INHERITANCE OF COTTON FIBER LENGTH AND DISTRIBUTION

A Dissertation

by

CHRIS ALAN BRADEN

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

DOCTOR OF PHILOSOPHY

August 2005

Major Subject: Plant Breeding

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ABSTRACT

Inheritance of Cotton Fiber Length
and Distribution. (August 2005)

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Dr. Eric F. Hequet

Fiber quality data from five upland cotton (*Gossypium hirsutum* L.) genotypes, which were grown at College Station, TX during 2001 and 2002, were subjected to diallel and generation means analyses to determine the potential for improvement of fiber length and to determine the inheritance of length distribution data. Four near-long staple (NLS) upland cotton genotypes and one short-staple genotype were crossed in all combinations, excluding reciprocals. Estimates of general (GCA) and specific combining ability (SCA) for fiber length based on Griffing's diallel Model I, Method 4 were calculated for high volume instrumentation (HVI) upper-half mean (UHM) fiber length and advance fiber information system (AFIS) mean fiber length by weight (FLw), mean fiber length by number (FLn), upper quartile length by weight (Uqlw), fiber length distribution cross entropy (using 3 different standard or check distributions - CEA, CEB, and CEC), fiber length distribution kurtosis (FLwKurt), and fiber length distribution skewness (FLwSkew) for FLw. Across environments, GCA effects were significant for fiber length measurements of UHM, FLw, FLn, Uqlw, and SFCw and distribution measurements of CEA, CEB, FLwKurt, and FLwSkew. On the basis of GCA effects, TAM 94L-25 was the best parent to be used in a cross to improve upland fiber length, while Acala 1517-99 was the parent of choice to improve distribution among the 4 parents tested.

The inheritance of AFIS fiber length measurements and distribution data was estimated using parents, F_1, F_2, and backcross generations. The magnitude and significance of the estimates for non-allelic effects in the parental combinations suggest that epistatic gene effects are present and important in the basic mechanism of AFIS fiber length and length distribution inheritance for the populations studied. Gene effects and variances for all AFIS fiber length and distribution data measurements were inherited differently in different environments and specific parental combination, suggesting environmentally specific mechanisms. Developing genotypes with enhanced fiber length and an optimal fiber length distribution should be a priority to improve spinning performance and product quality of U.S. upland cotton.

DEDICATION

This dissertation is in loving memory of my grandfather, Elmer Braden, Sr., who taught and raised seven sons on the family farm. The oldest one, my Dad, taught me that agriculture is more than tractors, plows, and soil; it is love of the land, family, and God. This work is dedicated to my parents for all their love and support, for molding me into the man I am today, and for instilling in me a hard work ethic, a level head, and a gentle heart.

I would also like to dedicate this dissertation to the love of my life, Heather Jo Wilde, (soon to be Braden). Your unconditional love and support has overfilled my heart with happiness and joy. You are my best friend, someone who understands and knows me inside and out. I knew from the first moment that, "It must have been meant to be."

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I gratefully acknowledge the help of Matt Jakubik, Chad Eixmann, and Dawn Deno, Cotton Improvement Lab personnel, and fellow graduate students for their support and assistance in completing this project. Thanks are also due to all the student workers for their help with data collection. I would like to express my most sincere gratitude to Cotton Incorporated for providing the fellowship and financial support that allowed me to complete my graduate studies at Texas A&M University.

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TABLE OF CONTENTS

CHAPTER Page

LIST OF FIGURES

FIGURE Page

FIGURE Page

FIGURE Page

LIST OF TABLES

CHAPTER I

INTRODUCTION

Cotton, an oilseed and fiber crop, is grown in more than 17 states in the U.S. and in more than 70 countries world wide. The natural fiber of upland cotton, *Gossypium hirsutum* L., constitutes over 95% of the value of the cotton crop (Cotton Incorporated, 2005). It is a high-value crop that is grown by producers as raw material for the textile industry. Global competition in the production and consumption of cotton fiber combined with technological advancements in yarn manufacturing has accelerated efforts to enhance cotton fiber quality. Cotton fiber quality can be improved through genetics and crop management (Behery, 1993; Anthony, 1999). Knowledge of the effects of fiber properties on processing and their inheritance, relationships, and environmental influences is necessary to devise improvement strategies and techniques. Breeders do not conduct direct selection for yarn properties because it is not feasible. The quantity of fiber required for a spinning test is not attainable from 40 foot experimental plots and larger plots would increase the expense and time of an already costly procedure. Thus, breeders select for fiber properties that influence processing. The plant breeding industry should focus on enhancing fiber properties and reducing variation since variability in fiber properties is detrimental to fiber processing.

Connotation of fiber quality is different from the perspective of the cotton producer, ginners, and spinner. For a cotton grower, the word implies the economic

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This dissertation follows the style and format of Crop Science.

return of the fiber properties (premium and discounts) of his product based upon the United States Department of Agriculture (USDA) classing office when delivered to the yarn mill, merchant, or cooperative marketing association. Spinners are concerned with fiber quality impact on costly disruptions in yarn-spinning processes and with the presence of significant defects in yarn and finished fabrics. Spinners criticize the general tendency of producers and ginners to increase the premium by producing higher-grade cotton or lowering the cost of processing by increasing the speed of ginning (Anthony, 1994). By drying the seed cotton to the extreme and increasing lint cleaning, the cotton processed is cleaner and more marketable. However, short fibers and neps have been increased, lowering the spinnability of the cotton, which may lower the quality of cotton products. The cotton producer's production and ginning practices are more influenced by the government loan program and cotton merchants than by the ultimate customers for their fiber. As a result, the price of cotton cannot be directly correlated with the quality of yarn produced. Spinners want to change and raise the standards, but the marketplace is not sending the right signals to growers, ginners, and breeders. The valuation of cotton in the future may be based on the true spinning value of fibers, changing the present cotton marketing system from its present grade and staple orientation to a system based on the fiber characteristics that the spinner, weaver, and consumer demands (El Mogahzy, 1999; ICAC 2004).

Fiber properties of Texas cotton must be improved continually to remain competitive in world markets and meet the needs of new spinning and weaving methods. Cotton producers in Texas are confronted, in general, with lower yields and poorer fiber quality than are producers in other sections of the cotton belt, especially when considering the hectares grown under dryland conditions. Short staple and micronaire outside the premium range account for the majority of the discounts when calculating the Commodity Credit Corporation (CCC) loan value for any given bale. In Texas during the 2003-04 crop year, only 44.1% of the bales classified achieved a U.S. base staple length of 34 (26.7 mm) (Hequet, 2004). This number has substantially increased over the past few years with the private sector commercializing new long staple picker varieties that are capable of being grown across all regions of Texas. However, considering the U.S. is exporting two-thirds of our cotton to overseas mills, a minuscule 8.1 and 0.9% of classified Texas bales attained the International and International Cotton Advisory Committee (ICAC) base staple length of 35 (27.4 mm) and 36 (28.2 mm), respectively (Hequet, 2004). Part of this problem is caused by more stressful and highly unpredictable environmental conditions (i.e., drought, adverse temperatures, hail, early frost, etc.) a crop will endure during the growing season. A second problem may be the narrow genetic base and lack of adaptability that exists in current cotton cultivars (Van Esbroeck et al., 1999).

Fiber length is one of the most important properties of cotton fibers in both marketing and processing (Bragg and Shofner, 1993). A premium is paid for longer fiber length. Length, i.e., the average length of all fibers in the sample or the average length of a given percentage, is related to other cotton fiber characteristics such as strength, fineness, maturity, and uniformity. Longer staple cottons are generally stronger, finer, and more uniform than shorter staple cottons. A few parameters affected by length, or staple, during spinning are production efficiency, amount of waste, and fly generation. Yarn quality parameters such as strength, elongation, hairiness, and evenness are correlated strongly with the length of cotton fibers (Perkins et al., 1984; El Mogahzy, 1999; El Mogahzy and Chewning, 2001). Fiber length uniformity, or its distribution, has increased importance for the newer technologically advanced spinning systems, such as air-jet.

Knowledge of fiber length is critical to manufacturing yarn of a specific size on ring spinning systems (Rusca and Reeves, 1968; El Mogahzy and Chewning, 2001). The known fiber length is used to set the distance between rollers in the drafting procedure during yarn manufacturing (Perkins et al., 1984; Behery, 1993; El Mogahzy and Chewning, 2001). The draft setting should not be longer than the staple length to avoid floating fibers and unevenness or fibers flowing at undetermined speeds. On the other hand, the setting should not be shorter than the staple length to avoid stretching and breaking of fibers.

Inter-fiber friction is dependent upon fiber length, specific surface area, and surface characteristics of the fibers. Longer fibers will improve the frictional resistance because of increased area of contact that they have with adjoining fibers, thus enhancing yarn strength. Shorter fibers have a higher probability of slippage than longer fibers, therefore, if the frictional hold is less than the breaking load, the fiber will slip rather than break and will not make its full contribution to the strength of the yarn (Balasubramanian, 1995). Holding other fiber properties constant, longer fibers require less twist to produce maximum yarn strength. Fiber length and length uniformity are the primary factors in yarn uniformity and defect level, while fineness dictates the spin limit and the number of fibers per yarn cross section (Deussen, 1993; El Mogahzy and Chewning, 2001). Lack of fiber strength can be compensated partially by longer fibers to improve spinnability.

Fiber length and its distribution is a quantitative trait. Detection of gene action and inheritance among current near-long staple (NLS) genotypes will expedite the search and development of allelic or gene combinations necessary for the selection of parents and new germplasm. Knowledge of heritability, magnitude, and type of genetic variance controlling fiber length in current NLS upland genotypes would allow a breeder to choose effective parents for developing segregating populations. Maximizing fiber length while minimizing its variance in upland cotton will create a value added agricultural commodity.

By studying the type of gene action and heritability among four NLS upland cotton genotypes and one short-staple genotype, the inheritance of NLS fiber length in upland cotton was determined. Genetic information was obtained from a diallel mating design for estimates of general (GCA) and specific (SCA) combining ability. The inheritance of cotton fiber length was studied using AFIS data and generation means analysis of the five parents, F_1, F_2, and backcross generations. Growing the material for two years provided estimates of various genetic components controlling Advanced Fiber Information System (AFIS) fiber length. The length distribution data available with the AFIS appeared to contain information that would be useful to both cotton breeders and spinners. Mode of gene action for fiber length distribution data also was investigated.

The length distribution data may provide a new tool for cotton breeders in their efforts to reduce short fiber content, since it clearly appears to be cultivar related (Hequet and Ethridge, 2000).

Objectives

The objectives of this research project are to:

1. Determine HVI and AFIS fiber length combining ability of the selected parents.
2. Estimate gene effects, genetic variance, and heritability of AFIS fiber length in near-long x near-long and near-long x short staple upland parental combinations.
3. Determine combining ability of AFIS distribution data measurements with the selected parents
4. Determine the mode of gene action and inheritance of AFIS distribution data measurements in near-long x near-long and near-long x short staple upland parental combinations.

CHAPTER II

REVIEW OF LITERATURE

Factors affecting fiber length and length distribution

Enhancing fiber length is a complex issue because fiber samples from field research or cotton bales contain a range or distribution of fiber lengths (Behery, 1993), the variability of which generally is not measured. Environmental conditions within a growing year affect the length distribution of cotton fibers. The length of cotton fibers varies not only among cultivars, but also within a cultivar due to growth environment, within the same plant due to position of the boll, within the same boll due to individual seed nutrients, and within the same seed due to the positions of fibers on the seed (Bradow et al., 1997). Besides genotypic selection and environmental conditions affecting fiber length, harvesting, ginning, and processing methods can also change the length distribution of cotton.

Fiber quality, in general, plays an important role in how well the fiber withstands gin processing. Cotton fiber strength is indirectly related to short fiber content (SFC). The strength of fiber contributes to its ability to withstand mechanical stresses during harvesting and ginning. Weak fibers are prone to break during processing. Stronger fibers reduce the potential for breakage during harvesting and ginning, thus the existence of fewer short fibers in the bale. However, even with stronger fiber we have the potential to break fibers because of increasing stresses on the fiber that are caused by changes in harvesting and ginning. Length distributions are influenced by fiber maturity, and maturity is directly related to growing conditions. Immature fibers have underdeveloped, weak, thin walls that are apt to break during harvesting and ginning. Fully mature fibers are less likely to be damaged or broken. Thus, a growing season that has an early frost, water stress, or disease affects the fiber length distribution in a bale (Behery, 1993).

Cotton lint possesses its highest fiber quality and best potential for spinning when the bolls are mature and freshly opened (Anthony, 1994). Production practices and the degree of weathering after boll maturation will alter the length distribution (Anthony, 1999). The method of harvest (picker vs. stripper) and harvest speed impact fiber quality and length distributions (Garner et al., 1970; Cocke et al., 1977; Behery, 1993; ICAC, 2001). Stripping cotton reduces the fiber length and contains more foreign matter than picked cotton (Garner et al., 1970; El Mogahzy and Chewning, 2001). The type of ginning (hand, saw, or roller) used will also influence fiber length distributions. Roller ginned cotton fibers are removed from the seed with little movement of the fibers among each other whereas the saw gin produces much more blending or fiber to fiber movement (Hertel and Craven, 1960). Fransen and Verschrage (1985) reported roller ginning decreased the fiber length by several millimeters and the percentage of fibers shorter than 13 mm increased 6 to 8 times the corresponding value for hand-ginning cotton samples. This same source showed hand-ginned cotton had a nearly normal length distribution and it changes to a skew distribution for mechanically roller-ginned cotton. Bradow et al. (1999) summarized more than 1,000 samples of hand-picked fiber samples ginned by hand, saw, and roller. They concluded short fiber content by weight

(SFCw) for hand ginned samples was 6.2%, 10.2% for saw ginned, and 11.8% for roller ginned.

Post-harvest management will introduce alterations to fiber length and the length distribution (Anthony, 1999). Gin processing, especially the preliminary cleaning, and the effects of moisture content, processing rate, and gin machinery type can have a substantial effect on fiber length distribution (Anthony, 1985; Anthony, 1996a; Anthony, 1996b; Anthony, 1998; Anthony, 1999; Behery, 1993; Gordon, 2001; ICAC, 2001). The combination of heat and lint cleaning at the gin to improve producer's grades can result in excessive fiber damage and cause an increase in SFC (Anthony, 1985; Columbus et al., 1989). SFC has a negative influence on the manufacturing performance and end-use value of the cotton. Anthony and Bragg (1987) reported that only one lint cleaner should be used at the gin in order to minimize SFC.

Fiber length measurements

Determining the length of individual fibers is difficult and time consuming so various methods of estimating fiber length have been devised (Steadman, 1997). Most test methods and instruments for fiber length analysis measure the length and mass or weight of each group of fibers. Fiber length characteristics can then be determined. Instruments measuring fiber length can be classified into two general categories on the basis of their capability to measure one or a few related properties. The Suter-Webb fiber array method is the most difficult and expensive method since the fibers are first manually sorted by length group using a set of combs, then each length group is weighed and the length distribution by weight derived (ASTM, 1994a). Fibrograph, High

Volume Instrumentation (HVI), and AFIS systems have been developed for fast measurements and contain inherent advantages and disadvantages. The Fibrograph, a single-instrument measurement, evaluates fiber length parameters such as mean length, 2.5%, and 50% span lengths (ASTM, 1994b). HVI and AFIS measure a relatively complete profile of fiber properties. HVI provides estimates of length, strength, and micronaire reading on the same fiber sample (ASTM, 1994c). Compared with single-instrument testing, the HVI technology for evaluation of fiber properties is faster and costs less per measurement. Fiber property measurements by HVI have been beneficial to yarn manufacturers, especially when combined with bale selection software such as the Engineered Fiber Selection System (Chewning, 1994).

Without knowledge of heritability and selection response data, instrument choice to evaluate fiber properties in breeding programs may be based on cost and availability. Breeders need information on which instrument will result in the fastest genetic gain in fiber length. Green and Culp (1990) did not detect any significant GCA or SCA effects for any of the HVI fiber measurements, but did for standard laboratory instrumentation. They concluded that HVI was not useful to breeders in detecting small genetic differences. In contrast, Latimer et al. (1996) reported measurements of fiber traits using HVI analyses provide higher heritability estimates than those obtained from conventional fiber quality techniques, and HVI is suitable for improvement of fiber quality traits. May and Jividen (1999) reported that heritability estimates for 2.5% span length and UHM fiber length were similar between single- and HVI-instruments and of a magnitude to expect progress from selection. Although 2.5% span length and upper-half mean length are not the same measure of fiber length distribution, both give information on the length of the longest fibers in a sample of cotton (Kerr, 1961). The current research will be the first to assess the inheritance and heritability of AFIS fiber length measurements.

The fiber length of a cotton sample can only be fully described by its distribution, but fiber length distribution is a complex way to compare cotton lengths. Various aspects of a length distribution are important for different reasons. Different measurement techniques have resulted in more than one desired parameter from a length distribution. Yarn characteristics and spinning parameters are affected by several aspects of the length distribution, and therefore certain fiber characteristics (statistical parameters) of a fiber length distribution have been developed over the years to be used in both trading and processing of cotton fiber. Classer staple length (length estimated in 32nd inches), effective length, mean length, upper-quartile length (UQL), span length, uniformity index, uniformity ratio, SFC, and upper-half mean (UHM) length are the most common length distribution parameters.

Staple length

Staple length is the most commonly used parameter for characterizing cotton fiber length (Woo, 1967; El Mogahzy and Chewning, 2001). Staple length was originally defined as a quality estimated by personal judgment by which a sample of fibrous raw material was characterized with regards to its technically most important fiber length (Woo, 1967). It was never formally defined in terms of any statistical value of length distribution, but considered a measurement of the long fiber content. The concept of staple length was used long before satisfactory methods of measuring fibers had been developed, so that the merchants, spinners or graders would have a common language relative to fiber length (Munro, 1987; Behery, 1993; Steadman, 1997). Staple length was estimated by the hand stapling process performed by the classer with the aid of some official standards. The classer would pull a tuft of fibers from the sample, and by a process of lapping, pulling, and discarding, would make parallel a typical portion of the fibers.

Mean length

ASTM defines the mean length as, "in testing of cotton fibers the average length of all fibers in the test specimen based on weight-length data" (ASTM, 1994a). As an alternative, the mean length can be calculated by number-length data, too, and it is acknowledged to be the most important in engineering the yarn. Depending on the type of cotton, there exist different relationships between these two lengths. The length by number (FLn) data tends to emphasize the short fibers in the sample, whereas the length by weight (FLw) data tends to hide them. Cui et al. (1998) showed theoretically and experimentally that number-based and weight-based statistics may give opposite rank orders in some cases when they are used to compare cotton fiber lengths. They showed that FLw is always greater than FLn with the assumption that fiber length and linear density are statistically independent. However, SFC and UQL by number and by weight may give opposite rank orders.

Mean length by weight is not as straight-forward as it seems because cotton, being a natural fiber, varies in diameter (fineness) at the same time as it varies in length.

If fibers all had the same fineness then there would be no difficulty in calculating the mean fiber length. The only step necessary would be to add up all the individual fiber lengths and divide this sum by the number of fibers. However, if the fibers have different diameters, then the thicker fibers will have a greater mass so that there is a case for taking the mass into account when calculating the mean length by weight.

Hequet et al. (1998) reported a strong correlation ($R^2 = 0.93$) between the old AFIS (length and diameter module) FLw and HVI mean length. The AFIS FLw was slightly higher than those obtained with the HVI.

Upper-quartile length

ASTM defines the upper-quartile length as the fiber length which is exceeded by 25% of the fibers by weight in the test specimen when tested by the array method (ASTM, 1994a). As discussed above, upper-quartile length by weight is not always greater than upper-quartile by number. Cui et al. (1998) found that 8.33% of measurements gave opposite ranks.

Effective length

Effective length is longer than the average length and is a measure of the length of the majority of the longer fibers in the sample. Effective length is statistically defined as the upper quartile of a numerical length distribution from which some of the short fibers have been eliminated by an arbitrary construction (Woo, 1967; Behery, 1993). Thus, the effective length is more independent of the tail of short fibers than is the upper-quartile of the complete fiber. According to Woo (1967), the effective length is equal to 0.859 of the maximum length in the sample.

Modal length

Modal length is the length in a fiber length frequency diagram that has the highest frequency of occurrence. The modal length for long staple cottons is more than the mean length because of the progressive increase in skewness of the fiber length distributions with increasing staple length. The modal or most frequent length of the fibers when measured in a straightened condition corresponds very closely to the staple length (Woo, 1967).

Span length

Span length is the distance spanned by a specified percentage of the fibers in the test beard when tested by the Fibrograph, taking the amount reading at the starting point of the scanning as 100% (ASTM, 1994b). There are an infinite number of reference points for span lengths. The 50 and 2.5% are used most commonly by industry. The 2.5% span length is that length at which only 2.5% of the fibers are that long or longer and likewise for the 50% span length. The 2.5% span length references the shortest distance to which roller drafting ratch settings can be adjusted so that few, if any, fibers are broken (Hertel and Craven, 1960). Behery (1993) stated that the draft setting should be set to the fiber length attained by 1% of the fibers (distribution according to number). Audivert and Castellar (1971) found that the 2.5% span length was less variable than others and increasing span lengths tended to increase the coefficient of variation from 1% to 4%. The 50% span length is more valuable as a potential measure of spinning performance and number of ends down. Hertel and Carven (1960) emphasized that the 67% span length was as good as mean length in describing breaking strength of yarns.

The 2.5% span length parameter has a strong relationship with HVI UHM (Hequet et al., 1998).

Uniformity index

Uniformity Index is obtained by dividing the mean length by the UHM length. It is a measure of the uniformity of fiber lengths in the sample expressed as a percent. Thus, this uniformity value is the ratio of the average length of all fibers to the average length of the longest one half (ASTM, 1994c).

Uniformity ratio

Uniformity ratio is determined by dividing the 50% span length by the 2.5% span length and expressed as a percentage (ASTM, 1994b). It is a smaller value than the uniformity index by a factor close to 1.8. Larger values indicate a more uniform fiber length distribution. Lower values tend to be associated with manufacturing waste, more difficult processing, and lower the product quality.

Short fiber content

The percentage of fibers, by number or weight, shorter than 12.7 mm (½ inch long) is associated with increased waste during combing and other processing steps. In addition, short fibers produce weaker, hairier, less uniform yarns with higher CV% and poor surface integrity, resulting in poorer quality fabric (Backe, 1986; El Mogahzy, 1999; Hequet and Ethridge, 2000). Various attempts have been made to use measurements obtained from the fibrograph for estimating SFC. However, the American Society of Testing and Materials (ASTM) only acknowledges one method for measuring short fiber content in cotton, the Suter Webb Array (ASTM, 1994a). AFIS is also capable of determining SFC but currently is not accepted as ASTM standard.

Traditionally, the SFCw has been used for most spinning quality experiments concerning SFC. However, the number basis, short fiber content by number (SFCn), also has been used for comparisons because it is believed that the number of short fibers is more important than their small weight fraction implies. The importance of SFC in determining fiber-processing success, yarn properties, and fabric performance has led the post-harvest sector of the U.S. cotton industry to assign top priority to minimizing SFC, whatever the cause (Rogers, 1997). Behery (1993) reported that documentation of post-ginning SFC at the bale level would reduce the cost of textile processing and increase the value of raw fiber.

HVI and UHM

Since 1980, USDA classing offices have relied almost entirely on HVI for measuring fiber length and other fiber properties (Moore, 1996). The HVI system provides measures of cotton fiber length on the basis of the familiar Fibrograph method (Hertel, 1940) in which a span length of a cotton beard is tested (El Mogahzy and Chewning, 2001). The standard device currently used by both fibrographs and HVIs is similar to that originally developed by Hertel. This device uses a fiber comb with parallel needles attached with a spacing of 13 needles/inch (twice the spacing of Hertel hand comb). The sample is placed in the fibrosampler so as to protrude through holes on a sampling plate, and the fibers are picked up by the needles on the comb as the comb is moved over the sample. The fibers are then carded as they pass over a section of card wire; this produces a fiber beard of parallel fibers and is similar to Hertel's hand comb process.

The outcome is that the fibers are placed on the comb in such a way that they are caught at random points along their length to form a beard. The fibers in the test beard are assumed to be uniform in cross-section, but this is a false assumption because the cross section of each individual fiber in the beard varies significantly from tip to tip. The fibers are combed and brushed to form a fiber beard. The density along the beard is then photoelectrically scanned from the base to the tip (ASTM, 1994c). The light attenuation is assumed to be related to the fiber mass between the lenses. If we assume that fibers have uniform linear density or fineness, the measured amount is proportional to the number of fibers. The sample density is then plotted against distance from the comb. The HVI fiber-length data are converted into the percentage of the total number of fiber present at each length value and into other length parameters, such as mean length, UHM length, and length uniformity (Behery, 1993; Steadman, 1997). When tested on HVI, the UHM length is the average length by number of the longest (50%) of the fibers when they are divided on a weight basis (ASTM, 1994c). The UHM length was chosen because it approximates the classer staple length. This measure is slightly lower than the 2.5% span length (El Mogahzy and Chewning, 2001).

The HVI and fibrograph measurements are not “length biased” samples according to Chu and Riley (1997), contradicting ASTM (1994b) and Zeidman et al. (1991) which stated fibers are extracted from the population in direct proportion to their length. Chu and Riley (1997) showed that the length of the fibers sampled with the fibrosampler were almost identical to the original fiber sample. They assumed that the fibrosamplers used to prepare fiber beards have an equal probability of selecting any length fiber rather than being proportional to the fiber length, because the fibers are sampled in clumps rather than individually.

Advanced fiber information system

The accurate measurement of fiber length is important in evaluating cotton quality and in optimizing fiber processing. The USTER® AFIS is a sophisticated and versatile laboratory instrument that was designed for single fiber measurements and results from this instrument are distinguishable from other methods. The applications are useful not only in the context of commercial textile manufacturing operations, but they are proving to be valuable to the process of selection superior cotton cultivars (Ethridge and Hequet, 1999). The USTER® AFIS utilizes small samples (usually 3,000 or 5,000 fibers per rep), which is advantageous for testing cotton breeders' fiber samples, and can be used extensively in research at the plant, boll, lock, or even seed level. An optimized minimum AFIS sample size has been set empirically at ≥ 500 fibers or ≥ 100 mg per analysis (Wartelle et al., 1995).

A simple schematic diagram of an AFIS instrument was given by Ghorashi et al. (1994), Steadman (1997), and Bragg and Shofner (1993), which illustrated the basic components of the measurement system. USTER® AFIS is based on aeromechanical fiber processing, similar to opening and carding, followed by electro-optical sensing. The fibers are separated from microdust and trash and individualized using specially designed pinned, perforated cylinders and stationary carding flats. Airflow into the perforations of the cylinder allows efficient dust and trash removal by the combination of combing via the stationary carding flat and the airflow drawn through the cylinder (Hinohosa and Thibodeaux, 1994).

Electro-optical sensors installed in the fiber channel use advanced signal processing technology to identify and characterize several thousand individual cotton fibers. The Electro-optical sensor consists of three basic elements: tapered entrance and exit nozzles, beam-forming and collecting optics, and the detection circuitry. Individual fibers are transported pneumatically from the fiber individualizer by a high-velocity air stream. As the material enters the tapered nozzle, it is accelerated and aligned by the airflow. As the fibers leave the entrance nozzle, they penetrate a collimated beam of light. As the fibers pass through, they scatter light in relation to their size and cross sectional shape. This light is detected and generates voltages characteristic of their length and cross sectional dimension. The light blocked by an individual fiber is directly proportional to its mean optical diameter and length or time-of-flight in the sampling volume (Bragg and Shofner, 1993). The light-attenuation signal is analyzed in AFIS-length and maturity module. The modular concept of the USTER® AFIS system provides comprehensive information on the frequency distribution of pertinent dimensional parameters. The abundance of information provided by the USTER® AFIS is a result of determining the complete frequency distribution of each measurement. Such distributions include information on the mean values, standard deviations, the number of observations, and several other parameters that can be calculated using these few basic characteristics of a frequency distribution (Behery, 1993).

There are a number of error sources in AFIS measurements. Fiber damage may occur during the separation of fibers by the individualizer on the AFIS prior to actual measurement. Bragg and Shofner (1993) indicated that the length distribution of fibers passing through the fiber individualizer is much the same as the length distribution of cotton passing through the cotton card. Cui et al. (2004) stated that there are fiber breakages in the opening unit between 1 to 4%. Bragg and Shofner (1993) concluded that the UHM is reduced by 1-2 mm and that the SFC readings increase approximately 7% in comparison with slower, hand-sorting methods. Furthermore, only a portion of the fibers may be counted since both entangled and hooked fibers are excluded. Cui et al. (2004) reported only 9 to 33% of fibers were counted in the measurement unit, depending on the sample type (sliver or lint) and fiber properties (short or long) when using the recommended sliver density. The percentage was significantly increased with a decrease in sliver density. Average fiber length in their experiment was reduced by 0.25 to 1.02 mm after AFIS measurement. This reduction in the average fiber length is due to fiber breakage. Therefore, there could be a bias for longer or shorter fiber lengths.

Cui et al. (2004) measured AFIS accuracy using acrylic filaments cut to lengths of 6.35, 12.7, 19.1, 25.4, and 31.8 mm long. Samples of different length were mixed (20% by number of each) and the percentage of each fiber length group was measured by AFIS. They reported that only a portion of the fibers were counted by AFIS, however, the data represented the sample population well with a slight bias towards the mean (19.1) and a negative bias towards longer fibers. They observed also that lower sample density increased the percentage of fibers counted, while higher density reduced testing time. The length measurement was not affected significantly based on the densities and samples used.

Hequet and Ethridge (2000) stated that AFIS tended to measure fibers longer than 50.8 mm whereas neither the Peyer nor the Array showed any fibers in this category. The authors concluded that fibers measured longer than 50.8 mm from AFIS were not anomalous since they exhibited the highest correlation with yarn count strength product but that their length was overestimated. The AFIS tends to underestimate the length of the shorter fibers and to overestimate the length of the longest fibers because the speed difference between short and long fibers (more air - fiber friction with long fibers) is not totally compensated by the speed sensor. Bragg and Shofner (1993) compared length measurements from AFIS to the Sutter-Webb method, and found that AFIS measurement of cotton fiber length is biased toward the shorter fiber lengths. They explained this bias as a breakage of fibers in the fiber individualizer of the instrument. The UHM length was reduced by 1 to 2 mm, and SFC increased almost 7% compared with the traditional hand-sorting method. Comparing AFIS and Sutter-Web Array measurements from 14 standard cottons, Hequet and Ethridge (2000) determined that the instruments correlate well for the shortest fiber percentages, although the levels were different. The length distributions obtained were very similar for short staple cottons, however, as the staple length increased the Array reflected a higher percentage of the longest fibers, and the discrepancy between the instruments substantially increased as staple length increased.

