20		-0.22		1.41		0.56		0.19	
M9651 x FM832	-0.59	*	-0.12		-1.25	***	-0.24		-0.69		1.11		0.13		-0.22	
M9651 x HS624	0.83	**	0.46		1.39	***	0.28		0.85		-1.54		0.49		0.77	
M9651 x HSMD9	0.29		-0.39		-0.11		-0.25		-0.42		0.94		0.12		-1.15	**
M9651 x SID84	0.13		-0.16		0.10		0.25		0.13		-0.47		-0.33		-0.79	
M9651 x TAM22	0.10		0.06		0.42		0.13		0.49		-1.06		0.48		0.05	
SID84 x FM832	0.04		-0.22		0.37		0.01		0.21		-0.33		-0.15		0.36	
SID84 x HS624	-0.90	***	0.11		-1.36	***	-0.43		-0.98	*	2.79		0.19		0.54	
SID84 x HSMD9	0.73	**	0.58	*	1.07	**	0.57		0.64		-0.59		0.41		0.33	
FM832 x HSMD9	-0.31		-0.64	*	-0.09		-0.43		0.08		-1.31		0.42		-0.44	
FM832 x M24	0.15		0.06		-0.15		0.21		-0.41		1.53		-0.32		-0.07	
TAM22 x ELS17	-0.42		0.14		-0.35		0.02		-0.74		2.35		0.18		-0.07	
TAM22 x ELS33	-0.07		-0.87	**	0.24		-0.14		0.77		-3.15	*	0.19		-1.21	**
TAM22 x FM832	0.14		-0.07		0.63		-0.49		-0.13		0.34		0.05		0.41	
TAM22 x SID84	-0.23		-0.11		-0.49		0.13		0.81		-3.13	*	-0.23		0.52	
$LSD_{0.05}$ s_{ij}-s_{ik}[†]	0.76		0.77		1.00		0.89		0.04		3.53		0.95		1.25	
$LSD_{0.05}$ s_{ij}-s_{kl}[‡]	0.70		0.70		0.92		0.81		0.04		3.22		0.87		1.14	

*Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

***Significant at the 0.001 probability level.

[†]s_{ij}-s_{ik}, least significant difference of SCA for parental combination *ij* and SCA for parental combination ik at the 0.05 probability level.

[‡]s_{ij}-s_{kl}, least significant difference of SCA for parental combination *ij* and SCA for parental combination kl at the 0.05 probability level.

Table 9. Estimates of general combining ability (GCA) for fiber bundle strength (Str), fiber elongation at break (Elon), micronaire (Mic), immature fiber content (IFC), maturity ratio (MR), standard fineness (Hs), and lint percentage (LP) of nine parents when grown near College Station, TX, in 2009 and 2010.

Genotype	Str		Elon		MR	Hs	LP	
	2009	2010	2009	2010			2009	2010
	---- kN m kg-1 -----		------- % -------		-- ratio --	-- mtex --	------- % -------	
ELS17 x FM832	5.77	0.70	-0.19 *	-0.17	-0.009	-0.7	0.09	-0.06
ELS17 x HSMD9	-4.17	-6.54	-0.02	0.04	-0.006	-0.1	-1.42 ***	-0.14
ELS17 x M24	-2.87	3.53	0.02	-0.18	0.009	-1.2	-0.46	-0.21
ELS17 x M9651	-7.75	-7.15	-0.02	0.01	0.019	1.0	1.75 ***	0.47
ELS17 x SID84	-5.33	-0.60	0.15	-0.05	-0.005	-3.7 **	-0.77 *	-1.10 **
ELS33 x ELS17	-3.37	2.63	0.14	0.01	0.001	1.5	0.89 *	1.24 ***
ELS33 x FM832	6.47	7.26	0.03	-0.09	0.005	-0.1	0.37	0.34
ELS33 x HSMD9	14.43 **	-3.73	-0.08	-0.11	-0.010	0.6	-0.05	1.19 ***
ELS33 x M9651	3.98	-1.08	-0.03	0.16	-0.015	-1.1	-1.69 ***	-1.16 **
ELS33 x SID84	-2.67	-7.03	-0.16	-0.20 *	-0.012	-1.6	0.52	-0.89 *
HS624 x ELS17	10.25	8.12	0.17	0.27 **	-0.006	-0.7	-0.19	-0.14
HS624 x ELS33	-5.23	-3.46	0.13	0.17	0.012	-0.5	0.15	0.58
HS624 x FM832	-1.97	4.90	-0.02	-0.02	-0.011	-0.3	0.12	0.09
HS624 x TAM22	-1.24	-6.55	0.10	-0.09	0.006	-1.1	0.12	0.10
HSMD9 x HS624	-9.21	4.53	0.33 ***	0.06	0.001	1.8	0.09	-0.75 *
HSMD9 x M24	7.27	6.31	-0.12	-0.19 *	0.020	1.0	0.93 *	0.90 *
HSMD9 x TAM22	-4.63	3.79	-0.06	0.05	-0.019	-4.0 ***	-0.09	-1.58 ***
M24 x ELS33	-6.10	3.48	0.21 *	0.05	0.009	0.1	-0.54	-1.81 ***
M24 x HS624	5.08	-4.28	0.02	-0.03	-0.004	-1.6	-0.67	-0.22
M24 x M9651	-7.53	-4.59	0.11	0.13	-0.012	2.0	0.67	-0.59
M24 x SID84	-4.63	-5.15	-0.13	0.04	-0.010	-0.6	0.52	1.09 **

Table 9. Continued

Genotype	Str				Elon				MR		Hs		LP			
	2009		2010		2009		2010						2009		2010	
	---- kN m kg-1 -----				------- % -------				-- ratio --		-- mtex --		------- % -------			
M24 x TAM22	5.74		-5.26		-0.05		0.03		-0.005		0.0		-0.14		0.11	
M9651 x FM832	3.56		-5.47		0.25	**	0.04		0.009		2.0		0.47		-0.07	
M9651 x HS624	-1.52		1.96		-0.25	**	-0.10		0.006		-1.2		-0.85	*	-0.50	
M9651 x HSMD9	-0.25		-2.41		-0.01		-0.03		0.003		-1.0		1.24	***	1.63	***
M9651 x SID84	-1.66		6.97		-0.09		-0.15		0.003		-1.9		-1.60	***	0.28	
M9651 x TAM22	11.16	*	11.77	*	0.04		-0.06		-0.012		0.1		0.01		-0.07	
SID84 x FM832	4.02		2.31		0.14		0.28	**	0.004		0.8		0.22		-0.48	
SID84 x HS624	3.84		-5.22		-0.48	***	-0.26	**	-0.004		3.6	**	1.23	**	0.84	*
SID84 x HSMD9	8.54		1.44		0.06		0.24	*	0.002		0.4		-0.38		-0.64	
FM832 x HSMD9	-11.98	*	-3.39		-0.10		-0.08		0.009		1.0		-0.33		-0.63	
FM832 x M24	3.04		5.95		-0.07		0.15		-0.006		0.3		-0.32		0.73	*
TAM22 x ELS17	7.48		-0.70		-0.25	**	0.06		-0.004		3.9	***	0.11		-0.06	
TAM22 x ELS33	-7.51		1.93		-0.25	**	0.01		0.010		1.1		0.34		0.51	
TAM22 x FM832	-8.91		-12.26	**	-0.03		-0.11		0.000		-2.9	*	-0.62		0.08	
TAM22 x SID84	-2.11		7.28		0.51	***	0.11		0.023	*	2.9	*	0.27		0.90	*
$LSD_{0.05}$ s_{ij}-s_{ik}[†]	15.36		13.60		0.24		0.28		0.02		3.11		1.06		1.03	
$LSD_{0.05}$ s_{ij}-s_{kl}[‡]	14.02		12.41		0.22		0.25		0.02		2.84		0.97		0.94	

*Significant at the 0.05 probability level.
** Significant at the 0.01 probability level.
***Significant at the 0.001 probability level.
[†]s_{ij}-s_{ik}, least significant difference of SCA for parental combination *ij* and SCA for parental combination ik at the 0.05 probability level.
[‡]s_{ij}-s_{kl}, least significant difference of SCA for parental combination *ij* and SCA for parental combination kl at the 0.05 probability level.

The cross SID84 x HS624 exhibited negative SCA effects in both years and performed worse than both parents in 2009 for Elon (Table 9). TAM22 x SID84 had the greatest Elon with 5.4 and 5.3%. In 2009 it was significantly better than all other genotypes but was not different than SID84 x HSMD9, SID84, and SID84 x FM832 in 2010.

The only hybrid to express a significant SCA effect for MR was TAM22 x SID84 with a value of 0.023 (Table 9). No significant high-parent heterosis was observed. Of the 45 genotypes, 37 had a MR of 0.95 or higher.

SCA effects for Hs were significant for six hybrids (Table 9). HSMD9 x TAM22 had the most negative (favorable) effect at -4.0 mtex. TAM22 x ELS17 was 3.9 mtex coarser than the GCA effects of its parents predicted. No high-parent heterosis was observed. SID84 exhibited the finest fiber at 138 mtex (Table 5). ELS33 x SID84 was the next closest genotype with a mean of 152 mtex.

Six F_1s expressed significant SCA effects for LP in both 2009 and 2010 (Table 9). Among them, M9651 x HSMD9 had the largest SCA for improving LP, but with a mean of 36.9% in 2009 and 38.1% in 2010 it was not a significant improvement over its high-parent, HSMD9 (Table 5). It is important to remember that SCA does not identify the highest performing F_1s rather measures the deviation of an F_1's performance from what would be expected given the GCA effects of its two parents. Thus, SCA is useful for trait improvement only when combined with desirable mean trait performance. The highest performing cross, HS624 x TAM22, did not possess significant SCA effects and was not different from its high-parent, TAM22. Five hybrids did exhibit high-parent

heterosis in 2009 but only one, M24 x SID84, also possessed it in 2010. Unfortunately, its mean performance is still rather low at 31.4 and 32.8% in 2009 and 2010, respectively.

Mid-Parent and High-Parent Heterosis

There was very little overall mid-parent heterosis observed (Table 4, 5, and 10). LP was the only trait where mid-parent heterosis exceeded 5% with 7.1% exhibited in 2009 and 5.2% in 2010. Average high-parent heterosis occurred at a much lower percentage and was negative for most traits. The presence of heterosis, albeit very low levels, agree with previous reports of low levels of heterosis for various fiber quality traits (Al-Rawi and Kohel, 1970). Such a low level of heterosis suggests that these traits are predominantly controlled by additive gene action within these populations.

SID84 was responsible for a large portion of mid-parent heterosis for LP, Ln, and SFCn. When only F_1s with SID84 as a parent are considered, the average of mid-parent heterosis for LP is 15.1% in 2009 and 15.7% in 2010. However, the overall average of mid-parent heterosis for LP was only 7.1% and 5.2% in 2009 and 2010, respectively, which dropped to 4.8% and 2.2% in 2009 and 2010, respectively, when F_1s with SID84 as a parent were removed. Average mid-parent heterosis for combinations including SID84 compared with non-SID84 combinations was 6.5% versus 2.1% and 11.5% versus 1.3% for Ln and SFCn, respectively. Since SID84 is the worst performer for these traits, it likely differs at more loci affecting each trait compared with other parents, than do the other parents among themselves. Thus, the difference in heterosis between the two groups, F_1s sharing SID84 as a parent versus all other F_1s which did not have SID84

Table 10. Percentage of mid-parent and high-parent heterosis for selected fiber properties and lint percentage (LP) of nine parents when grown near College Station, TX, in 2009 and 2010.

Trait	Year	Mid-parent heterosis			High-parent heterosis		
		Non-SID84 combinations[†]	SID84 combinations	Overall	Non-SID84 Combinations	SID84 Combinations	Overall
		%					
UHML[‡]	2009	1.1	3.1	1.5	-3.6	-1.0	-3.0
	2010	2.8	4.3	3.1	-1.8	0.1	-1.4
UQLw	2009	2.3	4.2	2.7	-3.2	0.0	-2.5
	2010	2.2	2.5	2.2	-2.1	-1.4	-2.0
Ln		2.1	6.5	3.0	-0.7	2.0	-0.1
SFCn		1.3	11.5	3.5	-4.8	-11.3	-6.2
UI	2009	0.1	0.4	0.2	-0.4	0.1	-0.2
	2010	1.3	0.8	1.2	0.2	0.0	0.1
Str	2009	-0.5	0.3	-0.3	-5.0	-2.9	-4.5
	2010	1.4	-1.7	0.7	-3.2	-5.4	-3.7
Elon	2009	-3.0	0.7	-2.2	-8.2	-6.5	-7.8
	2010	-0.4	2.8	0.3	-3.9	-4.9	-4.1
IFC		-0.9	1.2	-0.4	-14.3	-16.7	-14.9
MR		0.0	1.6	0.4	-1.6	-2.6	-1.9
Hs		-0.1	-2.9	-0.7	-3.4	-15.5	-6.1
LP	2009	4.8	15.1	7.1	-0.7	-4.5	-1.5
	2010	2.2	15.7	5.2	-2.7	-4.8	-3.2

[†] Non-SID84 combinations, all F1s that do not have SID84 as a parent; SID84 combinations, all F1s that do have SID84 as a parent;

[‡] UHML, Upper-half mean length; UQLw, upper-quartile length by weight; Ln,fiber length by number; SFCn, percentage of fibers by number shorter than 12.7 mm; UI, uniformity index; Str, fiber bundle strength; Elon, fiber elongation at break; IFC, immature fiber content; MR, maturity ratio; and Hs, standard fineness.

as a parent, was likely caused by the accumulation of non-additive genetic effects across the additional loci. This conclusion is logical since SID84 is the only parent in this study that has *G. barbadense*, biotype Sea Island, in its immediate pedigree.

This argument fits well with LP and SFCn. However, SID84 and TAM22 performed almost exactly the same for Ln, but TAM22 did not show the elevated levels of heterosis. Pleiotropy could be the genetic reason but it is difficult to demonstrate. SID84 possesses the biological potential for higher lengths whereas TAM22 does not as can be seen by looking at the other fiber length traits as discussed above. Unfortunately, SID84 did not reach its phenotypic length potential likely because of its lower fiber maturity which led to decreased individual fiber strength. These weaker, immature fibers likely were broken during processing leading to an increase in short fiber content and subsequent lower Ln. TAM22 possesses the fiber maturity and, consequently, a lower level of short fiber content. However, without the biological length potential, its overall Ln remains low. Not surprisingly, the only hybrids expressing high-parent heterosis for Ln were SID84 x HSMD9 and TAM22 x SID84.

Interaction Analysis

Anytime a plant breeder observes a significant interaction of G x Y or locations (environments), the question arises of cause. It would be informative to know if only one genotype responded differently to environments or if an experimental genotype responded differently than accepted commercial cultivars used as checks. Smith (1978) proposed that such information could be obtained for any two environments by separating interaction elements rather than simply observing rank changes within

environments. A negative interaction element indicates that the genotype performed better in year two than year one, while a positive interaction element indicates performance was better in year one than year two for that genotype.

Significant interactions of GxY were observed for LP, all five HVI fiber quality measurements, and AFIS UQLw (Tables 2 and 3). Two parental lines, M9651 and HS624, along with three F_1s, M9651xSID84, ELS33xHSMD9, and ELS17xHSMD9, exhibited interaction elements different from zero for LP (Table 11). In each case, LP was higher in 2010 than 2009. Only M9651 was different from both FM832 and TAM22 and FM832 was different than TAM22, suggesting that these unique fiber quality parents and their F_1s responded similarly to the cultivar parents for LP across years.

Only HSMD9xTAM22 was different than both checks for UHML but was not different than zero (Table 11). Two parents and four F_1s were different from zero but were not different from both of the cultivar checks. ELS33 was a common parent in three of these F_1s with the other hybrid being M24xSID84.

Five F_1s were different from both FM832 and TAM22 but were not different than zero for UI, again suggesting stability across years (Table 11). It is notable that only MD9xTAM22 and ELS17xMD9 had higher UI values in 2010 than 2009. Five F_1s and four parental lines including FM832 and TAM22 were different than zero suggesting less stability across years. TAM22 exhibited the largest interaction element with UI decreasing 4.1 percent from 2009 to 2010 and was significantly different from FM832. No genotype had interaction elements for Str differ ($p<0.05$) from both FM832 and TAM22. FM832 was different from TAM22. FM832, M9651, and four F1s had

Table 11. Interaction elements, representing the differences of genotypic means across years, for fiber properties with significant genotype x year (GxY) interactions involving 36 F1 combinations and nine parents from a diallel without reciprocals when grown near College Station.