The sampling process of AFIS is a primary strength over other systems. The fiber length reported from the AFIS instrument is based on the number-frequency methodology since it involves measurement of individual fibers. First the length distribution by number is determined. Then the apparatus computes the length distribution by weight assuming that all the fibers within the tested specimen have the same fineness. Therefore, the distribution by weight is actually a length-biased distribution. The frequencies obtained from the original measurement (by number) are weighted (multiplied) by the fiber length they represent. In addition, construction of an array is not necessary for AFIS numerical sampling. Any inaccuracy in the fibers' alignment should be reflected in the length distribution, with short fibers being affected more than longer fibers (Bragg and Shofner, 1993; Krifa, 2004).

Length distribution

The length characteristics of a cotton sample can only be fully described by its fiber length distribution. Two cotton length distributions may differ in either shape and range, or both as is more often true. Two distributions having the same range and shape are identical; thus, all their corresponding parameters are the same. If the range is the same but the shape is different, some of the parameters of both location and dispersion (mean value, variance, skewness, uniformity index, etc.) may be different also. Two distributions with different ranges cannot have the same shape. At best, they can be "similar" if they comply with the following definition: if each fiber in a population has a corresponding fiber *k* times longer in another population, the distributions of the two populations are called similar. To make comparisons, a number of different numerical parameters are derived from the length distribution. About ten parameters have practical applications and specific uses**.** If a sample of fibers is sorted into common length groups onto a velvet board, the length distribution can be observed.

Genetic diversity

Many crops have a narrow genetic base relative to their undomesticated progenitors. In cotton, successful cultivars are developed most frequently from closely-related parents that further narrows the genetic base (Meredith et al., 1997). Thus, limited progress in cultivar improvement in recent years has led some to advocate that cotton breeders expand the range of germplasm used in crosses (Meredith, 1991). The genetic base of cotton may be decreasing due to the increasingly proprietary nature of germplasm, the large number of reselections in the pedigrees of modern cotton cultivars, the tendency to frequently use the same parents for the creation of new cultivars, and the planting of only a small portion of the available cultivars (Bowman et al., 1996; Van Esbroeck et al., 1998). This narrowed genetic base in cotton germplasm results in a limited supply of alleles for traits of interest, and until the genetic diversity is expanded by the introgression of favorable and novel alleles from other populations, the trend to greater uniformity will continue. May et al. (1995) assessed the diversity among 126 upland cotton cultivars released between 1980 and 1990 by use of coefficient of parentage (CP). They reported that the mean CP among the 126 cultivars was 0.07, implying a genetically diverse group. However, the cluster analysis revealed 12 distinct gene pools, in which the analysis recommended that breeders consider the pedigree of parents to use in crosses and plan crosses that will provide genetic diversity. Bowman et al. (1996) determined the average CP for 260 upland cotton cultivars released between 1970 and 1990 to be 0.07, suggesting substantial remaining diversity and ample opportunities for cultivar improvement. However, the validity of the CP estimates were not verified until Van Esbroeck et al. (1999), who stated if relationships among ancestors are unknown, CP may not accurately estimate the true level of genetic diversity within a crop species. The agronomic and fiber data from this study supported isozyme and DNA data showing a narrow genetic base in cotton.

Tools for crop improvement

Many genetic phenomena, such as linkage, influence expression of traits. Genes controlling the expression of many traits lie close together on a chromosome linkage and therefore have a higher than random probability of being transmitted together to progeny. Multiple alleles for each gene can exist in a population. Epistasis can be present in which the expression of one gene is affected by the genotype of another gene at a separate locus. Pleiotropy is a phenomenon in which a single gene affects multiple traits. Finally, heterosis can exist in which progeny between unrelated parents perform better than would be expected based on the average performance of the parents.

Crop improvement requires that genetic variation exist to select higher performing individuals from a population. Within upland cotton, genetic variability for fiber quality exists among cultivars (USDA, 1995), among germplasm lines (Percival, 1987), and in primitive germplasm converted to non-photoperiodic flowering habit (McCarty and Jenkins, 1993). Quantitative traits, such as fiber quality, are controlled by multiple genes, such that as the gene number for a trait increases, the probability of finding an individual with beneficial alleles at all of the genetic loci decreases. Sustained genetic advance requires that genetically diverse parents be mated to form segregating populations for selection followed by phenotypic screening.

Heritability

The likelihood of improvement is determined by the amount of and type of genetic control of the trait, which is referred to as heritability. Broad-sense heritability is the ratio of the genetic variance to phenotypic variation, while narrow-sense heritability is the ratio of additive genetic variance to total phenotypic variation (Fehr, 1991). Highly heritable traits are easier to improve than those that are lowly heritable. Low heritability can be caused by lack of genetic variation or high environmental variation or combination of both.

When determining heritability estimates for fiber length measurements from a diverse collection of cotton populations and various selection units, May (1999) stated that selection for various length parameters should be effective. Narrow-sense heritability estimates from eight experiments for 2.5% span length ranged from 0.10 to 1.00, averaging 0.52. Broad-sense heritability estimates from four experiments for 2.5% span length ranged from 0.54 to 0.91, averaging 0.77. Calculating heritability and selection response from two populations derived from mating excellent fiber quality germplasm with lesser quality germplasm, May and Jividen (1999) reported similar heritability estimates for 2.5% span length and UHM length, and of a magnitude to expect progress from selection. Herring et al. (2004) reported a narrow-sense heritability range of 0.29 to 0.46 for UHM fiber length from a chemically mutated population of Paymaster HS 200. May and Jividen (1999) reported a low heritability (0.19) for SFCn from parent-offspring regression in two populations.

Environment

The environment in which a crop is grown will affect trait performance. Attempts should be made to minimize environmental effects on selections through use of replications, locations, years, and sampling unit, thus increasing probability of selecting superior genotypes. A good genotype evaluated in poor conditions often can be overlooked. Many quantitative traits display interactions between genetic and environmental effects known as genotype by environment interaction (GxE). This phenomenon can pose difficulties in selecting superior genotypes that are adapted to wide geographic areas, a goal of most crop improvement programs.

However, most studies involving breeder fiber samples have considered the GxE interaction variance as small relative to genetic variation and thus do not consider GxE to be a serious bias in estimating heritability or response to selection (Meredith et al., 1996; May and Taylor, 1998; May and Jividen, 1999; Meredith, 2003). Analyzing 14 experiments for the genetic and environmental influences on various measures of fiber length across the cotton belt, May (1999) reported a strong genetic basis for fiber length. Regardless of the instrument, classers staple, Suter-Webb array, or fibrograph (UHM or span length) used to measure fiber length the magnitude of genetic variance was greater than that of non-genetic influences in cases where genetic differences existed. Interactions of genotypes with locations, years, or higher-order were minor in magnitude when compared with genetic variation. May (1999) concluded that extensive environmental replication is not necessary to evaluate and select breeding material on the basis of fiber length parameters. May (1999) also noted that in some studies the experimental error was of similar or greater magnitude as the genotypic variance, however, these non-genetic influences should not preclude the identification of genotypes with desired fiber length. Meredith (2003) summarized breeding progress for fiber traits over 36 years of the USDA Regional High Quality Tests and concluded that the genetic variance component was comprised of 30.6% for UHM length and 29.3% for 2.5% span length. The location variance component contributed approximately 50% of the total variance component and the genetics by location interaction made up the remaining 19%.

Diallel analysis

The diallel crossing scheme, i.e., the mating of parents in all possible combinations, is a method that can be used to determine genetic variance components and heritability if the parents were selected randomly, to calculate repeatability, and to identify lines to serve as parents in a breeding program for trait improvement (Fehr, 1991; Kearsey and Pooni, 1996). Griffing (1956) described that the basic methods of the diallel analysis could be conducted with or without reciprocal crosses and with or without parental lines. Method 1 involves parents and all F_1 combinations including reciprocals. Method 2 is composed of the parents and all F_1 combinations without reciprocals. Method 3 consists of all F_1 combinations including reciprocal crosses but without parents, and Method 4 comprises only F_1 combinations without reciprocals or parents. Each method provides estimates of different genetic parameters and can be evaluated as Model 1 or 2 (fix or random). Fixed effects are required when the population is small (i.e., fewer than 10 parental lines) and/or the parental lines were selected prior to diallel mating. Such a model is limiting in two ways. First, the parameters that can be estimated with a fixed effects model are reduced. Variance due to genetic sources cannot be estimated. No conclusion regarding genetic control of the trait can be drawn. Second, the scope of estimates is reduced to the genotypes in the study, the parental lines, and their F_1 progeny. No inferences can be made regarding the population as a whole.

Baker (1978) stated that a diallel analysis can provide useful information regarding the combining ability of a quantitative trait, but from a genetic perspective two key assumptions must be made for interpretations to be valid. First, the assumption concerning the independent distribution of genes in parents, presence or absence of an allele at a particular locus is statistically independent of the presence or absence of an allele at any other locus. This is critical for proper interpretation and seems to be the least acceptable in actual practice. Second, epistasis must not affect the trait, which may frequently be incorrect. Difficulty in accepting these assumptions can bias genetic parameter estimates. Baker (1978) stated that additive and dominance genetic variance and the number of genes for a trait could not be estimated from any diallel.

Although genetic control of quantitative traits cannot be determined from a fixed diallel analysis, many researchers use the relative magnitude of GCA and SCA effects to obtain an approximation. The GCA effects reflect performance of parental lines in combination with all other lines, so the parents with the highest GCA effects should have the greatest impact on trait improvement. SCA effects identify the best hybrid combinations, but they also identify complementary alleles for trait performance (Kearsey and Pooni, 1996). GCA is associated with additive genetic effects whereas SCA reflects dominant genetic effects.

Cheatham et al. (2003) evaluated the GCA among nine diverse cotton lines and reported that Fibermax 832, a parental line also being evaluated in the current experiment, had the numerically highest positive predicted GCA effect for 50% span length at 0.12, although not different from zero. For 2.5% span length, Fibermax 832 had the highest predicted effect of 0.58, which was significantly different from zero. The homozygous SCA for Fibermax 832 in the Cheatham et al. (2003) paper stated its predicted effects for 50 and 2.5% span length, 0.04 and 0.18 respectively, were significantly different from zero but less than the predicted effect for Suregrow 501. In their discussion, they stated that Fibermax 832 combined well with the selected U.S. cultivars and would be good parental germplasm for improving fiber quality in cotton breeding programs in the United States. Gutierrez et al. (2002), in a study with the same lines as Cheatham et al. (2003) plus two additional Australian cultivars, showed that the eleven cultivars had a low genetic distance based upon molecular markers (0.06 to 0.34). They suggested that genetic distance, based upon his set of 90 simple sequence repeat markers, was not a good indication of what to expect from crosses among these lines.

Genetic control/gene action

Generation means analysis is important tool in determining the gene action controlling the expression of traits in order to develop appropriate breeding procedures.

Several models have been developed for analysis of generation means (Anderson and Kempthorne, 1954; Hayman, 1958; Hayman, 1960; Gamble, 1962; Gardner and Eberhart, 1966a; Mather and Jinks, 1982). Genetic improvement of a quantitative trait is based on effective selection among individuals that differ in genotypic value. The amount and type of genetic control influences improvement because only certain types of genetic control can be reliably transmitted to progeny and the next generation. An understanding of the various types of genetic control that determine the genotypic value of individuals in a population would be helpful in understanding the concept of genetic variance. Genotypic value can be considered on the basis of a single locus (Falconer and Mackay, 1996) or the value of all loci considered together (Fehr, 1991). In the formula for all loci considered together ($G = A + D + I$), G is the genotypic value, A is the additive effect of genes, D is the dominance effect of genes, and I is epistatic effect of the genes or the portion attributable to the interaction of alleles among loci. Of these, epistatic effects for two loci can be further described as additive x additive, additive x dominance, and dominance x dominance. Epistatic interactions are dependent on the average effects of genes and dominance deviations at individual loci. As a result, they are dependent on the degree of dominance and the gene frequency in the population (Fehr, 1991).

Numerous studies in which the genetic variation for cotton fiber length, measured as 50% span length, 2.5% span length or UHM, concluded that additive variance within upland cotton genotypes tended to be more prominent than non-additive variance (Miller and Marani, 1963; Ramey and Miller, 1966; Lee et al., 1967; Al-Rawi and Kohel, 1969; Al-Rawi and Kohel, 1970; Meredith and Bridge, 1972; Green and Culp, 1990; Tang et al., 1993). Quisenberry (1975) stated that genetic control for fiber length contained additive and non-additive genetic variance, but that the greater portion was additive. He reported that 41% of the phenotypic variance from Acala cultivars was additive genetic variance compared to only 13% for Texas High Plains cultivars. However, a few older experiments and two more recent studies have found non-additive variance to be more important (Verhalen and Murray, 1969; Baker and Verhalen, 1973; May and Green, 1994; Cheatham et al., 2003). May and Green (1994), using a Design II mating scheme and variances from the F_2, F_3, and F_4, found dominance genetic variance to be greater than additive genetic variance for 50 and 2.5% span length in the Pee Dee cotton population. Cheatham et al. (2003) using an extended additive-dominance model, also stated genetic variance for 50 and 2.5% span lengths was primarily dominance. Of the sources cited above, none detected epistasis for fiber length except May and Green (1994), which reported additive x additive epistatic variance for 2.5% span length.

Heterosis

Heterosis, another method by which gene action can be determined, is measured usually as the deviation of the F_1 from the high parent of mid-parent. A significant heterosis would indicate the existence of non-additive gene effects caused either by dominance, or epistasis, or both. Lee et al. (1967) reported heterosis for fiber length and Al-Rawi and Kohel (1969) reported heterosis for 50 and 2.5% span length. Summarizing nine experiments, May (1999) reported that heterosis for fiber length can occur, however, the deviation is small and apparently of no biological significance.

The disparity of genetic variation for fiber length from experiment to experiment must be due to different parental material used and different environments, since a large environment variance component would simply drive heritability toward zero. The presence of additive effects suggests that selection for fiber length improvement can be obtained successfully from pedigree selection schemes and without the use of hybrid cultivars (Culp, 1982).

Textile industry

Yarn manufacturing is the first step in the construction of cotton textile products, and it continues to undergo technological advance to produce more yarn at less unit cost to remain profitable (Deussen, 1993; Faerber, 1995). With the technological evolution of yarn manufacturing from solely ring-based spinning to predominately rotor in the U.S. (Smith and Zhu, 1999), and potentially in the near future to air-jet spinning (El-Mogahzy, 1998), needs for fiber profiles have been revised. Breeders need to understand fiber property needs of different spinning systems. Each yarn manufacturing method has distinct fiber profile needs in terms of the basic fiber properties to produce strong yarn for subsequent textile construction. These profiles should guide breeding objectives that must evolve in tandem with processing methods.

Technologically advanced equipment requires fibers to spin into consistent, high-strength yarn at speeds unheard of just 20 years ago. Newer textile mills can spin nearly 272 kilograms of yarn/spinning position each year, when just a few years ago each spindle only transformed about 91 kilograms of cotton (National Cotton Council, 2004). Dramatic changes have been made in the speed of processing over the last 40 years.

Spindle speeds have risen from 12,000 rpm in the early 1970s to 25,000 rpm in the 1990s through the development of automatic doffing and link-winding (Bragg, 1991).

Ring spinning

Ring spinning is a continuous system in which the fiber strand fed to the spinning system follows a continuous path throughout the entire spinning process from the feeding point to the yarn package. Ring spinning is characterized by two main features, the continuity of fiber flow from roving to yarn and a tension-controlled spinning process (El Mogahzy and Chewning, 2001). Because of these two features, ring spinning produces yarn quality that is unsurpassed by other spinning systems. It is the only system that can produce yarns at the lowest twist possible without sacrificing yarn strength. This method yields optimum comfort and is therefore the preferred system in the knit apparel market. Another major advantage for ring spinning, its primary factor for survival, is its flexibility and capability of producing virtually any yarn count or any yarn style within the spun yarn range. However, ring spinning is also the slowest spinning system primarily due to the use of the ring/traveler system for twisting and winding. Ring spinning mandates respectable fiber length and length uniformity for more twists, followed by fiber strength and fineness (Deussen, 1993). The increase in twists produces yarn and fabric strong enough to spin at finer yarn counts for higher quality cotton products and improves the overall spinning performance.

Compact spinning

Compact, also called condensed spinning, is a continuous system and is a new concept of yarn forming that represents a fundamental modification of the conventional ring-spinning system. This method better controls the dimensions and minimizes the change in width of the fiber strand entering the delivery point of the drafting zone through the use of aerodynamic condensation (Artzt, 2000). This results in a near elimination of the spinning triangle, the area between the clamping line of the delivery rollers of the drafting system and the point of twist insertion by the ring spindle. From the quality perspective, when compared to the conventional ring-spun yarn, compact spinning results in a significant reduction in yarn hairiness, increases in yarn strength and elongation, considerable improvement in abrasion resistance, better yarn evenness, lower yarn imperfections, higher draft ratios, and better yarn performance in further processing steps (Artzt, 2000; El Mogahzy and Chewning, 2001; Krifa et al., 2002).

Compact spinning is currently replacing conventional ring spinning for all yarn styles where ring spinning is utilized. Compact spinning can tolerate more short fibers, thus reducing the amount of waste, and produce stronger yarns at lower twist levels, which improves yarn performance during weaving and knitting and increasing the range textile products produced. Aside from a few added input costs, the use of an aerodynamic system, additional rollers, and frequent cleaning, compact spinning offers substantial economical advantages in terms of yarn quality, processing performance, and diversity of end products created.

Rotor spinning

Rotor spinning, commonly called open-end, is a non-continuous spinning system in which the fiber strand undergoes a complete or partial separation before it is finally reconsolidated into a yarn. (El Mogahzy and Chewning, 2001). Rotor spinning uses a direct spinning system in which a drawn sliver is directly spun into a yarn, eliminating the roving process and breaking the linkage between twisting and winding to overcome the low production rates in ring and compact spinning systems. Rotor spinning consists of a drafting mechanism, a consolidation mechanism, and a winding mechanism.

Rotor spinning has become the dominant U.S. yarn manufacturing process, replacing ring spinning, because of its economic superiority. Its advantages include more yarn per unit of time combined with less labor and fewer prespinning fiber preparation operations. Since the introduction of rotor spinning in the late 1960s, rotor speeds have increased from 25,000 rpm in 1967 to 130,000 rpm in the 1990s (Faerber, 1995). The anticipation of higher processing speeds in rotor spinning will have to be accompanied with improved fiber properties to counterbalance the increase in tensile and yarn strain. The quality of fibers used is critical, and the processing equipment is very sensitive to the cleanliness of cotton. Trash content is the primary cause of spinning endsdown. For rotor spinning, good fiber strength is the primary quality factor, closely followed by fiber fineness (Deussen, 1993). In regard to fiber length, rotor spinning has altered its importance. Rotor spinning can handle a short UHM yet produce a strong coarse count. Longer fibers are likely to be more disturbed by turbulent airflow than shorter fibers, resulting in lower yarn strength, and more unevenness compared to ring spun yarn. However, a high percentage of short fibers will result in low yarn strength and excessive endsdown (El Mogahzy and Chewning, 2001).

Air-jet spinning

Air-jet spinning technology, specifically the Murata Vortex Spinning system, is the latest development in spinning technology and may become the dominant form of yarn manufacturing because of its productivity and ability to spin a broad range of yarn counts. This system uses the principle of air vortex to produce a yarn similar in structure to that of the ring-spun yarn. The two main actions in air-jet spinning are false twisting and end-opening. False twisting aims at gathering and packing the fibers in the yarn structure, while end-opening action aims at separating some of the fibers from the bundle to form a wrapper. El Mogahzy and Chewning (2001) stated it is necessary to balance the two actions by optimizing various spinning parameters. Compared with older air-jet systems, the Murata Vortex Spinning system offers improvements in the number and length of wrapper fibers.

This relatively new spinning method can spin a fine count yarn of similar quality to that of the same size of ring spun yarn (El Mogahzy, 1998). In addition, it offers impressive manufacturing productivity gains and may push spinning speeds past 300 m min^{-1} as compared with 100 m min^{-1} for rotor and 20 m min^{-1} with ring spinning for 30 count yarn (El Mogahzy and Chewning, 2001). These elevated production speeds must be maintained to justify the cost of the high-tech processing equipment. Similar to rotor spinning, the quality of the fibers used is vital, and this system in particular is very sensitive to dust and fine trash. Strength of air-jet yarns requires effective fiber wrapping because of its ‘false twist’ yarn structure (El Mogahzy, 1998), thus air-jet spinning requires reputable fiber length and length uniformity so that the fascinating fibers can lock the parallel fiber bundle together. Fiber fineness, fiber strength, and fiber friction then follow these properties in importance (Deussen, 1993). The Murata Vortex Spinning system also removes a significant percentage of short fibers, which gives the yarn a combed-like surface structure (El Mogahzy and Chewning, 2001).

Yarn properties cannot be directly selected through breeding because their measurement is precluded in early generation breeding material by available lint sample size, genetic population size, and cost. Breeders must therefore conduct indirect selection for yarn properties by selection of one or more fiber properties that influence yarn manufacturing (Meredith et al., 1991; May and Taylor, 1998). Therefore, the challenge to the breeder is improving selection effects on yarn strength, the most important yarn property influencing textile performance.

CHAPTER III

MATERIALS AND METHODS

Experimental material

Genotypes selected on the basis of their HVI UHM length of fibers and programmatic origins were TAM 94L-25, TTU 202, Acala 1517-99, Fibermax 832, and Tamcot CAMD-E (Table 1).

Generation development

Potential parental plants were screened for UHM length prior to the initiation of the crossing scheme. Seed cotton was harvested from 10 individual plants of each genotype in the fall of 1999. These plants were then stumped from the field, potted, and placed in a greenhouse. Fiber samples were ginned and sent to the International Textile Center for HVI analysis. To ensure long fiber phenotypes, TAM 94L-25, TTU 202, Fibermax 832, and Acala 1517-99 plants having an UHM fiber length 1.5 mm shorter than that of the parent plant with the longest UHM in each genotype were discarded. To ensure that all Tamcot CAMD-E plants were short fiber phenotypes, plants having an UHM fiber length greater than 1.5 mm than the plant with the shortest UHM were discarded. Parent plants thus selected were hybridized in a half-diallel during the winter of 2000. The ten crosses made were: near-long x near-long staple (Fibermax 832 x TAM 94L-25, TAM 94L-25 x TTU 202, Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, TAM 94L-25 x Acala 1517-99, Acala 1517-99 x TTU 202), near-long x short staple (TAM 94L-25 x Tamcot CAMD-E, Fibermax 832 x Tamcot CAMD-E, Acala 1517-99 x Tamcot CAMD-E, and TTU 202 x Tamcot CAMD-E). During the

Table 1. Pedigrees of the genotypes used in the diallel and generation means analysis study.

● TAM 94L-25	An early-fruiting upland cotton line that has superior fiber length and strength even under dryland conditions. It is a cross between two breeding lines, TAM 870^3-37 and TAM $87G^3$-27 (Smith, 1994). TAM 870^3-37 has a complex pedigree that includes Stoneville 1023, 'Lankart 57', Rogers Acala, Lankart 3840, 'Gregg', 'Fox 4', and Acala 5675 (Smith, 2003). TAM $87G^3$-27 resulted from the cross of a breeding line developed by the Texas Agriculture Experiment Station and having AE 179, 'Tideland 501', 'DeltaPine 14', and a New Mexico Acala strain in its pedigree, along with PD 6992 (Culp et al., 1985). Both parents of TAM $87G^3$-27 have G. *barbadense* in their pedigree and may be the source of the near-long staple trait of TAM 94L-25.
● TTU 202	A gemplasm line developed by Texas Tech University and released in 1999. It was created as a part of a mutation breeding program at Texas Tech University and this line has a HVI UHM fiber length 8% greater than that of the original cultivar HS 200 (Auld et al., 2000).
● Acala 1517-99	A high quality cultivar with released by the New Mexico Agricultural Experiment Station in 1999. This cultivar originated from a single-plant selection from experimental B2541. B2541 was derived from the cross B742/E1141. The pedigree of B742 is Acala 9136/250. Acala 9136 has significant introgression from G. *barbadense*. Parents E1141 and 250 are of unknown origin (Cantrell et al., 2000).
● Fibermax 832	An okra-leaf cultivar bred by Commonwealth Scientific and industrial Research Organisation (CSIRO) in Australia and sold by Bayer CropScience. Fibermax cotton varieties currently have a reputation for very good fiber properties, and they continue to provide acceptable yields in the USA and Australia (Constable, 2001).
● Tamcot CAMD-E	A short-season, early-maturing, agronomically determinate cultivar with short fiber length, developed by the Texas Agricultural Experiment Station (Bird, 1979).

2000 growing season, parent plants were moved from the greenhouse to the field to increase the F_1 seed base, and F_1 seeds were planted to generate F_2, BC_1P_1, and BC_1P_2 populations. Selfed progeny of each parent plant was tested for homogeneity of UHM fiber length in a complete block design during the summer of 2000. Fiber evaluation of selfed progeny of each parent plant confirmed homozygosity except for TTU 202.

The parents used herein were specifically chosen and did not represent a random sample of all upland cultivars. Thus, inferences derived from the data apply in the strict sense to the parents, crosses, and generations studied. The degree to which the conclusions may be extended to the species as a whole is unknown.

Experimental design

In 2001 and 2002, parents and their filial generations (family) were grown at the Texas Agricultural Experiment Station Research Farm located near College Station in a randomized complete block design with four replications. For each family and replication, the experimental unit for each non-segregating generations (P_1, P_2, and F_1) consisted of 1 row, each back-cross generation (BC_1P_1 and BC_1P_2) of 2 rows, and the F_2 generation of 4 rows. Each row, 12 m x 1.0 m, was thinned to contain 25 plants spaced 0.50 m apart to minimize inter- and intra- plot competition. Soil type for both years was a Westwood silt loam, a fine-silty, mixed thermic Fluventic Ustochrept, intergraded with Ships clay, a very fine, mixed, thermic Udic Chromustert. Genotypes were planted on 20 April 2001 and 25 April 2002. Cultural practices, including furrow irrigation, were designed to maximize boll retention

For HVI analysis, five plants of each non-segregating generation per family and replication were harvested individually and ginned on a laboratory saw gin. HVI fiber quality parameters with 1 replication for mike and 2 replications for length amd strength were determined at the Texas Tech University International Textile Center.

For AFIS analysis, five bolls/ plant from the middle fruiting zone were harvested. Across families and replications, a total of 10 plants of each parent and F_1 were collected. For each family, a total of 100 plants in the BC_1P_1 and BC_1P_2 populations and 200 F_2 plants were accumulated across replications. Fiber samples were processed on a 10 inch roller gin. AFIS fiber properties were determined at the International Textile Center at Texas Tech University in Lubbock, Texas. The non-segregating generation samples collected for the generation means analysis were also used to conduct a diallel analysis using AFIS data.

Fiber length measurements

A diallel test for each fiber length measurement, i.e., UHM fiber length from HVI, and FLw, FLn, Uqlw, SFCw, and SFCn from AFIS, was conducted and results compared. A generation means analysis test was performed using FLw, FLn, and Uqlw fiber measurements from AFIS.

Fiber length distribution measurements

In addition to providing an abundance of fiber measurements, AFIS also provides comprehensive information on the frequency distribution of FLw, FLn, maturity, and fineness. Efforts were made in this study to find practical and effective applications of the distribution data provided. FLw was the measurement selected to be analyzed by the various distribution statistical parameters of cross entropy, kurtosis, and skewness. Microsoft Excel 2000 macros (Microsoft Corporation, 1999) were used to remove trivial information and organize the FLw distribution data of each sample, which contained 40 length classes.

Cross entropy is a method to measure how good one distribution approximates another distribution, with a value of 0 being a perfect match. Scientific quandary with this procedure surrounds the proposition of what shall serve as the ideal cotton fiber length distribution to be compared with all other samples. No published material exists identifying the optimal length distribution. Questions arise as should the distribution be artificially fabricated, what genotype, how many samples or environments shall be appropriate. In the current study, two genotypes grown in a single environment and one genotype grown in two environments were examined as possible cross entropy check candidates.

To have a valid comparison of distributions from different samples, all FLw distributions were standardized with a mean of 0 and a variance of 1. However, AFIS does not record the length of the 9,000 fiber observations needed to standardize the distribution for each sample. AFIS does provide the percentage of fibers for each of the defined forty length classes. Therefore, a SAS program (SAS, 2004) was created to generate random numbers corresponding to the frequency and range of each length class. The 9,000 fiber observations randomly generated were then uniformly divided into 40 new length classes. The 40 new length classes for each sample were then used to standardize the distribution. Cross entropy values according to Shore and Johnson (1980) were then calculated using a C++ program (Hequet, 2004).

Acala 1517-99 was one check candidate contingent upon its reputation of spinning high quality yarn and spinning tests conducted for the Texas A&M Cotton Improvement Lab. The average percentage of fibers for each of the forty length classes from 10 plant samples in 2002 was used to construct cross entropy A (CEA). In 2002, Acala 1517-99 was grown in large spinning test experimental plots in Weslaco and College Station, TX. Test plots were machined picked and saw ginned. The average percentage of fibers for each of the forty length classes from both locations (environments) were combined to constitute cross entropy C (CEC). Tamcot CAMD-E was another candidate chosen based upon possessing a large percentage of fibers in a narrow length range. The average percentage of fibers for each of the forty length classes from ten plant samples in 2002 was used to construct cross entropy B (CEB).

Two other distribution statistical parameters, kurtosis and skewness, were evaluated. Kurtosis is a measure of whether the distribution data are peaked (narrow) or flat (wide) relative to a normal distribution. Positive kurtosis indicates a relatively peaked distribution whereas a negative kurtosis signifies a relatively flat distribution. A positive FLwKurt would indicate more fibers attained within a narrow length range, potentially indicating higher spinning speeds and yarn quality if all other fiber characteristics are equal. Skewness is a measure of the asymmetry of a distribution. The normal distribution is symmetric, and has a skewness value of zero. Positive skewness indicates a distribution with a long asymmetric right tail. A distribution with a negative skewness has a long asymmetric left tail. A skewness value greater than 1 generally indicates a distribution that differs significantly from a normal distribution. A negative FLwSkew would indicate genotypes with longer fibers. Kurtosis and skewness were calculated according to the formulas of Pearson (1895 and 1905).