Genotype	LP[†]			UHML			UI			Str			Elon			UQLw		
	----- % -----			---- mm ----			---- % ----			kN m kg-1			---- % ----			---- mm ----		
ELS17 x FM832	-0.13		f-m[‡]	0.010		a-i	0.30		a-e	0.27		a-g	-0.45	*	a-f	0.008		d-i
ELS17 x HSMD9	-2.25	*	a-e	0.045		f-l	-0.25		a-b	0.13		a-f	-0.65	*	a-b	0.030		g-j
ELS17 x M24	-0.40		f-m	0.030		c-k	1.15		a-i	-0.38		a-d	-0.35		a-h	-0.008		c-i
ELS17 x M9651	1.14		k-m	0.008		a-i	0.00		a-c	-0.23		a-e	-0.48	*	a-e	-0.018		a-h
ELS17 x SID84	-0.73		e-j	0.045		f-l	1.05		a-h	0.57		a-i	-0.38		a-g	0.036		h-j
ELS33 x ELS17	-1.03		b-i	0.053	*	h-l	1.63		c-i	0.13		a-f	-0.43		a-f	0.015		d-j
ELS33 x FM832	-0.60		e-k	-0.017		a-c	0.17		a-e	0.80		a-i	-0.13		d-i	-0.068	*	a-b
ELS33 x HSMD9	-2.55	*	a-c	0.034		d-k	1.08		a-h	2.86	*	i-k	-0.37		a-g	0.025		g-j
ELS33 x M9651	-1.01		b-i	0.009		a-i	0.79		a-h	1.47		c-k	-0.45	*	a-f	0.020		e-j
ELS33 x SID84	0.01		f-m	0.040		e-l	1.18		a-i	2.63	*	h-k	-0.35		a-h	0.035		h-j
HS624 x ELS17	-0.43		f-m	0.020		b-k	0.30		a-e	1.13		a-j	-0.55	*	a-d	0.010		d-j
HS624 x ELS33	-1.15		b-h	0.067	*	k-l	2.80	*	i-j	1.85		d-k	-0.30		b-i	0.045		i-j
HS624 x FM832	-0.30		f-m	0.043		f-l	1.15		a-i	0.35		a-h	-0.13		d-i	0.023		f-j
HS624 x TAM22	0.37		g-m	0.013		a-j	0.95		a-h	1.38		b-j	0.03		g-i	-0.017		a-h
HSMD9 x HS624	-0.17		f-m	-0.013		a-d	0.45		a-f	-0.23		a-e	-0.02		f-i	-0.033		a-f
HSMD9 x M24	-0.75		d-j	0.000		a-f	1.05		a-h	0.64		a-i	-0.33		b-i	-0.015		a-h
HSMD9 x TAM22	1.26		l-m	-0.030		a	-0.52		a	-1.05		a	-0.43		a-f	-0.050		a-c
M24 x ELS33	0.79		j-m	0.025		b-k	0.55		a-g	0.42		a-h	-0.20		c-i	0.020		e-j
M24 x HS624	-0.65		e-j	0.030		c-k	1.07		a-h	2.53	*	g-k	-0.20		c-i	0.023		f-j
M24 x M9651	1.31		m	0.003		a-g	1.05		a-h	0.20		a-f	-0.28		b-i	-0.035		a-e
M24 x SID84	-1.44		b-f	0.050	*	g-l	2.15	*	f-i	1.78		d-k	-0.55	*	a-d	0.030		g-j
M24 x TAM22	0.34		g-m	0.028		b-k	1.48		c-i	1.33		b-j	-0.35		a-h	-0.035		a-e
M9651 x FM832	0.46		h-m	-0.020		a-b	1.15		a-i	0.90		a-i	0.08		h-i	-0.070	*	a
M9651 x HS624	-0.53		e-k	0.028		b-k	1.13		a-i	0.78		a-i	-0.30		b-i	0.047		i-j
M9651 x HSMD9	-1.16		b-h	0.030		c-k	2.30	*	h-j	0.33		a-h	-0.28		b-i	-0.007		c-i

Table 11. Continued

Genotype	LP[†]			UHML			UI			Str			Elon			UQLw		
	----- % -----			---- mm ----			---- % ----			kN m kg-1			---- % ----			---- mm ----		
M9651 x SID84	-2.74	*	a-b	0.033		d-k	1.78	*	d-i	0.40		a-h	-0.23		b-i	0.000		c-i
M9651 x TAM22	0.67		i-m	0.000		a-f	1.68		c-i	-0.30		a-d	-0.07		e-i	-0.025		a-g
SID84 x FM832	-0.30		f-m	0.030		c-k	0.05		a-c	1.38		b-j	-0.40		a-g	0.013		d-j
SID84 x HS624	-0.71		e-j	-0.005		a-f	0.80		a-h	3.28	*	j-k	-0.50	*	a-e	-0.005		c-i
SID84 x HSMD9	-1.43		b-f	0.030		c-k	0.88		a-h	2.05		e-k	-0.60	*	a-c	0.035		h-j
FM832 x HSMD9	-0.61		e-k	0.015		a-j	1.13		a-i	-0.85		a-b	-0.30		b-i	-0.008		c-i
FM832 x M24	-1.14		b-h	0.015		a-j	0.42		a-e	0.13		a-f	-0.45	*	a-f	-0.040		a-d
TAM22 x ELS17	-0.45		f-l	-0.008		a-e	0.80		a-h	0.38		a-h	-0.78	*	a	-0.033		a-f
TAM22 x ELS33	-0.11		f-m	0.055	*	i-l	2.80	*	i-j	-0.30		a-d	-0.55	*	a-d	0.005		c-i
TAM22 x FM832	-0.24		f-m	0.005		a-h	0.13		a-d	0.03		a-f	-0.08		e-i	0.000		c-i
TAM22 x SID84	-0.95		c-j	0.015		a-j	0.25		a-e	0.02		a-f	0.10		i	-0.033		a-f
04SID84	-0.30		f-m	0.047		f-l	0.83		a-h	0.42		a-h	-0.23		b-i	-0.013		b-h
06WE624	-2.51	*	a-d	0.025		b-k	1.02		a-h	2.13		f-k	-0.20		c-i	-0.023		a-g
94L25M24	-1.48		b-f	0.039		e-l	1.83	*	d-i	1.38		b-j	-0.10		e-i	0.012		d-j
94L25M405	-3.80	*	a	0.085	*	l	1.70		c-i	3.78	*	k	-0.45	*	a-f	0.065	*	j
B13917ELS	-0.11		f-m	0.060	*	j-l	2.25	*	g-i	-0.80		a-c	-0.50	*	a-e	0.002		c-i
B18233ELS	0.13		f-m	0.023		b-k	1.27		b-i	-0.33		a-d	-0.33		b-i	-0.008		c-i
FM832	-1.35		b-g	0.025		b-k	1.88	*	e-i	3.38	*	j-k	-0.07		e-i	0.003		c-i
MD9ne	-0.70		e-j	0.010		a-i	1.13		a-i	0.00		a-f	-0.35		a-h	-0.070	*	a
Tamcot22	0.63		i-m	0.040		e-l	4.09	*	j	-0.20		a-e	0.14		i	-0.035		a-e

*Values different from zero at $p < 0.05$ according to Fisher LSD.

[†] LP, lint percentage; UHML, upper half mean length; UI, uniformity index; Str, fiber bundle strength; Elon, percent elongation at break; UQLw, upper quartile length on a weight basis.

[‡] Values within a column followed by the same letter are not different at the 0.05 probability level according to Fisher's LSD.

interaction elements different than zero exhibiting greater fiber strength in 2009 than 2010.

M9651, ELS17, and eleven F_1s, all of which had a either an ELS line or SID84 as a parent, displayed Elon interaction elements different than zero (Table 11). In addition to these thirteen genotypes, HSMD9 and eight F_1s responded differently ($p<0.05$) to years than did FM832 and TAM22. It is important to remember that HVI does not currently have standard cotton to calibrate Elon. Typically Elon is consistent on a given HVI machine but tends to drift over large periods of time. Thus these data for Elon can only be considered as indicators and the data per se are suspect, since no records exist that documents the same machine and same operator across years. However, this concern only applies to Elon.

M9651xFM832, ELS33xFM832, and HSMD9 produced significantly negative interaction elements, i.e., 2010 was greater than 2009, for UQLw (Table 11). Interestingly, while these two F_1s had FM832 as a common parent, they responded differently to years than did FM832 but not TAM22. M9651 exhibited a significantly positive interaction element which was also different than both cultivar checks.

M9651 deserves more attention as its interaction elements were different from zero for four fiber quality parameters, UHML, Str, Elon, and UQLw, and LP. This suggests that it is less stable across years for fiber quality than the other genotypes. SID84 and ELS33, on the other hand, exhibited no interaction elements different than zero, indicating that across years they tended to be stable for fiber quality (Table 11). However, each was a parent for five and seven F_1s, respectively, which did respond

differently ($p<0.05$) to years for at least one fiber quality parameter and multiple parameters for some F_1s.

Out of the 31 F_1s that produced interaction elements different than zero, 27 had ELS17, ELS33, M24, or SID84 as a parent, which were the parents exhibiting the greatest UHML (Table 11). This should not prohibit breeders from utilizing these lines to improve fiber quality, since only one or a few interaction elements of any particular F_1 are different ($p<0.05$) from zero. Rather, breeders should be sure to evaluate fiber quality over multiple years to identify both superior fiber quality that is stable over environments.

4. GENERATION MEANS ANALYSIS

Materials and Methods

Genotypes

Parents were selected based upon their HVI UHML and Str as well as genetic background (Table 1). Genetic backgrounds included extra-long staple uplands, mutated uplands, high strength uplands, and interspecific hybrids.

Generation Development

In the summer of 2008, approximately 25 plants of each parent were planted approximately 0.5 m apart at the Texas Agrilife Research Farm near College Station, TX. These plants were used simultaneously to verify parental phenotypes and to produce F_1 seed. Open-pollinated bolls were harvested from each plant, ginned, and submitted to HVI analysis at the Fiber and Biopolymer Research Institute in order to verify the phenotype of each parental plant. Standard deviations were calculated across plants for each genotype for UHML and Str. To ensure fiber length phenotypes of ELS33, M24, and SID84, any parent plant having UHML two standard deviations below the parent plant with the highest UHML within each genotype was discarded. For the same genotypes, any plant with Str two standard deviations above or below the mean Str for each genotype was also discarded. To ensure fiber strength phenotype of HS624, any parent plant having Str two standard deviations below the parent plant with the highest Str was discarded. For these genotypes, any plant with UHML two standard deviations above or below the mean UHML for each genotype also was discarded.

The parents were crossed in a diallel without reciprocals. Flower buds, called candles, were emasculated by hand the afternoon prior to the day of anthesis. To prevent outcrossing, paper straws with the top pinched shut were placed over stigmas after emasculation and after pollination. Selfed seeds of each parental plant were obtained by clipping candles shut with metal clips the afternoon prior to anthesis. Since parental phenotypes of each plant had not yet been verified, the specific male and female plant used in each individual cross was recorded on the tag identifying the cross. Any F_1 or selfed seeds obtained on discarded plants were discarded. Selfed parental seeds and F_1 seeds from verified parental plants were planted during the 2009 and 2010 growing seasons to increase F_1 seeds and to produce the F_2, BC_1P_1 and BC_1P_2 generations. The F_1 was used as the female to produce the BC_1P_1 and BC_1P_2 generations with the exception of combinations involving TAM 94L-25-M24. Since the majority of flowers obtained from TAM 94L-25-M24 during the 2009 growing season failed to dehisce, TAM 94L-25-M24 was designated as the female parent in all of its backcrosses.

Since all parents were selected specifically, rather than at random, from all upland, mutated upland, and interspecific cultivars, inferences made will apply solely to genotypes included in the study.

Field Study

All six generations for each parental combination were planted 27 April 2010 and 20 April 2011 at the Texas Agrilife Research Farm near College Station, TX on a Weswood silt loam, a fine-silty, mixed, superactive, thermic Udifluventic Haplustepts integrated with Ships silty clay, a very-fine, mixed, active, thermic Chromic Hapluderts.

A split plot arrangement within a randomized complete block design was utilized where generations were randomized within each parental combination and parental combinations were randomized within each replication. Plots were 6.1 m x 1.0 m and 13.0 m x 1.0 m in 2010 and 2011, respectively. To minimize inter-plant competition and increase boll retention, plots were thinned to a plant spacing of 0.3 to 0.5 m. Any skips due to lack of germination were planted with a filler genotype having red foliage. The experimental unit for each parental combination and replication consisted of one row for non-segregating generations (P_1, P_2, and F_1), three rows in 2010 and one row in 2011 for each of the back-cross generations (BC_1P_1 and BC_1P_2), and six rows in 2010 and three rows in 2011 for the F_2 generation. Cultural practices, such as furrow irrigation, weed control, and insect control, including boll weevil, *Anthonomus grandis*, eradication, were normal for cotton production in Central Texas.

For non-segregating generations (P_1, P_2, and F_1) up to three individual plants were harvested per parental combination per replication per year. Up to 19 individual plants were harvested for each of the back-cross generations (BC_1P_1 and BC_1P_2) per parental combination per replication per year, and approximately 50 individual plants per parental combination per replication were harvested for the F_2 generation. Since each parent appeared in four different families, a total of twelve individual plants of each parent potentially were harvested per replication per year. Due to poor germination in some plots and insufficient lint production of certain individual plants, the intended number of individual plants for each respective generation listed above was unattainable in some parental combinations.

Individual plants were harvested from 30 September through 19 October 2010 and 6 September through 5 October 2011. Samples were ginned on a laboratory saw-gin without lint cleaner and sent for HVI analysis at Cotton Incorporated in Cary, NC.

Statistical Analysis

The GLM procedure of SAS (2004) was utilized to carry out analyses of variance on plot means for HVI UHML and Str. The Brown-Forsythe F-test revealed heterogeneity of variance in the F_2 generation for parental combinations HS624xELS33, SID84xHS624, and TAM22xELS33 across years for UHML and SID84 x HS624, HS624 x TAM22, and SID84 x TAM22 for Str. Therefore data for these parental combinations are presented by year. Further statistical analysis also was separated by year for parental combinations in which generations responded differently to years, i.e., a significant Gen x Y interaction.

Frequency distributions for UHML were created to gain a deeper understanding of the generation means and to determine transgressive segregation. Individual plants were separated into classes by rounding to the nearest mm which is plotted along the x-axis, and the number of plants falling into each class is plotted along the y-axis. Each class across all figures and generations within figures are the same size, 1 mm, but the number of classes varies from figure to figure dependent on the range of UHML observed within each parental combination. For parental combinations which required analysis by year due to either significant Gen x Y interactions or heterogeneity of variances, separate series for each year were plotted within the same graph for each generation in order to observe differences in distribution from year to year along with

from generation to generation within years. Transgressive segregation was defined as any observation within the F_2, BC_1P_1, or BC_1P_2 generations which was either longer (positive transgressive segregation) or shorter (negative transgressive segregation) than the longest or shortest parental or F_1 plant, respectively.

The best estimates of additive and dominance gene action occur in the absence of epistasis. In order to test for the presence of epistasis, the ABCD scaling tests were utilized (Hayman and Mather, 1955; Mather, 1949):

$$A = 2BC_1P_1 - P_1 - F_1$$

$$B = 2BC_1P_2 - P_2 - F_1$$

$$C = 4F_2 - 2F_1 - P_1 - P_2$$

$$D = 2F_2 - BC_1P_1 - BC_1P_2$$

with the following variances:

$$V_A = 4V(BC_1P_1) + V(P_1) + V(F_1)$$

$$V_B = 4V(BC_1P_2) + V(P_2) + V(F_1)$$

$$V_C = 16V(F_2) + 4V(F_1) + V(P_1) + V(P_2)$$

$$V_D = 4V(F_2) + V(BC_1P_1) + V(BC_1P_2)$$

In the absence of epistasis, each of the scaling tests should not be different from zero. The simple additive-dominance model of genetic control was deemed inadequate when one of the scaling tests was significant, and a more complex, six-parameter model was utilized.

The six parameters of genetic effects were estimated from the six basic generations using the following equations (Kearsey and Pooni, 1996):

$m = ½P_1 + ½P_2 + 4\ F_2 – 2BC_1P_1 – 2BC_1P_2$

$a = ½P_1 – ½P_2$

$d = 6BC_1P_1 + 6BC_1P_2 – F_1 – 8F_2 – 1\ ½\ P_1 – 1\ ½\ P_2$

$aa = 2BC_1P_1 + 2BC_1P_2 – 4F_2$

$ad = 2BC_1P_1 – 2BC_1P_2 – P_1 + P_2$

$dd = P_1 + P_2 + 2F_1 + 4F_2 – 4BC_1P_1 – 4BC_1P_2$

These parameters were defined using the F_∞ metric (van der Veen, 1959) where *m* was the reference point and was defined as the overall mean of all possible inbred lines arising from a given cross. The remaining genetic parameters were defined as follows: *a* = the amount of variation among means due to additive genetic effects, *d* = the amount of variation among means due to dominance genetic effects, *aa* = the amount of variation among means due to additive x additive epistatic genetic effects, *ad* = the amount of variation among means due to additive x dominance epistatic genetic effects, and *dd* = the amount of variation among means due to dominance x dominance epistatic genetic effects. Since variances and number of individuals observed per generation differed, the means were weighted using the reciprocal of variances of the respective generation means (Kearsey and Pooni, 1996).

The joint scaling test, proposed by Cavalli (1952) as a comprehensive test to replace the ABCD scaling tests, was used to confirm the presence or absence of epistasis. The goodness-of-fit of the three-parameter model (*m*, *a*, and *d*) was tested using a chi-square test with three degrees of freedom. In all cases except M24 x TAM22, the results from the joint scaling test agreed with those obtained from ABCD scaling

tests. The six-parameter model was used whenever an ABCD scaling test or the joint scaling test was significant.

Since the number of observations in the non-segregating generations were unequal, environmental variances (σ^2_E) were calculated by summing the sums of squares for P_1, P_2, and F_1 then dividing by their combined degrees of freedom, i.e. $\sigma^2_E = (SS_{P1} + SS_{P2} + SS_{F1})/(df_{P1} + df_{P2} + df_{F1})$ (Kearsey and Pooni, 1996). Additive and dominance variance (σ^2_A and σ^2_D) were estimated according to Warner (1952) where $\sigma^2_A = 2\sigma^2_{F2} - (\sigma^2_{BC1P1} + \sigma^2_{BC2P2})$ and $\sigma^2_D = \sigma^2_{F2} - (\sigma^2_A \text{ and } \sigma^2_E)$. Broad-sense and narrow-sense heritability (H^2 and h^2) were estimated on a single-plant basis as follows (Fehr, 1991; Warner, 1952):

$$H^2 = \sigma^2_G / (\sigma^2_G + \sigma^2_E)$$

$$h^2 = \sigma^2_A / (\sigma^2_G + \sigma^2_E) = \sigma^2_A / (\sigma^2_A + \sigma^2_D + \sigma^2_E)$$

Results and Discussion

Upper Half Mean Length

UHML varied (p <0.05) for all parental combinations with the exception of M24 x ELS33 (Table 12). As expected, the greatest variation among generations was observed when the three high-length parents were crossed to TAM22, the parent with the shortest length. M24 x ELS33 exhibited no differences for UHML suggesting that they carry similar alleles for UHML which may be a result of their close relation; M24 is a selection from a mutated population of TAM 94L-25, and TAM 94L-25 is a parent of ELS33. Years were not a significant source of variation for any parental combination. Parental combinations ELS33 x SID84, M24 x HS624, SID84 x TAM22, and SID84 x

Table 12. Mean squares for HVI upper half mean length (UHML) measured on P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 for 10 parental combinations at College Station, TX in 2010 and 2011.

A.

		Parental Combinations†				
Source	df	ELS33 x SID84	ELS33 x HS624	ELS33 x TAM22	M24 x ELS33	M24 x SID84
Year (Y)	1	44.76	19.34	0.36	4.39	6.44
Reps(Y)	6	45.69	46.52	25.12	31.58	27.91
Generation (Gen)	5	182.50	393.41 ***	662.16 ***	3.73	16.87
Gen x Y	5	37.93 **	5.98	0.18	3.53	3.84
Error	30	8.93	2.46	1.91	2.67	1.75

B.

		Parental Combinations				
Source	df	M24 x HS624	M24 x TAM22	SID84 x TAM22	SID84 x HS624	HS624 x TAM22
Year (Y)	1	18.96	0.81	17.14	2.21	5.46
Reps(Y)	6	12.74	30.25	6.99	34.08	24.71
Generation (Gen)	5	429.41 ***	748.41 ***	608.96 ***	342.58 ***	124.15 ***
Gen x Y	5	13.56 *	5.74	5.82 *	4.28 *	1.54
Error	30	4.33	2.27	1.89	1.63	1.59

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

† ELS33, TAM B182-33 ELS; SID84, 04 SID 84-2; HS624, 06 WE 62-4; TAM22, Tamcot 22; M24, TAM 94L-25-M24.

HS624 responded differently across years and thus further analyses on these parental combinations were separated by year. For all parental combinations except M24 x ELS33, differences among generations explained a much larger portion of the variation than did Gen x Y interactions when magnitudes of respective mean squares were considered.