A diallel for the FLw distribution measurements of CEA, CEB, CEC, FLwKurt, and FLwSkew was conducted and results of CEA, CEB, and CEC compared. A generation means analysis test was performed and results compared using the FLw distribution measurements of CEA, FLwKurt, and FLwSkew.

AFIS sample preparation and variability

Preparing AFIS specimen involved hand-drawing a 500 mg tuft of fibers into a 25-cm length, which yields a silver of approximately 800 mtex. Only a portion of the fibers in the silver is analyzed by the AFIS. AFIS sample size can be set anywhere between 1 and 10,000 fibers, according to fiber availability and experimental design requirements. In this study, 3,000 fibers per specimen were analyzed. The stipulated number of fibers, however, does not represent the total number of fibers fed into the system. Each specimen requires less than 5 min to produce, and for each sample, three specimens were prepared. Conditioning and testing were carried out under constant standard atmospheric conditions. The standard temperature for textile testing is 20 ± 2 °C and 65 ± 2% relative humidity. Prior to testing, the samples were arranged in single layers and allowed to equilibrate for 48 h under constant standard atmospheric conditions.

To control or reduce the experimental error involving AFIS fiber properties, the same technician and AFIS machine (USTER AFIS) was used to prepare and analyze the fiber. A daily cleaning regimen with standard cottons was done to provide reliable and repeatable measurements. Although the AFIS requires no external adjustments or daily calibration, three referenced samples were run each morning to monitor the consistency and ensure the AFIS machine was properly calibrated. The data showed that the behavior of measurements on the three standard cottons was similar. Therefore, it was concluded that the best way to monitor instrument changes was by taking the average over all three standard cottons. All subsequent results are based on this average.

The exponentially weighted moving average was calculated according to the formula of Montgomery (1985) to measure the long-term accuracy of the AFIS over the time frame the samples were analyzed in 2002 and 2003. The exponentially weighted moving averages for FLw, FLn, Uqlw, SFCw, and SFCn in 2001 are shown in figures 1-5. The exponentially weighted moving averages for FLw, FLn, Uqlw, SFCw, and SFCn in 2002 are shown in figures 6-10. In all cases, even small trends, drifts, or level shifts in the data are clearly revealed. The boundary lines drawn above and below the mean value line in each figure encompass three standard deviations for the exponential moving average series. The interval encompassing three standard deviations is narrow (Table 2). This could be attributed to the slight smoothing applied to the data series (moving average span = 2), but most of it is due to the remarkable stability of the AFIS instrument over a long period of time.

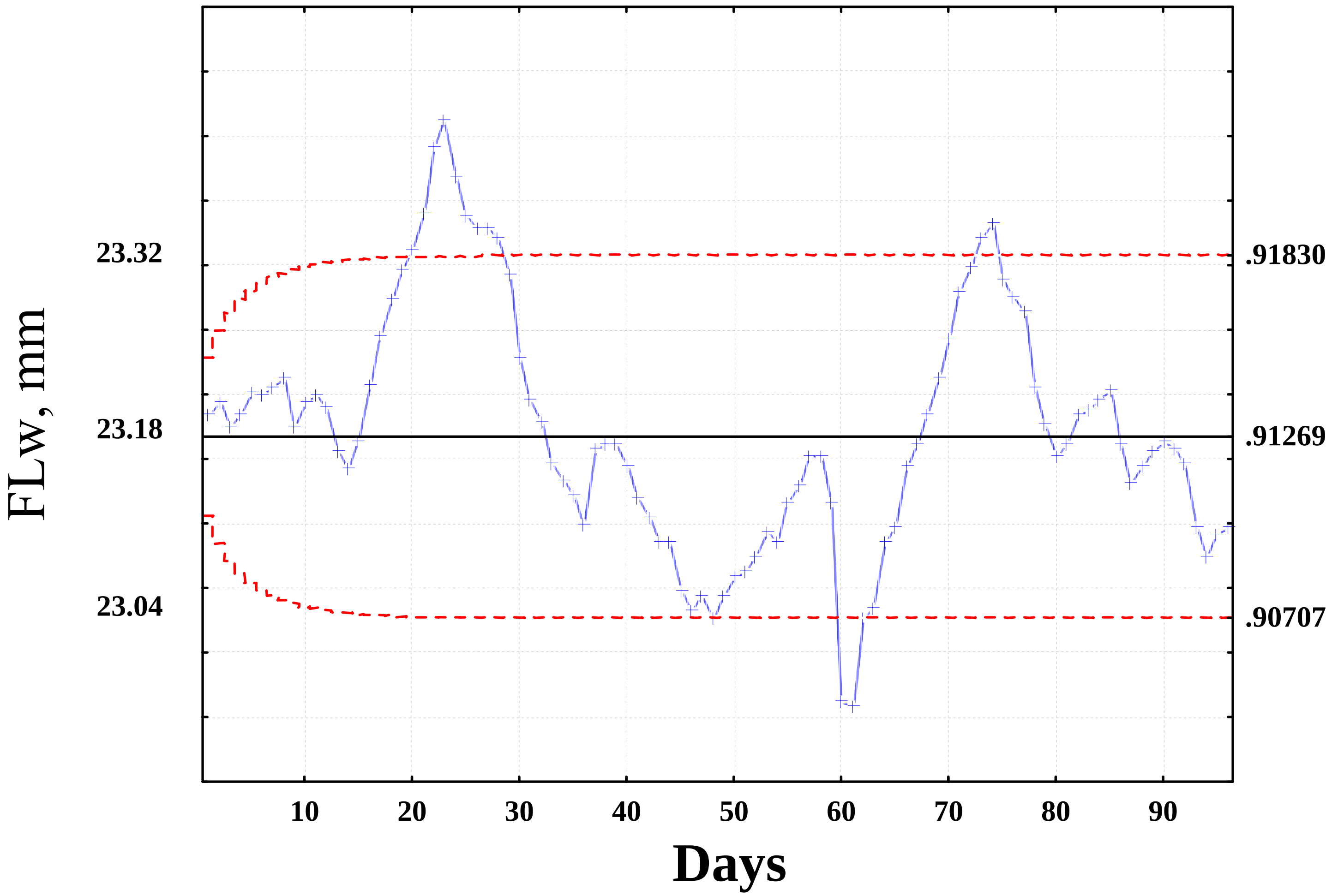

Fig. 1. FLw exponentially weighted moving averages versus time for standards analyzed in 2002.

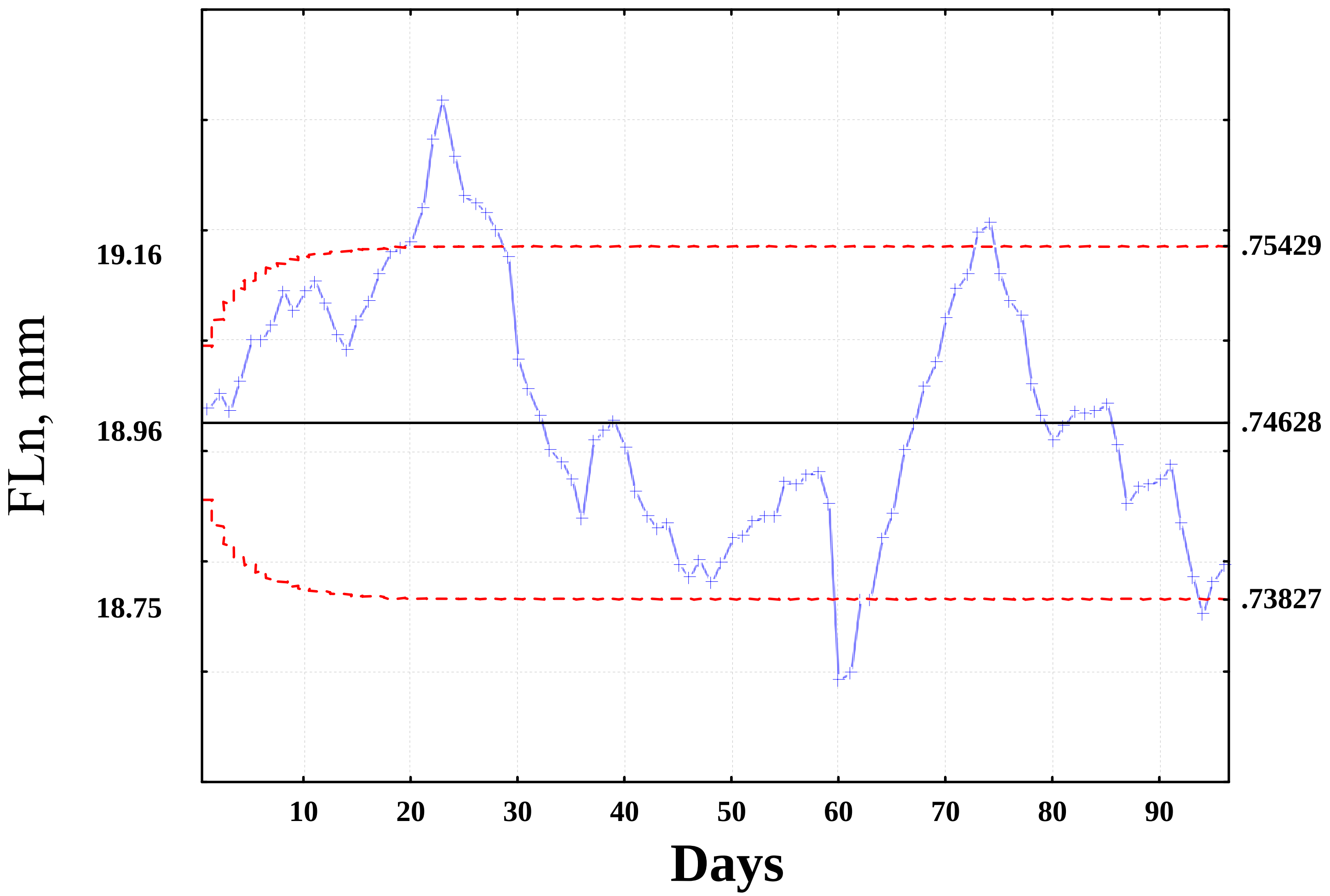

Fig. 2. FLn exponentially weighted moving averages versus time for standards analyzed in 2002.

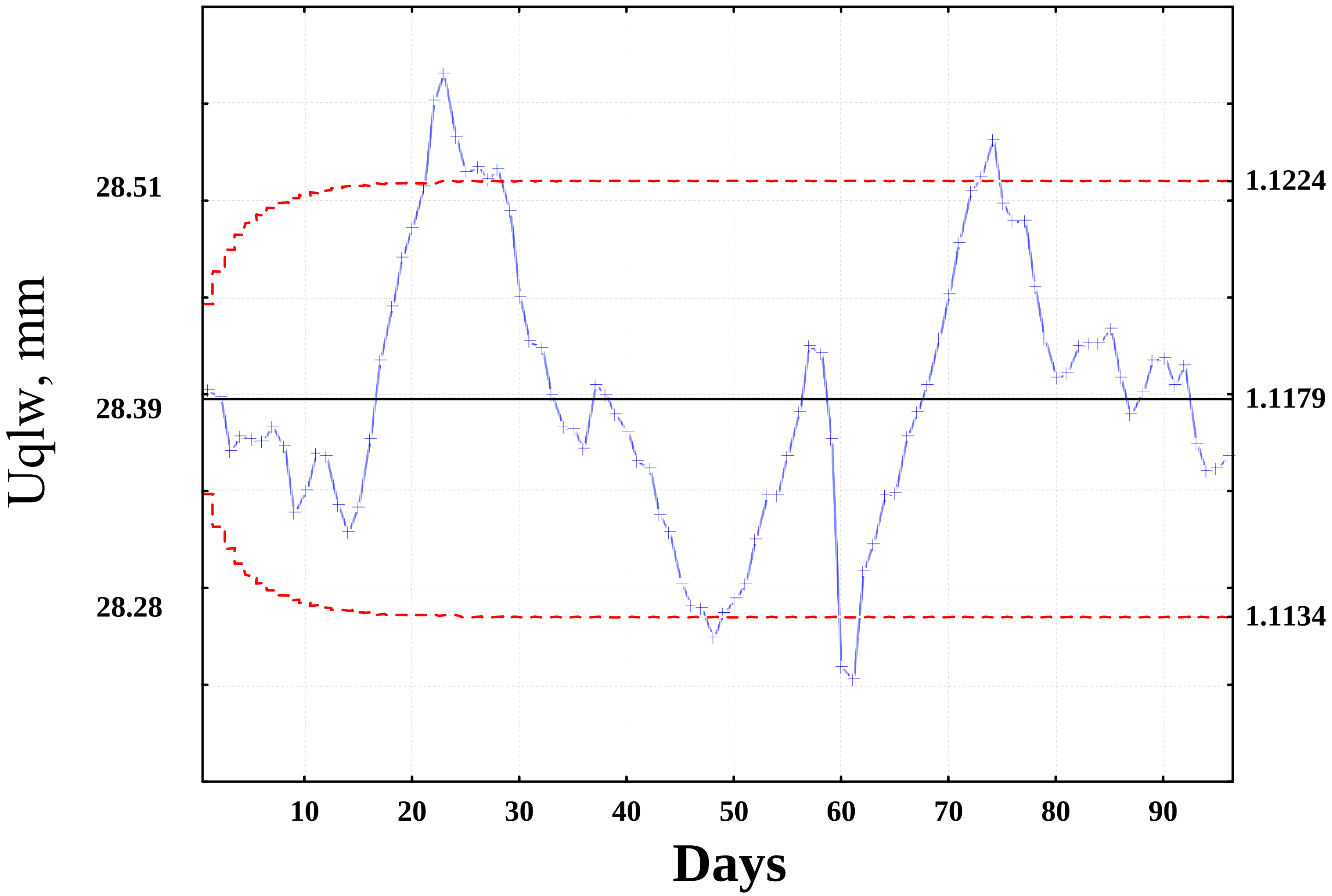

Fig. 3. Uqlw exponentially weighted moving averages versus time for standards analyzed in 2002.

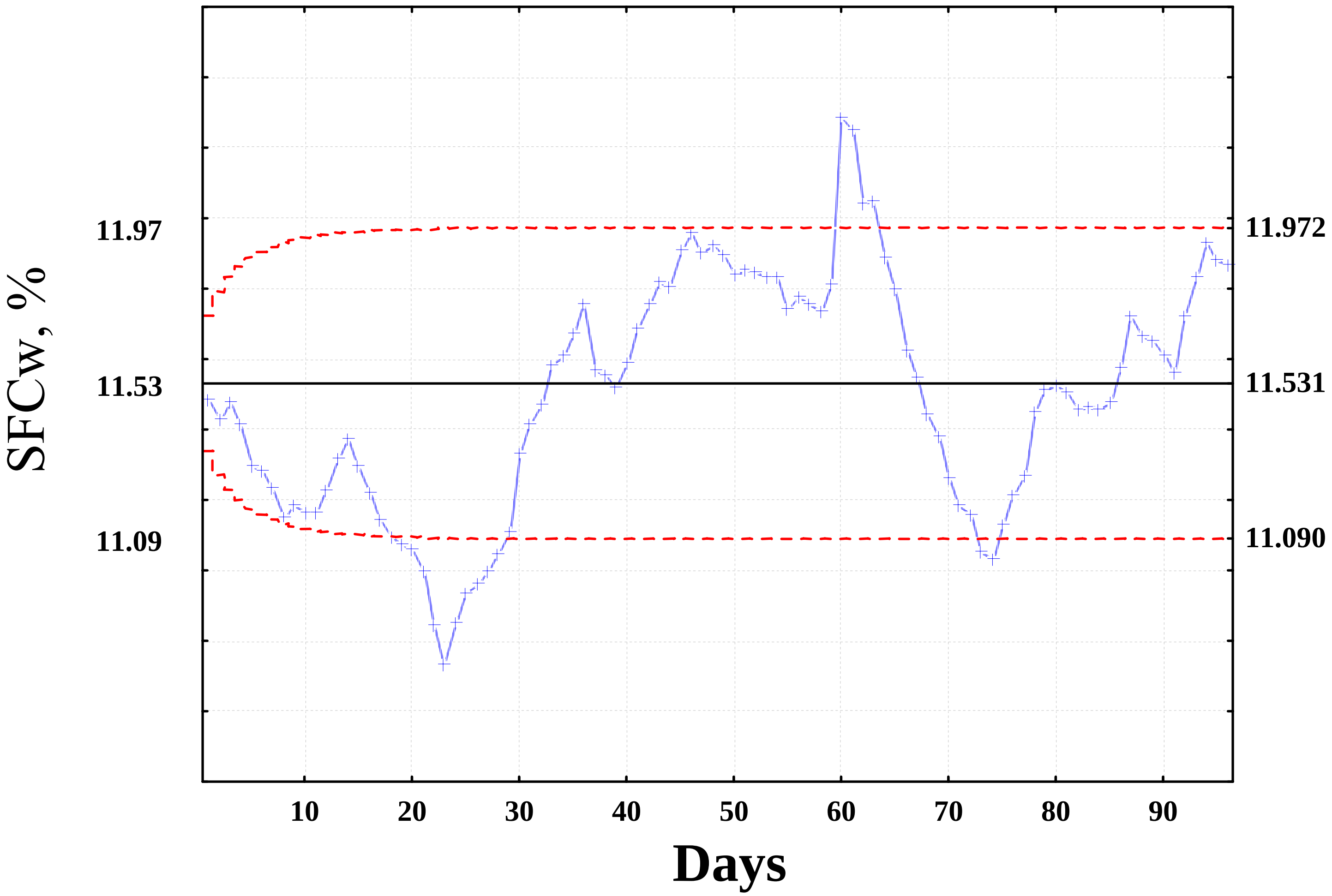

Fig. 4. SFCw exponentially weighted moving averages versus time for standards analyzed in 2002.

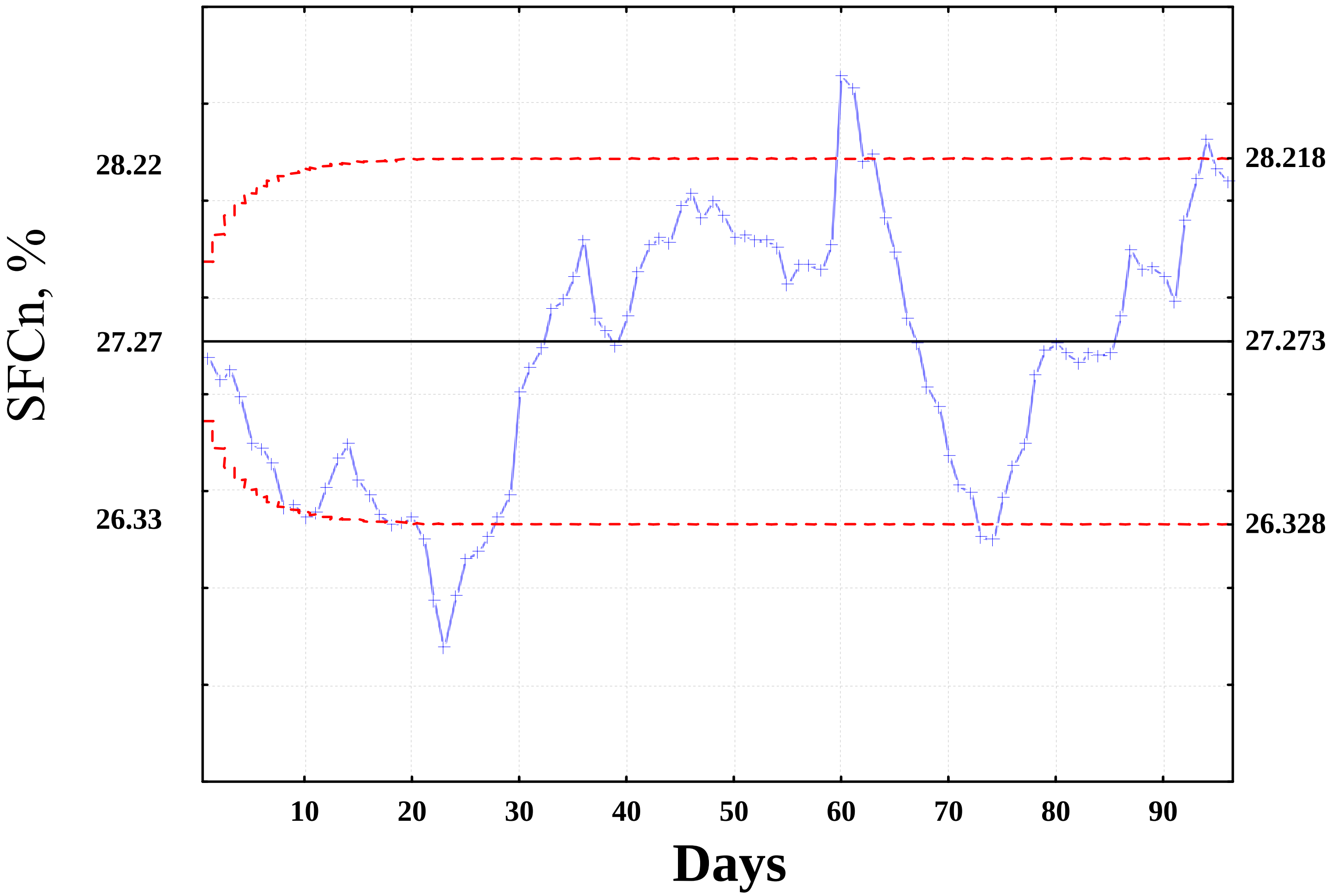

Fig. 5. SFCn exponentially weighted moving averages versus time for standards analyzed in 2002.

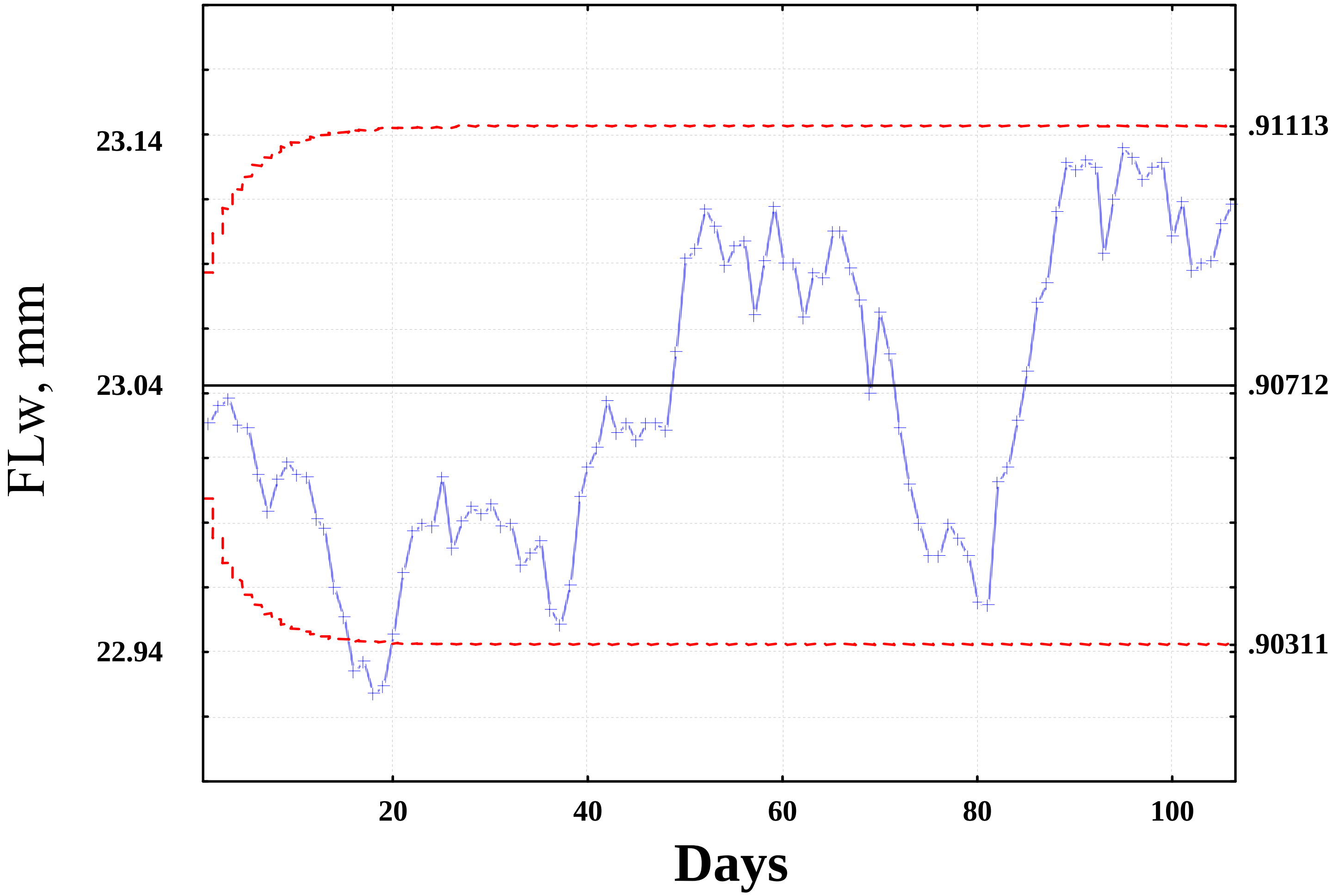

Fig. 6. FLw exponentially weighted moving averages versus time for standards analyzed in 2003.

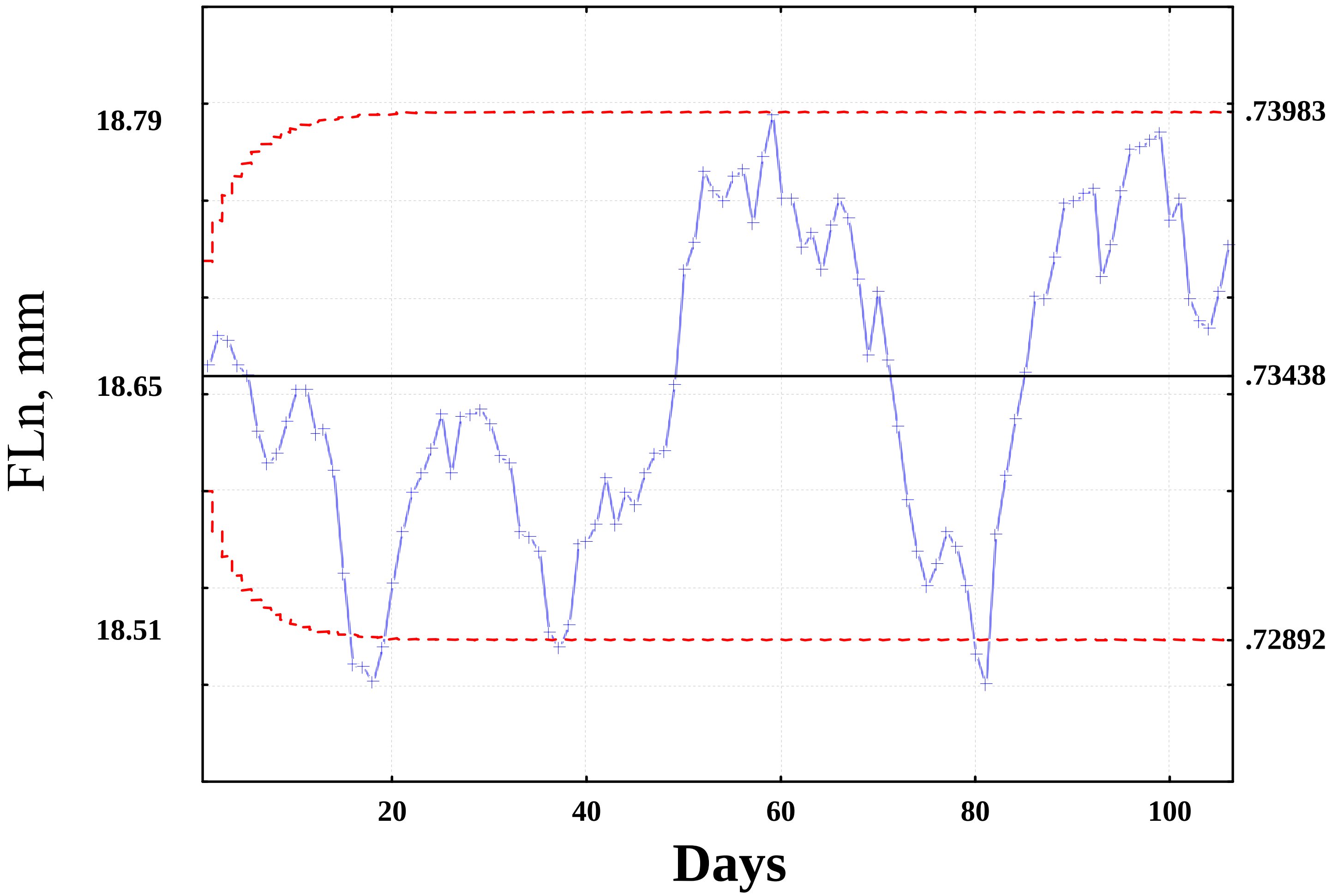

Fig. 7. FLn exponentially weighted moving averages versus time for standards analyzed in 2003.