Means of P_1 and P_2 differed ($p < 0.05$) for all parental combinations except crosses among the three high-length parents, ELS33, M24, and SID84 (Table 13). The F_1 was equal to or greater than the longest parent for all combinations except ELS33 x HS624 in 2010, ELS33 x TAM22, M24 x HS624 in 2010, M24 x TAM22, and SID84 x TAM22, suggesting dominance gene action. The only instances of significant high-parent heterosis were ELS33 x SID84 in 2010 and M24 x SID84 where the UHML of the F_1 significantly exceeded the longer parent by 5% and 4% respectively. The means of the F_2 generation were intermediate to the two parents for most parental combinations and years. The exceptions were the combinations between the three longest parents, ELS33, M24, and SID84, which exhibited F_2 means that were not different than either parent except ELS33 x SID84, in 2010 which was shorter than both parents. For all parental combinations except those between the three longest parents, the backcross generations tended to be different from one another with values in the direction of the respective recurrent parent. Several means of backcrosses to the longer parent were similar to the means of the recurrent parent, but the mean of backcrosses to the shorter parent was always greater than the mean of the recurrent parent except for the parental combinations among the three longest parents. The BC_1P_1 of ELS33 x SID84 in 2010

Table 13. Least square means of P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 for HVI upper half mean length (mm) per parental combination at College Station, TX in 2010 and 2011. First parent listed is P_1, second parent is P_2.

A.

	Parental combination†														
	ELS33 x SID84				ELS33 x HS624				ELS33 x TAM22		M24 x ELS33				M24 x SID84	
Generation‡	2010		2011		2010		2011		2010/11		2010		2011		2010/11	
P_1	33.6	c§	33.6	ab	33.7	a	33.5	a	33.5	a	33.9	a	33.7	ab	33.8	c
P_2	33.5	c	34.4	ab	29.8	e	29.5	d	27.6	f	33.7	a	33.5	b	33.7	c
F_1	35.2	a	35.3	a	33.0	b	32.7	a	31.1	c	33.7	a	34.2	a	35.2	a
F_2	30.9	d	33.1	b	32.3	c	31.6	b	30.6	d	33.6	a	33.7	b	33.9	c
BC_1P_1	34.3	b	34.5	a	33.0	b	33.2	a	32.3	b	33.5	a	34.0	a	34.3	b
BC_1P_2	34.3	b	34.2	ab	31.4	d	31.1	c	29.5	e	33.4	a	33.6	b	34.0	c

B.

	Parental combination															
	M24 x HS624				M24 x TAM22				SID84 x TAM22				SID84 x HS624				HS624 x TAM22	
Generation	2010		2011		2010/11				2010		2011		2010		2011		2010/11	
P_1	33.8	a	33.7	a	33.7	a			33.7	a	33.8	a	33.6	ab	33.5	a	29.6	a
P_2	29.8	e	29.4	d	27.5	e			27.6	f	27.5	e	29.8	e	29.5	d	27.5	c
F_1	32.2	b	33.2	a	31.3	c			31.5	c	32.5	b	32.8	bc	33.8	a	29.7	a
F_2	31.5	c	32.2	b	31.3	c			30.2	d	30.8	c	32.5	c	31.9	b	29.1	b
BC_1P_1	32.6	b	33.0	a	32.7	b			32.4	b	32.7	b	33.9	a	33.5	a	29.9	a
BC_1P_2	30.8	d	30.7	c	29.8	d			29.4	e	29.4	d	31.4	d	30.9	c	29.0	b

† ELS33, TAM B182-33 ELS; SID84, 04 SID 84-2; HS624, 06 WE 62-4; TAM22, Tamcot 22; M24, TAM 94L-25-M24.

‡ P_1, parent one; P_2, parent two; F_1, P_1 x P_2; F_2, selfed F_1; BC_1P_1, backcross to P_1; BC_1P_2, backcross to P_2.

§ Means within a column followed by the same letter are not different at p = 0.05 according to Fisher LSD.

and M24 x SID84 across years was longer than P_1. The means of the BC_1P_2 for the combinations of the three longest parents were similar to the means of their recurrent parent and often to the means of the BC_1P_1.

Frequency distributions for UHML were created to gain a deeper understanding of the generation means and to determine transgressive segregation (Figures 3-12). As expected, the range of values for the segregating generations tended to be wider than for the non-segregating generations. Frequency distributions do not appear to differ greatly from 2010 to 2011 within each parental combination except for the F_2 generation for ELS33 x SID84 in which case 2010 and 2011 follow a similar distribution with 2011 shifted to the right of 2010. Frequency distributions of the segregating generations roughly align with a normal distribution suggesting the UHML is a quantitative trait.

Only one plant exhibited positive transgressive segregation which came from the BC_1P_2 of the M24 x SID84 parental combination (Figure 7). Negative transgressive segregation was observed at low levels (<1%) in the F_2 for ELS33 x SID84 in 2010, ELS33 x HS624 in 2011, SID84 x TAM22 in 2010, and HS624 x TAM22 in 2010 (Figures 3, 4, 10, and 12) and in both the F_2 and BC_1P_2 for ELS33 x TAM22 in 2010 and SID84 x HS624 in 2011 (Figures 5 and 11). Such low levels of transgressive segregation suggest that further improvement for UHML relative to the better parent is possible but likely difficult in these populations.

ABCD and joint scaling tests were performed to determine the adequacy of the three-parameter model, i.e., the absence of epistasis (Table 14). Results from the ABCD scaling tests agreed with results from the joint scaling test for all parental and year

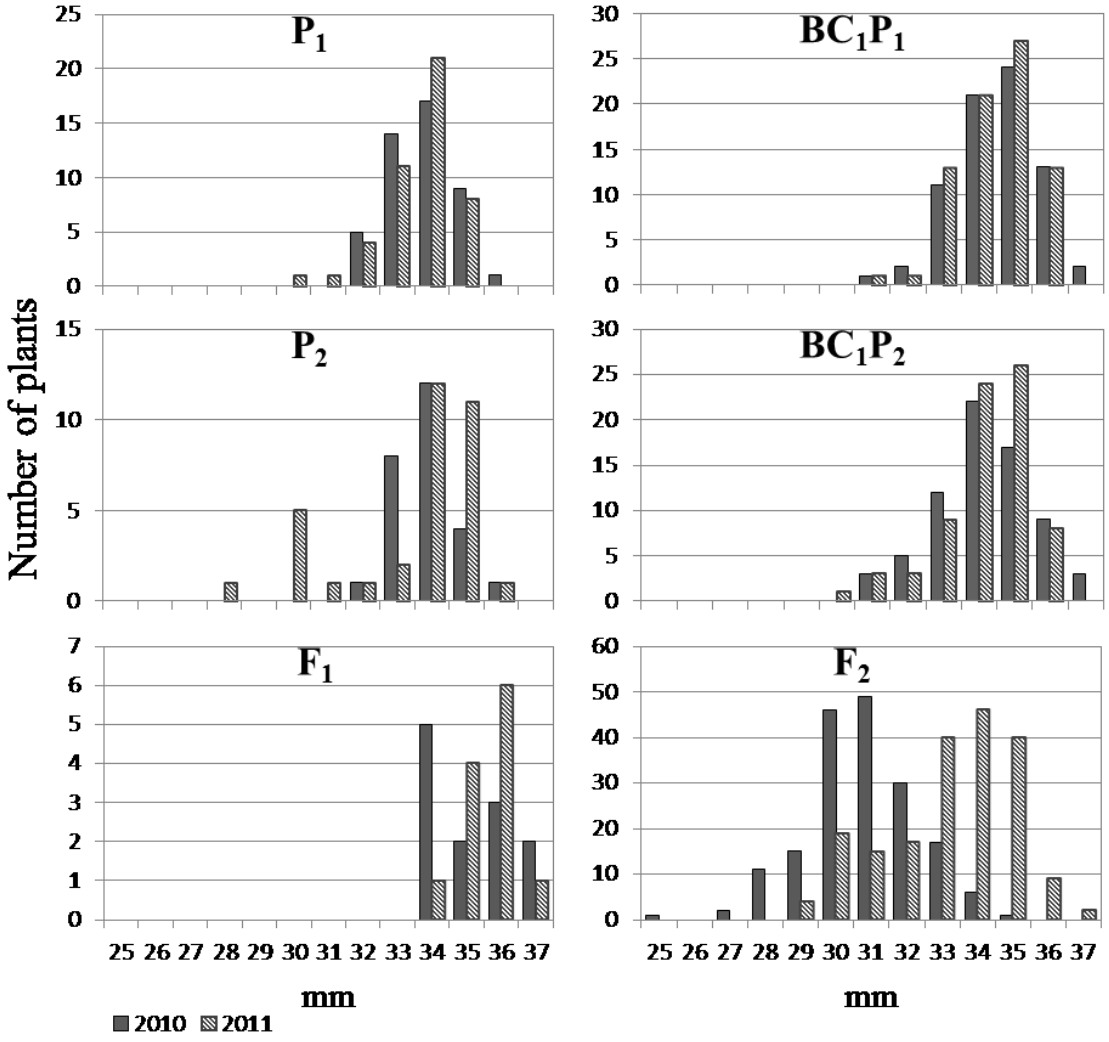


Figure 3. Frequency distribution of upper half mean length (UHML) in the P1, P2, F1, BC1P1, BC_1P_2, and F_2 generations for the parental combination of ELS33 (P_1) x SID84 (P_2) in 2010 and 2011.

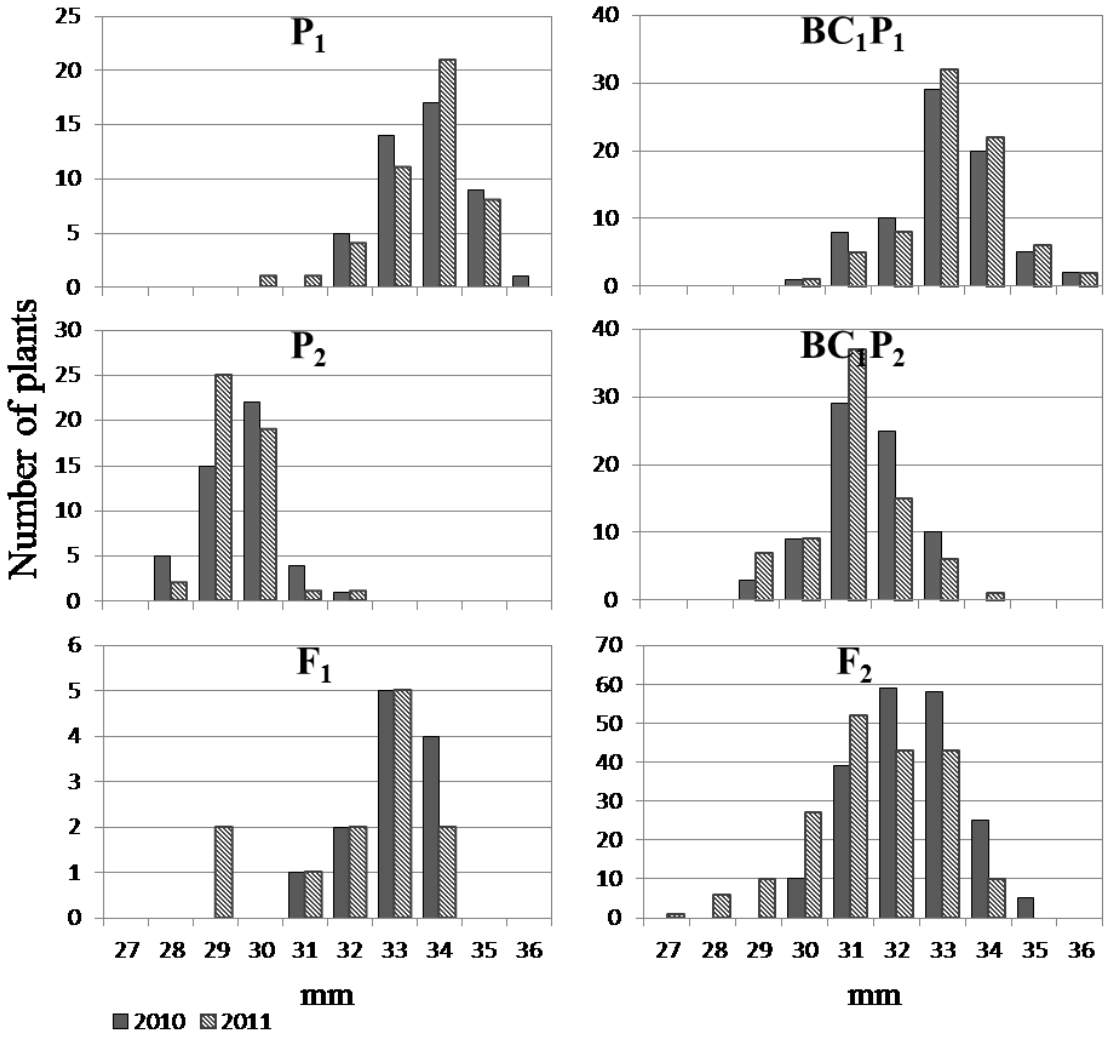


Figure 4. Frequency distribution of upper half mean length (UHML) in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of ELS33 (P_1) x HS624 (P_2) in 2010 and 2011.

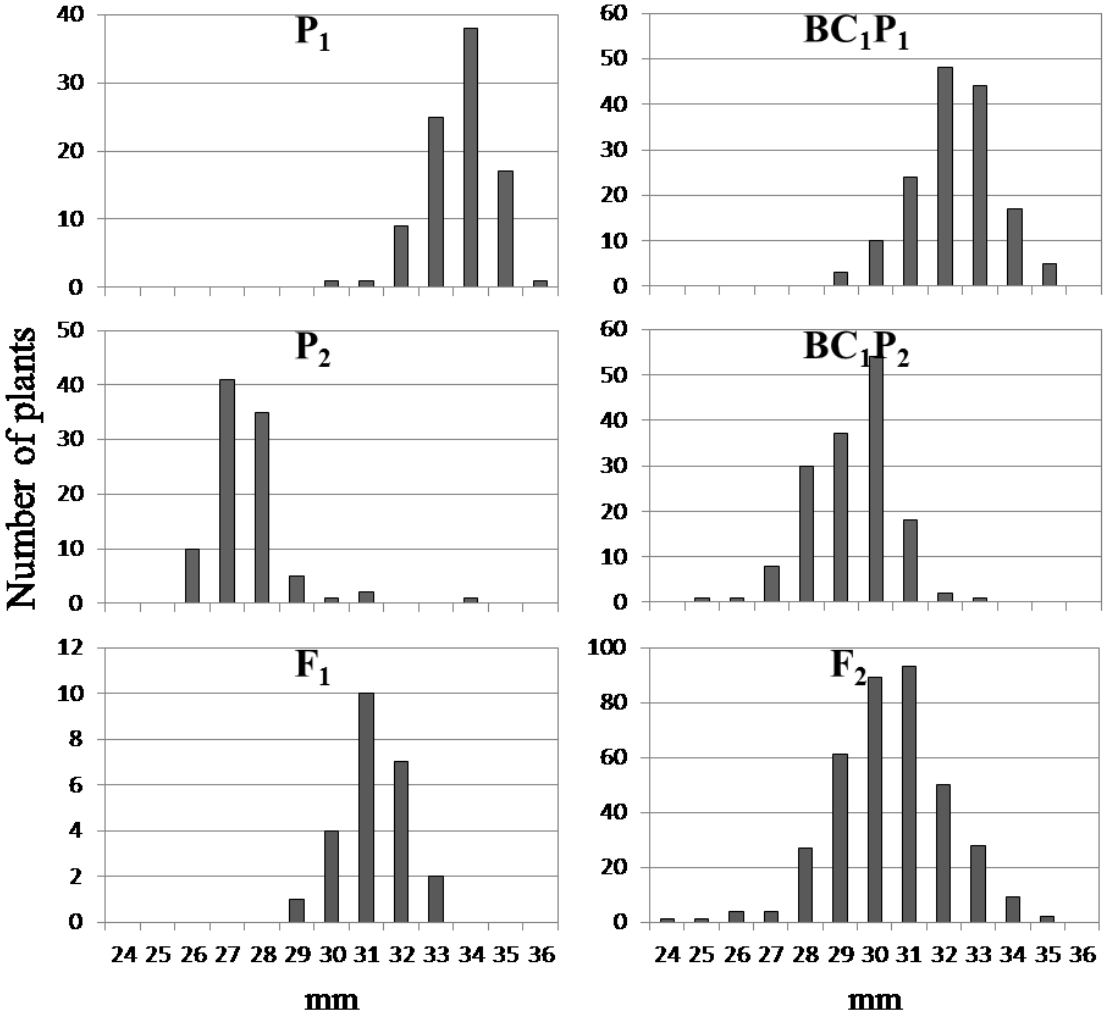


Figure 5. Frequency distribution of upper half mean length (UHML) in the P1, P2, F1, BC1P1, BC_1P_2, and F_2 generations for the parental combination of ELS33 (P_1) x TAM22 (P_2) in 2010 and 2011.

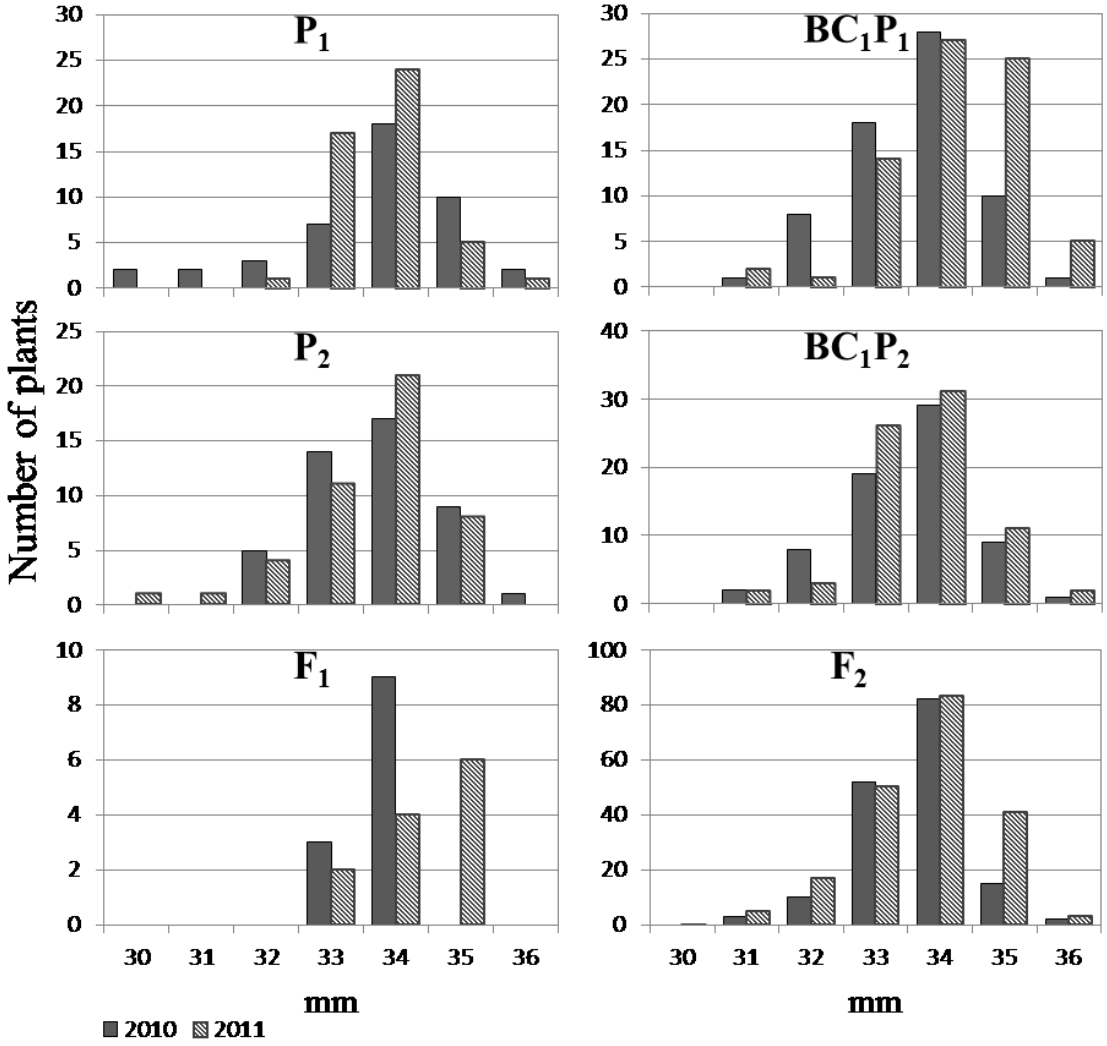


Figure 6. Frequency distribution of upper half mean length (UHML) in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of M24 (P_1) x ELS33 (P_2) in 2010 and 2011.

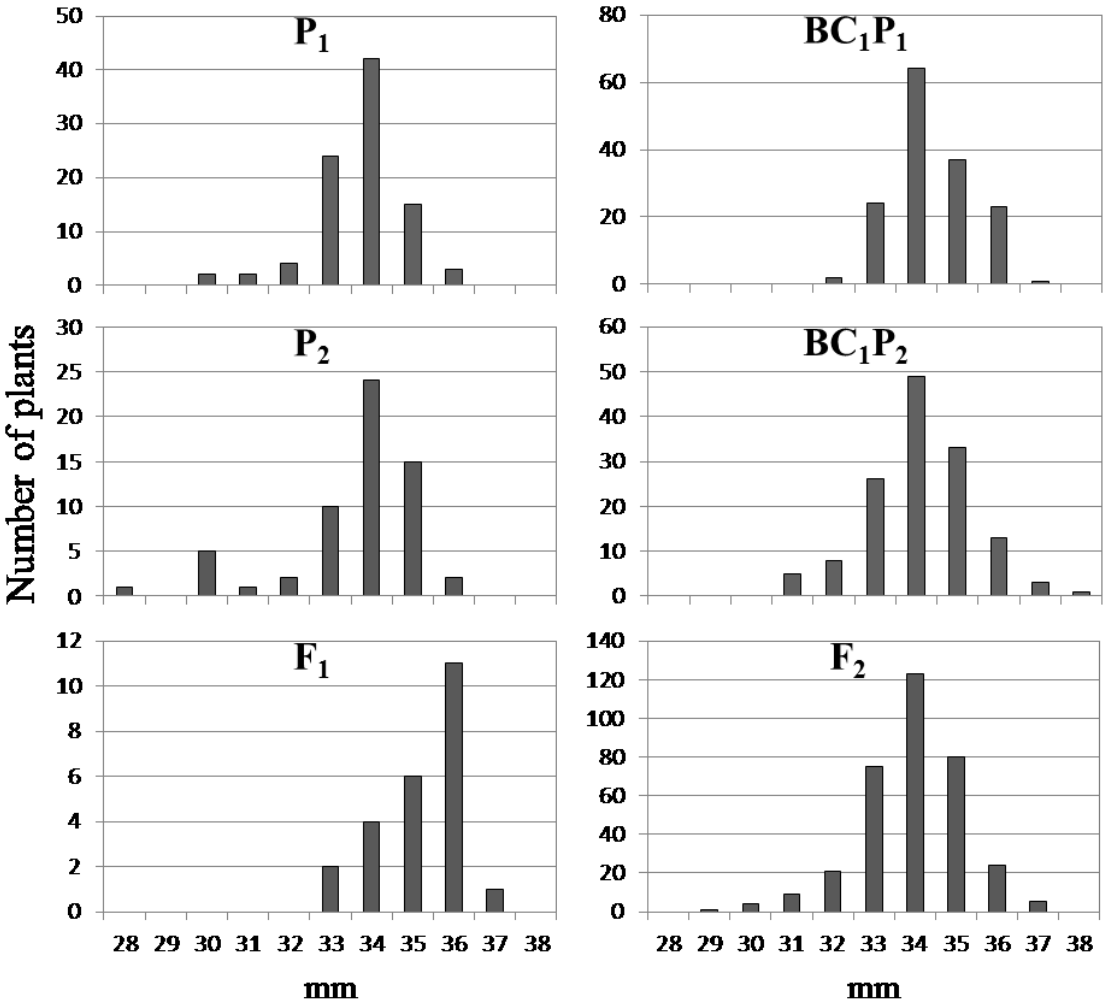


Figure 7. Frequency distribution of upper half mean length (UHML) in the P1, P2, F1, BC1P1, BC1P2, and F2 generations for the parental combination of M24 (P1) x SID84 (P2) in 2010 and 2011.

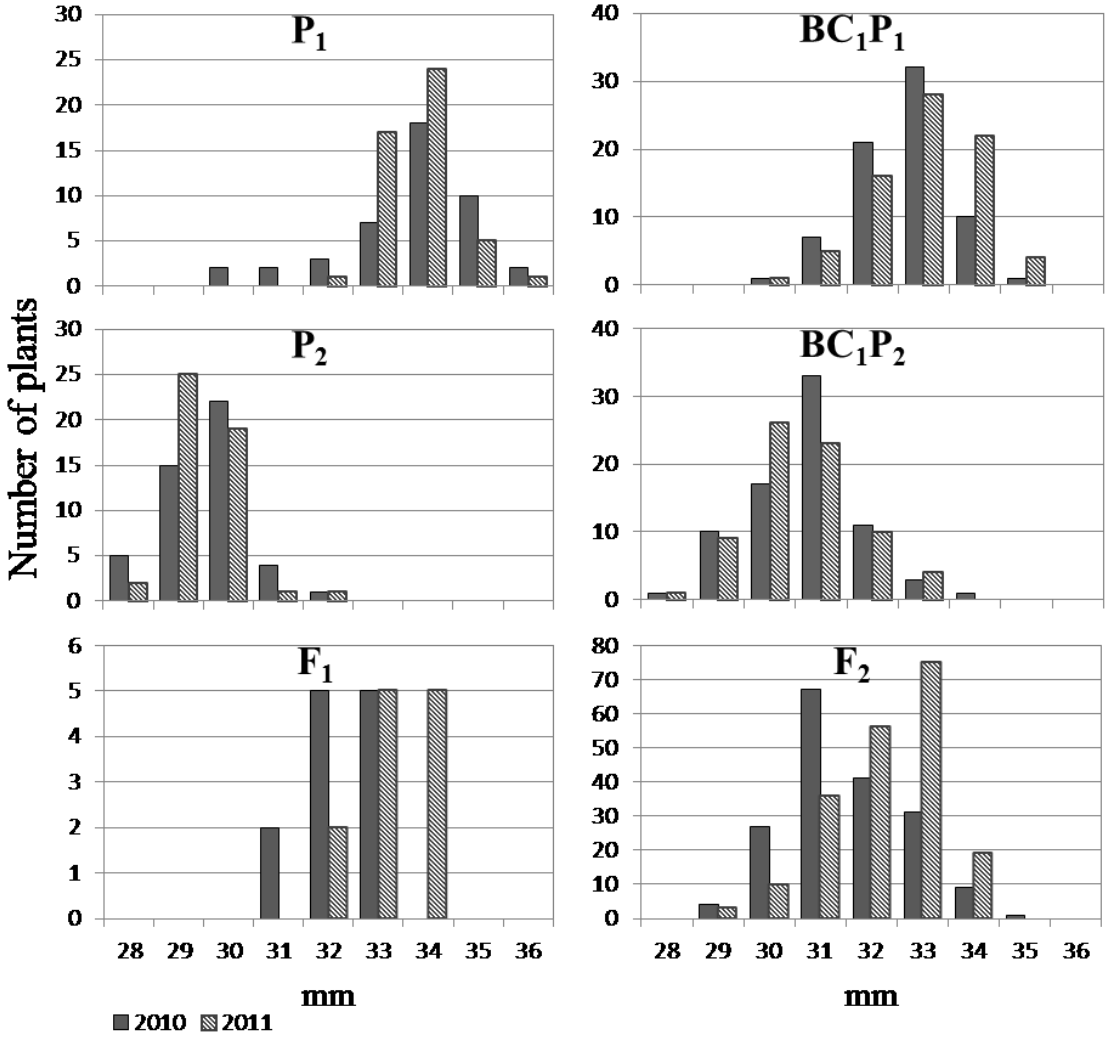


Figure 8. Frequency distribution of upper half mean length (UHML) in the P1, P2, F1, BC1P1, BC_1P_2, and F_2 generations for the parental combination of M24 (P_1) x HS624 (P_2) in 2010 and 2011.

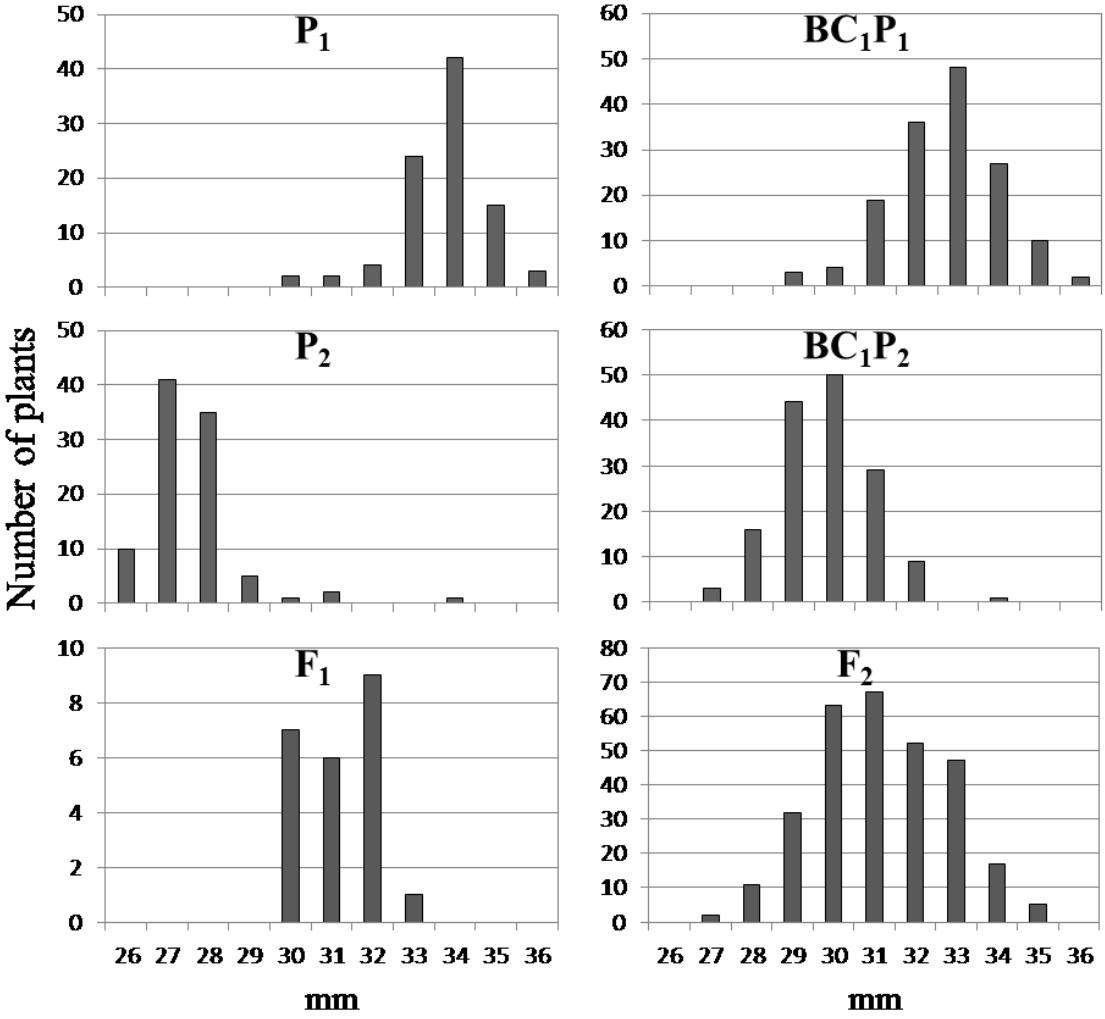


Figure 9. Frequency distribution of upper half mean length (UHML) in the P1, P2, F1, BC1P1, BC_1P_2, and F_2 generations for the parental combination of M24 (P_1) x TAM22 (P_2) in 2010 and 2011.

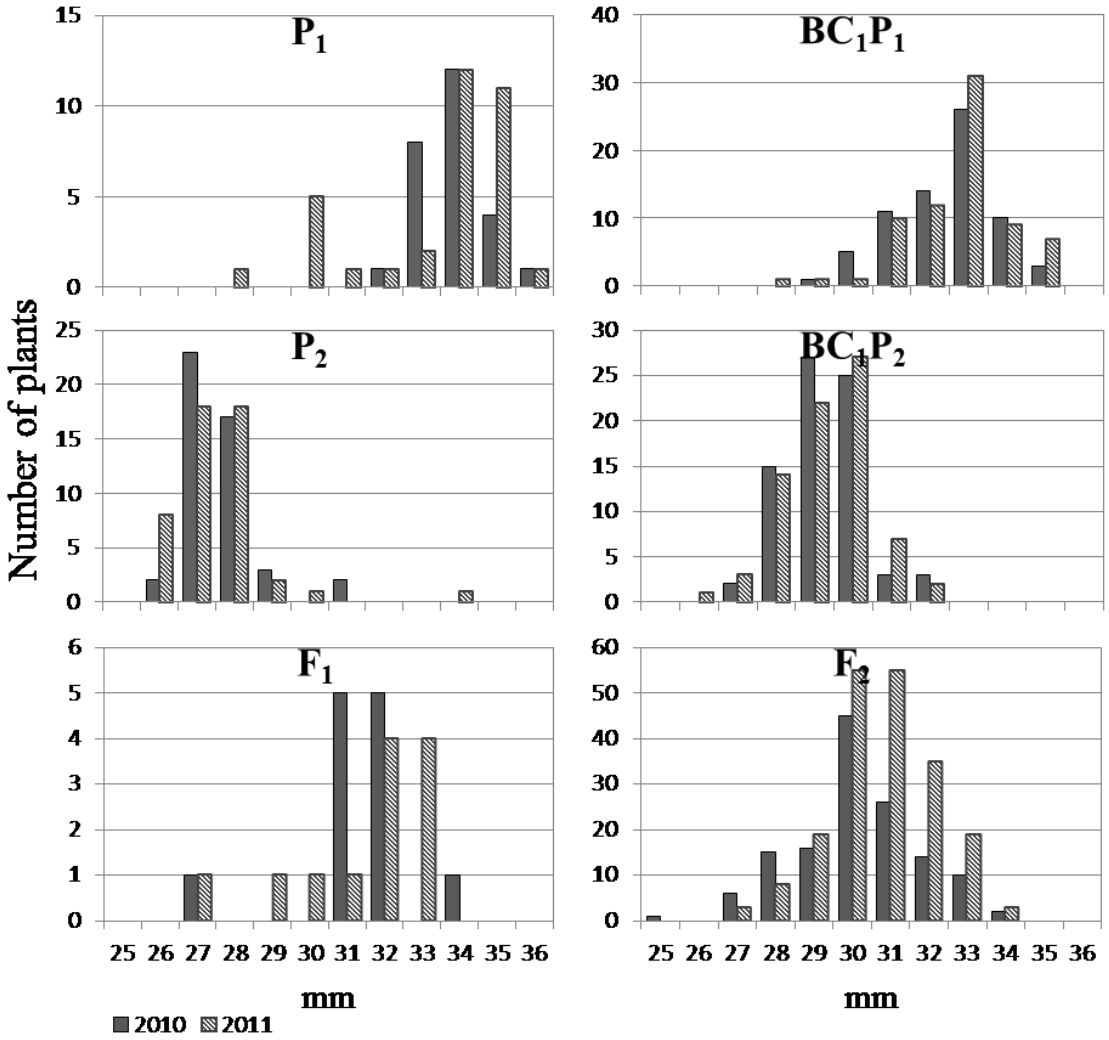


Figure 10. Frequency distribution of upper half mean length (UHML) in the P1, P2, F1, BC1P1, BC_1P_2, and F_2 generations for the parental combination of SID84 (P_1) x TAM22 (P_2) in 2010 and 2011.

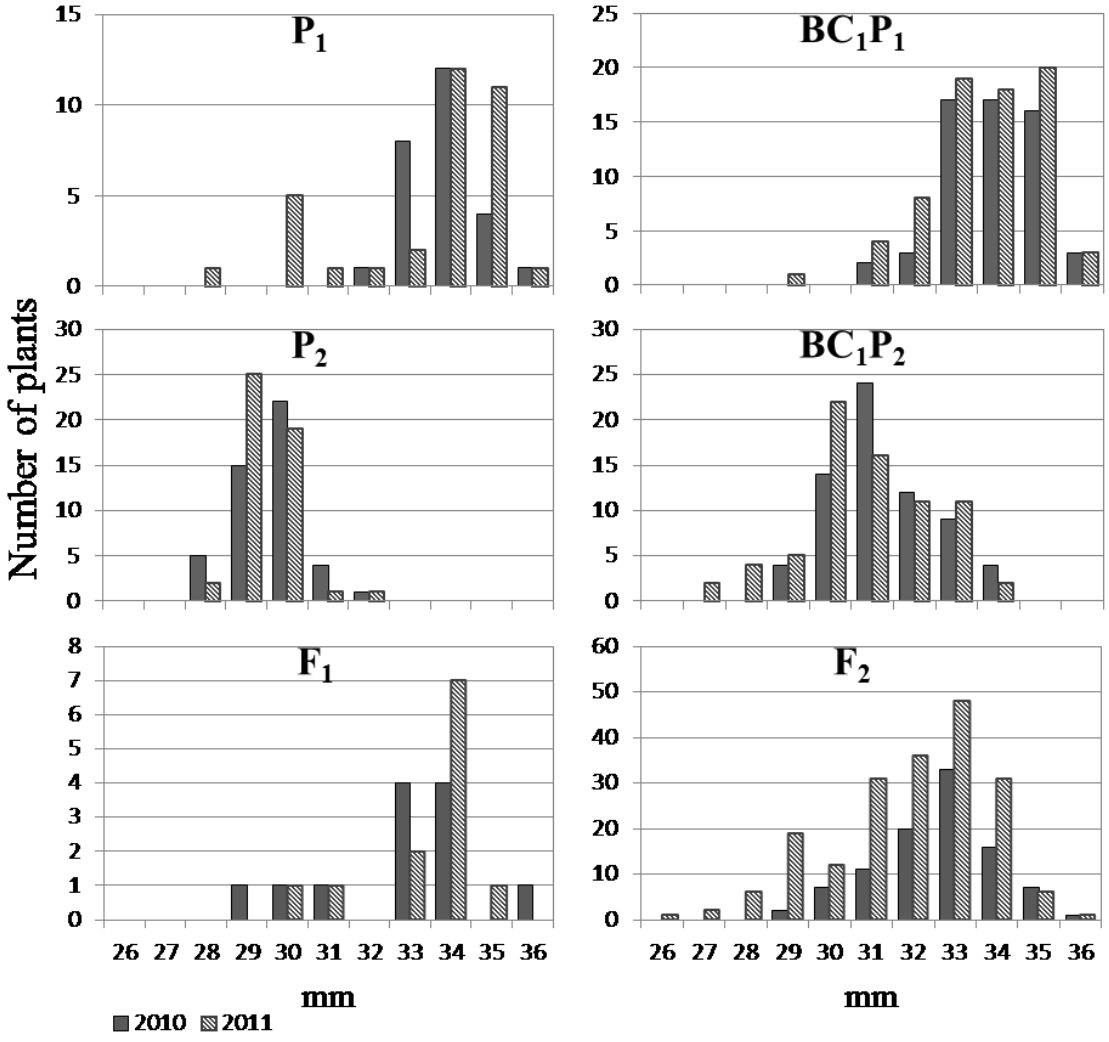


Figure 11. Frequency distribution of upper half mean length (UHML) in the P1, P2, F1, BC1P1, BC_1P_2, and F_2 generations for the parental combination of SID84 (P_1) x HS624 (P_2) in 2010 and 2011.