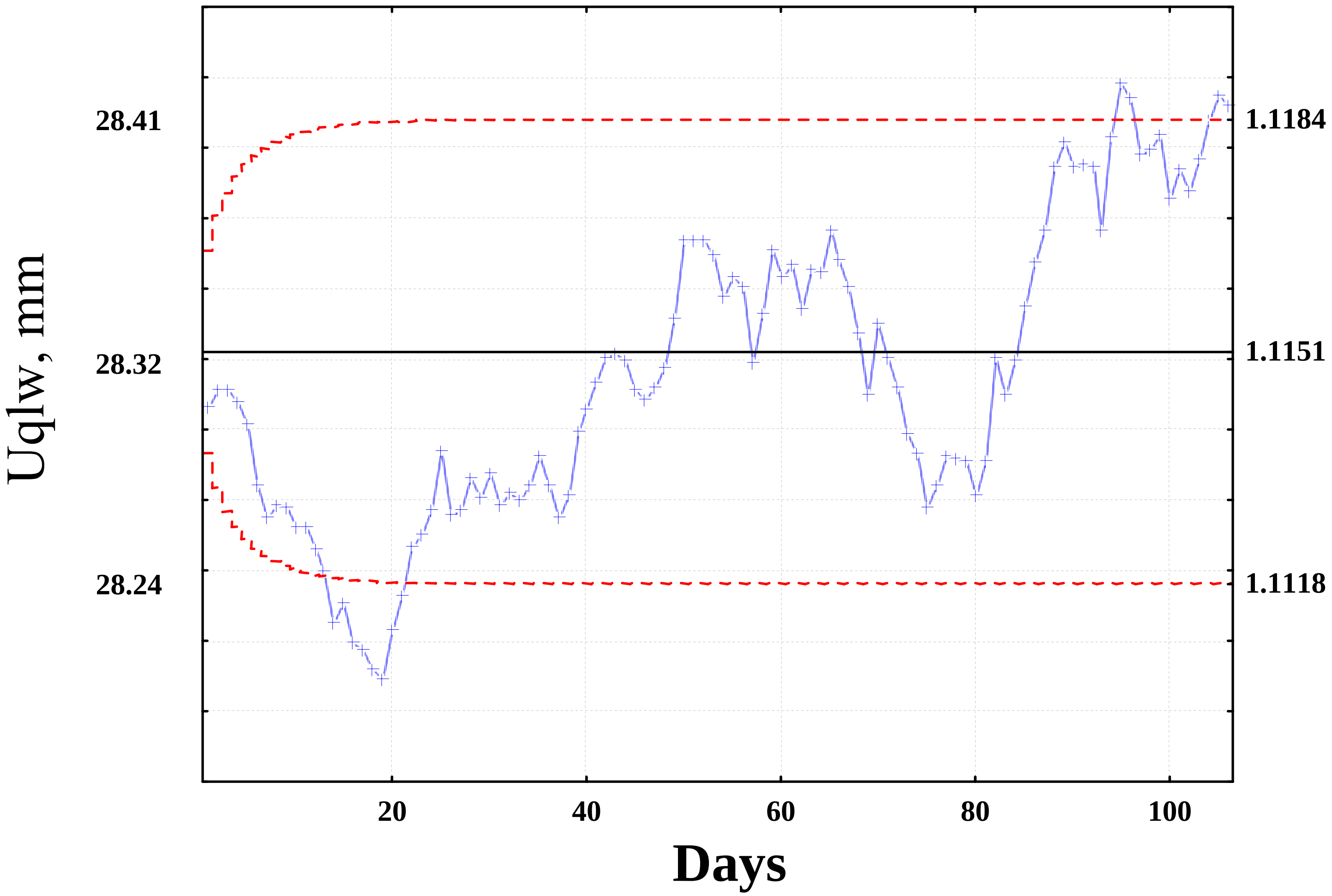

Fig. 8. Uqlw exponentially weighted moving averages versus time for standards analyzed in 2003.

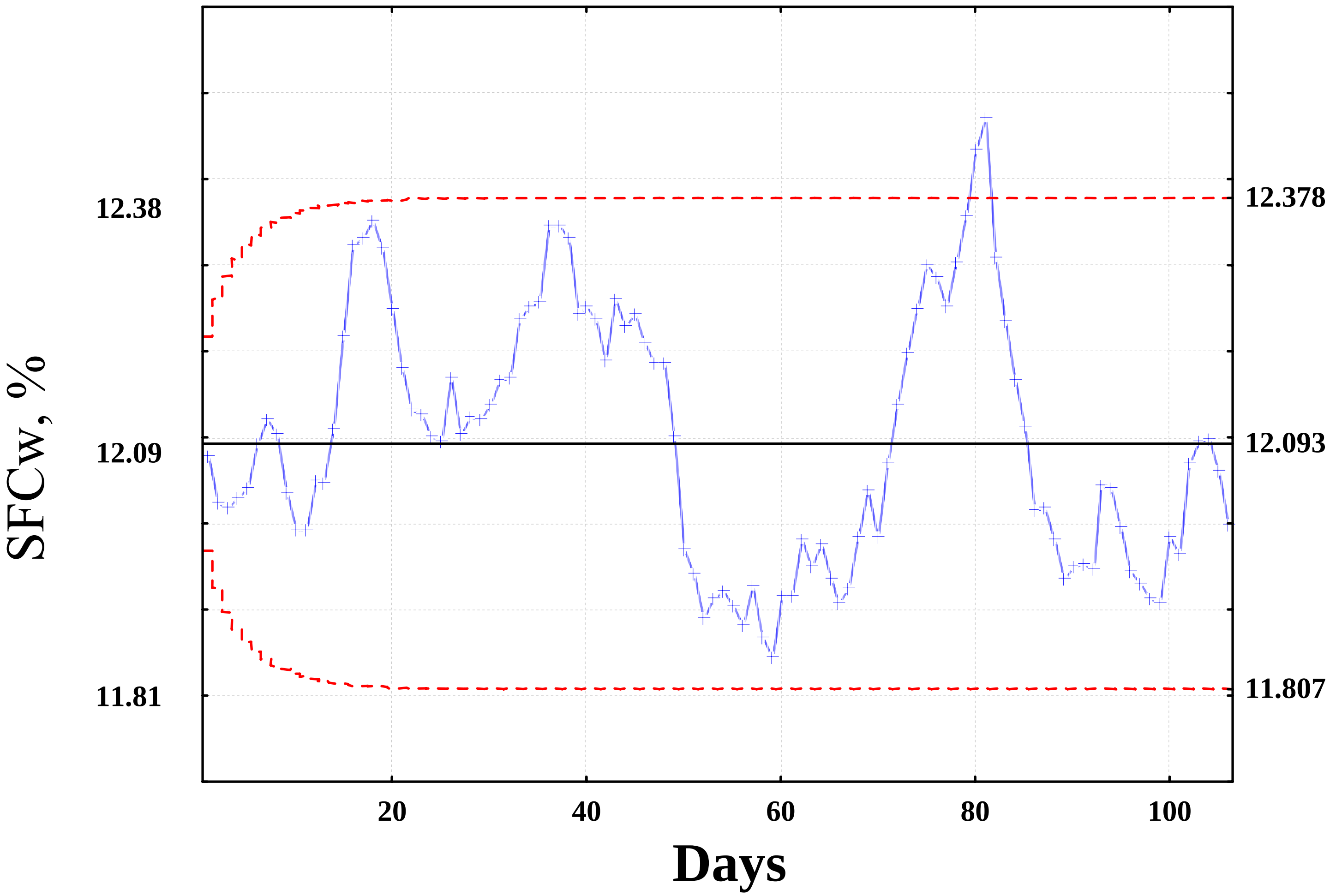

Fig. 9. SFCw exponentially weighted moving averages versus time for standards analyzed in 2003.

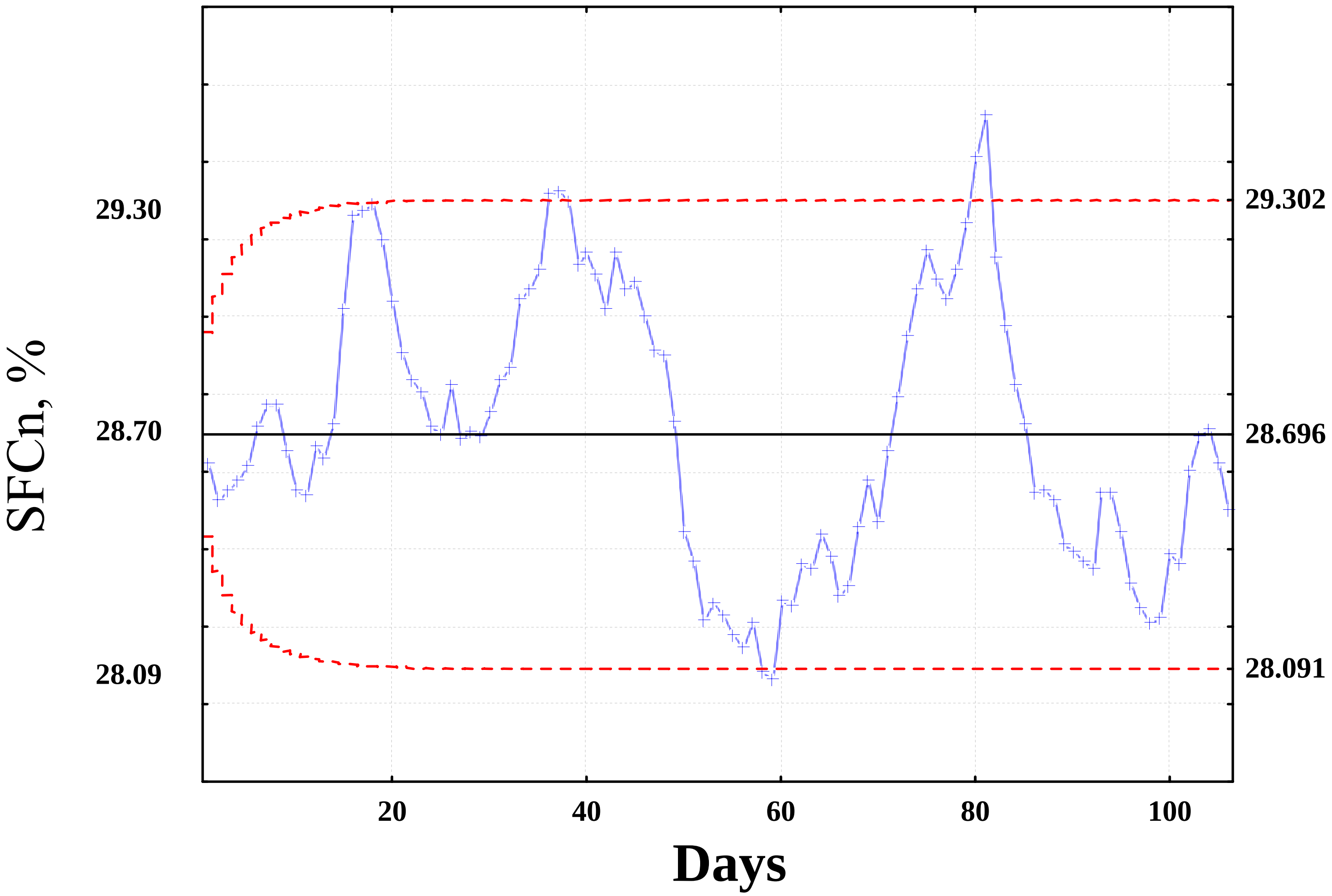

Fig. 10. SFCn exponentially weighted moving averages versus time for standards analyzed in 2003.

Table 2. Range of AFIS fiber length measurements [Upper Control Limit (+3σ) – Lower Control Limit (-3σ)].

Trait	**2002**	**2003**
FLw	0.28 mm (σ = 0.05 mm)	0.20 mm (σ = 0.03 mm)
FLn	0.41 mm (σ = 0.07 mm)	0.28 mm (σ = 0.05 mm)
UQLw	0.23 mm (σ = 0.04 mm)	0.17 mm (σ = 0.03 mm)
SCFw%	0.88 % (σ = 0.15 %)	0.57 % (σ = 0.10 %)
SFCn%	1.89 % (σ = 0.32 %)	1.21 % (σ = 0.20 %)

In 2002, the data revealed slight level shifts up and down for FLw, FLn, and Uqlw (Figs. 1-3) that could be attributed to the natural variability of cotton slivers. All three measurements had the same trend over the course of 96 days. SFCw and SFCn showed the same level shifts in the contrasting direction (Figs. 4-5). In 2003, the data were more within the boundaries with a slight trend toward longer fibers and reduced short fiber content over the course of 104 days (Figs. 6-10). In conclusion, we detected no instrument malfunction, shift, or drift that could impact the values of the results presented in this work.

As a tool to detect non-normality and trends, this exponentially weighted moving average is quite sensitive. Because of its lagging behavior, however, it is not appropriate for deciding exacting when there should be an operator intervention to check and clean the instrument for the purpose of determining whether it is necessary to recalibrate it. A short-term protocol is needed for this purpose (Ethridge and Hequet, 2001).

Statistical analysis

Diallel

Analyses of variance were completed for all fiber length and distribution measurements using plot mean data. Individual ANOVA across environments and per environment were conducted using PROC GLM (SAS, 2004). Replications were considered random, and genotypes and environment were considered fixed effects in the ANOVA. Significances of main effects and partitions of the main effects were tested against their respective interaction with environment, whereas the interaction with environment terms was tested against the error term. The average heterosis effect was estimated by partitioning the total entry sums of squares into a single degree of freedom contrast between parents vs. crosses (Griffing, 1956; Gardner and Eberhart, 1966b). General combining ability effects of the parents and SCA effects for the crosses, as well as their mean squares at each environment and across environments, were estimated following Griffing's Method 4 diallel analysis (Griffing, 1956).

Generation means

Analyses of variance were completed for all fiber length and distribution measurements using plot mean data. The GLM procedure of SAS was used to perform a combined analysis of variance across environments for each upland parental combination and among all parental combinations. Generations and environments were considered fixed effects, while replications were random.

Generation means analysis was performed by the PROC MIXED procedure of SAS (SAS, 2004) to assess the inheritance of AFIS fiber length measurements and distributions. The generation means were used to perform simple and joint scaling tests (Kearsey and Pooni, 1996).

The scaling test is based on the assumption that generation means depend only on the additive and dominance gene effects and linear relationships among the means. To test this assumption, the adequacy of the additive-dominance model in each cross was determined by the ABCD scaling tests (Mather, 1949; Singh and Chaudhary, 1985). Within the ABCD scaling test, A and B are contrasts of backcross means and provide tests for additive x dominance epistasis ($A = 2BC_1P_1 - P_1 - F_1$, $B = 2BC_1P_2 - P_2 - F_1$), C is a contrast among parental, F_1, and F_2 generation means and largely tests for dominance x dominance epistasis ($C = 4F_2 - 2F_1 - P_1 - P_2$), and D indicates additive x additive epistasis ($D = 2F_2 - BC_1P_1 - BC_1P_2$). Generation means are assumed independent, so that variances (V) are $V(A) = 4V(BC_1P_1) + V(P_1) + V(F_1)$, $V(B) = 4V(BC_1P_2) + V(P_2) + V(F_1)$, $V(C) = 16V(F_2) + 4V(F_1) + V(P_1) + V(P_2)$, and $V(D) = 4V(F_2) + V(BC_1P_1) + V(BC_1P_2)$. In the ABCD scaling test, a simple t-test determined the presence or absence of gene interactions. If the additive-dominance model is adequate, quantities A, B, C, and D will each equal zero within the limits of sampling error. The standard errors were obtained by taking the square root of the corresponding variances. This step is important because, in most cases, the estimation of additive and dominance components of variances was made assuming the absence of gene interaction.

Gene effects

The joint scaling test is based on a three-parameter model (*m*, *a*, and *d*). The three genetic parameters were defined as follows: *m* = midparent value, *a* = the amount of variation among the means resulting from the additive effect of the genes, and *d* = the amount of variation among the means resulting from the dominance effect of the genes. This model was used and tested for goodness of fit by a weighted chi-square test with three degrees of freedom. In this procedure, the weights were the reciprocal of the respective variances of generation means. A six-parameter model (*m*, *a*, *d*, *aa*, *ad*, and *dd*) was used if a significant chi-square value (poor fit; $P \geq 0.05$)) was obtained for the three-parameter model. The six genetic parameters were defined as follows: *m* = the mean of the inbred population, *a* and *d* as defined for the three parameter model, *aa* =

the amount of variation among the means attributed to additive x additive epistasis, *ad* = the amount of variation among the means resulting from additive x dominance epistasis, and *dd* = the amount of variation among the means resulting from dominance x dominance epistasis. These genetic parameters were tested for significance using a t-test. The adequacy of the six parameter model cannot be tested by a chi-square test because of the absence of degrees of freedom. The relative importance of different gene effects on AFIS fiber length and distribution measurements was determined based on the magnitude and significance of the estimates. Estimates of the six parameters can be calculated by the equations:

m = mean = $\frac{1}{2}P_1 + \frac{1}{2}P_2 + 4\,F_2 - 2BC_1P_1 - 2BC_1P_2$

a = additive effect = $\frac{1}{2}P_1 - \frac{1}{2}P_2$

d = dominance effect = $6BC_1P_1 + 62BC_1P_2 - 8F_2 - F_1 - 3/2P_1 - 3/2P_2$

aa = additive x additive = $2BC_1P_1 + 2BC_1P_2 - 4F_2$

ad = additive x dominance = $2BC_1P_1 - 2BC_1P_2 - P_1 + P_2$

dd = dominance x dominance = $P_1 + P_2 + 2F_1 + 4F_2 - 4BC_1P_1 - 4BC_1P_2$

Variances and heritability

In the generation means analysis, additive and dominance (non-additive) genetic variances (σ^2_A and σ^2_D) were estimated following the method of Warner (1952), in which $\sigma^2_A = 2\sigma^2_{F2} - (\sigma^2_{BC1P1} + \sigma^2_{BC2P2})$, $\sigma^2_D = \sigma^2_{F2} - (\sigma^2_A + \sigma^2_E)$. Environmental variance were calculated by $\sigma^2_E = (\sigma^2_{P1} + \sigma^2_{P2} + 2\,\sigma^2_{F1})/4$ (Wright, 1968). The estimate of the genetic variance (σ^2_G) is equal to the variance of the F_2 generation minus the environment variance (σ^2_E). In the variance components and heritability estimate, a negative variance was interpreted as zero.

Broad-sense heritability on a single-plant basis was estimated according to the equation:

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

The method used to estimate narrow-sense heritability on a single-plant basis was as follows (Warner, 1952; Fehr, 1991):

$$h^2 = [2(\sigma^2_{F2}) - (\sigma^2_{BC1P1} + \sigma^2_{BC1P2})] / \sigma^2_{F2}$$

Where:

σ^2_{F2} = the variance among F_2 plants of the single-cross population; σ^2_{BC1P1} and σ^2_{BC1P2} are the variance among plants from the backcrosses of the single cross F_1 to P_1 and to P_2. The numerator of the equation represented additive genetic variance, and σ^2_{F2} in the denominator represented the phenotypic variance among plants. A standard error for h^2 was derived as the square root of the following (Ketata et al, 1976).

$$\sigma^2(h^2) = 2\{[(\sigma^2_{BC1P1} + \sigma^2_{BC1P2})^2 / df_{F2}] + [(\sigma^2_{BC1P1})^2 / (df_{BC1P1})] + [(\sigma^2_{BC1P2})^2 / (df_{BC1P2})]\} / (\sigma^2_{F2})^2$$

Where:

σ^2_{F2}, σ^2_{BC1P1}, and σ^2_{BC1P2} are the variance of the F_2, backcross to P_1 and backcross to P_2. The terms df_{F2}, df_{BC1P1}, and df_{BC1P2} refer to degree of freedom associated with σ^2_{F2}, σ^2_{BC1P1}, and σ^2_{BC1P2}, respectively.

CHAPTER IV

FIBER LENGTH DIALLEL

Results and discussion

Parents differed ($P \leq 0.05$) for all fiber length measurements with the exception of SFCw and SFCn, for which these parents were not selected (Table 3). The parent x environment interactions, except for SFC, were not significant, suggesting that parents tended to be consistent across the two environments and allowing environments to be combined for comparison of genotypic means (Table 4). Fibermax 832 exhibited the longest UHM at 31.6 mm followed by TAM 94L-25 with an UHM fiber length of 31.2 mm, Acala 1517-99 at 30.3, TTU 202 at 30.0, and Tamcot CAMD-E had the shortest UHM fiber length of 26.9 mm. These data supported the rationale for selecting these parents for a diallel study. Fibermax 832 had the longest FLw at 28.4 mm, followed by TAM 94L-25, Acala 1517-99, and TTU 202 at 27.3, 26.9, and 26.6 mm respectively. Tamcot CAMD-E produced the shortest FLw at 23.8 mm. Fibermax 832 exhibited the numerically longest FLn at 22.7 mm and not different than Acala 1517-99. TAM 94L-25 and TTU 202 were similar in FLn to Acala 1517-99 and longer than Tamcot CAMD-E. Fibermax 832 had the longest upper quartile length by weight (Uqlw) at 34.4 mm and was followed by TAM94L-25 with an Uqlw measurement of 33.5 mm. Acala 1517-99 and TTU 202 were similar in Uqlw and Tamcot CAMD-E produced the shortest Uqlw at 28.5 mm.

Table 3. Combined analyses of variance of diallel crosses among five upland cotton genotypes for fiber length measurements at College Station, TX in 2001 and 2002.†

		Mean squares					
Source	df	UHM	FLw	FLn	Uqlw	SFCw	SFCn
		--------------------- mm		-----------------------		---------- %	------------
Environment (E)	1	24.61**	83.38**	162.49**	46.84**	169.19**	1155.13**
Reps/E	6	0.94**	0.50	0.82	0.47	1.75	9.82
Genotypes (G)	14	14.45**	15.28**	7.90*	26.54**	6.61	18.72
Parents (P)	4	27.07**	23.48**	12.06*	41.16**	10.38	33.91
P vs. F_1	1	14.45	26.90	9.01	46.65*	25.07	13.09
F_1	9	8.84**	10.35**	5.93**	17.80**	2.89**	12.60
GCA	4	19.33**	21.69**	10.09**	39.02**	2.69**	3.54
SCA	5	0.45	1.28*	2.61*	0.83	3.05*	19.84
G x E	14	0.19**	0.81	2.86**	0.37	9.49**	54.57**
P x E	4	0.10	0.70	1.66	0.17	4.34**	18.77*
P vs. F_1 x E	1	0.62**	6.53**	30.70**	0.10	111.77**	648.15**
F_1 x E	9	0.18*	0.23	0.30	0.49	0.41	4.53
GCA x E	4	0.21*	0.28	0.28	0.54	0.15	2.93
SCA x E	5	0.16	0.19	0.32	0.44	0.62	5.81
Error	84	0.08	0.46	0.70	0.49	1.30	6.66
Mean		30.51	27.27	21.70	33.05	7.33	24.30
CV, %		0.94	2.49	3.85	2.11	15.53	10.62

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

† UHM, HVI upper half mean length; FLw, AFIS fiber length by weight; FLn, AFIS fiber length by number; Uqlw, AFIS upper quartile length by weight; SFCw, AFIS short fiber content by weight; SFCn, AFIS short fiber content by number; GCA, general combining ability; SCA, specific combining ability.

Table 4. Means of five upland parental genotypes for fiber length measurements evaluated near College Station, TX in 2001 and 2002.†

Genotype	UHM	FLw	FLn	Uqlw	SFCw		SFCn	
					2001	2002	2001	2002
Fibermax 832	31.6 a‡	28.4 a	22.7 a	34.4 a	8.4 a	5.2 ab	27.9 a	18.7 ab
TAM 94L-25	31.2 b	27.3 b	21.4 b	33.5 b	12.5 a	5.1 ab	35.8 a	18.4 ab
Acala 1517-99	30.3 c	26.9 b	21.9 ab	32.4 c	9.2 a	4.1 b	28.8 a	15.2 b
TTU 202	30.0 d	26.6 b	21.2 b	32.1 c	10.8 a	6.1 a	31.7 a	20.2 a
Tamcot CAMD-E	26.9 e	23.8 c	19.4 c	28.5 d	11.7 a	6.5 a	31.6 a	19.3 ab

† UHM, HVI upper half mean length; FLw, AFIS fiber length by weight; FLn, AFIS fiber length by number; Uqlw, AFIS upper quartile length by weight; SFCw, AFIS short fiber content by weight; SFCn, AFIS short fiber content by number.

‡ Means within a column followed by the same letter are not different at K = 100 (approximates $p = 0.05$) according to Waller-Duncan LSD.

GCA effects were observed ($P \leq 0.05$) for all fiber length measurements except SFCn (Table 3). The ANOVA revealed a significant GCA x environment interaction for UHM fiber length. The preponderance of GCA effects implied that progeny performance relative to fiber length improvement can be predicted from GCA alone (97.2%, 93.1%, 75.6%, and 97.4% of total F_1 sums of squares were attributable to GCA for UHM, FLw, FLn, and Uqlw respectively). TAM 94L-25 had the highest significant GCA effects for improving HVI and AFIS fiber length measurements and for reducing short fiber content (Table 5). Estimates of TAM 94L-25 GCA effects for HVI UHM were 0.77 and 1.06 in 2001 and 2002, respectively. GCA effects for AFIS fiber measurements of FLw, FLn, and Uqlw were 1.03, 0.71, and 1.45 respectively, complemented with a significant -0.27 estimate for SFCw and non-significant -0.12 for SFCn. Fibermax 832 also exhibited significant positive GCA effects for enhancing UHM, FLw, and Uqlw cotton fiber length. Although not significant, Fibermax 832 GCA effects were negative (desirable) and positive (undesirable) for SFCw and SFCn, respectively. As expected, Tamcot CAMD-E combined for shorter fiber lengths and higher SFCw. Acala 1517-99 and TTU 202 exhibited no significant GCA effects for any of the fiber length measurements, although the trend for TTU 202 as a combiner was for shorter UHM, longer AFIS fiber length measurements, and a reduction of short fiber content.

F_1 differed ($P \leq 0.05$) for all fiber length measurements except SFCn (Table 3). Yet, the test for average heterosis (parents vs. F_1) was significant only for Uqlw, where three F_1 exhibited an Uqlw mean greater than the longest parent, which supports

Table 5. Estimates of general combining ability (GCA) effects of five upland parents for fiber length measurements evaluated near College Station, TX in 2001 and 2002.†

Genotype‡	UHM		FLw	FLn	Uqlw	SFCw	SFCn
	2001	2002					
	mm					%	
832	0.53**	0.57**	0.53**	0.24	0.73**	-0.04	0.41
L-25	0.77**	1.06**	1.03**	0.71**	1.45**	-0.27*	-0.12
1517	0.06	-0.02	-0.14	-0.10	-0.24	-0.06	-0.03
202	-0.03	-0.07	0.08	0.18	0.03	-0.20	-0.56
CD-E	-1.34**	-1.54**	-1.50**	-1.03**	-1.96**	0.57*	0.30
LSD (0.05) $(g_i - g_j)$	0.17	0.22	0.23	0.23	0.32	0.35	0.75

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

† UHM, HVI upper half mean length; FLw, AFIS fiber length by weight; FLn, AFIS fiber length by number; Uqlw, AFIS upper quartile length by weight; SFCw, AFIS short fiber content by weight; SFCn, AFIS short fiber content by number.

‡ 832, Fibermax 832; L-25, TAM 94L-25; 1517, Acala 1517-99; 202, TTU 202; CD-E, Tamcot CAMD-E.

previous reports of heterosis for fiber length in upland cotton (Lee et al., 1967; Al-Rawi and Kohel, 1969). Except for UHM, all F_1 x environment interactions and all SCA x environment effects were not significant. For SFCw and SFCn, 58.6% and 87.5% of the total F_1 sums of squares were attributable to SCA.

The F_1 of Fibermax 832 x Acala 1517-99 had significant SCA effects for increasing fiber length of all measurements except for Uqlw and reducing both SFCw and SFCn (Table 6). The UHM and Uqlw means of Fibermax 832 x Acala 1517-99 were 31.6, 32.1, and 34.3 mm, respectively (Table 7). FLw and FLn means were similar to the longest F_1 at 28.5 and 22.8 mm, and SFC means similar to the F_1 with the smallest percentage of short fibers. The cross between the best two general combiners, TAM 94L-25 and Fibermax 832, exhibited significant negative SCA effects for AFIS FLw, FLn, and Uqlw, and significant positive SCA effects for SFCw and SFCn. The F_1 UHM was the longest of all crosses in 2001, 31.6 mm, and numerically exhibited the longest UHM in 2002 and Uqlw, 32.7 and 35.2 mm respectively. The FLw mean, 28.7 mm, was not different from the longest F_1 mean. Of concern within this combination were the short FLn measurement of 22.2 mm and the high percentage of short fibers by weight and number. This clearly indicates an undesirable length distribution and proves that breeding on UHM length alone can be misleading. The current premium and discount schedule is rewarding this type of cotton whereas it should be discounted. The wide distribution range of cotton lengths will encounter increased waste, loss of production efficiency during spinning processes, and inferior yarn quality.

Table 6. Estimates of specific combining ability (SCA) effects of 10 upland F_1 crosses for fiber length measurements evaluated near College Station, TX in 2001 and 2002.†

F_1 cross‡	UHM	FLw	FLn	Uqlw	SFCw	SFCn
	mm				%	
832 x L-25	-0.07	-0.50**	-0.62**	-0.43*	0.61*	1.47*
L-25 x 202	0.05	0.28*	0.51**	0.11	-0.56*	-1.52*
832 x 1517	0.28*	0.53**	0.80**	0.36	-0.87**	-2.22**
832 x 202	0.05	-0.01	-0.22	0.16	0.35	0.94
L-25 x 1517	-0.24*	-0.02	-0.17	0.06	0.20	0.69
1517 x 202	-0.07	-0.29*	-0.30	-0.26	0.28	0.64
L-25 x CD-E	0.25*	0.24	0.28	0.26	-0.25	-0.64
832 x CD-E	-0.26*	-0.03	0.04	-0.09	-0.08	-0.19
1517 x CD-E	0.03	-0.22	-0.33*	-0.16	0.39	0.89
202 x CD-E	-0.03	0.01	0.01	-0.01	-0.06	-0.06
LSD (0.05) ($s_{ij} - s_{ik}$)	0.37	0.40	0.52	0.61	0.73	2.23
LSD (0.05) ($s_{ij} - s_{kl}$)	0.26	0.28	0.37	0.43	0.51	1.57

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

† UHM, HVI upper half mean length; FLw, AFIS fiber length by weight; FLn, AFIS fiber length by number; Uqlw, AFIS upper quartile length by weight; SFCw, AFIS short fiber content by weight; SFCn, AFIS short fiber content by number.

‡ 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x Acala 1517-99; 832 x 202, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202; L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamocot CAMD-E.

Table 7. Means of F_1 crosses for fiber length measurements evaluated near College Station, TX in 2001 and 2002.†

F_1 cross‡	UHM		FLw	FLn	Uqlw	SFCw	SFCn
	2001	2002					
	mm					%	
832 x L-25	31.6 a§	32.7 a	28.7 ab	22.2 cd	35.2 a	7.3 ab	25.8 a
L-25 x 202	31.1 b	32.2 ab	29.0 a	23.3 a	35.1 a	6.0 c	21.9 d
832 x 1517	31.1 b	32.1 b	28.5 ab	22.8 ab	34.3 b	6.0 c	22.2 cd
L-25 x 1517	31.0 b	31.6 c	28.5 ab	22.3 bc	34.8 ab	6.9 b	24.6 ab
832 x 202	30.8 b	32.1 b	28.2 b	22.1 cd	34.4 b	7.1 b	24.9 ab
1517 x 202	30.4 c	30.9 d	27.3 c	21.7 de	33.0 c	7.0 b	24.1 ab
L-25 x CD-E	30.1 c	30.8 d	27.4 c	21.8 cd	33.2 c	7.1 b	23.6 bcd
832 x CD-E	29.2 d	30.0 e	26.6 d	21.1 ef	32.2 d	7.5 a	24.6 ab
1517 x CD-E	29.2 d	29.5 f	25.7 e	20.4 g	31.1 e	7.9 a	25.2 ab
202 x CD-E	28.8 e	29.7 ef	26.2 de	21.1 f	31.6 de	7.3 ab	23.8 bc

† UHM, HVI upper half mean length; FLw, AFIS fiber length by weight; FLn, AFIS fiber length by number; Uqlw, AFIS upper quartile length by weight; SFCw, AFIS short fiber content by weight; SFCn, AFIS short fiber content by number.

‡ 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x Acala 1517-99; 832 x 202, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202; L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamocot CAMD-E.

§ Means within a column followed by the same letter are not different at K = 100 (approximates p = 0.05) according to Waller-Duncan LSD.

TAM 94L-25 x TTU 202 combined well as it produced a significant positive SCA effect for FLw and FLn, 0.28 and 0.51 mm, respectively. This parental combination exhibited also significant negative SCA effects for SFCw and SFCn, -0.56 and -1.52 mm, respectively. The FLw and FLn means of TAM 94 L-25 x TTU 202 were numerically the longest of all 10 crosses, and its UHM length of 32.2 mm in 2002 and Uqlw of 35.1 mm were not different from the longest F_1 mean. The SFCw and SFCn means were also superior as the lowest of all 10 crosses. This parental combination had fiber characteristics that were favorable for a well-balanced distribution and should provide reputable yarn quality if all other parameters are equal. Parental combinations TAM 94L-25 x Acala 1517-99, TAM 94L-25 x Tamcot CAMD-E, and Fibermax 832 x Tamcot CAMD-E exhibited significant SCA effects for UHM. For FLw, Acala 1517-99 x TTU 202 had a negative SCA effect.

Summary and conclusions

Successful breeding approaches are a direct consequence of the gene action prevalent in the breeding population under consideration. The relative importance of additive vs. non-additive effects for fiber length measurements, HVI and AFIS, in diallel crosses is an indication of the type of gene action (Baker, 1978). GCA estimates additive genetic effects. The GCA effects reflect performance of parental lines in combination with all other lines evaluated, so the parents with the highest GCA effects should have the greatest impact on trait improvement. The diallel reported herein demonstrated that there is sufficient genetic variation among the parents for fiber length to facilitate improvement though selection, but not for the percentage of short fibers.

The absolute SFC used in this study measured the percentage of fibers, by number or weight, shorter than 12.7 mm (½ inch long). What is proposed is a relative SFC measurement because absolute SFC in not staple independent, shorter staple cottons will have more short fibers than long staple genotypes. A relative SFC measurement by weight or number could be the percentage of fibers that are shorter than one-half the UHM length. This staple independent SFC parameter would enable breeders to make more accurate selections for genotypes across a range of UHM lengths.

The GCA effects for all fiber length measurements, except for SFCn, were significant (Table 3). TAM 94L-25 was the best overall combiner, i.e., the best parent to be used in a cross to improve all fiber length measurements. TAM 94L-25 showed positive GCA effects for UHM (both years), FLw, FLn, Uqlw, and negative GCA effects for SFCw. SFCn was also lowered when TAM 94L-25 was utilized as a parent. Fibermax 832 combined well with selected U.S. cultivars to enhance fiber length, which agreed with Cheatham et al. (2003) but it did not exhibit the magnitude of TAM 94L-25 in this study. This study also indicated that additive genetic effects tended to be more prominent within upland cotton genotypes than non-additive genetic effects, as numerous other diallel studies have concluded (Miller and Marani, 1963; Lee et al., 1967; Al-Rawi and Kohel, 1969; Al-Rawi and Kohel, 1970; Meredith and Bridge, 1972; Green and Culp, 1990; Tang et al., 1993). Genotype x environment interactions were minimal, agreeing with May (1999), who reported a strong genetic basis for fiber length. Among these parents, only SFCw and SFCn measurements exhibited significant parent x environment interactions, which appear based more on magnitude than changes in rank.

Only HVI UHM fiber length, which was saw ginned, exhibited a F_1 x environment and GCA x environment interaction with significance at $P \leq 0.05$.

SCA reflects dominant gene effects. SCA effects represent the deviation of hybrid performance from that expected from the GCA effects of each parent. SCA effects can identify the best hybrid combination, but they can also identify complementary alleles for trait performance (Kearsey and Pooni, 1996). SCA effects were significant for only FLw, FLn, and SFCw (Table 3). Of interest are combinations of lines with good to superior mean trait performance and beneficial GCA effects which also have beneficial SCA effects. No such combination was observed for HVI UHM fiber length, but two combinations for AFIS fiber length measurements were prevalent. For FLw and Uqlw, the TAM 94 L-25 x TTU 202 cross exhibited positive SCA effects and means greater than the longest parent (Tables 6 and 7). For FLn, this F_1 exhibited the longest length, among parents and crosses, with a significant positive SCA effect of 0.51 mm. For FLw, the Fibermax 832 x Acala 1517-99 cross exhibited a mean greater than the longest parent and a significant positive SCA effect of 0.53 mm.

The genetic interpretation of a diallel with a reduced number of parental inbreds, such as this one, can be biased by the lack of independent distribution of genes in the parental lines (Baker, 1978). Therefore, combining abilities reported here could be biased by the correlation of gene frequencies and should be interpreted with caution. Despite these limitations, this diallel was useful in determining which near-long staple upland parent had the most desirable GCA expression of fiber length traits. Where non-additive gene action was prevalent, this diallel identified certain combinations that might be useful since the parental performance would not necessarily be indicative of the performance in cross combination.

Most current cotton breeding programs use HVI data for selection and advancements because of cost and availability. Conclusions of past studies regarding instrument choice and probability for genetic gain have been variable. Green and Culp (1990) did not detect any significant GCA or SCA effects for any HVI measurement but did for standard laboratory instrumentation, suggesting that HVI was not useful to breeders in detecting small genetic differences. In contrast, Latimer et al. (1996) reported that HVI analyses provided higher heritability estimates than those obtained from single instrument techniques, and that HVI thus was suitable for improvement of fiber quality traits. May and Jividen (1999) also reported that heritability estimates of HVI UHM fiber length were of a magnitude to expect progress from selection. Uster's AFIS is the newest instrument to be used by breeders, and it offers a plethora of fiber information, including distribution data. However, high cost is a deterent to utilizing AFIS data for selections, especially during early generations. In this study we detected significant GCA effects for both HVI and AFIS instruments, but only significant SCA effects were found with AFIS measurements.

The whole plant samples for the diallel and HVI test were ginned on a laboratory saw gin to handle the bulk and acquire the mandatory 30 g lint sample needed for HVI analysis. For the generation means analysis, AFIS was the preferred method to measure the fiber length from roller ginned samples because of its ability to analyze a small collection of bolls (Wartelle et al., 1995). Parental and F_1 samples in the generation means analysis presented interesting comparisons. Accordingly, a diallel for AFIS measurements was conducted to compare HVI and AFIS fiber length measurements. Behery (1993) noted that HVI UHM lengths do not always agree with AFIS length data due to effects of sample pooling, fiber crimp, specimen crimp characteristics, and other factors. In the current study, even though HVI and AFIS measurements were ginned differently and varied in sample size, sound conclusions can plausibly be made concerning HVI and AFIS fiber length measurements.

When comparing the HVI measurement of UHM to AFIS fiber trait measurements of FLw, FLn, and Uqlw, Uqlw most closely followed the mean separation order and magnitude of difference among the parents. FLw attained the same rank as UHM, but magnitude differed slightly. Overall, the three length by weight measurements, UHM, FLw, and Uqlw, discriminated the parental genotypes. Also worth noting, the magnitude of difference between Acala 1517-99 and TTU 202 averaged 0.33 mm for all three measurements. Comparing the F_1 data, the Waller-Duncan LSD test for the three length by weight measurements clearly discriminated the longest five F_1 from the shorter five, whereas FLn measurement did not. The actual output recorded by the AFIS machine is the FLn for each fiber passing through the sensor, providing an un-bias measurement of fiber length and percentage of short fibers in a sample. The FLw measurement is calculated from the recorded FLn assuming all fibers in the sample have the same linear density. However, Hequet (2004) knows that this assumption is false, therefore creating a FLw bias in which the measurement can then hide the measured short fibers. For example, the Fibermax 832 x TAM 94L-25 cross ranked near the top for all length by weight measurements, however its high percentage of short fibers lowered its FLn rank.

Developing genotypes with superior fiber length is a priority of most breeding programs across the Cotton Belt. In Texas during the 2003-04 crop year, only 44.1% of the bales classified achieved a U.S. base staple length of 34 (26.7 mm) (Hequet, 2004). This number has substantially increased over the past few years with the private sector commercializing new long staple picker varieties that are capable of being grown across all regions of Texas. However, considering the U.S. is exporting two-thirds of our cotton to overseas mills, a minuscule 8.1 and 0.9% of classified Texas bales attained the International and ICAC base staple length of 35 (27.4 mm) and 36 (28.2 mm), respectively (Hequet, 2004).

Knowledge of which instrument results in the fastest genetic gain and the type of genetic action controlling fiber length in current near-long staple genotypes would allow a breeder to choose effective parents for developing segregating populations. Increasing the fiber length a few more millimeters into well-adapted genotypes would be valuable for the Texas cotton industry, even more so if our premiums and discounts were comparable with other cotton producing regions across the Cotton Belt. Our results show considerable variation in GCA effects among the four near-long staple genotypes. U.S. breeders could benefit from using TAM 94L-25 to improve fiber length. Since the cultivars chosen represented diverse programmatic origins, we conclude that most U.S. cotton breeding programs should gain from using TAM 94L-25 in crosses with their lines.

CHAPTER V

AFIS FLw GENERATION MEANS ANALYSIS

Results and discussion

The parental, F_1, F_2, and backcross generations differed ($P \leq 0.01$) in FLw for all parental combinations except Acala 1517-99 x TTU 202 (Table 8). The ANOVA also revealed a significant generation x environment interaction in all parental combinations except Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, Acala 1517-99 x TTU 202, and Acala 1517-99 x Tamcot CAMD-E, thus these four parental combinations were pooled over years. The other parental combinations indicated that some generations reacted differently to each environment, suggesting that selection and evaluation should be conducted within environment if reliable knowledge of FLw is to be obtained.

FLw means from P_1 and P_2 were different ($P \leq 0.05$) in each parental combination except Fibermax 832 x TAM 94L-25 in 2002, TAM 94L-25 x TTU 202 in 2001, TAM 94L-25 x Acala 1517-99 in 2001, and Acala 1517-99 x TTU 202 combined across years (Table 9). Generally, F_1 hybrids had FLw similar to the longest parent, although some parental combinations had means intermediate to the parents. In 2001, F_1 means of TAM 94L-25 x TTU 202, TAM 94L-25 x Acala 1517-99, and TAM 94L-25 x Tamcot CAMD-E were greater than the longest parent, thus demonstrating heterosis. Depending upon the parental combination and environment, F_2 means were either similar to the longest parent or intermediate. The Fibermax 832 x TAM 94L-25 F_2 mean in 2001 and Fibermax 832 x TTU 202 F_2 mean combined across years was similar to the

Table 8. Mean squares for FLw measured on P_1, P_2, F_1, F_2, BC_1P_1, and BC_2 P_2 (per parental combination and among all combinations) at College Station, TX in 2001 and 2002.

A.

		Parental Combinations†					
Source	df	832 x L-25	L-25 x 202	832 x 1517	832 x 202	L-25 x 1517	1517 x 202
Environment (E)	1	96.27**	75.25**	38.80**	62.03**	103.32**	51.83**
Reps/E	6	0.67	0.36	0.37	0.20	0.27	0.44
Generation (Gn)	5	1.88**	4.86**	3.09**	3.80**	2.65**	0.36
Gn x E	5	1.90**	1.46**	0.35	0.46	2.44**	0.76
Error	30	0.37	0.26	0.40	0.51	0.28	0.49

B.

		Parental Combinations‡				
Source	df	L-25 x CD-E	832 x CD-E	1517 x CD-E	202 x CD-E	Among
Environment (E)	1	38.56**	55.28**	58.32**	19.20**	57.55**
Reps/E	6	0.41	0.22	0.09	0.38	0.04
Generation (Gn)	5	16.15**	21.11**	10.24**	9.72**	4.90**
Gn x E	5	1.87**	0.96*	0.17	1.30**	0.37**
Error‡	30	0.21	0.32	0.23	0.29	0.09

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

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

Table 9. Means of P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 for FLw (mm) per parental combination and among all combinations at College Station, TX in 2001 and 2002. First parent listed is P_1, second parent is P_2.

A.

	Parental Combinations†									
	832 x L-25		L-25 x 202		832 x 1517	832 x 202	L-25 x 1517		1517 x 202
Gen.‡	2001	2002	2001	2002	2001/02	2001/02	2001	2002	2001/02
P_1	27.5 ab§	29.2 ab	25.6 b	28.9 ab	28.4 a	28.4 a	25.6 b	28.9 ab	29.9 a
P_2	25.6 c	28.9 b	25.5 b	27.8 c	26.9 d	26.6 b	25.7 b	28.1 c	26.6 a
F_1	27.9 a	29.5 ab	28.5 a	29.5 a	28.5 a	28.2 a	28.0 a	29.0 ab	27.3 a
F_2	25.9 c	29.9 a	26.2 b	29.1 ab	27.7 bc	27.3 b	25.3 b	29.4 ab	26.9 a
BC_1P_1	26.6 bc	29.8 a	26.2 b	29.5 a	28.3 ab	28.1 a	26.1 b	29.6 a	27.1 a
BC_1P_2	26.6 bc	29.8 a	26.4 b	28.8 b	27.5 cd	27.2 b	25.4 b	28.8 bc	26.9 a

B.

	Parental Combinations¶								
	L-25 x CD-E		832 x CD-E		1517 x CD-E	202 x CD-E		Among	
Gen.	2001	2002	2001	2002	2001/02	2001	2002	2001	2002
P_1	25.6 b	28.9 a	27.5 a	29.2 a	26.9 a	25.5 a	27.8 a	26.4 ab	28.8 a
P_2	22.8 d	24.8 d	22.8 c	24.8 e	23.8 d	22.8 c	24.8 d	24.5 e	26.8 d
F_1	26.6 a	28.2 a	25.8 b	27.4 c	25.7 c	25.7 a	26.7 b	26.9 a	28.3 b
F_2	25.9 ab	26.8 b	24.8 b	26.3 d	26.3 b	25.8 a	25.9 c	25.8 cd	28.0 b
BC_1P_1	25.9 ab	28.3 a	25.3 b	28.4 b	26.6 ab	25.8 a	27.1 ab	26.2 bc	28.7 a
BC_1P_2	24.9 c	25.6 c	23.4 c	26.4 d	25.5 c	24.3 b	25.4 cd	25.3 d	27.7 c

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ Gen., generation; 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 K = 100 (approximates p = 0.05) according to Waller-Duncan LSD.

¶ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

shorter parent, TAM 94L-25 and TTU 202, respectively. In most parental combinations, the mean values of the backcrosses were different and shifted toward the values observed for the recurrent parent. However, the BC_1P_1 means were not different from BC_1P_2 means of Fibermax 832 x TAM 94L-25 in 2001 and 2002, TAM 94L-25 x TTU 202 in 2001, TAM 94L-25 x Acala 1517-99 in 2001, and Acala 1517-99 x TTU 202 combined across years.

The parental combinations were divided into two categories, near-long x near-long and near-long x short staple parental combinations. For each parental combination, P_1 was assigned accordingly to the parent with the longest FLw. The near-long x near-long parental combinations consisted of Fibermax 832 x TAM 94L-25, TAM 94L-25 x TTU 202, Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, TAM 94L-25 x Acala 1517-99, and Acala 1517-99 x TTU 202. The near-long x short staple parental combinations were Fibermax 832, TAM 94L-25, Acala 1517-99, and TTU 202 crosses with Tamcot CAMD-E.

FLw frequency distributions of each parental combination were constructed to visually gain a more comprehensive understanding into the generation means and to determine transgressive segregation (Figs. 11-28). For each figure the y-axis is the number of plants, and the x-axis is FLw in mm divided into 10 length classes. Within each figure classes are the same for the non-segregating and segregating populations. However, the overall range and class size does change from figure to figure.

Examination of the frequency distribution of individual plant values of each parental combination indicated that the segregating populations followed a normal distribution, suggesting that FLw is quantitatively inherited. Transgressive segregation, individual F_2 or backcross plant observations with values exceeding the longest parent or F_1 observation (Kearsey and Pooni, 1996), was visible in both near-long x near-long and near-long x short staple parental combinations.

At least one segregating population in all near-long x near-long parental combinations exhibited transgressive segregation. Averaging the percent of plants exhibiting transgressive segregation for each segregating population among the near-long x near-long parental combinations, the BC_1P_1 had the highest percent transgressive segregation at 3.6%, followed by the F_2 at 2.4%, and the BC_1P_2 at 1.7%. In 2002, the BC_1P_1 population of TAM 94L-25 x TTU 202 had the highest percentage of transgressive segregation, 10.0% (Fig. 14). In 2002, Fibermax 832 x TAM 94L-25 had the highest percent of transgressive segregation among the BC_1P_2 and F_2 populations, 7.0 and 8.0%, respectively (Fig. 12). It is interesting to note that a high percentage of transgressive segregation for FLw was observed in Fibermax 832 x TAM 94L-25 parental combination in 2002. This suggests that the two longest genotypes in this study have different alleles for FLw and that further improvement of fiber length is possible.

Fewer transgressive segregates appeared in the near-long x short staple segregating populations, and none appeared in the backcross to Tamcot CAMD-E (Figs. 20-28). In 2001, TAM 94L-25 x Tamcot CAMD-E had the highest percentage of BC_1P_1 and F_2 transgressive segregation, 6.0 and 8.0%, respectively (Fig. 20). Other near-long x short staple parental combinations either displayed no or a very low percentage of transgressive segregation.

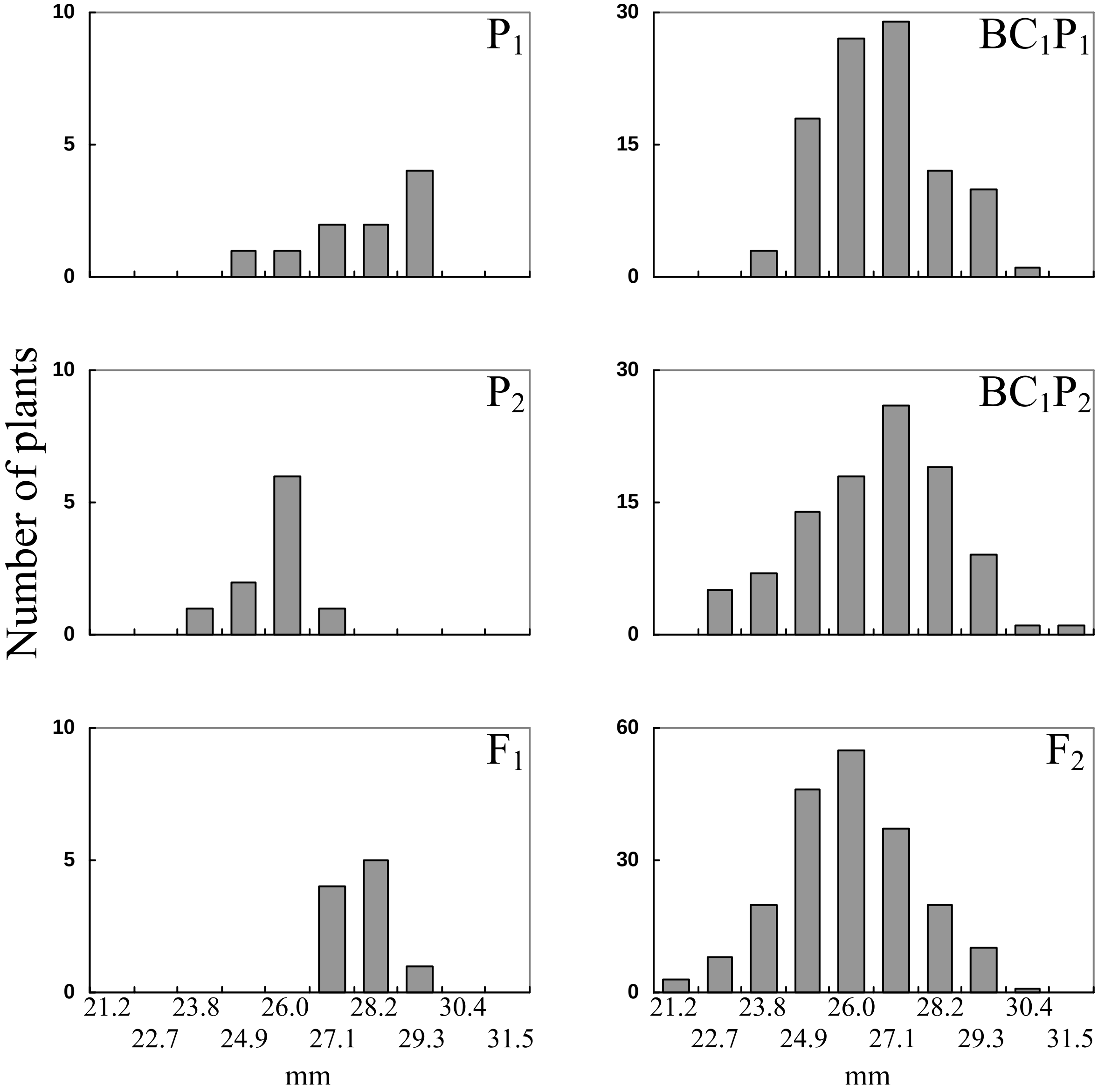

Fig. 11. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x near-long parental combination of Fibermax 832 (P_1) x TAM 94L-25 (P_2) in 2001.

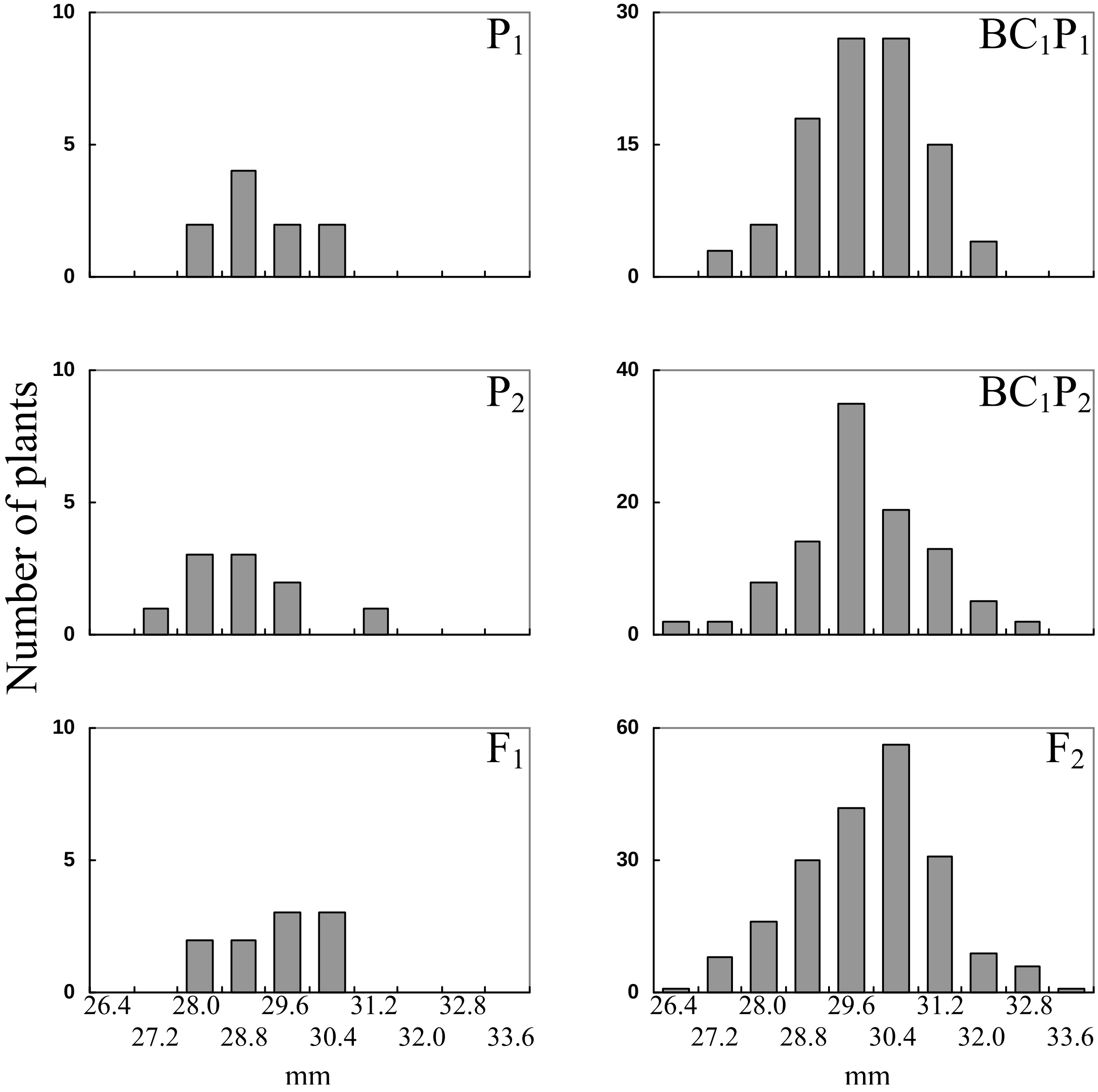

Fig. 12. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x near-long parental combination of Fibermax 832 (P_1) x TAM 94L-25 (P_2) in 2002.

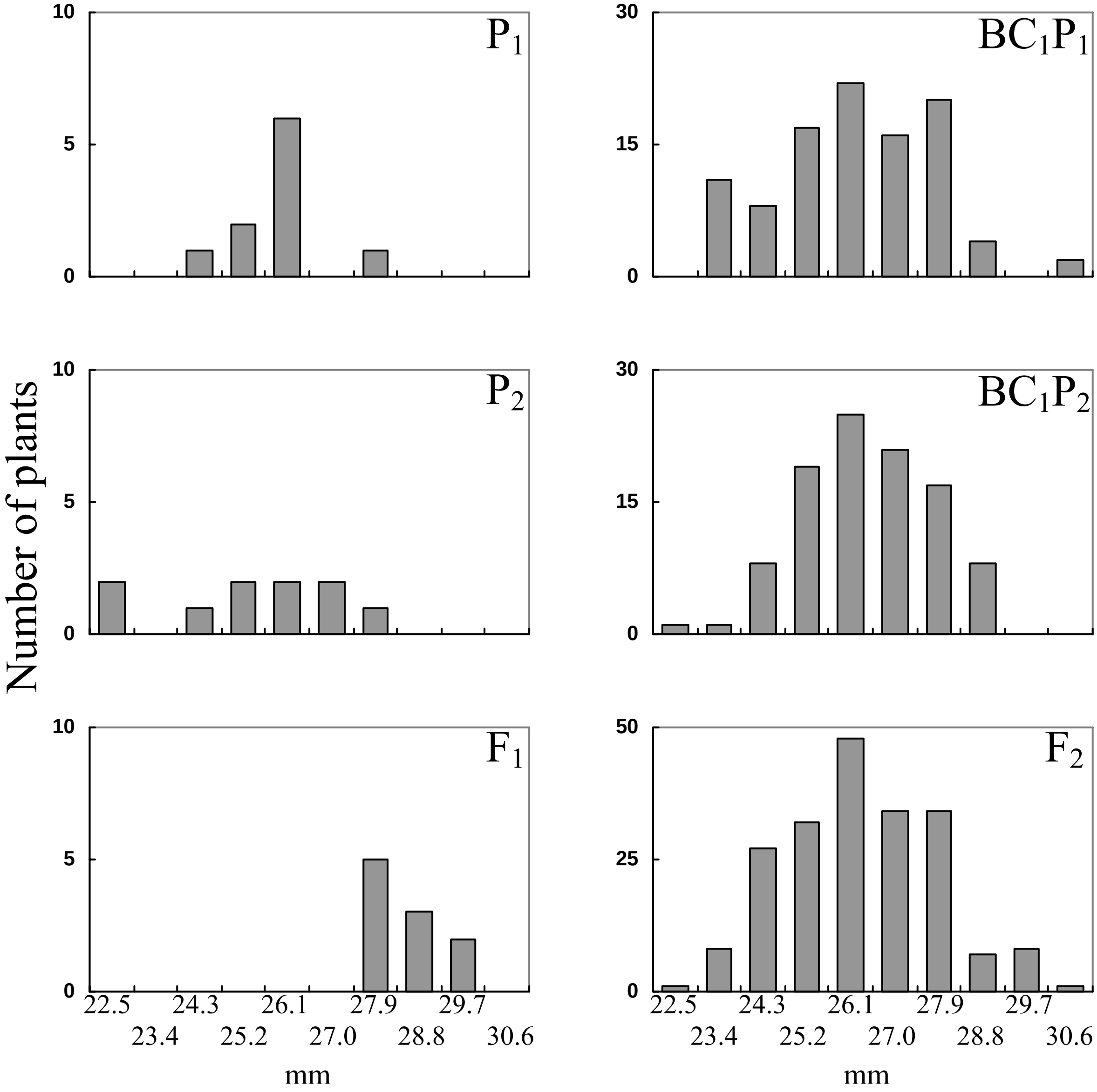

Fig. 13. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x near-long parental combination of TAM 94L-25 (P_1) x TTU 202 (P_2) in 2001.