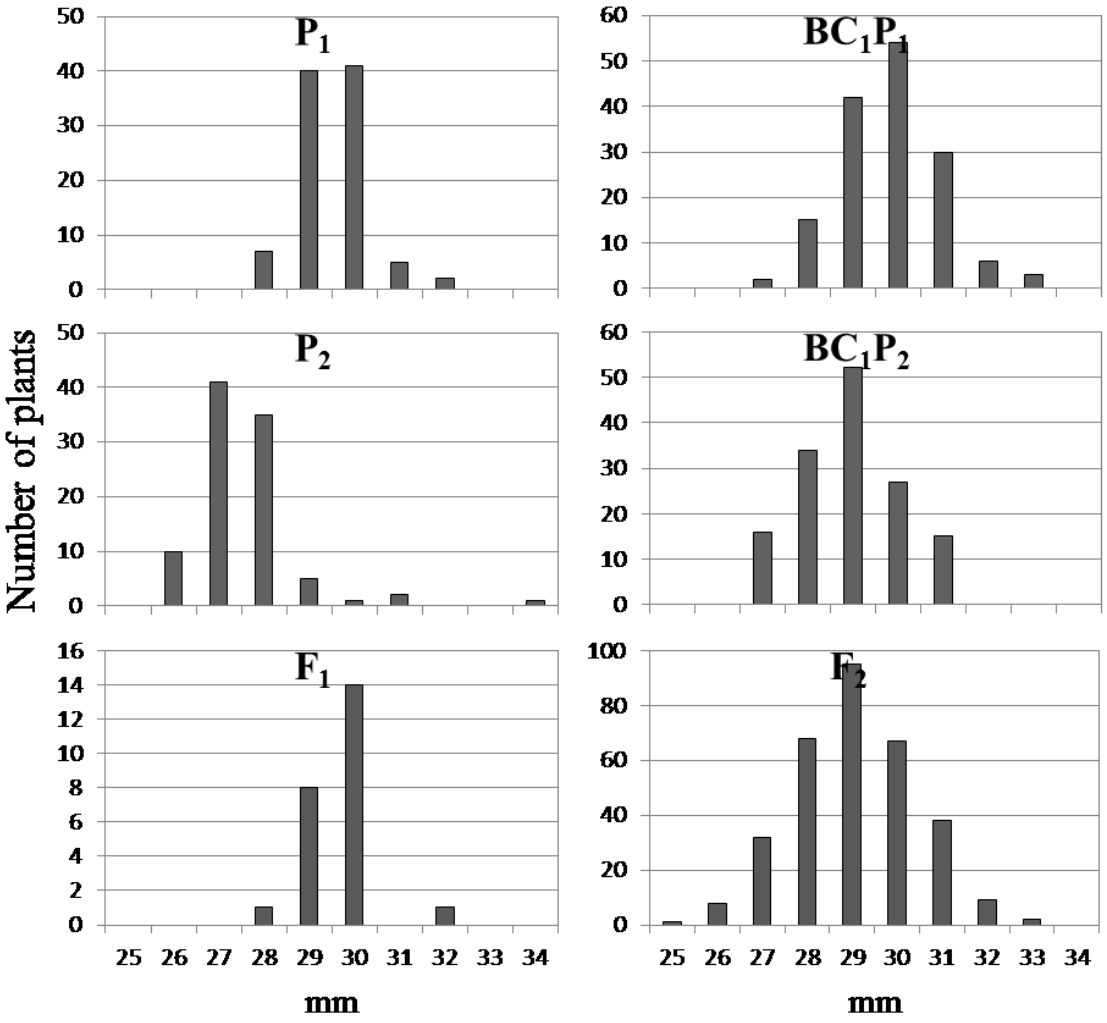


Figure 12. Frequency distribution of upper half mean length (UHML) in the P1, P2, F1, BC1P1, BC_1P_2, and F_2 generations for the parental combination of HS624 (P_1) x TAM22 (P_2) in 2010 and 2011.

Table 14. ABCD and joint scaling tests for HVI upper half mean length per parental combination at College Station, TX in 2010 and 2011.

		ABCD scaling tests				
Parental combination†	Year	A	B	C	D	Joint scaling test
ELS33 x SID84	2010	ns	ns	*	*	*
ELS33 x SID84	2011	ns	ns	*	*	*
ELS33 x HS624	2010	ns	ns	ns	ns	ns
ELS33 x HS624	2011	ns	ns	ns	*	*
ELS33 x TAM22	2010/11	ns	ns	*	*	*
M24 x ELS33	2010	ns	ns	ns	ns	ns
M24 x ELS33	2011	ns	ns	*	ns	*
M24 x SID84	2010/11	ns	ns	*	*	*
M24 x HS624	2010	*	ns	*	ns	*
M24 x HS624	2011	*	*	ns	*	*
M24 x TAM22	2010/11	ns	*	ns	ns	ns
SID84 x TAM22	2010	ns	ns	*	*	*
SID84 x TAM22	2011	ns	ns	ns	ns	ns
SID84 x HS624	2010	ns	ns	ns	ns	ns
SID84 x HS624	2011	ns	ns	ns	*	*
HS624 x TAM22	2010/11	ns	*	ns	*	*

† ELS33, TAM B182-33 ELS; SID84, 04 SID 84-2; HS624, 06 WE 62-4; TAM22, Tamcot 22; M24, TAM 94L-25-M24.

combinations with the exception of M24 x TAM22 in 2010/11 where the B scaling test indicated significant epistasis, but no epistasis was detected by the joint scaling test. When the generation means from this parental combination were fitted to the six-parameter model, no significant epistasis was indicated. Scaling tests also indicated significant epistasis for M24 x ELS33 in 2011 and M24 x HS624 in 2010 but was not confirmed in the six parameter model measuring gene effects.

The simple additive-dominance model was sufficient to explain the variation in UHML among generation means for parental combinations M24 x ELS33 in 2010, M24 x HS624 in 2010, and M24 x TAM22 (Table 14). All other combinations were fit to the six-parameter model which accounts for epistatic interactions between two loci. Additive genetic effects were significant for all parental combinations and environments except crosses between the three high-length parents (Table 15). As expected, additive genetic effects for UHML were greatest when TAM22 was crossed to one of the three high-length parents followed by crosses between HS624 and one of the three high-length parents. Additive genetic effects were insignificant for crosses between the three high-length parents. Dominance effects were highly significant for ELS33 x SID84 in 2010 and 2011 and M24 x SID84, but insignificant for ELS33 x M24 in 2010 and 2011. Parameter *a* accounts for the summation of all loci controlled by additive effects for UHML and is highly impacted by gene dispersion between parents. A small value of *a* might suggest that the two parents are very similar genetically for UHML, which cannot be given the large value of *d*. Such a small value of *a* coupled with such a large value for *d* suggests that a high level of gene dispersion is occurring between ELS33 and SID84

Table 15. Estimates of gene effects for HVI upper half mean length (UHML) for ten parental combinations at College Station, TX in 2010 and 2011.

		Gene effects†											
Parental combination‡	Year	m		a		d		aa		ad		dd	
ELS33 x SID84	2010	20.0	***	0.0		28.3	***	13.7	***	0.6		-13.2	***
ELS33 x SID84	2011	29.0	***	0.1		10.3	***	4.5	***	0.3		-3.9	***
ELS33 x HS624§	2010	31.7	***	1.9	***	1.2	***	-		-		-	
ELS33 x HS624	2011	29.1	***	2.0	***	6.7	***	2.4	***	0.1		-3.8	**
ELS33 x TAM22	2010/11	29.4	***	3.0	***	2.7	*	1.2	**	-0.3		-0.9	
M24 x ELS33§	2010	33.6	***	0.0		-0.1		-		-		-	
M24 x ELS33	2011	32.8	***	0.1		1.9		0.8		0.6		-0.6	
M24 x SID84	2010/11	32.3	***	0.1		3.3	**	1.3	***	0.4		-0.5	
M24 x HS624	2010	31.1	***	2.0	***	0.7		0.6		-0.5		0.4	
M24 x HS624	2011	33.2	***	2.1	***	-4.0	***	-1.6	***	0.4		4.0	***
M24 x TAM22	2010/11	30.5	***	3.0	***	2.1		0.2		-0.4		-1.2	
SID84 x TAM22	2010	28.0	***	3.0	***	5.4	**	2.7	***	0.1		-1.9	
SID84 x TAM22§	2011	30.5	***	3.0	***	0.7	*	-		-		-	
SID84 x HS624§	2010	31.8	***	2.1	***	1.5	***	-		-		-	
SID84 x HS624	2011	29.9	***	1.9	***	4.5	*	1.5	*	1.6	**	-1.2	
HS624 x TAM22	2010/11	27.3	***	1.0	***	5.0	***	1.4	***	-0.3		-2.5	***

*, ** Significant at the 0.05 and 0.01 probability levels, respectively.

† *m* = mean; *a* = additive; *d* = dominance; *aa* = additive x additive; *ad* = additive x dominance; *dd* = dominance x dominance.

‡ELS33, TAM B182-33 ELS; SID84, 04 SID 84-2; HS624, 06 WE 62-4; TAM22, Tamcot 22; M24, TAM 94L-25-M24.

§ Three parameter model sufficiently fitted the six-generation means.

and between M24 and SID84 (Kearsey and Pooni, 1996). Thus, UHML likely is still controlled by additive genetic effects to some degree in these parental combinations. While the responses between these two parental combinations were similar, the magnitude of dominance and epistatic effects was much larger for ELS33 x SID84 than M24 x SID84. Insignificant levels of both additive and non-additive genetic effects for M24 x ELS33 in combination with differing responses when they are individually crossed to SID84, implies that M24 and ELS33 are very similar but not identical genetically for UHML and might suggest the question whether or not the ELS selections by Smith et al. (2009b) were the result of naturally occurring mutations within TAM 94L-25.

There were fewer significant epistatic gene effects than additive and dominance gene effects (Table 15). Additive x additive epistasis was the predominant form observed among these parental combinations in these environments. Of the nine significant parental combinations and environment combinations, all but one, HS624 x TAM22 in 2010/11, had a high-length parent. HS624 served as a parent in four of the nine instances of significant additive x additive epistasis. Significant additive x dominance gene interaction was observed only for SID84 x HS624 in 2011, and thus does not appear to be a major contributor to variability for UHML within the parental combinations studied. Dominance x dominance epistasis was significant in five cases, four of which were in the negative direction. For ELS33 x SID84 in 2010 and 2011, ELS33 x HS624 in 2011, and HS624 x TAM22 in 2010/11, dominance gene effects were positive and dominance x dominance gene effects were negative indicating

duplicate epistasis between dominant increasers, i.e., complete dominance at both gene pairs and one dominant allele at either gene masks the effect of the other gene (Kearsey and Pooni, 1996). M24 x HS624 exhibited the opposite signs indicating duplicate epistasis between dominant decreasers. Additive genetic effects were more consistent from parental combination to parental combination and from year to year than were dominance and epistatic gene effects. The dominance effects were the largest in magnitude. Selection for improved UHML may be most successful if progeny are evaluated after a couple of generations of inbreeding to reduce the variability due to dominance. Advanced progeny should then be evaluated in multiple years or environments to ensure superior and stable UHML.

Estimates of variance components and heritability were calculated to ascertain the relative importance of different factors affecting phenotype (Table 16). Assuming that individuals within the P_1, P_2, and F_1 generations are identical genetically, their combined variance is an estimate of environmental variance. Environmental variance for UHML ranged from 0.61 to 2.63 with an average of 1.24. Environmental variance among parental combinations with SID84 as a parent was higher compared to all other parental combinations, 1.61 versus 0.96. While efforts were made to ensure homogeneity of parental lines, it is possible that some level of heterogeneity remained which impacted variance of the assumed non-segregating generations. Additionally, SID84 is an interspecific hybrid between a Sea Island, *G. barbedense*, parent and an upland, *G. hirsutum*, parent. The relative adaptation of the Sea Island germplasm compared to the other parental material also may be playing a role in the difference. Additive variance

Table 16. Variance components and broad (H^2) and narrow (h^2) sense heritability estimates for HVI upper half mean length for 10 parental combinations grown at College Station, TX in 2010 and 2011.

		Variance components†			Heritability estimates	
Parental combination‡	Year	σ^2_E	σ^2_A	σ^2_D	H^2§	h^2
ELS33 x SID84	2010	0.90	1.44	0.00	0.61	0.61
ELS33 x SID84	2011	1.95	2.93	-2.04	0.60	0.60
ELS33 x HS624	2010	0.78	0.33	0.00	0.30	0.30
ELS33 x HS624	2011	0.93	1.64	-0.72	0.64	0.64
ELS33 x TAM22	2010/11	1.05	2.10	-0.63	0.67	0.67
M24 x ELS33	2010	1.23	-0.31	-0.27	0.00	0.00
M24 x ELS33	2011	0.75	0.15	0.07	0.22	0.15
M24 x SID84	2010/11	1.60	0.41	-0.56	0.21	0.21
M24 x HS624	2010	1.18	0.51	-0.58	0.30	0.30
M24 x HS624	2011	0.61	0.06	0.33	0.39	0.06
M24 x TAM22	2010/11	1.17	2.19	-0.91	0.65	0.65
SID84 x TAM22	2010	1.12	2.22	-0.96	0.66	0.66
SID84 x TAM22	2011	2.63	0.53	-1.36	0.17	0.17
SID84 x HS624	2010	1.13	1.15	-0.42	0.50	0.50
SID84 x HS624	2011	1.93	1.99	-0.91	0.51	0.51
HS624 x TAM22	2010/11	0.91	1.16	-0.23	0.56	0.56

† σ^2_E, environmental variance; σ^2_A, additive variance; σ^2_D, dominance variance. Negative variance assumed zero in heritability estimates.

‡ ELS33, TAM B182-33 ELS; SID84, 04 SID 84-2; HS624, 06 WE 62-4; TAM22, Tamcot 22; M24, TAM 94L-25-M24.

§ H^2 = broad-sense heritability; h^2 = narrow-sense heritability.

ranged from 0.00 to 2.93 with an average of 1.16. Additive variance coming from crosses between the three high-length parents was less than the average additive variance coming from all other combinations. All estimates of dominance variance were less than or equal to 0.00 except M24 x ELS33 in 2011 and M24 x HS624 in 2011. This may be due to sampling error or the inability of this method to estimate dominance variance (Braden, 2006). Environmental, additive, and dominance variances typically were greater in 2011 than 2010.

Broad-sense heritability (H^2) for UHML ranged from 0.00 to 0.67 with an average of 0.44. Crosses involving TAM22 exhibited the highest average H^2 followed by SID84 (Table 16). These same groups also exhibited the highest environmental variances. H^2 is simply the ratio of genotypic to phenotypic variance (i.e., environmental plus genotypic variance). In order to obtain a higher ratio, genotypic variance increased at a greater proportion than environmental variance. TAM22 exhibits the shortest UHML among parents included in the study and thus carried the fewest alleles contributing to improved fiber length. Therefore, the greatest genotypic variance was created by crossing TAM22 to the high-length parents. The higher average H^2 for SID84 suggests that it carries unique genetic variability for UHML when compared to the upland parents included in this study.

Higher average heritability and environmental variance were observed in 2011 when compared to 2010 (Table 16). While environmental variance was greater in 2011, it was a more suitable environment to select for genetic potential of UHML as it led to greater expression of genotypic variance. It is noteworthy that ELS33 x SID84 in 2010

and 2011 expressed heritability estimates of 0.61 and 0.60 respectively. This population expressed high levels of additive genetic variance and may prove beneficial for increasing UHML. The cross between high-length parent ELS33 and high-strength parent HS624 expressed the second highest heritability estimate for UHML and may prove helpful in simultaneously improving fiber UHML and Str. Since most dominance variance estimates were negative, all but two narrow-sense heritability estimates were equal to their respective H^2 estimates.

Fiber Bundle Strength

Str varied (p <0.05) in all parental combinations with the exception of ELS33 x M24 (Table 17). Much like UHML, the greatest variation for Str among generations was observed when the three high-length parents were crossed to TAM22 followed by the high-length parents crossed to HS624, the strongest parent in the study. Years were not significantly different. However, generations for parental combinations ELS33 x SID84, M24 x HS624, SID84 x TAM22, and SID84 x HS624 did respond differently to years, thus further analysis for these parental combinations was done by year. Differences among generations explained a much larger portion of the variation than did Gen x Y interactions when magnitudes of respective mean squares were considered.

Means of P_1 and P_2 differed (p<0.05) for all parental combinations except M24 x ELS33 for UHML (Table 18). The F_1 was intermediate to the two parents for ELS33 x TAM22, M24 x TAM22, SID84 x HS624 in 2011, and HS624 x TAM22 in 2010 and 2011. The F_1 was not different than P_1 for ELS33 x SID84 in 2010 and 2011, M24 x SID84, SID84 x TAM22 in 2010 and 2011, and SID84 x HS624 in 2010. The F_1 was not

Table 17. Mean squares for HVI fiber bundle strength (Str) measured on P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 for 10 parental combinations at College Station, TX in 2010 and 2011.

A.

		Parental combinations				
Source	df	ELS33 x HS624	ELS33 x SID84	ELS33 x TAM22	M24 x ELS33	M24 x SID84
Year (Y)	1	19.34	44.76	0.36	4.39	6.44
Reps(Y)	6	46.52	45.69	25.12	31.58	27.91
Generation (Gen)	5	393.41 ***	182.50 ***	662.16 ***	3.73	16.87 ***
Gen x Y	5	5.98	37.93 **	0.18	3.53	3.84
Error	30	2.46	8.93	1.91	2.67	1.75

B.