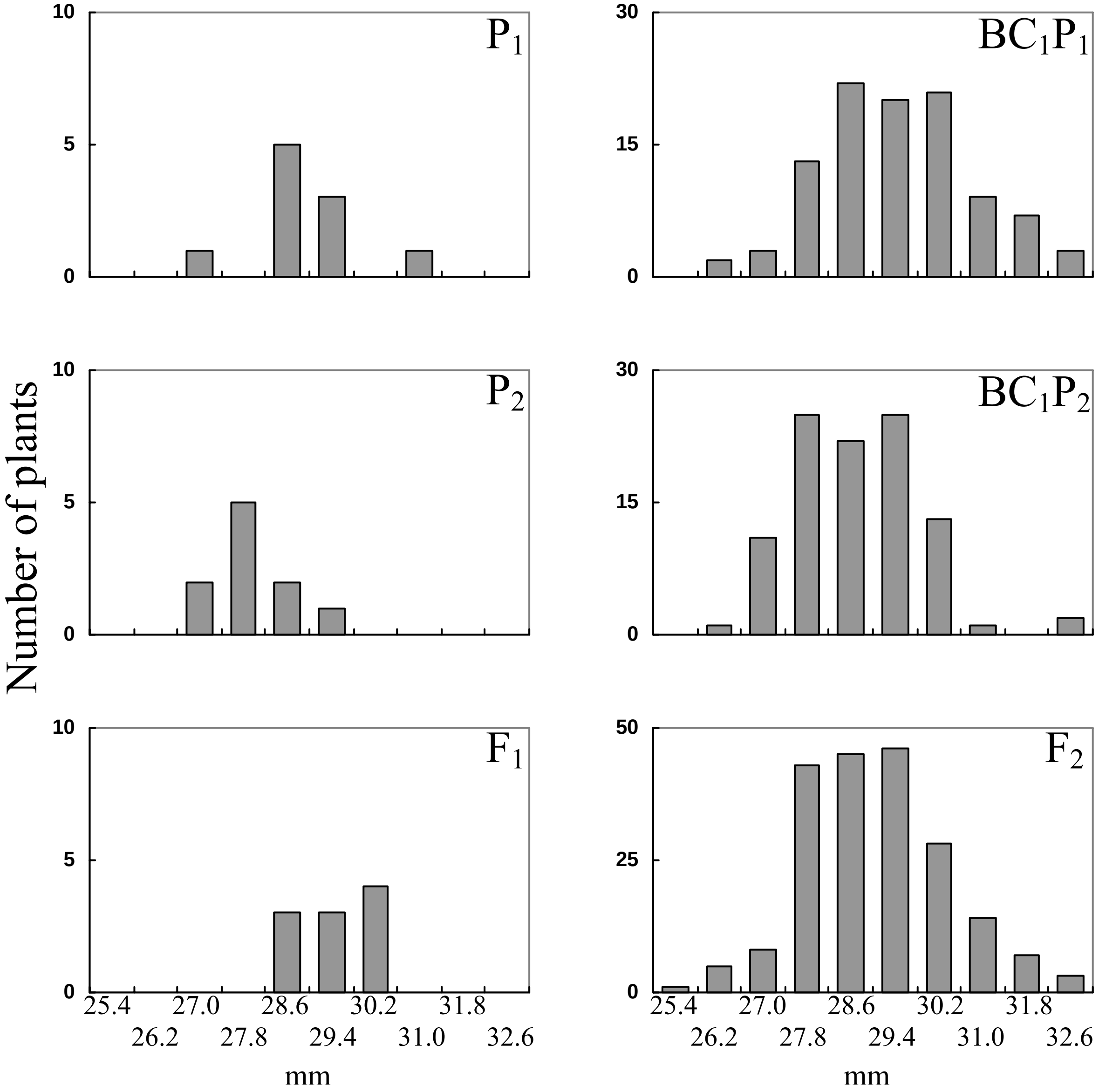

Fig. 14. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x near-long parental combination of TAM 94L-25 (P_1) x TTU 202 (P_2) in 2002.

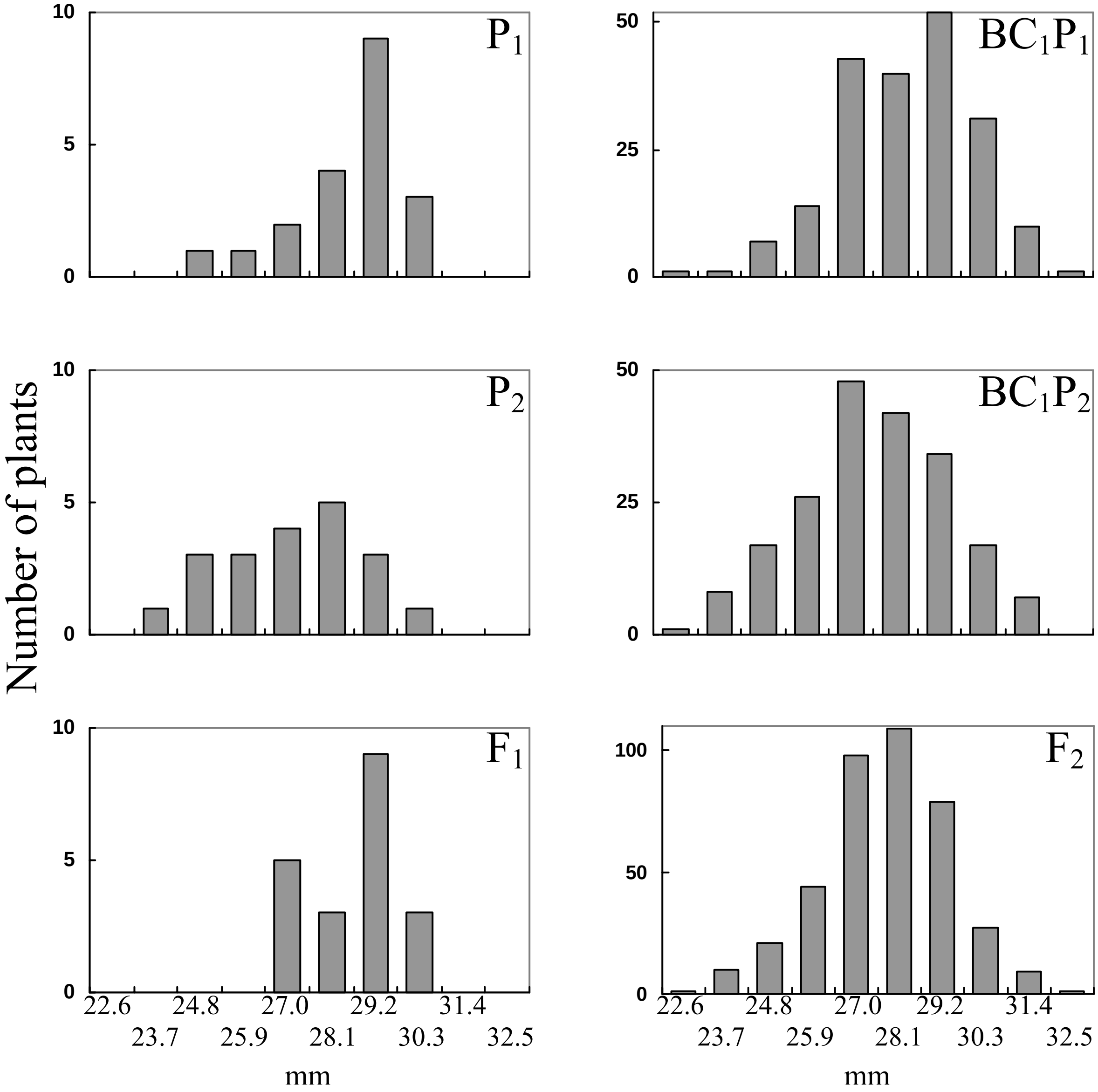

Fig. 15. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x near-long parental combination of Fibermax 832 (P_1) x Acala 1517-99 (P_2) across 2001 and 2002.

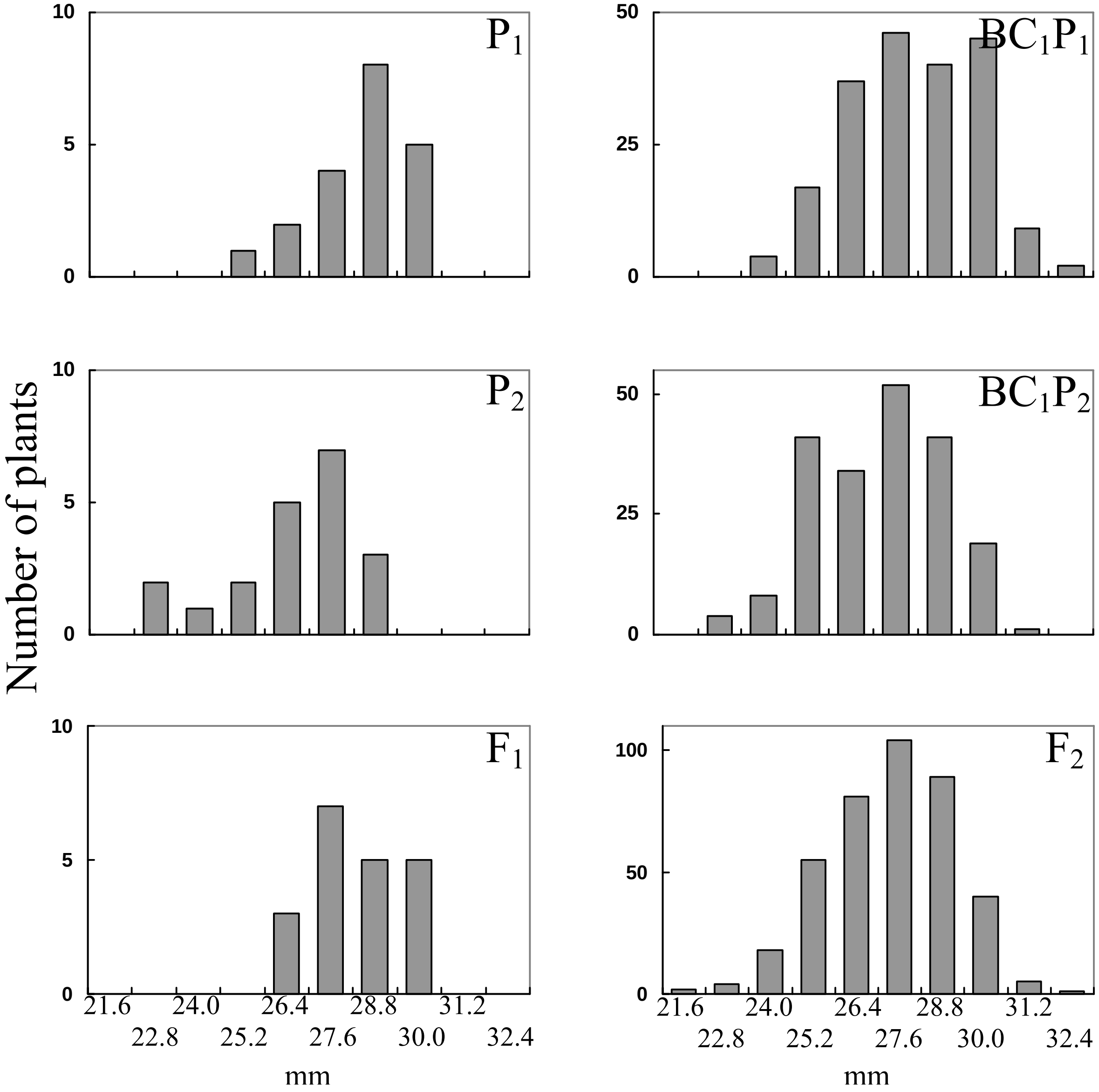

Fig. 16. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x near-long parental combination of Fibermax 832 (P_1) x TTU 202 (P_2) across 2001 and 2002.

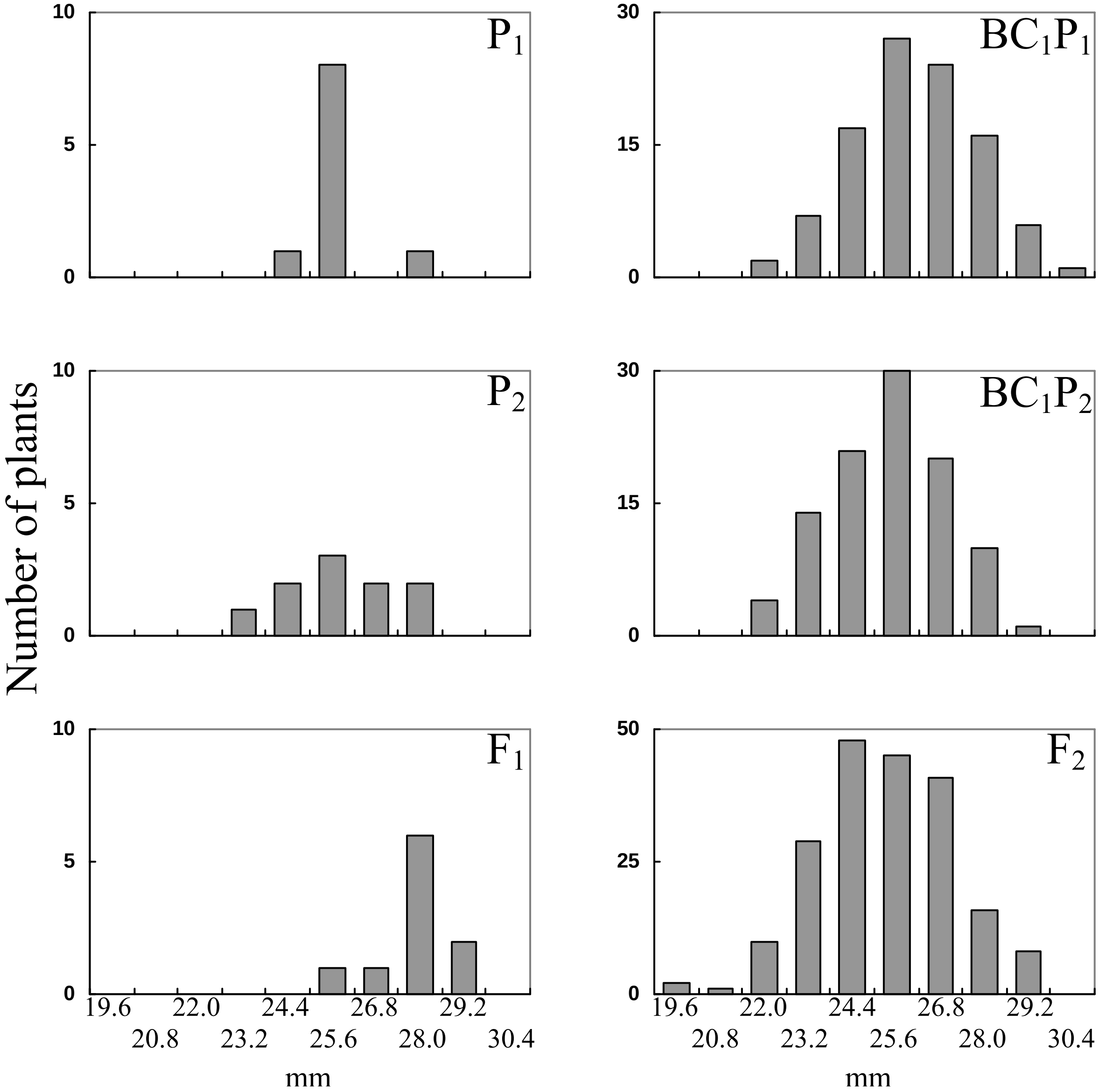

Fig. 17. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_1, and F_2 generations for the near-long x near-long parental combination of TAM 94L-25 (P_1) x Acala 1517-99 (P_2) in 2001.

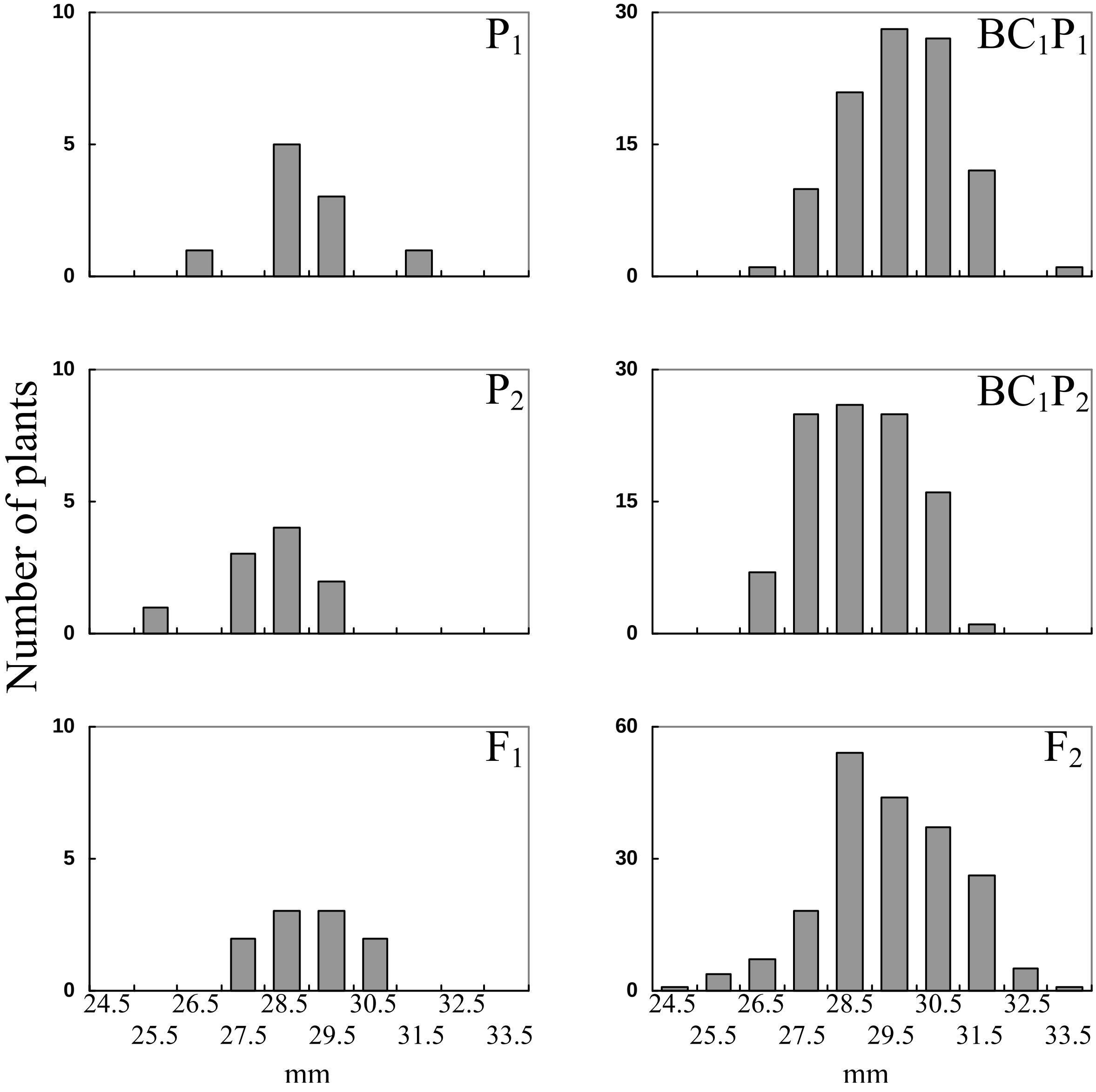

Fig. 18. Frequency distribution of FLw in the P$_1$, P$_2$, F$_1$, BC$_1$P$_1$, BC$_1$P$_2$, and F$_2$ generations for the near-long x near-long parental combination of TAM 94L-25 (P$_1$) x Acala 1517-99 (P$_2$) in 2002.

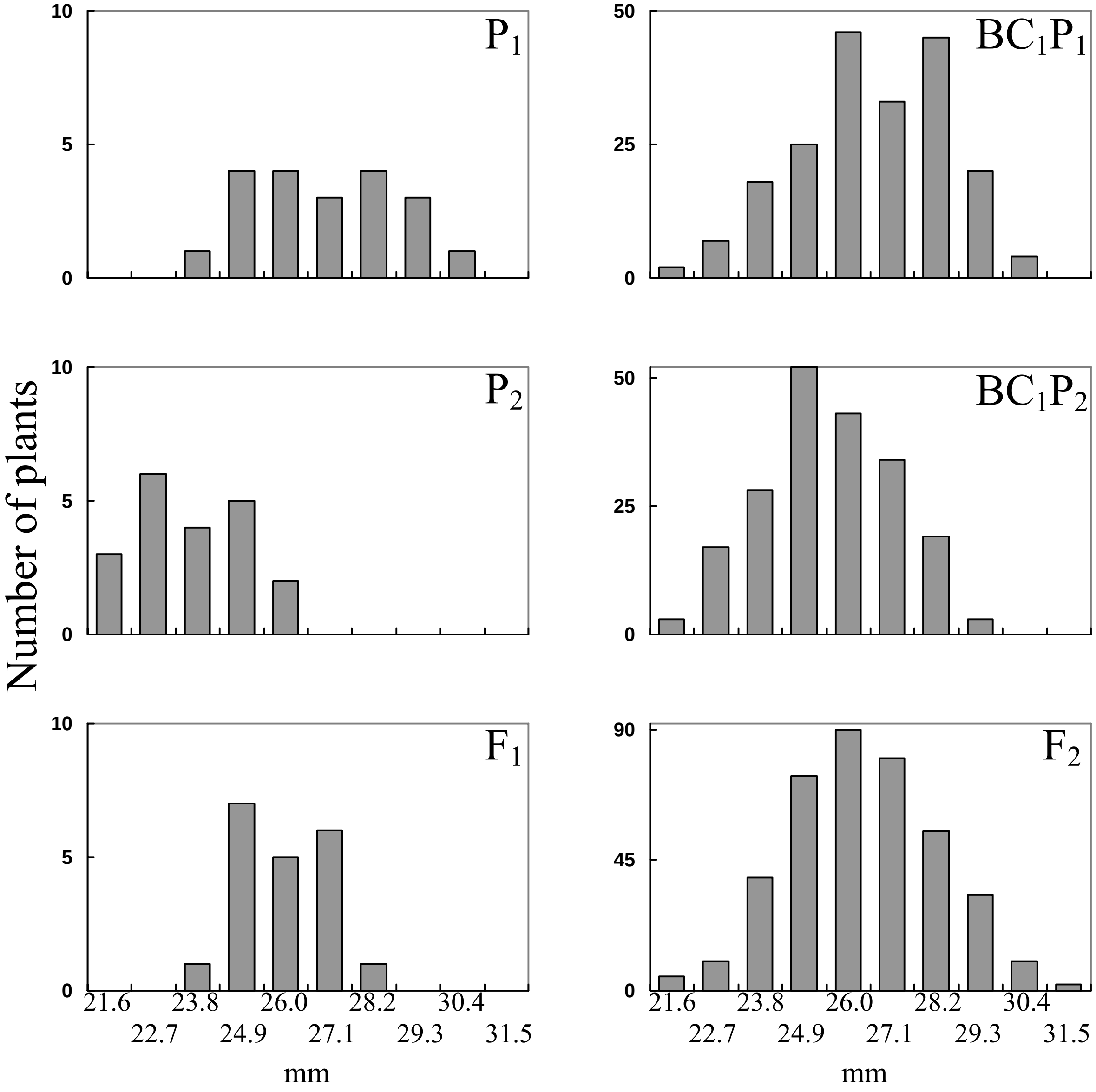

Fig. 19. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x near-long parental combination of Acala 1517-99 (P_1) x TTU 202 (P_2) across 2001 and 2002.

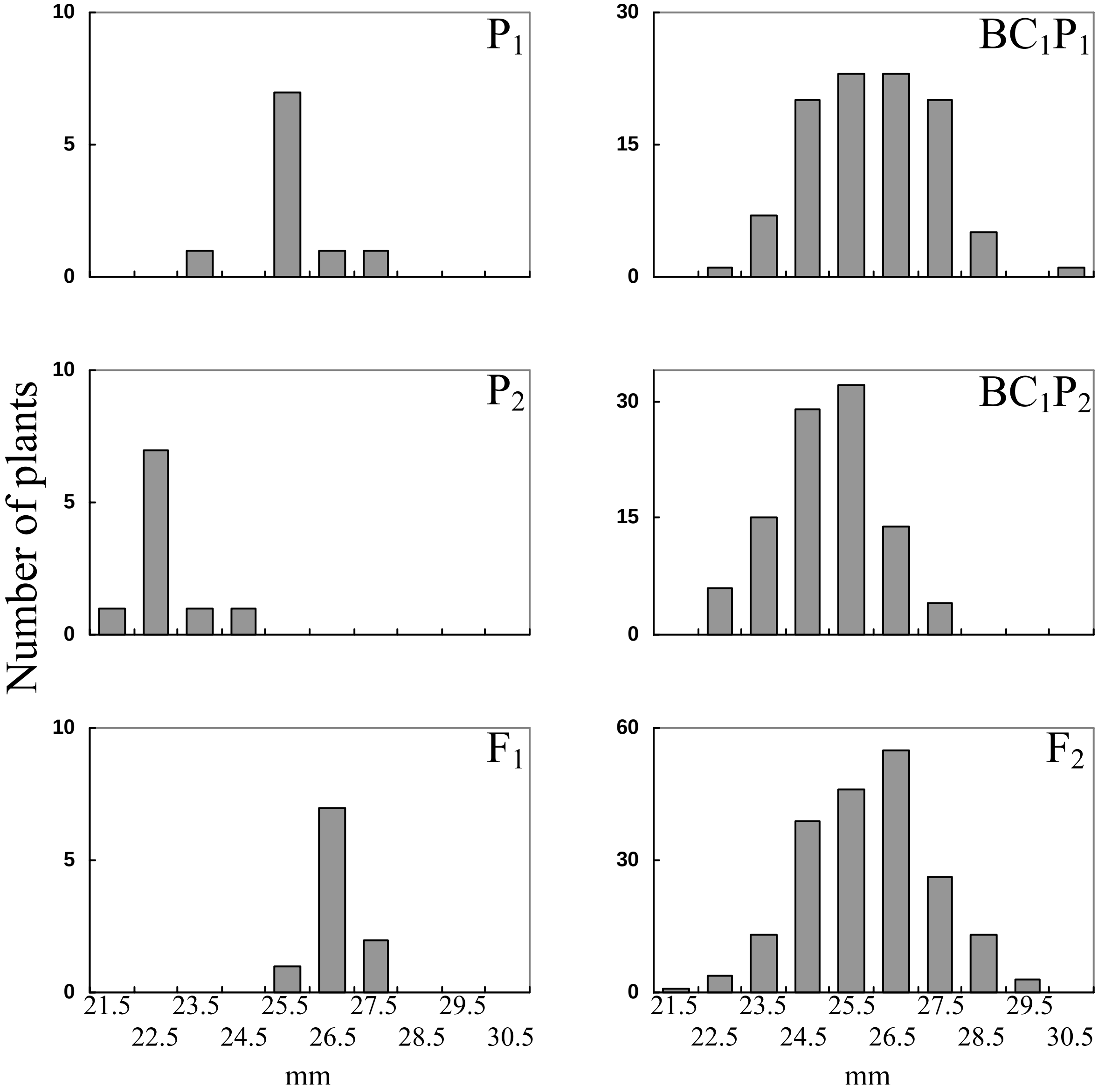

Fig. 20. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x short staple parental combination of TAM 94L-25 (P_1) x Tamcot CAMD-E (P_2) in 2001.

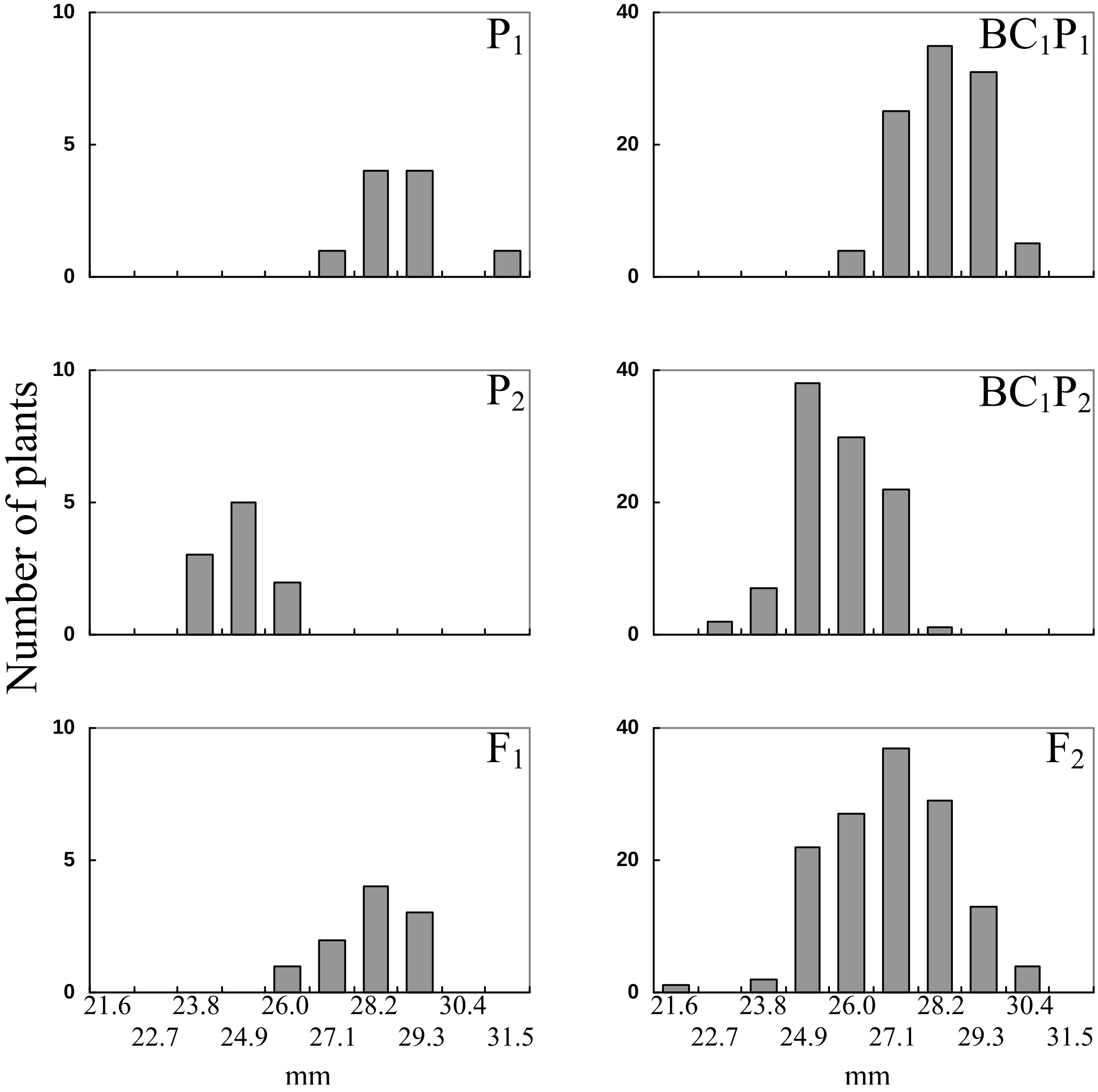

Fig. 21. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x short staple parental combination of TAM 94L-25 (P_1) x Tamcot CAMD-E (P_2) in 2002.