		Parental combinations				
Source	df	M24 x HS624	M24 x TAM22	SID84 x TAM22	SID84 x HS624	HS624 x TAM22
Year (Y)	1	18.96	0.81	17.14	2.21	5.46
Reps(Y)	6	12.74	30.25	6.99	34.08	24.71
Generation (Gen)	5	429.41 ***	748.41 ***	608.96 ***	342.58 ***	124.15 ***
Gen x Y	5	13.56 *	5.74	5.82 *	4.28 *	1.54
Error	30	4.33	2.27	1.89	1.63	1.59

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

† ELS33, TAM B182-33 ELS; SID84, 04 SID 84-2; HS624, 06 WE 62-4; TAM22, Tamcot 22; M24, TAM 94L-25-M24.

Table 18. Least square means of P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 for HVI fiber bundle strength (kN m kg^{-1}) per parental combination at College Station, TX in 2010 and 2011. First parent listed is P_1, second parent is P_2.

A.

	Parental combination													
	ELS33 x SID84		ELS33 x HS624		ELS33 x TAM22		M24 x ELS33		M24 x SID84		M24 x HS624			
Gen	2010		2011		2010/11		2010/11		2010/11		2010/11		2010		2011	
P_1	356.4	a	370.4	a	384.7	a	363.8	a	362.5	a	354.0	ab	377.5	a	393.0	a
P_2	325.5	b	347.3	b	362.9	bc	265.0	f	354.3	a	333.2	c	350.8	bc	356.7	c
F_1	349.5	a	373.2	a	361.4	c	321.2	c	351.1	a	354.5	ab	332.4	d	367.3	bc
F_2	318.3	b	360.0	ab	367.0	b	304.6	d	355.7	a	357.4	a	345.1	c	372.6	b
BC_1P_1	347.3	a	365.5	ab	377.0	a	336.4	b	358.1	a	354.7	ab	359.6	b	376.3	b
BC_1P_2	346.5	a	357.4	ab	360.0	c	296.9	e	353.6	a	348.9	b	340.3	cd	359.6	c

B.

	Parental combination											
	M24 x TAM22		SID84 x TAM22				SID84 x HS624				HS624 x TAM22			
Gen	2010/11		2010		2011		2010		2011		2010		2011	
P_1	354.6	a	331.2	b	344.1	a	377.9	a	392.6	a	377.9	a	395.2	a
P_2	264.5	e	266.2	d	263.3	d	324.0	c	337.0	e	265.3	e	263.1	f
F_1	323.9	c	320.3	b	338.5	a	361.9	ab	374.7	bc	325.4	c	342.0	c
F_2	321.4	c	348.8	a	327.2	b	376.0	a	367.5	cd	315.8	c	321.0	d
BC_1P_1	339.8	b	332.5	ab	345.5	a	374.8	a	380.9	b	347.2	b	357.4	b
BC_1P_2	303.4	d	301.4	c	302.6	c	359.1	b	364.8	d	297.6	d	298.4	e

† ELS33, TAM B182-33 ELS; SID84, 04 SID 84-2; HS624, 06 WE 62-4; TAM22, Tamcot 22; M24, TAM 94L-25-M24.

‡ P_1, parent one; P_2, parent two; F_1, P_1 x P_2; F_2, selfed F_1; BC_1P_1, backcross to P_1; BC_1P_2, backcross to P_2.

§ Means within a column followed by the same letter are not different at p = 0.05 according to Fisher LSD.

different than P_2 for ELS33 x HS624, M24 x ELS33, and M24 x HS624 in 2011 and was significantly weaker than P_2 for M24 x HS624 in 2010. The F_2 was intermediate to the two parents for ELS33 x TAM22, M24 x HS624 in 2011, M24 x TAM22, SID84 x TAM22 in 2011, SID84 x HS624 in 2011, and HS624 x TAM22 in 2010 and 2011. The F_2 was not different than P_2 for ELS33 x SID84 in 2010 and 2011, ELS33 x HS624, and M24 x HS624 in 2010 and not different than P_1 for M24 x SID84 and SID84 x HS624 in 2010. The F_2 was the strongest generation for SID84 x TAM22 in 2010. The backcross generations were different from one another with values in the direction of the recurrent parent with the exception ELS33 x SID84 in 2010 and 2011, M24 x ELS33, and M24 x SID84 in which cases the BC_1P_1 was not different from the BC_1P_2.

Evaluation of the frequency distributions for Str (Figures 13 to 22) revealed that the range of values for the segregating generations tended to be wider than for the non-segregating generations. In general, frequency distributions do not appear to differ greatly from 2010 to 2011 within each parental combination except for ELS33 x SID84 and M24 x HS624 in which case 2010 and 2011 follow a similar distribution with 2011 shifted to the right of 2010 indicating 2011 presented more favorable conditions for Str. Frequency distributions of the segregating generations roughly align with a normal distribution suggesting that Str is a quantitative trait.

Parental combinations ELS33 x SID84, M24 x ELS33, M24 x SID84, SID84 x TAM22, and SID84 x HS624 (Figures 13, 16, 17, 20, and 21) expressed positive transgressive segregation at low levels (1.7%, 0.2%, 0.2%, 1.2%, and 4.0% respectively). Positive transgressive segregation occurred most often in the F_2 and BC_1P_1

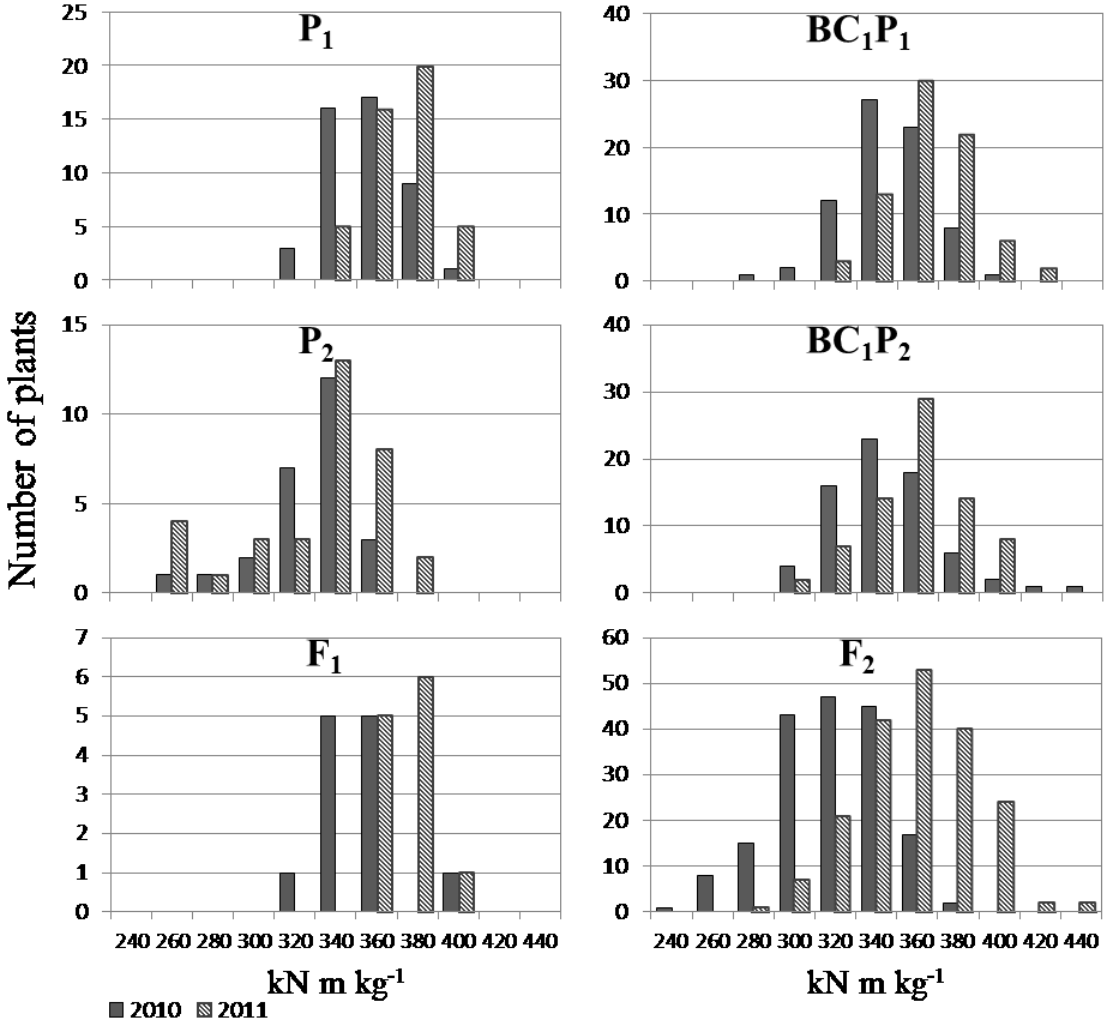


Figure 13. Frequency distribution of fiber bundle strength in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of ELS33 (P_1) x SID84 (P_2) in 2010 and 2011.

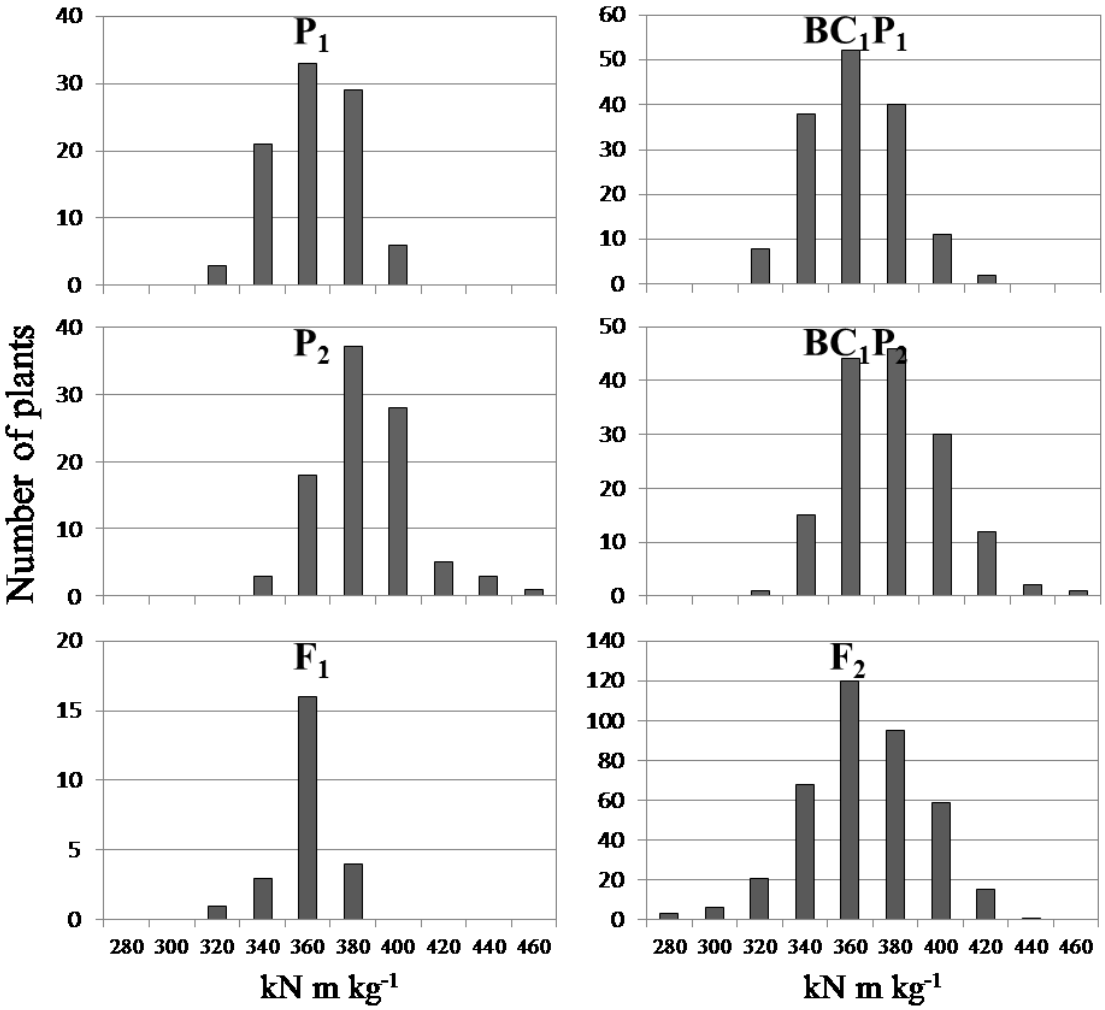


Figure 14. Frequency distribution of fiber bundle strength in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of ELS33 (P_1) x HS624 (P_2) in 2010 and 2011.

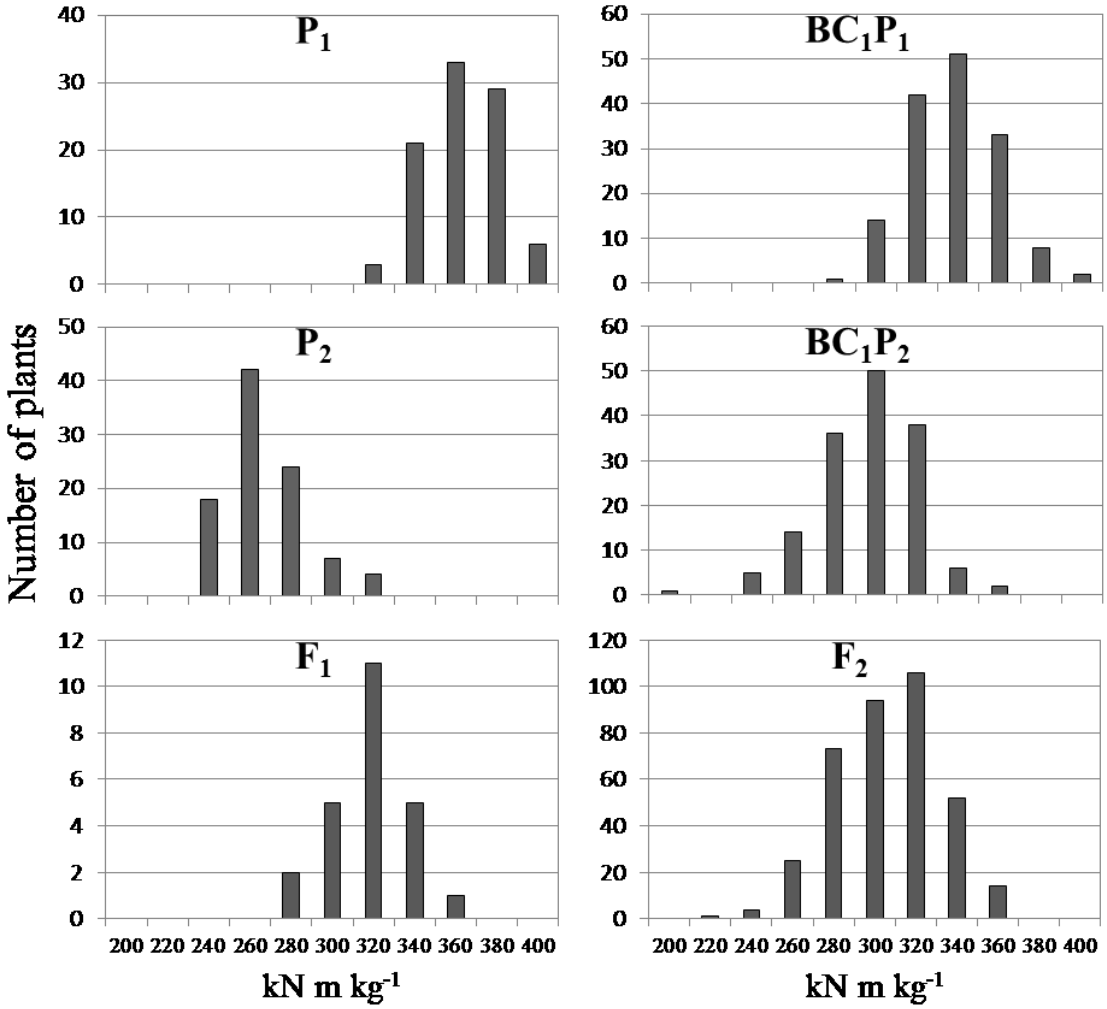


Figure 15. Frequency distribution of fiber bundle strength in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of ELS33 (P_1) x TAM22 (P_2) in 2010 and 2011.

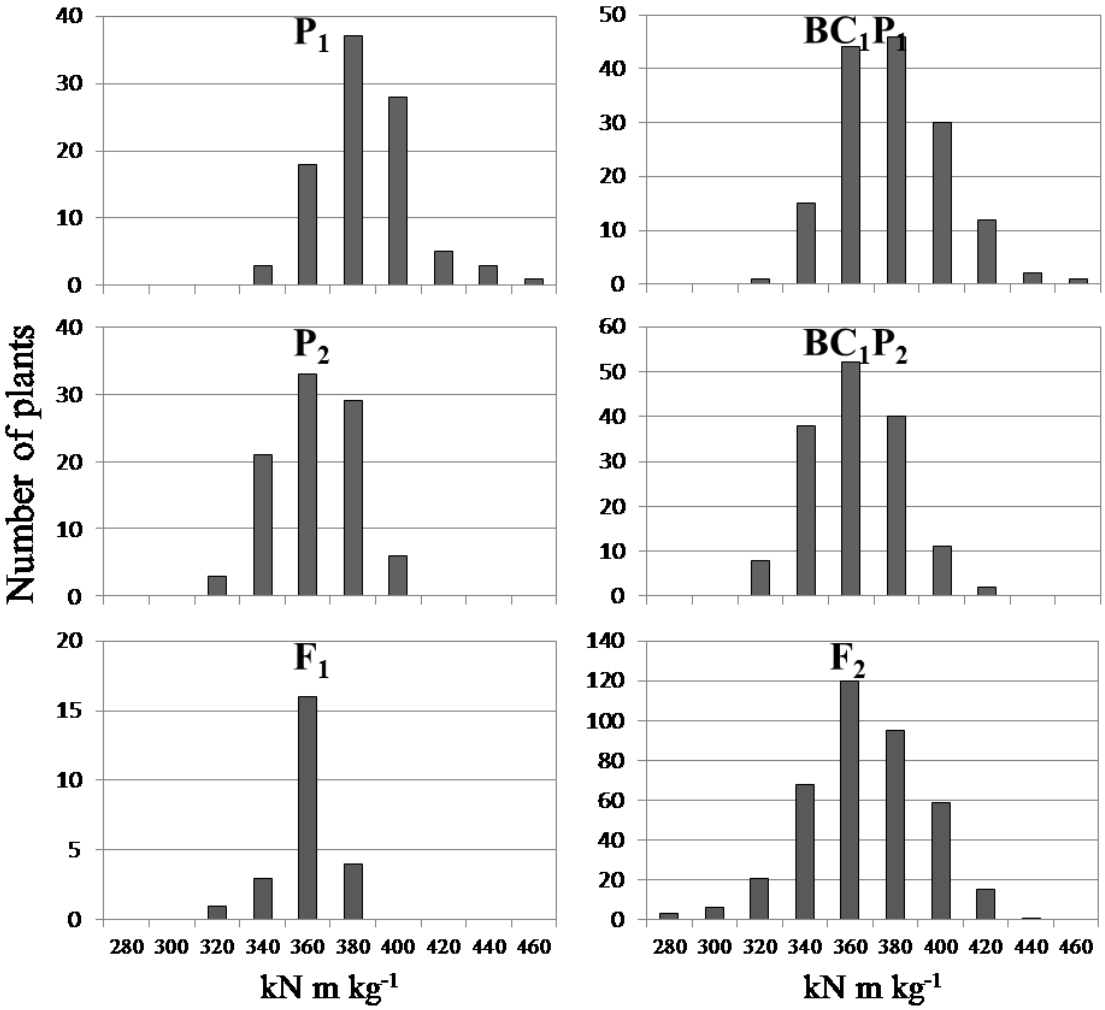


Figure 16. Frequency distribution of fiber bundle strength in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of M24 (P_1) x ELS33 (P_2) in 2010 and 2011.

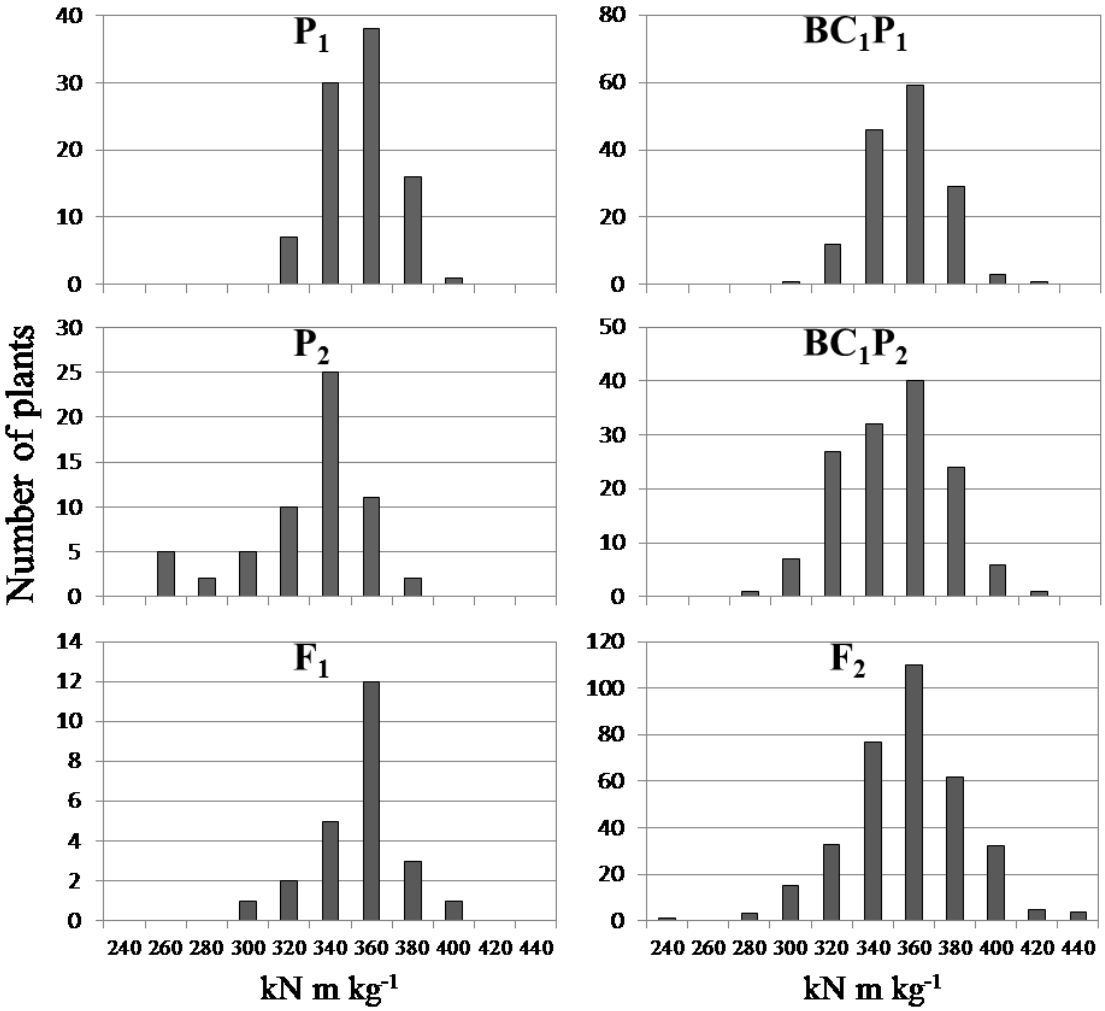


Figure 17. Frequency distribution of fiber bundle strength in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of M24 (P_1) x SID84 (P_2) in 2010 and 2011.

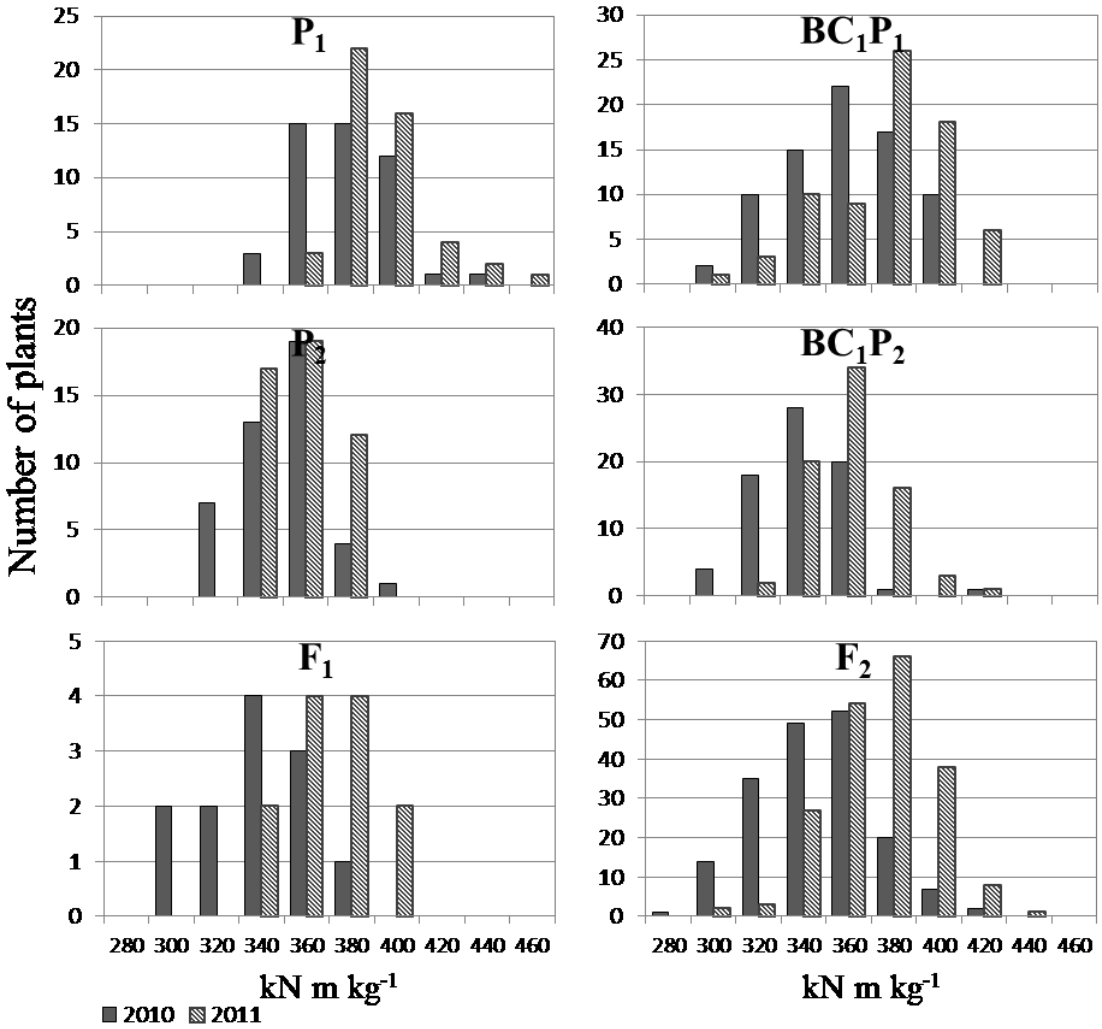


Figure 18. Frequency distribution of fiber bundle strength in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of M24 (P_2) x HS624 (P_1) in 2010 and 2011.

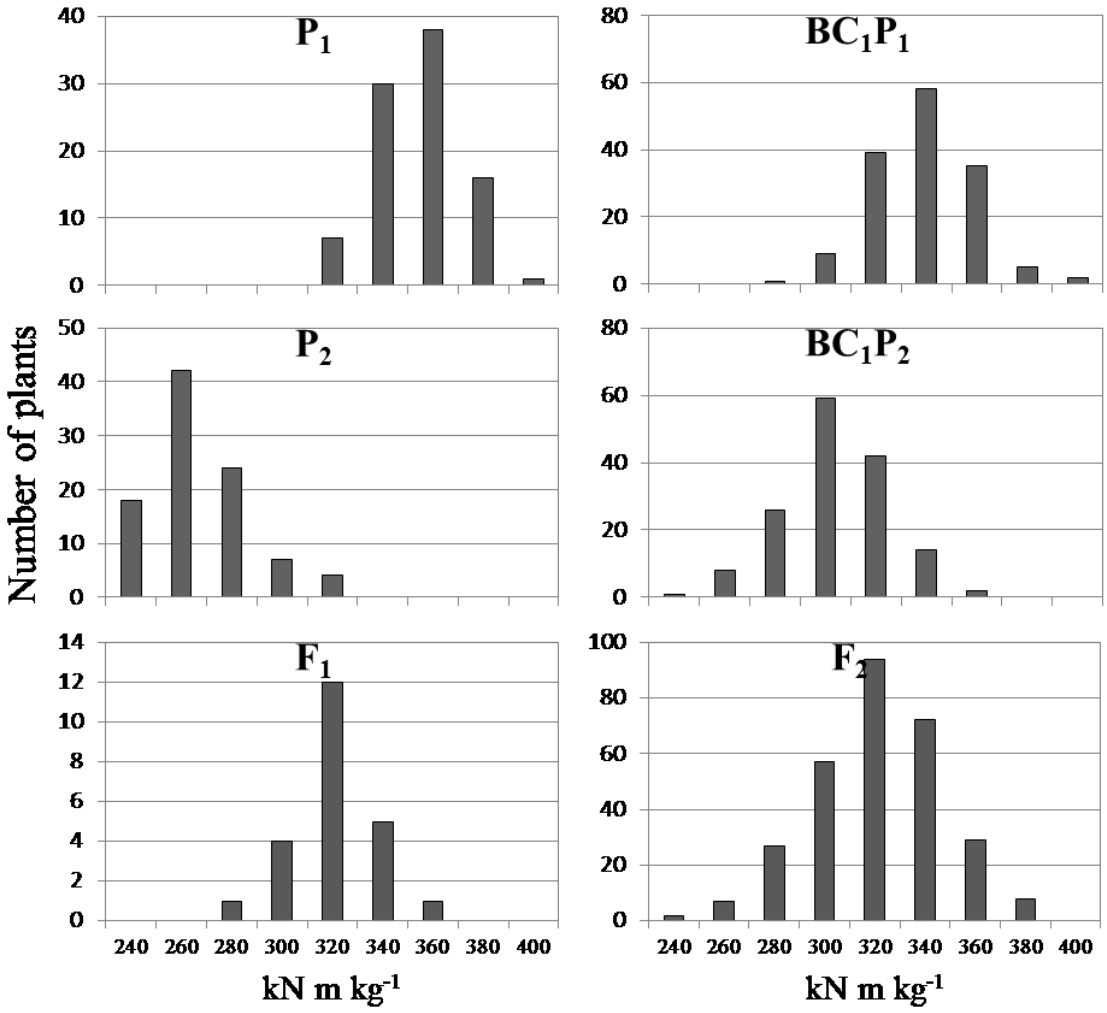


Figure 19. Frequency distribution of fiber bundle strength in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of M24 (P_1) x TAM22 (P_2) in 2010 and 2011.

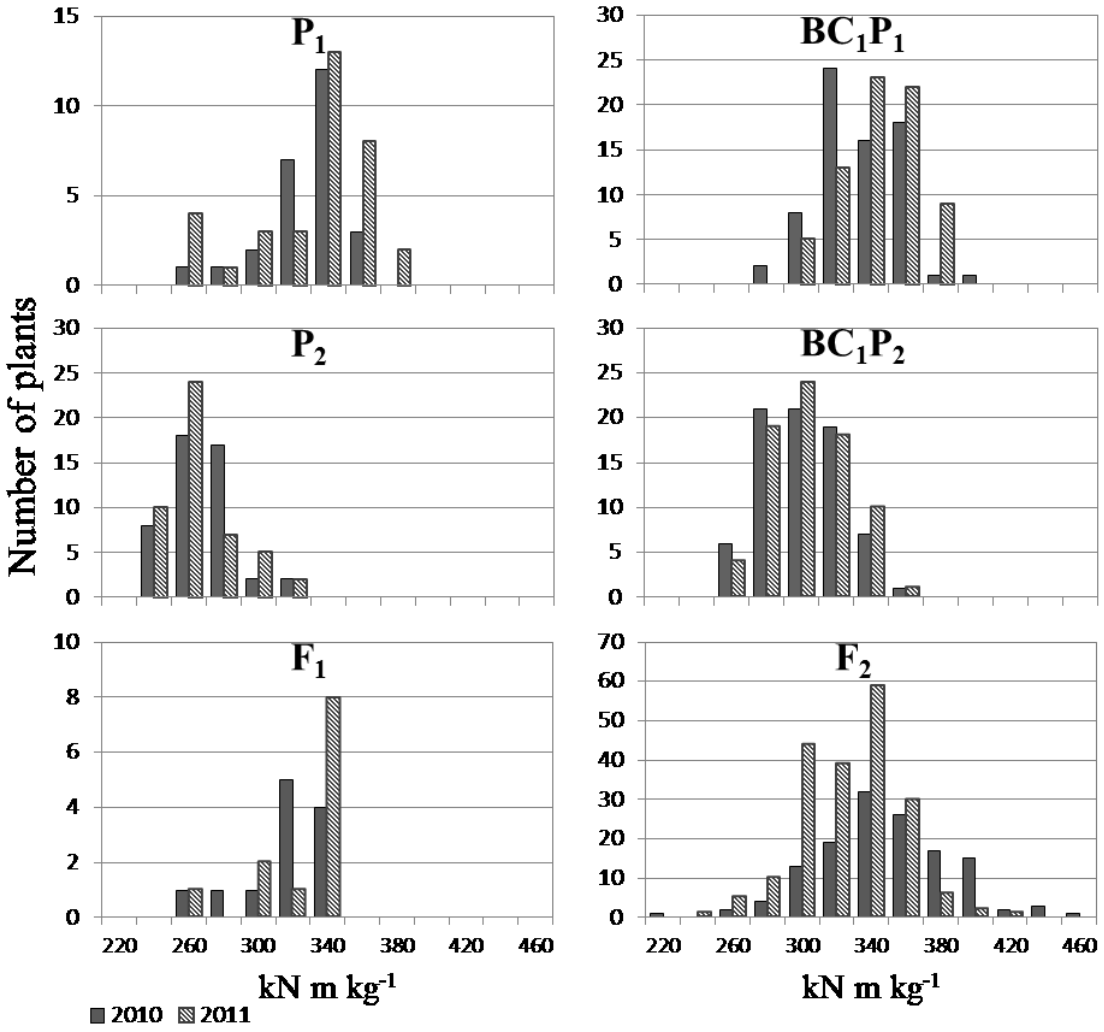


Figure 20. Frequency distribution of fiber bundle strength in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of SID84 (P_1) x TAM22 (P_2) in 2010 and 2011.

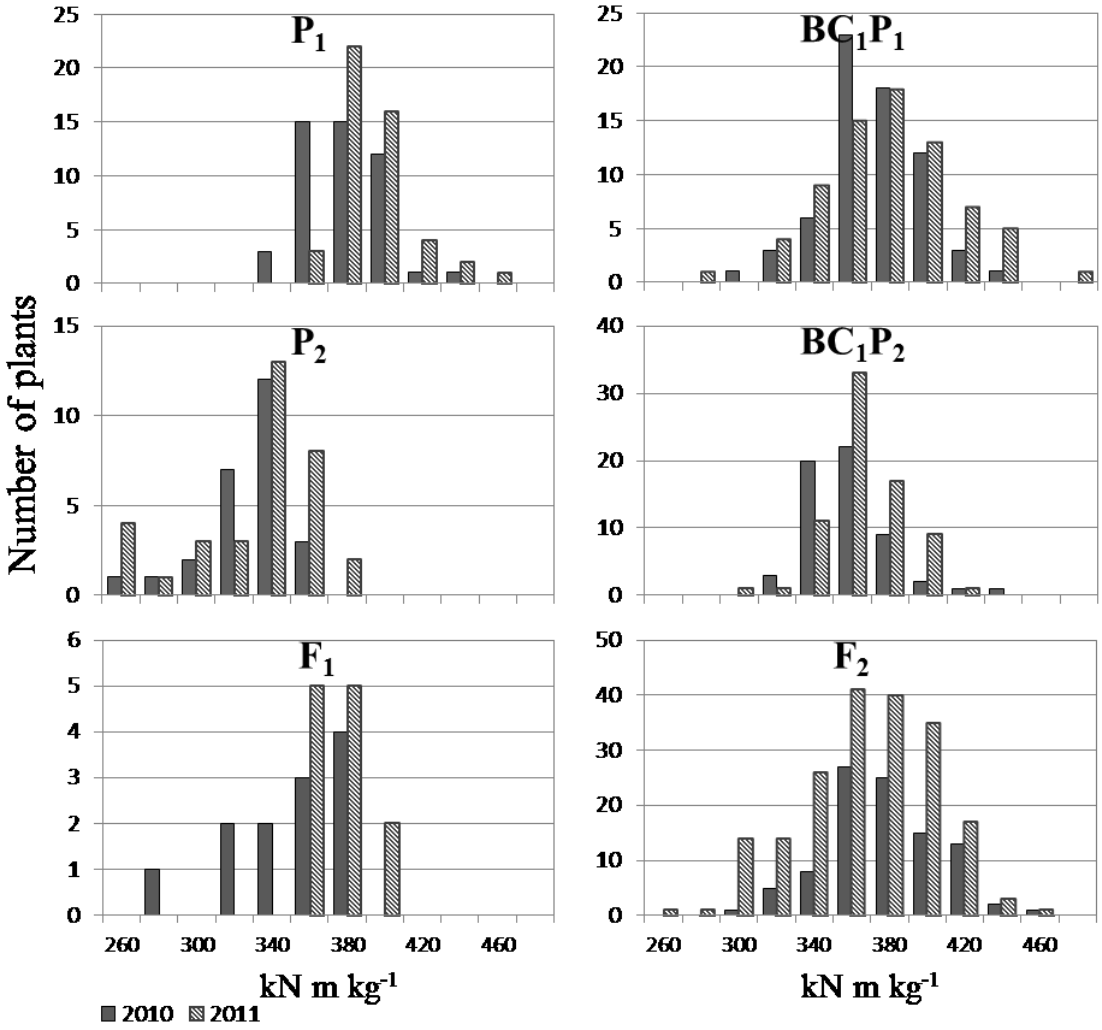


Figure 21. Frequency distribution of fiber bundle strength in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of SID84 (P_2) x HS624 (P_1) in 2010 and 2011.