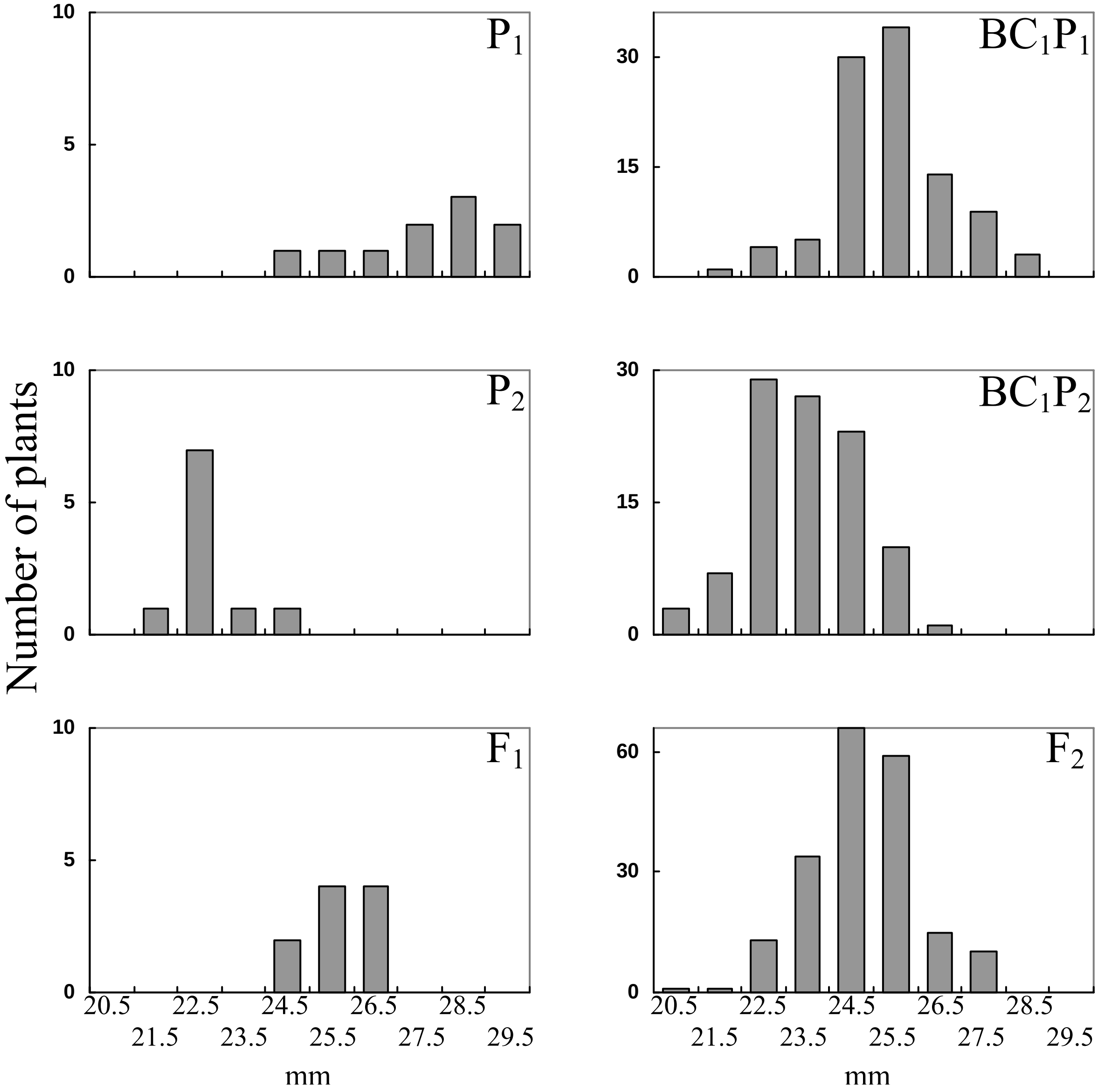

Fig. 22. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x short staple parental combination of Fibermax 832 (P_1) x Tamcot CAMD-E (P_2) in 2001.

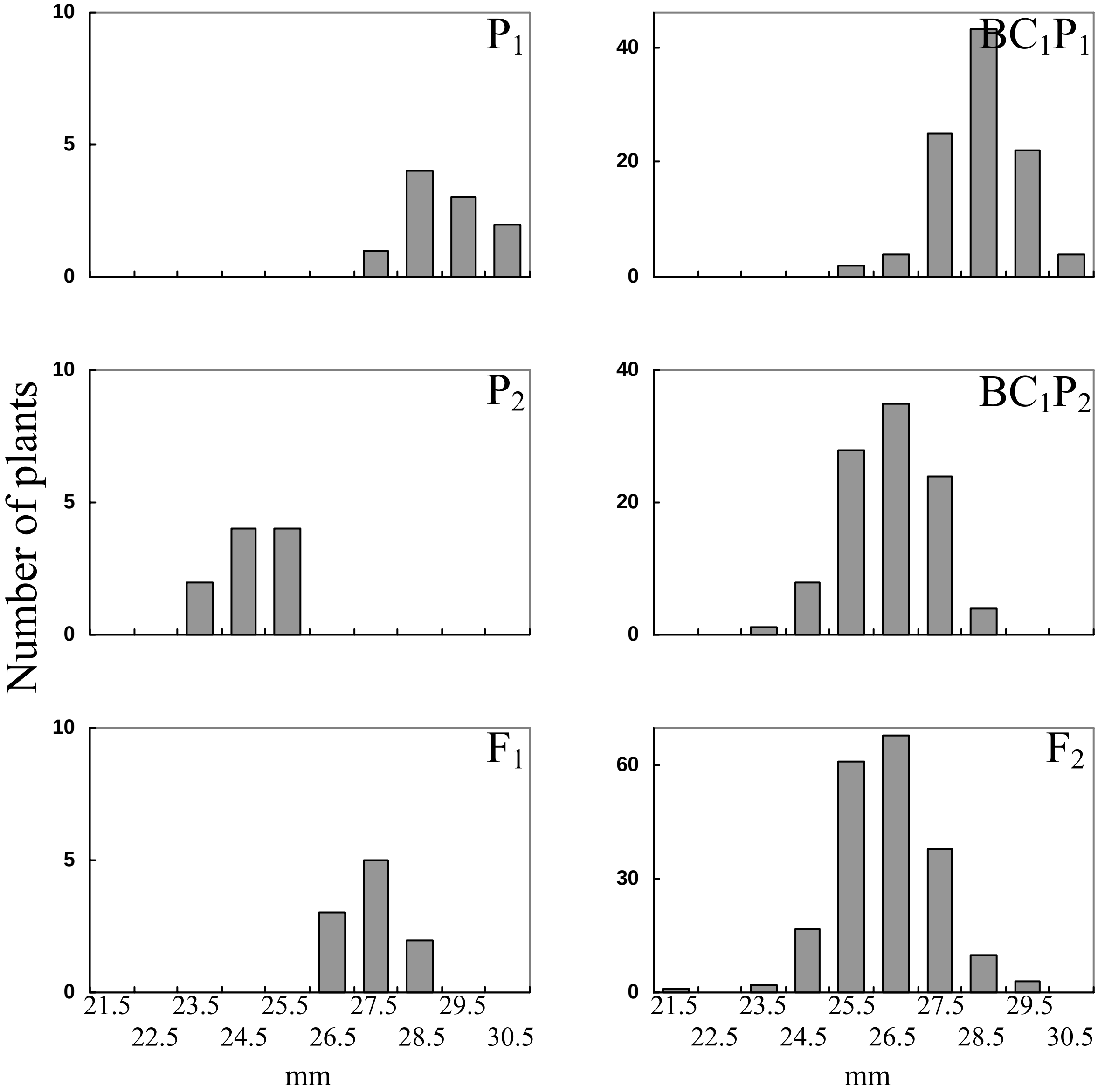

Fig. 23. Frequency distribution of FLw in the P$_1$, P$_2$, F$_1$, BC$_1$P$_1$, BC$_1$P$_2$, and F$_2$ generations for the near-long x short staple parental combination of Fibermax 832 (P$_1$) x Tamcot CAMD-E (P$_2$) in 2002.

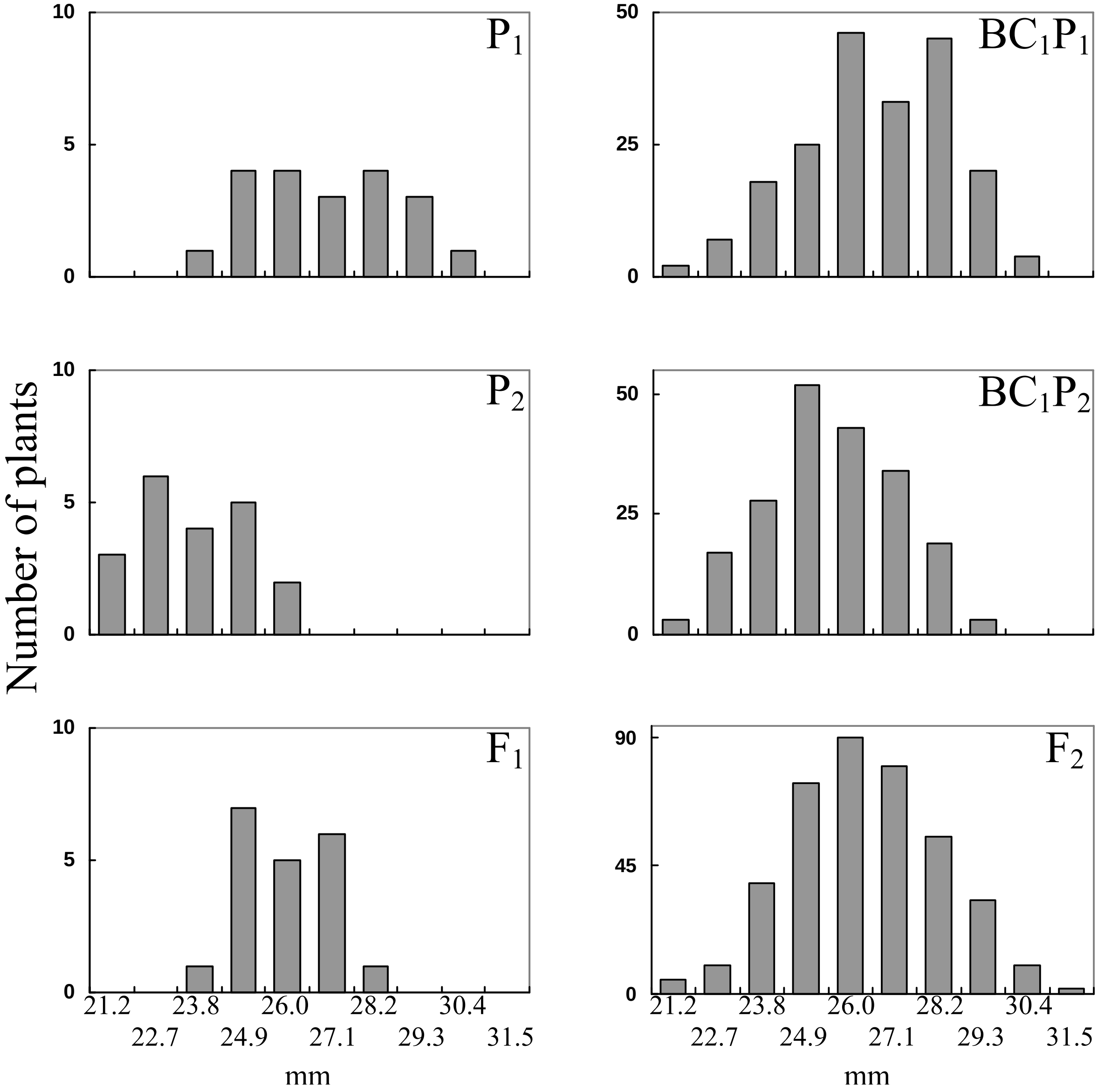

Fig. 24. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x short staple parental combination of Acala 1517-99 (P_1) x Tamcot CAMD-E (P_2) across 2001 and 2002.

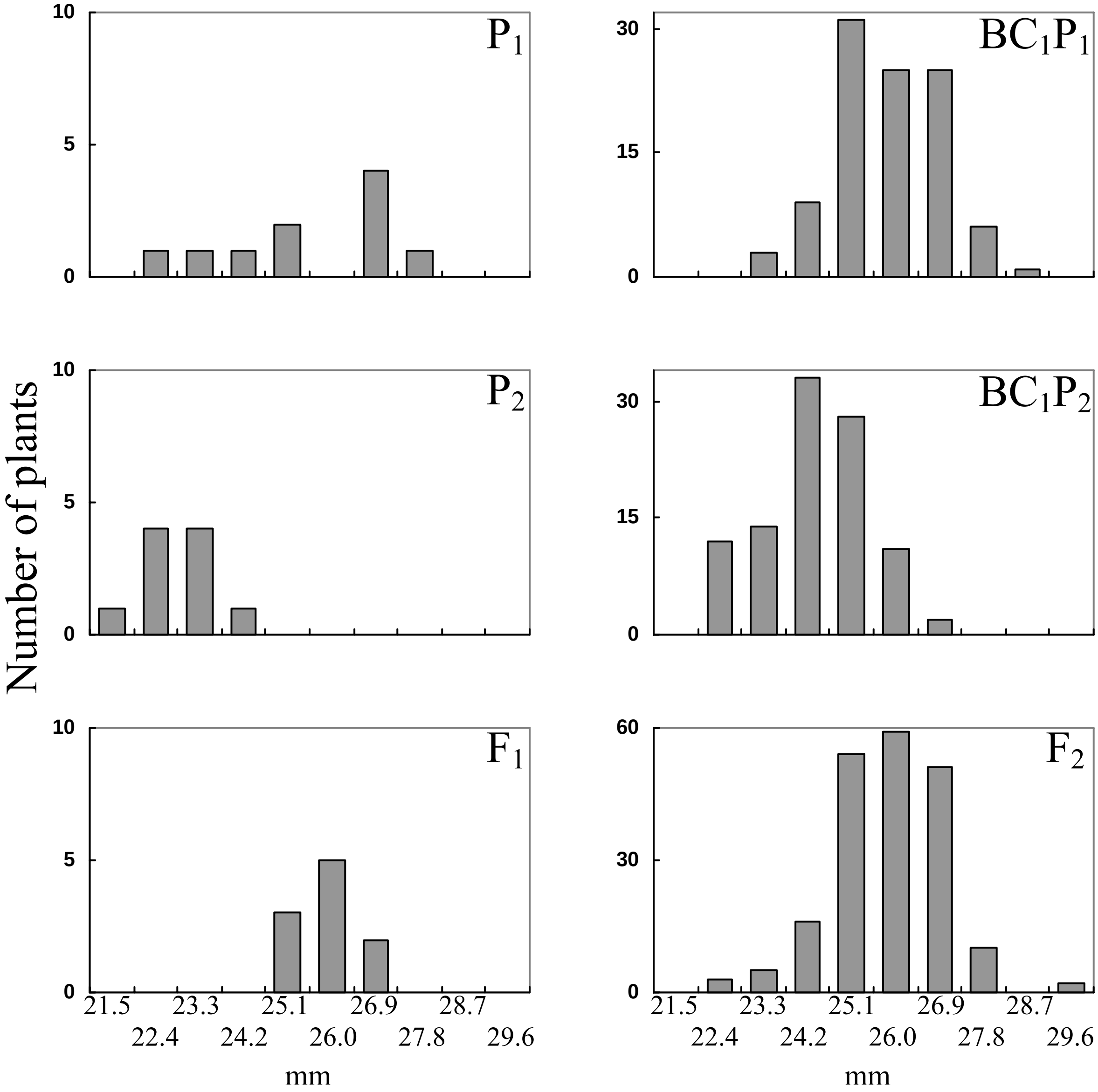

Fig. 25. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x short staple parental combination of TTU 202 (P_1) x Tamcot CAMD-E (P_2) in 2001.

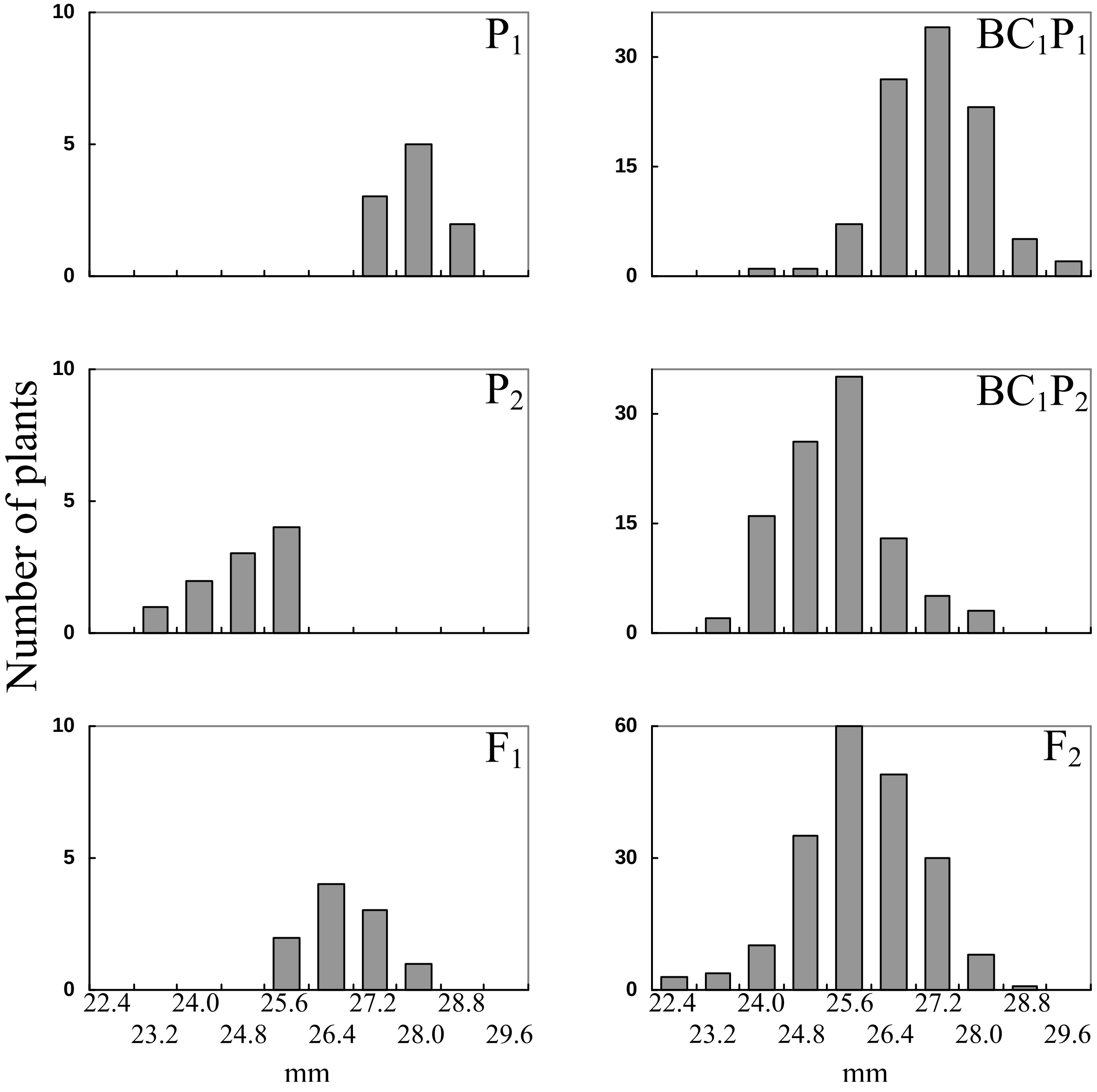

Fig. 26. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations for the near-long x short staple parental combination of TTU 202 (P_1) x Tamcot CAMD-E (P_2) in 2002.

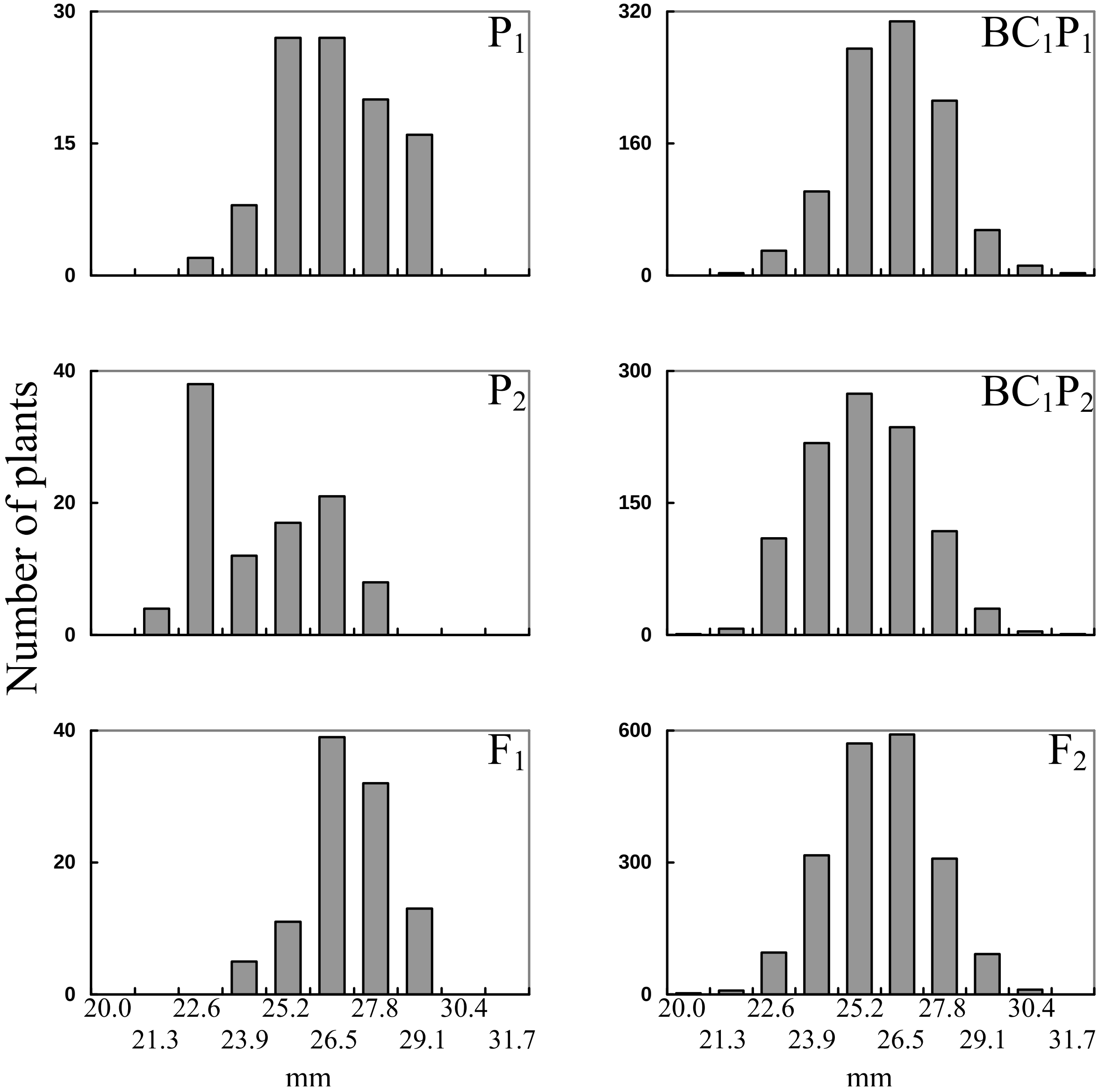

Fig. 27. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations among all parental combinations in 2001.

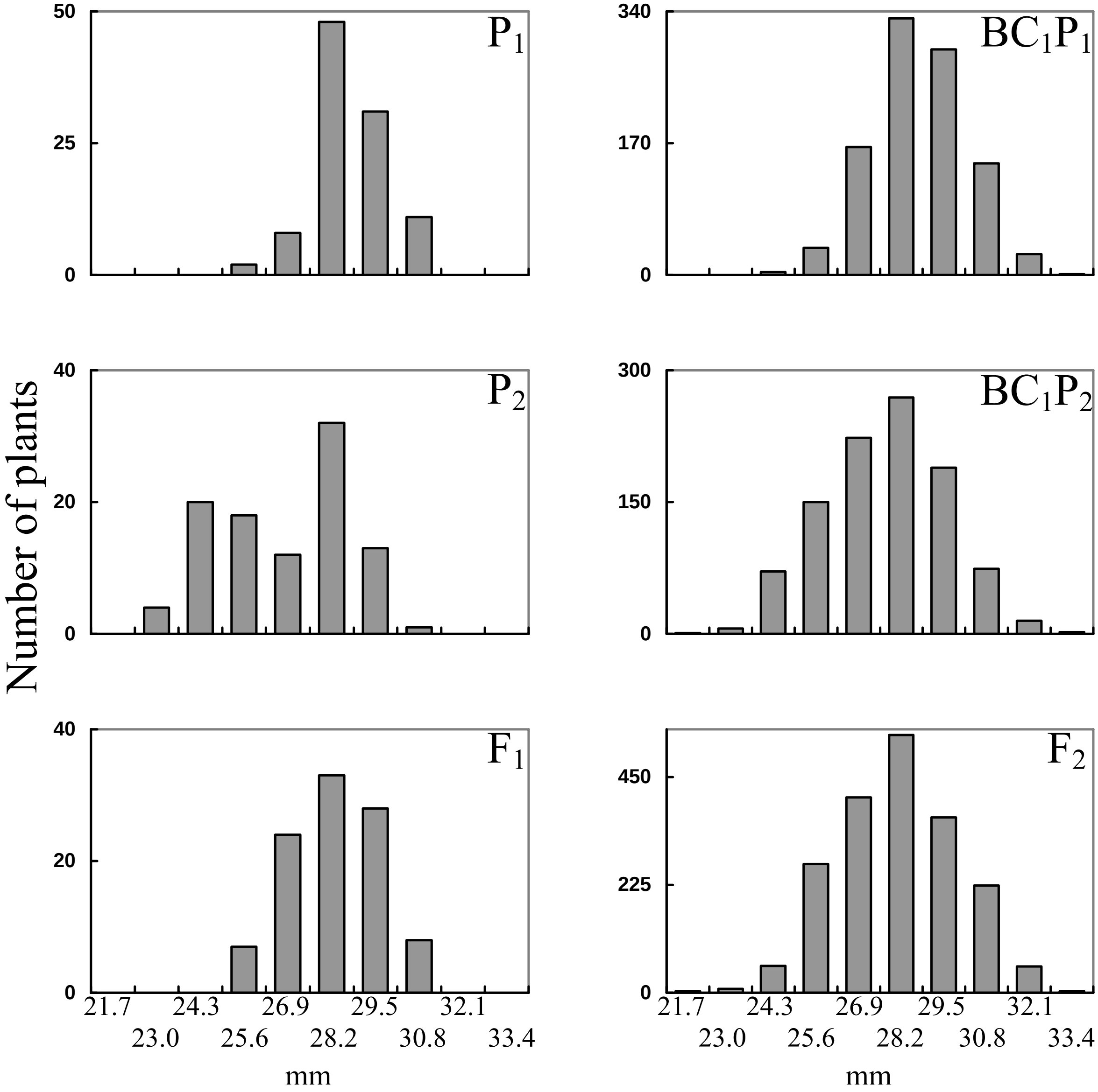

Fig. 28. Frequency distribution of FLw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generations among all parental combinations in 2002.

Generation mean analyses tested three- and six-parameter models for the best fit to explain genetic control of FLw in various upland parental combinations. Effects were first estimated with the three-parameter model and accepted if $P \geq 0.05$. The three-parameter model satisfactorily explained the genetic differences for FLw in TAM 94L-25 x TTU 202 in (Table 10). In this combination and environment, the variation among generation means was explained by the simple additive-dominance model, indicating that epistasis was not involved in the inheritance of the trait. The best approximation of additive and dominance effects can be obtained from the three-parameter additive-dominance model because these effects are unbiased due to the absence of epistasis (Hayman, 1958). TAM 94L-25 x TTU 202 in 2002 was the only near-long x near-long parental combinations to display significant additive effects with estimated values of 0.70 (Table 10). In 2002, TAM 94L-25 x TTU 202 was the only near-long x near-long parental combination to display a significant dominance effect with an estimated value two times larger than the additive effect.

In the near-long x near-long parental combinations for FLw, only significant additive x additive gene effect estimates were attained among the non-allelic interactions. Positive estimates were obtained in Fibermax 832 x TAM 94L-25 in 2001, Fibermax 832 x TTU 202 combined across years, TAM 94L-25 x Acala 1517-99 in 2001, and Acala 1517-99 x TTU 202 combined across years with values of 2.91, 0.98, 1.80, and 2.04, respectively, suggesting one parent contributed the alleles for FLw (Table 10). Among the near-long x near-long parental combinations, additive effects accounted for a smaller portion of the observed variability than dominance effects.

Table 10. Estimates of gene effects for FLw (per parental combination and among all combinations) at College Station, TX in 2001 and 2002.

		Gene effects†					
Parental Combinations	Year	*m*	*a*	*d*	*aa*	*ad*	*dd*
Fibermax 832 x TAM 94L-25‡	2001	23.80**	1.19	4.47	2.91**	-2.26	-0.67
Fibermax 832 x TAM 94L-25‡	2002	29.52**	0.18	1.25	-0.53	-0.30	-0.76
TAM 94L-25 x TTU 202‡	2001	25.41**	-0.10	0.76	-0.05	-0.20	1.80
TAM 94L-25 x TTU 202‡§	2002	28.38**	0.70**	1.38**	-	-	-
Fibermax 832 x Acala 1517-99‡	2001/02	27.52**	0.55	0.64	0.77	1.07	-0.24
Fibermax 832 x TTU 202‡	2001/02	27.22**	0.67	1.17	0.98*	0.22	0.72
TAM 94L-25 x Acala 1517-99‡	2001	23.85**	-0.03	1.18	1.80**	1.37	3.42
TAM 94L-25 x Acala 1517-99‡	2002	29.29**	0.16	0.86	-0.77	1.60	-1.44
Acala 1517-99 x TTU 202‡	2001/02	25.59**	0.30	3.38	2.04**	-0.73	-1.65
TAM 94L-25 x Tamcot CAMD-E¶	2001	25.96**	1.46**	-1.05	-1.82**	-1.18	1.87
TAM 94L-25 x Tamcot CAMD-E¶	2002	27.08**	2.06**	-1.81	-0.16	1.25	3.21*
Fibermax 832 x Tamcot CAMD-E¶	2001	26.62**	2.78**	-6.54**	-1.40**	-1.83	5.63**
Fibermax 832 x Tamcot CAMD- E¶	2002	22.68**	2.00**	9.97**	4.30**	-0.10	-5.50**
Acala 1517-99 x Tamcot CAMD-E¶	2001/02	25.85**	2.31**	2.51	-0.38	-2.01	-3.60**
TTU 202 x Tamcot CAMD-E¶	2001	27.29**	1.62*	-3.73	-2.92**	-0.33	1.61
TTU 202 x Tamcot CAMD-E¶	2002	24.96**	1.44**	2.10	1.31**	0.55	-0.51
Among all combinations	2001	25.39**	1.39**	-0.18	-0.45*	-0.79	1.80**
Among all combinations	2002	27.46**	0.66**	-0.30	0.61**	1.06*	2.35**

*, ** Significant at the 0.05 and 0.01 probability level on the basis of *t* test with n – 1 =5 degrees of freedom, respectively.