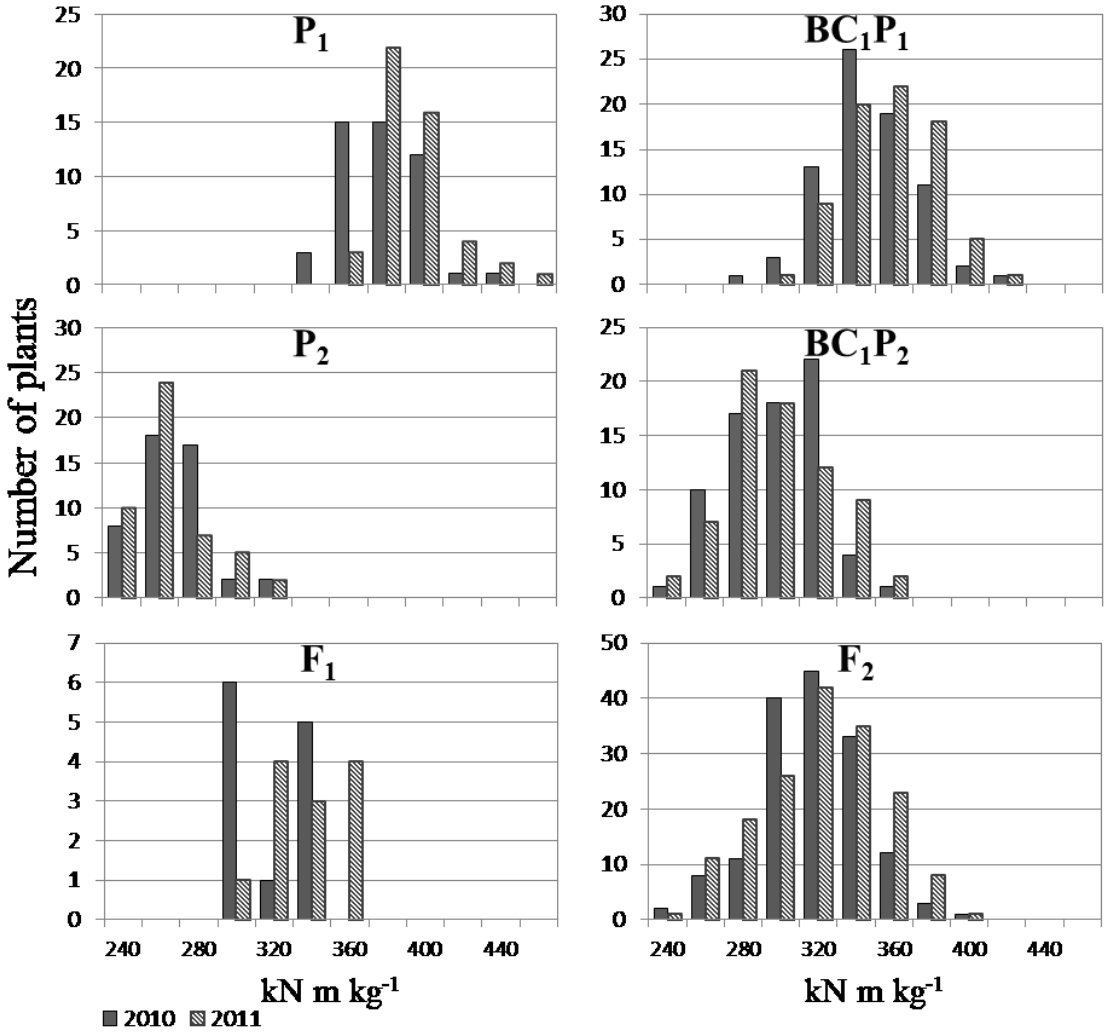


Figure 22. Frequency distribution of fiber bundle strength in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the parental combination of HS624 (P_1) x TAM22 (P_2) in 2010 and 2011.

generations but was also observed in the BC_1P_2 generation for parental combinations M24 x SID84 and ELS33 x SID84 in 2010. Four of the five parental combinations expressing positive transgressive segregation had SID84 as a parent suggesting it may carry novel alleles for Str not possessed by any of the upland parents used in this study. This may be a result of its low Hs (Table 5) in comparison to the other parents. The finer the fibers, the more fibers will be included in the fiber bundle, and thus increasing fiber bundle strength. Negative transgressive segregation was observed for M24 x SID84, M24 x ELS33, ELS33 x HS624, ELS33 x TAM22, ELS33 x SID84, M24 x HS624, and SID84 x TAM22 (0.2%, 0.9%, 1.3%, 0.3%, 0.2%, 0.1%, and 0.2% respectively). Negative transgressive segregation was more prevalent in 2010 than 2011 and in the F_2 and BC_1P_2 generations though it did occur in the BC_1P_1 for M24 x ELS33.

Results from the ABCD scaling tests agreed with results from the joint scaling test for all parental combinations except ELS33 x HS624, M24 x HS624 in 2011, and HS624 x TAM22 in 2010. Significant epistasis was observed for each of these parental combinations when the generation means were fit with the six-parameter model. SID84 x TAM22 in 2011 failed the scaling tests but did not exhibit significant epistasis when fit to the six-parameter model suggesting either higher-order epistasis or other complicating factor was at play.

The simple additive-dominance model was sufficient to explain the variation of Str among generation means for parental combinations ELS33 x SID84 in 2011, M24 x ELS33, and M24 x HS624 in 2010 (Table 19). All other combinations were fit to the six-parameter model which accounts for epistatic interactions between two loci. Additive

Table 19. ABCD and joint scaling tests for HVI fiber bundle strength per parental combination at College Station, TX in 2010 and 2011.

		ABCD scaling tests				
Parental combination†	Year	A	B	C	D	Joint scaling test
ELS33 x SID84	2010	ns	ns	*	*	ns
ELS33 x SID84	2011	ns	ns	ns	ns	ns
ELS33 x HS624	2010/11	*	ns	ns	ns	ns
ELS33 x TAM22	2010/11	ns	ns	*	*	ns
M24 x ELS33	2010/11	ns	ns	ns	ns	ns
M24 x SID84	2010/11	ns	*	*	*	ns
M24 x HS624	2010	ns	ns	ns	ns	ns
M24 x HS624	2011	ns	ns	ns	*	*
M24 x TAM22	2010/11	ns	*	*	ns	ns
SID84 x TAM22	2010	*	ns	*	*	ns
SID84 x TAM22	2011	*	ns	*	ns	ns
SID84 x HS624	2010	ns	*	*	*	ns
SID84 x HS624	2011	ns	*	ns	ns	ns
HS624 x TAM22	2010	ns	ns	ns	*	*
HS624 x TAM22	2011	*	ns	*	*	ns

† ELS33, TAM B182-33 ELS; SID84, 04 SID 84-2; HS624, 06 WE 62-4; TAM22, Tamcot 22; M24, TAM 94L-25-M24.

genetic effects were significant for all parental combinations and environments (Table 20). M24 x ELS33 expressed the lowest level of additive genetic effects, 4. 2 kN m kg^{-1}, and HS624 x TAM22 in 2011 expressed the highest level, 63.8 kN m kg^{-1}. As would be expected, additive genetic effects tended to be higher in crosses involving TAM22, the parent having the weakest fiber. Fewer significant dominance genetic effects were observed but with a much greater variability when compared to additive genetic effects having both positive and negative values. Dominance genetic effects are a measure of the deviation of the F_1 from the midparent value. A negative dominance effect indicates that the P_2 was contributing to the dominance effect while a positive dominance effect indicates a greater contribution by P_1. ELS33 x SID84 exhibited the greatest dominance of 237.9 kN m kg^{-1} in 2010 but only 16.7 kN m kg^{-1} in 2011. SID84 x TAM22 expressed the largest negative dominance genetic effect in 2010, -195.0 kN m kg^{-1}, but expressed a dominance effect of 54.8 kN m kg^{-1} in 2011.

Fewer epistatic genetic effects were observed for Str as compared to additive and dominance genetic effects (Table 20). Additive x additive genetic effects were significant in eight cases spread across all five parents and in both years. They ranged from -126.0 to 113.7 kN m kg^{-1}. Additive x dominance epistasis was less prevalent and was negative or not different from zero in all cases. Three of the four instances of significant dominance x dominance genetic effects involved ELS33 as a parent. ELS33 x SID84 in 2010 and ELS33 x TAM22 expressed a significant positive dominance genetic effect but a negative dominance x dominance genetic effect indicating duplicate epistasis between dominance increasers. Duplicate epistasis between dominant decreasers was

Table 20. Estimates of gene effects for HVI fiber bundle strength (Str) for ten parental combinations at College Station, TX in 2010 and 2011.

		Gene effects											
Family	Year	m		a		d		aa		ad		dd	
ELS33 x SID84	2010	228.2	***	13.8	***	237.9	***	113.7	***	-26.6	**	-115.5	***
ELS33 x SID84	2011	352.6	***	15.8	***	16.7	***	-		-		-	
ELS33 x HS624	2010/11	360.8	***	11.3	***	25.8		13.5		10.8		-28.7	*
ELS33 x TAM22	2010/11	268.9	***	48.3	***	96.9	***	45.7	***	-15.0	*	-47.2	***
M24 x ELS33	2010/11	358.8	***	4.2	***	-6.4	*	-		-		-	
M24 x SID84	2010/11	364.9	***	12.2	***	-17.7		-22.4	**	-14.2	*	6.5	
M24 x HS624	2010	363.8	***	14.4	***	-31.5	***	-		-		-	
M24 x HS624	2011	396.0	***	17.5	***	-65.0	*	-20.7	*	-3.8		36.6	
M24 x TAM22	2010/11	307.2	***	44.2	***	39.7	*	3.2		-18.2	***	-24.5	
SID84 x TAM22	2010	423.8	***	30.3	***	-195.0	***	-126.0	***	2.7		90.0	***
SID84 x TAM22	2011	309.2	***	33.5	***	54.8		-10.7		15.7		-39.8	
SID84 x HS624	2010	405.9	***	25.1	***	-60.2		-52.8	***	-22.4	*	5.3	
SID84 x HS624	2011	342.6	***	30.4	***	67.6		19.8		-30.9	**	-36.3	
HS624 x TAM22	2010	298.2	***	55.3	***	51.4		24.6	*	-13.2		-29.3	
HS624 x TAM22	2011	299.5	***	63.8	***	46.7		29.4	*	-13.9		-7.2	

*, ** Significant at the 0.05 and 0.01 probability levels, respectively.

† *m* = mean; *a* = additive; *d* = dominance; *aa* = additive x additive; *ad* = additive x dominance; *dd* = dominance x dominance.

‡ ELS33, TAM B182-33 ELS; SID84, 04 SID 84-2; HS624, 06 WE 62-4; TAM22, Tamcot 22; M24, TAM 94L-25-M24.

§ Three parameter model sufficiently fitted the six-generation means.

observed for SID84 x TAM22 in 2010 as it expressed a negative dominance genetic effect but a positive dominance x dominance genetic effect. Additive genetic effects were more consistent from parental combination to parental combination and from year to year than were dominance and epistatic genetic effects. The dominance effects were the largest in magnitude.

Estimates of variance components and heritability were calculated to ascertain the relative importance of different factors affecting phenotype for Str (Table 21). Environmental variance ranged from 298.32 to 713.80 with an average of 437.52. As with UHML, crosses with SID84 as a parent expressed a higher average environmental variance, 538.88, when compared to the average of all other crosses, 348.83. Additive variance ranged from 0.00 to 2038.72 with an overall average of 535.29. Additive variance for Str was the highest among crosses having SID84 as a parent followed by those having TAM22 as a parent. Dominance variance ranged from 0.00 to 224.06. The estimate of dominance variance was less than zero in ten instances suggesting either sampling error or the inability of this method to effectively measure dominance variance. In general, environmental, additive, and dominance variances were greater in 2011 than 2010.

H^2 for Str ranged from 0.22 to 0.82 with an average of 0.52 (Table 21). Crosses involving TAM22 exhibited the highest average H^2, 0.59, followed by SID84, 0.54. These same parental combinations also exhibited the highest environmental variances, but exhibited an even greater genotypic variance to produce the highest H^2. The higher average H^2 for SID84 suggests that it carries unique genetic variability for Str when

Table 21. Variance components and broad (H^2) and narrow (h^2) sense heritability estimates for HVI fiber bundle strength (Str) for 10 parental combinations grown at College Station, TX in 2010 and 2011.

		Variance components†			Heritability estimates§	
Parental combination‡	Year	σ^2_E	σ^2_A	σ^2_D	H^2	h^2
ELS33 x SID84	2010	400.04	281.56	35.36	0.44	0.39
ELS33 x SID84	2011	510.87	542.82	-282.12	0.52	0.52
ELS33 x HS624	2010/11	338.07	410.25	-41.97	0.55	0.55
ELS33 x TAM22	2010/11	337.30	313.02	25.39	0.50	0.46
M24 x ELS33	2010/11	319.04	-73.08	89.30	0.22	0.00
M24 x SID84	2010/11	493.63	635.17	-301.84	0.56	0.56
M24 x HS624	2010	424.80	313.73	-52.99	0.42	0.42
M24 x HS624	2011	298.32	0.88	224.06	0.43	0.00
M24 x TAM22	2010/11	319.50	489.18	-155.46	0.60	0.60
SID84 x TAM22	2010	462.70	2038.72	-988.65	0.82	0.82
SID84 x TAM22	2011	713.80	484.60	-449.16	0.40	0.40
SID84 x HS624	2010	604.78	505.28	-260.05	0.46	0.46
SID84 x HS624	2011	586.33	950.03	-278.44	0.62	0.62
HS624 x TAM22	2010	354.59	367.10	26.80	0.53	0.49
HS624 x TAM22	2011	398.98	770.11	-138.82	0.66	0.66

† σ^2_E, environmental variance; σ^2_A, additive variance; σ^2_D, dominance variance. Negative variance assumed zero in heritability estimates.

‡ ELS33, TAM B182-33 ELS; SID84, 04 SID 84-2; HS624, 06 WE 62-4; TAM22, Tamcot 22; M24, TAM 94L-25-M24.

§ H^2 = broad-sense heritability; h^2 = narrow-sense heritability.

compared to the upland parents included in this study. Parental combination SID84 x TAM22 in 2010 exhibited the highest H^2, 0.82, but exhibited the second lowest H^2, 0.40 in 2011. H^2 was very similar between 2010 and 2011. Since most dominance variance estimates were negative, all but five narrow-sense heritability estimates were equal to their respective H^2 estimates. H^2 was similar between 2010 and 2011, but 2010 exhibited a higher narrow-sense heritability than 2011.

5. CONCLUSIONS

Diallel

The diallel reported herein identified sufficient genetic variation among the parents to aid in the improvement of the traits through selection. Rankings of parental means often did not correspond to the rankings of GCA effects. Thus, the prediction of combining ability by making of the crosses contributed valuable information not available from analysis of parental means alone. HS624 was the parent of choice to improve LP and Str. SID84 was the best general combiner to improve UHML and UQLw, but exhibited problematic length distributions as indicated by its GCA estimates for Ln and SFCn, likely caused by fiber maturity issues. Still SID84 might be the parent of choice if attempting to improve fiber length along with Elon and Hs. If attempting to improve fiber length simultaneously with Str, ELS33 would be the parent of choice among the parents in this study as it was among the best general combiners for all length measurements in addition to Str. HSMD9, HS624, or FM832 would be the parent of choice to improve fiber maturity as indicated by their GCA estimates for IFC and MR.

The traits reported herein appear to be predominantly controlled by additive gene action as indicated by the comparison of variability due to GCA and low-level of heterosis. While nonadditive gene action was significant, based on SCA estimates, it is minimal and should not deter breeders from successfully selecting for these traits even in earlier generations. Significant G x Y interactions were observed for LP, all HVI measurements, and UQLw, thus breeders should evaluate for fiber quality in multiple years, or environments, prior to release to ensure superior and stable fiber quality.

HVI analysis alone was not sufficient to effectively evaluate these genotypes for fiber quality. Currently AFIS is the most feasible method for measuring cotton fiber length distribution, maturity and fineness, but unfortunately it is still too expensive and slow to evaluate large numbers of progeny necessary to successfully breed for improvement in these traits. This emphasizes the importance of developing faster, more economical methods of measuring these highly valuable traits. In the meantime, it may prove beneficial to perform AFIS evaluation on parents used in crossing which will highlight any populations with potential downfalls for length distribution or fiber maturity. Only these populations then would be evaluated using AFIS during early selection. All advanced lines should be evaluated for at least two generations before intended release to identify any unpredicted fiber quality problems.

Generation Means Analysis

The generation means analyses reported herein identified significant variation among generations for UHML and Str with the exception of M24 x ELS33. The two years of this study were not significantly different for any parental combination for UHML or Str. However, Gen x Y was significant for four parental combinations for both UHML and Str but represented a much smaller portion of the variation when compared with variation due to generation. Homogeneity of variance was violated in three parental combinations for both UHML and Str. Given the Gen x Y interaction and homogeneity of variance violation, it would be prudent for advanced lines to be tested in multiple environments prior to being released to confirm a superior and stable fiber quality phenotype.

Analyses of the frequency distributions of these parental combinations revealed that UHML and Str are inherited quantitatively. Only one positive transgressive segregate, individuals with values exceeding longest parent or F_1 plant, was observed for UHML. More frequent positive transgressive segregation was observed for Str, albeit at low levels. It was most often observed in the F_2 and BC_1P_1 generations. Parental combinations with SID84 as a parent accounted for four of the five instances of positive transgressive segregation for Str suggesting that SID84 carries favorable alleles for Str not found in the four upland parents included in this study. Thus, it may prove to be a valuable source of genetic improvement for Str in elite germplasm pools that appear to have exhausted genetic variability of upland germplasm.

A wide range for H^2 was observed for both UHML and Str and was not completely consistent among years. H^2 was the highest for both UHML and Str in crosses involving TAM22 indicating that in these populations effective selection among progeny for improved UHML and Str relative to the lower fiber quality parent, TAM22, is possible using pedigree breeding. Thus creating selection populations using one parent for yield potential and one parent for UHML and/or Str appears to be a viable strategy for breeding improved yield and quality as long as genetic linkages between these traits can be decoupled.

In general, gene action could not be best explained using a simple, additive-dominance model of inheritance, and the more complex, six parameter model was utilized in order to account for non-allelic interactions of two loci. Additive gene action was significant for all parental combinations for UHML and Str with the exception of

crosses between ELS33, M24, and SID84 for UHML. Dominance genetic effects for UHML were high for ELS33 x SID84 and less so for M24 x SID84. The low levels of additive genetic effects coupled with high levels of dominance genetic effects suggest a high level of gene dispersion for UHML within these parents. Generally, the significance and magnitude of additive genetic effects were more consistent among parental combinations and years than were non-additive genetic effects for both UHML and Str. Estimates of dominance and epistatic genetic effects often were of a greater magnitude than additive genetic effects but in an inconsistent manner, and in both positive and negative directions. Selection for UHML and Str may be most effective after a couple of generations of inbreeding in order to reduce undesirable variation due to dominance genetic effects.

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