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

‡ Near-long x near-long parental combination.

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

¶ Near-long x short staple parental combination.

When reviewing all genetic effects, the relative magnitude of dominance or dominance x dominance effects were larger, except for Fibermax 832 x Acala 1517-99, in which additive x dominance effects were larger.

In the near-long x short staple parental combinations, the results of the three-parameter model analysis indicated that epistasis was present in all parental combinations. Therefore, the six-parameter model was used to determine the type and magnitude of gene effects involved in the inheritance of FLw. In 2001 and 2002, additive effects were significantly positive for all parental combinations (Table 10). Dominance effects were only significant in Fibermax 832 x Tamcot CAMD-E. In 2001, the dominance estimate was negative with a value of -6.54, while in 2002 it was positive with an estimated value of 9.97. The direction of response of the dominance effect is a function of the F_1 mean value in relation to the mid-parent value and indicates which parent was contributing to the dominance effect. In 2001, the dominance effect was contributed by the alleles differing in Tamcot CAMD-E, while in 2002 the dominance effect was contributed by the alleles differing in Fibermax 832. Additive x additive effects were significant in all parental combinations except for TAM 94L-25 x Tamcot CAMD-E in 2002 and Acala 1517-99 x Tamcot CAMD-E in 2002. In 2001, negative additive x additive effects were obtained in TAM 94L-25 x Tamcot CAMD-E, Fibermax 832 x Tamcot CAMD-E, and TTU 202 x Tamcot CAMD-E, indicating gene pairs responsible for FLw are in dispersive form (Mather and Jinks, 1977). This means both parents contributed alleles for FLw. In 2002, positive additive x additive estimates were produced in Fibermax 832 x Tamcot CAMD-E, and TTU 202 x Tamcot CAMD-E.

Dominance x dominance effects were significant in all near-long x short staple parental combinations except for TAM 94L-25 x Tamcot CAMD-E in 2001 and TTU 202 x Tamcot CAMD-E in 2001 and 2002. Dominance x dominance effects were positive in TAM 94L-25 x Tamcot CAMD-E in 2002 and Fibermax 832 x Tamcot CAMD-E in 2001 with values of 3.21 and 5.63, respectively. Dominance x dominance effects were negative in Fibermax 832 x Tamcot CAMD-E in 2002 and Acala 1517-99 x Tamcot CAMD-E with values of -5.50 and -3.60, indicating a decrease of FLw. In 2001, the dominance effect of Fibermax 832 x Tamcot CAMD-E was negative while the dominance x dominance effect was positive. The contrasting direction of response among the dominance and dominance x dominance effects suggest negative duplicate epistasis (Kearsey and Pooni, 1996). For this same parental combination in 2002, the direction of response was reversed suggesting positive duplicate epistasis.

Generation means analysis indicated that genetic control for FLw among near-long x short staple parental combinations is complex, involving multiple alleles with several effects contributing significantly to the inheritance of FLw. Generally, dominance effects were larger than additive effects, but additive effects were significant more often than dominance effects because the generation means analysis produced larger standard errors for dominance than for additive effects (data not shown). Also, dominance x dominance effects accounted for a larger portion of the observed variability than additive x additive effects. Among all combinations in 2001, additive, additive x additive, and dominance x dominance effects were significant with dominance x dominance effects being the largest in magnitude (Table 10). Among all combinations in 2002, additive, additive x additive, additive x dominance, and dominance x dominance effects were significant with dominance x dominance effects being the largest in magnitude.

Variance components and broad- and narrow-sense heritability estimates for FLw were calculated to determine the relative importance of the various determinants of the phenotype, the extent to which individuals' phenotypes are determined by their genotypes, and the extent to which phenotypes are determined by the alleles transmitted from the parents (Falconer and MacKay, 1996). Environmental variance among the ten near-long x near-long parental combinations ranged from 0.62 to 2.09 with an average of 1.33, while the near-long x short staple parental combinations ranged from 0.42 to 1.84 with an average of 0.92 (Table 11). The additive variance among the near-long x near-long parental combinations ranged from 0.00 to 1.90 with an average of 0.68, while the near-long x short staple parental combinations ranged from 0.00 to 2.10 with an average of 0.72. The dominance variance among the near-long x near-long parental combinations ranged from 0.00 to 1.25 with an average of 0.67, while the near-long x short staple parental combinations ranged from 0.00 to 0.89 with an average of 0.32. Among all combinations in 2001, the environmental, additive, and dominance variance was 2.35, 0.00, and 0.11, respectively. Among all combinations in 2002, the environmental, additive, and dominance variance was 2.09, 1.40, and 0.00, respectively.

Among the near-long x near-long parental combinations in 2001 and 2002, broad- (H^2) and narrow-sense (h^2) heritability estimates averaged 0.50 and 0.24, respectively (Table 11). Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, and

Table 11. Variance components and broad (H^2) and narrow (h^2) sense heritability estimates for FLw for 10 parental combinations grown at College Station, TX in 2001 and 2002.

		Variance components†			Heritability estimates	
Parental Combinations	Year	σ^2_E	σ^2_A	σ^2_D	H^2	h^2
Fibermax 832 x TAM 94L-25‡	2001	1.07	0.39	1.25	0.61	0.14 ± 0.05
Fibermax 832 x TAM 94L-25‡	2002	0.93	0.59	0.11	0.43	0.36 ± 0.04
TAM 94L-25 x TTU 202‡	2001	1.16	0.45	0.73	0.50	0.19 ± 0.04
TAM 94L-25 x TTU 202‡	2002	0.62	0.10	0.95	0.63	0.06 ± 0.05
Fibermax 832 x Acala 1517-99‡	2001/02	2.00	-0.88	0.65	0.25	0.00 ± 0.05
Fibermax 832 x TTU 202‡	2001/02	1.95	0.16	1.00	0.37	0.05 ± 0.04
TAM 94L-25 x Acala 1517-99‡	2001	0.99	1.83	0.60	0.71	0.54 ± 0.03
TAM 94L-25 x Acala 1517-99‡	2002	1.14	1.90	-0.61	0.63	0.63 ± 0.02
Acala 1517-99 x TTU 202‡	2001/02	2.09	0.67	0.78	0.41	0.19 ± 0.03
TAM 94L-25 x Tamcot CAMD-E§	2001	0.42	0.83	0.89	0.80	0.39 ± 0.03
TAM 94L-25 x Tamcot CAMD-E§	2002	0.90	2.10	-0.82	0.70	0.70 ± 0.01
Fibermax 832 x Tamcot CAMD-E§	2001	0.95	-0.04	0.46	0.33	0.00 ± 0.05
Fibermax 832 x Tamcot CAMD- E§	2002	0.70	0.51	-0.10	0.42	0.42 ± 0.03
Acala 1517-99 x Tamcot CAMD-E§	2001/02	1.84	0.69	0.86	0.46	0.20 ± 0.03
TTU 202 x Tamcot CAMD-E§	2001	1.06	0.14	0.05	0.15	0.11 ± 0.05
TTU 202 x Tamcot CAMD-E§	2002	0.57	0.75	-0.05	0.57	0.57 ± 0.03
Among all combinations	2001	2.35	-0.36	0.11	0.04	0.00 ± 0.01
Among all combinations	2002	2.09	1.40	-0.10	0.40	0.40 ± 0.00

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

‡ Near-long x near-long parental combination.

§ Near-long x short staple parental combination.

1517-99 x TTU 202 were the three parental combinations in which the ANOVA indicated no significant generation x environment interaction and, thus, the data of 2001 and 2002 were pooled together. The lower heritability estimates for these three parental combinations is due to the generation x environment interaction being accounted for in the total phenotypic variance. Fibermax 832 x Acala1517-99 had the lowest genetic variance due to the absence of any additive variance and in conjunction with the highest environmental variance had low broad- and zero narrow-sense heritability estimates. TAM 94L-25 x TTU 202 and Fibermax 832 x TTU 202 had low additive variances which correlated into low narrow-sense heritability estimates of 0.06 and 0.05, respectively. Within the Fibermax 832 x TAM 94L-25 parental combination, the total genetic variance was higher in 2001 and corresponded to a higher broad-sense heritability estimate, however, the lower environmental variance, higher additive variance, and lower dominance variance translated to a higher narrow-sense heritability estimate in 2002 than in 2001. Within the TAM 94L-25 x TTU 202 parental combination, higher total genetic variance was attained in 2001, however, a higher broad-sense heritability estimate was obtained in 2002 because of a lower environmental variance. The narrow-sense heritability estimate was higher in 2001 due to the higher additive variance. In 2002, the zero dominance variance within the TAM 94L-25 x Acala 1517-99 parental combination led to an increased narrow-sense heritability estimate of 0.63, compared to the narrow-sense heritability estimate of 0.54 in 2001. The Acala 1517-99 x TTU 202 parental combination had the highest environmental variance which lowered the broad- and narrow-sense heritability estimates.

Among the near-long x short staple parental combinations in 2001 and 2002, broad- and narrow-sense heritability estimates averaged 0.49 and 0.34, respectively (Table 11). In 2002, the higher additive variance and zero dominance variance in TAM 94L-25 x Tamcot CAMD-E, Fibermax 832 x Tamcot CAMD-E, and TTU 202 x Tamcot CAMD-E parental combinations resulted in higher narrow-sense heritability estimates. In 2001, TAM 94L-25 x Tamcot CAMD-E had a lower environmental variance and positive dominance variance which translated into higher broad-sense heritability estimate. Also in 2001, the zero additive variance in Fibermax 832 x Tamcot CAMD-E corresponded to a 0.00 narrow-sense heritability estimate. Acala 1517-99 x Tamcot CAMD-E was analyzed across 2001 and 2002 and had the highest environmental variance among all near-long x short staple parental combinations. The broad- and narrow-sense heritability estimates took into account the generation x environment interaction in the total phenotypic variance. In comparing TTU 202 x Tamcot CAMD-E in 2001 to 2002, environmental variance was higher, additive variance was lower, and total genetic variance was lower which corresponded into the lower broad- and narrow-sense heritability estimates.

Among all combinations in 2001, the broad- and narrow-sense heritability estimates were 0.04 and 0.00 (Table 11). Among all combinations in 2002, the broad- and narrow-sense heritability estimates were 0.40 and 0.40.

Estimates of additive effects could be small due to a high degree of dispersion of alleles increasing FLw between parents. This might explain why the additive genetic components of variance varied greatly and a definitive relationship between additive effects and additive genetic variance could not be detected. The negative estimates of dominance variance seen in this study could have been due to sampling error and/or the fact that basic generations are inefficient when used for determining dominance variance.

Summary and conclusions

Cotton is a natural product with lint characteristics determined by environmental and genetic factors. There is limited information available about the native fiber length distribution (i.e., on the seed), however it is believe that cotton possesses a normal fiber length distribution (probably is highly heritable) when bolls are hand picked cautiously and ginned carefully with a razor, tweezer, and aid of a microscope. Whatever the genetic determination of length distribution, the mechanical operations in harvesting, ginning, and textile manufacturing alter the distribution by breaking longer fibers into shorter ones (Anthony and Griffin, 2001a; Anthony and Griffin, 2001b; Robert et al., 2000). These successive stages of mechanical handling and processing incrementally but unavoidably inflict some fractures upon fibers being processed.

The degree of fiber breakage is dependent primarily upon fiber length, maturity, strength, and elongation. Longer fibers allow for a greater chance of tension forces being held at both ends, so they therefore have a higher probability of breakage than shorter fibers. Length distributions are also influenced by fiber maturity, and maturity is directly related to growing conditions. Immature fibers have underdeveloped, weak, thin secondary walls that are prone to break during mechanical processes. Fully mature fibers are less likely to be damaged or broken. The load, a specimen of a single fiber or bundle of fibers in its axial direction, at which the specimen breaks provides a measure of fiber strength. Fiber elongation, the increase in length of fiber during tensile loading, is important in determining the processing propensity of fibers and the mechanical behavior of yarn. Two cottons with the same strength, but with different elongations will behave differently under mechanical stresses.

The environment influenced the magnitude of FLw in 2001 and 2002. The mean responses of the generations indicated that plants had longer fibers by weight in 2002 than in 2001. The climatological conditions of the two years were normal in terms of temperature and rainfall. However, rainfall events at physiological maturity during 2001 extended the harvesting period and thus weathering of the fiber might have shortened the mean fiber length (Hequet, 2004). Significant generation x environment interactions were detected in most parental combinations but mostly were due to changes in magnitude and not changes in genotype rank. No distinct relationship between genotypic means and gene effects could be detected. All near-long x near-long F_1 hybrids had an FLw mean similar to or greater than the longest parent suggesting dominance or overdominance, however, the generation means analysis does not substantiate this.

Frequency distributions of individual plant values revealed that the segregating populations followed a normal distribution, suggesting that FLw is quantitatively inherited. A higher percent of transgressive segregation appeared in the BC_1P_1 than in other segregating populations. However, most breeders will attempt to select superior individual plants among the F_2 population and continue selecting throughout subsequent generations with the goal of looking for transgressive segregants among a population of inbred lines derived from the selfing of an F_1 hybrid. The presence of transgressive segregation in the segregating populations of these near-long x near-long combinations suggest that the parental material chosen for this study contained different length alleles for FLw, thus suggesting that breeders could make further improvements for upland cotton fiber length among these near-long staple parental genotypes, but only if the appropriate breeding method is implemented. Cotton already has a narrow genetic base (Van Esbroeck et al., 1999) and limited progress in cultivar improvement has been made in recent years because closely-related parents have been used to make successful cultivars (Meredith, 1991; Meredith et al., 1997). Even though transgressive segregation was present in this study, it was at a low frequency and thus requires large populations for exploration. Most breeding programs use a pedigree method, in which seeds are harvested separately from each F_2 to produce F_3 families and continue to keep each F_2 pedigree distinct throughout successive generations. However, if any of the seeds are bulked between the F_2 to F_4 generation so that it is not possible to identify which seeds are derived from individual F_2 plants, considerable loss of already limited variability may occur.

In general, parental combinations were analyzed within individual environments for FLw. For most parental combinations, analyses of genetic effects indicated that a simple additive-dominance model did not account for most of the genetic variation for FLw. Therefore, a six-parameter model fit the generation means indicating that epistatic effects were present and suggested that inheritance is complex such that multiple alleles interacted to affect upland cotton fiber length. Among the near-long x near-long parental combinations, few significant gene effects were detected, possibly indicating a high degree of dispersion of alleles increasing FLw between parents. Among the near-long x short staple parental combinations, significant gene effects were numerous. Both additive and additive x additive effects were abundant in the expression of FLw, however the presence and magnitude of dominance x dominance effects can not be ignored. For the parental combinations that were controlled by additive gene action, simple selection in early segregating generations would be successful. Whereas for those parental combinations controlled by non-additive gene action, selection in later generations could prove to be more effective.

Several explanations of the inconsistent gene effects in this study can be proposed. First, parents used in this study were from vastly different genetic backgrounds. The dispersion of alleles in the parents, complete or partial, affects the magnitude and composition of the additive component. The mean and dominance components of the parents remain independent of gene dispersion. Two loci having an inter-allelic interaction will change the F_2 mean, the magnitude and direction of additive x additive and additive x dominance effects, and the magnitude and direction of the variances (Kearsey and Pooni, 1996). Higher order interactions, such as trigenic interactions, may be needed with enough generations to adequately understand the inheritance of cotton fiber length.

The environmental variance for FLw was moderate to high, contradicting May (1999) who concluded that extensive environmental replication is not necessary to evaluate and select breeding material on the basis of fiber length parameters. Among the near-long x near-long parental combinations, genetic control for FLw contained additive and non-additive genetic variance, but the greater portion was primarily non-additive, whereas among the near-long x short staple parental combinations, the additive gene effects were predominant. Numerous studies in the past concluded that additive variance within upland cotton genotypes tended to be more prominent than non-additive variance (Miller and Marani, 1963; Ramey and Miller, 1966; Lee et al., 1967; Al-Rawi and Kohel, 1969; Al-Rawi and Kohel, 1970; Meredith and Bridge, 1972; Quisenberry 1975; Green and Culp, 1990; Tang et al., 1993), however, a few experiments have found non-additive variance to be more important (Verhalen and Murray, 1969; Baker and Verhalen, 1973; May and Green, 1994; Cheatham et al., 2003).

The moderate broad-sense heritability estimates found in this study suggest that improvement for FLw can be realized through breeding if some of the genetic variation is additive in nature. Moderate to relatively high values for broad and narrow-sense heritability ($H^2 > 0.50$ and $h^2 > 0.50$) for fiber length parameters, 2.5% span length and UHM length, have been reported previously (May, 1999; May and Jividen, 1999; Herring et al., 2004). Depending upon the parental combination and environment, the sometimes moderate to high values for narrow-sense heritability found in this study suggest that conventional pedigree and early generation selection methods should be effective for initial improvements in FLw in cotton. However, most of the narrow-sense heritability estimates in this study were low, suggesting that the inheritance is complex and that selection of individual plants in an F2 population with improved FLw will not be as simple as indicated by the broad-sense heritability estimate.

Gene effects and variances for FLw were inherited quite differently in specific environments and specific parental combinations, suggesting environmentally specific mechanisms for FLw. This type of interaction would make selection of fiber length and superior genotypes that are adapted to wide geographic areas much more difficult. This would explain why improvement of fiber length in upland cotton has been slow, even though many genetic studies have indicated that fiber length is moderately to highly heritable. Cotton fiber length is a complex trait, and improved fiber length is the result of many different loci. These results show that both the adequacy of certain modes of inheritance as well as the importance and significance of gene effects were dependent upon the particular parental combination and environment, stressing the importance of the appropriate selection of both parents and environment for the success of a cotton breeding program.

CHAPTER VI

AFIS FLn GENERATION MEANS ANALYSIS

Results and discussion

The parental, F_1, F_2, and backcross generations differed ($P \leq 0.01$) in FLn, a length by number measurement, for all parental combinations except Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, TAM 94L-25 x Acala 1517-99, and Acala 1517-99 x TTU 202 (Table 12). The ANOVA also indicated a significant generation x environment interaction for all parental combinations except Fibermax 832 x Acala 1517-99 and Fibermax 832 x TTU 202, thus these two parental combinations were pooled over years. The other parental combinations indicated that some generations reacted differently to each environment, suggesting that selection and evaluation should be conducted with related environments if reliable knowledge of FLn is to be obtained.

FLn means from P_1 and P_2 were different ($P \leq 0.05$) in each parental combination except Fibermax 832 x TAM 94L-25 in 2002, TAM 94L-25 x TTU 202 in 2001, Fibermax 832 x Acala 1517-99 combined across years, TAM 94L-25 x Acala 1517-99 in 2002, and Acala 1517-99 x TTU 202 in both years (Table 13). Parents for this study were selected base upon HVI UHM, a length by weight measurement, and not a length by number measurement. In 2001, all F_1 hybrids had an FLn mean greater than or similar to the longest parent. In 2001, F_1 means of TAM 94L-25 x TTU 202, TAM 94L-25 x Acala 1517-99, TAM 94L-25 x Tamcot CAMD-E, and TTU 202 x Tamcot CAMD-E were greater than the longest parent, demonstrating heterosis. In 2002, no trend was observed in the F1 means. The F1 mean of TAM 94L-25 x Acala 1517-99 was shorter

Table 12. Mean squares for FLn measured on P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 (per parental combination and among all combinations) at College Station, TX in 2001 and 2002.

A.

		Parental Combinations†					
Source	df	832 x L-25	L-25 x 202	832 x 1517	832 x 202	L-25 x 1517	1517 x 202
Environment (E)	1	193.90**	169.21**	100.09**	134.35**	202.92**	106.00**
Reps/E	6	1.07	0.55	0.37	0.25	0.20	0.58
Generation (Gn)	5	1.56*	4.50**	1.30	2.54	0.91	0.79
Gn x E	5	3.86**	2.45**	1.23	1.11	5.05**	2.17*
Error	30	0.61	0.40	0.75	1.09	0.41	0.85

B.

		Parental Combinations‡				
Source	df	L-25 x CD-E	832 x CD-E	1517 x CD-E	202 x CD-E	Among
Environment (E)	1	86.22**	98.56**	120.29**	44.74**	121.43**
Reps/E	6	0.46	0.30	0.07	0.95	0.05
Generation (Gn)	5	6.98**	11.10**	6.89**	4.53**	2.25**
Gn x E	5	4.89**	2.11*	1.47**	3.45**	1.32**
Error	30	0.32	0.70	0.39	0.43	0.19

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

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

Table 13. Means of P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 for FLn (mm) per parental combination and among all combinations at College Station, TX in 2001 and 2002. First parent listed is P_1, second parent is P_2.

A.

	Parental Combinations†									
	832 x L-25		L-25 x 202		832 x 1517	832 x 202	L-25 x 1517		1517 x 202	
Gen.‡	2001	2002	2001	2002	2001/02	2001/02	2001	2002	2001	2002
P_1	21.3 a§	24.2 ab	18.8 c	24.0 a	22.7 a	22.7 a	18.8 c	24.0 a	19.9 a	23.9 a
P_2	18.8 b	24.0 ab	19.3 c	23.0 b	21.9 a	21.2 b	19.9 b	23.9 a	19.3 a	23.0 ab
F_1	21.3 a	23.2 b	22.3 a	24.3 a	22.8 a	22.1 ab	21.8 a	22.9 b	21.1 a	22.2 b
F_2	19.2 b	24.8 a	19.7 bc	23.9 a	22.1 a	21.7 ab	19.0 bc	24.4 a	19.9 a	23.0 ab
BC_1P_1	20.2 ab	24.5 a	19.7 bc	24.1 a	22.3 a	22.4 a	19.7 bc	24.0 a	20.5 a	23.0 ab
BC_1P_2	20.0 ab	24.2 ab	20.6 b	23.7 ab	21.9 a	21.7 ab	19.2 bc	23.8 a	19.4 a	22.9 ab

B.

	Parental Combinations¶									
	L-25 x CD-E		832 x CD-E		1517 x CD-E		202 x CD-E		Across	
Gen.	2001	2002	2001	2002	2001	2002	2001	2002	2001	2002
P_1	18.8 c	24.0 a	21.3 a	24.2 a	19.9 a	23.9 a	19.3 b	23.0 a	20.1 b	23.9 a
P_2	17.8 d	21.0 d	17.8 c	21.0 c	17.8 b	21.0 d	17.8 c	21.0 cd	18.8 c	22.4 c
F_1	20.8 a	22.9 b	20.5 ab	21.8 c	19.7 a	21.2 d	20.4 ab	21.7 bc	21.1 a	22.7 bc
F_2	20.5 ab	21.8 c	19.0 bc	21.0 c	19.8 a	23.0 b	20.9 a	20.9 cd	19.9 b	23.0 b
BC_1P_1	19.7 bc	23.1 b	19.0 bc	22.9 b	19.6 a	23.4 ab	20.3 ab	22.4 ab	20.0 b	23.6 a
BC_1P_2	19.6 bc	20.5 d	18.1 c	22.0 bc	18.7 ab	22.1 c	19.4 b	20.8 d	19.5 bc	22.7 bc

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ Gen., generation; 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 K = 100 (approximates p = 0.05) according to Waller-Duncan LSD.

¶ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

than all other generations. No trend was observed in F_2 means for either year. In 2001, the F_2 mean of TAM 94L-25 x Tamcot CAMD-E and TTU 202 x Tamcot CAMD-E, which were greater than either parents, once again suggesting heterosis. Among all parental combinations, BC_1P_1 and BC_1P_2 means were not different except for the 2002 combinations of TAM 94L-25 x Tamcot CAMD-E and TTU 202 x Tamcot CAMD-E.

As with FLw, the parental combinations were divided into two categories, near-long x near-long and near-long x short staple parental combinations. For each parental combination, P_1 was assigned accordingly to the parent with the longest FLw. The near-long x near-long parental combinations consisted of Fibermax 832 x TAM 94L-25, TAM 94L-25 x TTU 202, Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, TAM 94L-25 x Acala 1517-99, and Acala 1517-99 x TTU 202. The near-long x short staple parental combinations were Fibermax 832, TAM 94L-25, Acala 1517-99, and TTU 202 crosses with Tamcot CAMD-E.

FLn frequency distributions of each parental combination were constructed to visually gain a more comprehensive understanding of the generation means and to determine transgressive segregation (Figs. 29-48). For each figure the y-axis is the number of plants, and the x-axis is FLn in mm divided into 10 length classes. Classes within each figure are the same for the non-segregating and segregating populations. However, overall range and class size does change from figure to figure.

Examination of the frequency distribution of individual plant values of each parental combination indicated that the segregating populations followed a normal distribution, suggesting that FLn is quantitatively inherited. Transgressive segregation, i.e., individual F_2 or backcross plant observations with values exceeding the longest parent or F_1 observation (Kearsey and Pooni, 1996), was visible in near-long x near-long and near-long x short staple parental combinations. At least one segregating population in all near-long x near-long parental combinations exhibited transgressive segregation except for Fibermax 832 x Acala 1517-99 combined across years (Fig. 33). Averaging the percent of plants exhibiting transgressive segregation for each segregating population among the 10 near-long x near-long parental combinations, the BC_1P_1 had the highest transgressive segregation at 2.3%, followed by the F_2 at 2.0%, and the BC_1P_2 at 1.0%. In 2001, the BC_1P_1 population of Acala 1517-99 x TTU 202 had the highest percentage of transgressive segregation, 8.0% (Fig. 37). In 2002, TAM 94L-25 x Acala 1517-99 had the highest percent of transgressive segregation among the BC_1P_2 and F_2 populations at 5.0 and 7.0%, respectively (Fig. 36). Fewer transgressive segregates appeared in the near-long x short staple segregating populations, and negligible numbers appeared in the backcross to Tamcot CAMD-E (Figs. 39-46). In 2001, TAM 94L-25 x Tamcot CAMD-E and TTU 202 x Tamcot CAMD-E had high percentages of BC_1P_1 and F_2 transgressive segregation, 8.0 and 15.5% and 8.0 and 21.5%, respectively (Figs. 39 and 45). TAM 94L-25 x Tamcot CAMD-E also had 5% transgressive segregation in the BC_1P_2 population.

Generation mean analyses using three- and six-parameter models were utilized to explain the genetic control of FLn in these upland parental combinations across 2001 and 2002. Effects were first estimated with the three-parameter model and accepted if $P \geq 0.05$. The three-parameter model satisfactorily explained the genetic differences for

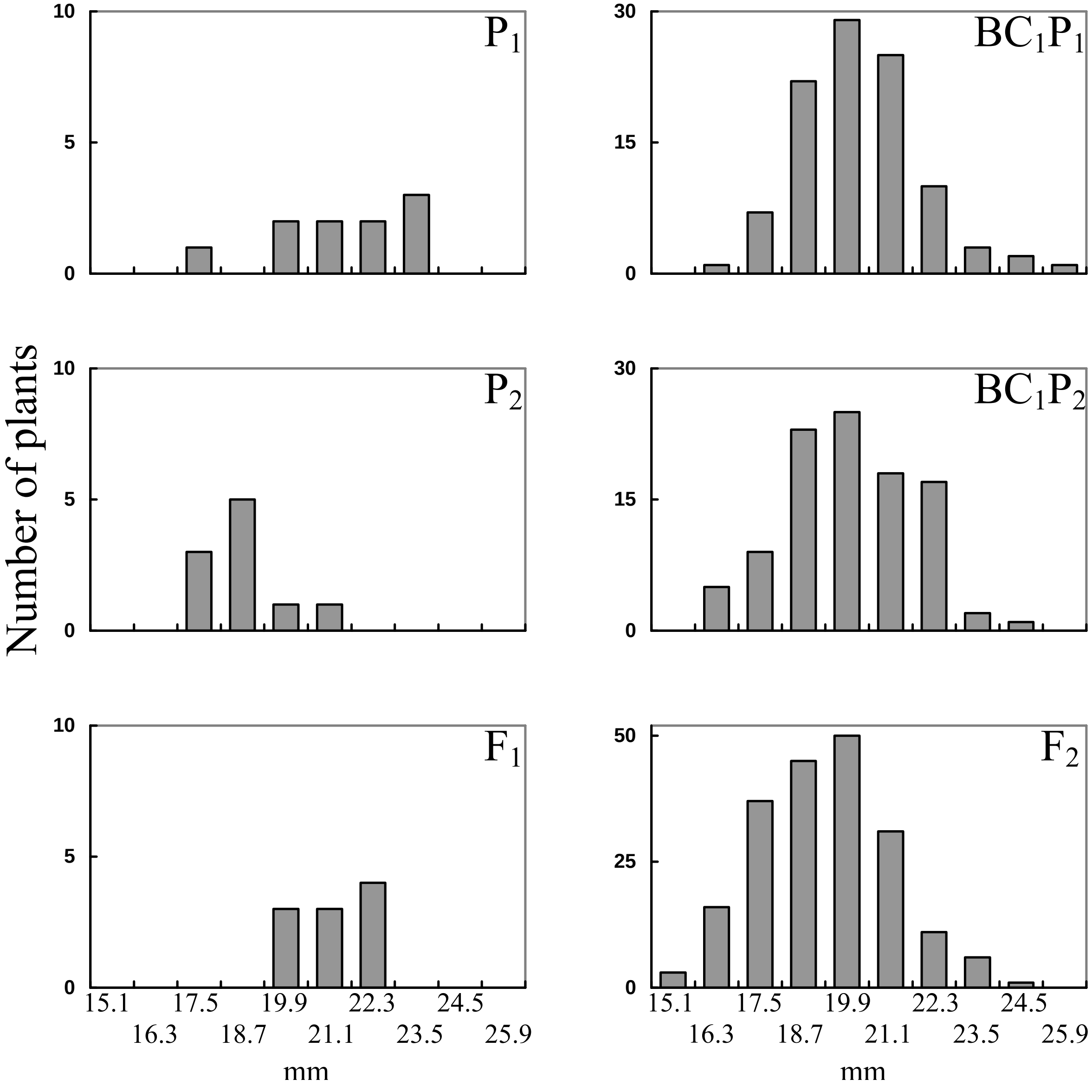

Fig. 29. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental of combination Fibermax 832 (P_1) x TAM 94L-25 (P_2) in 2001.

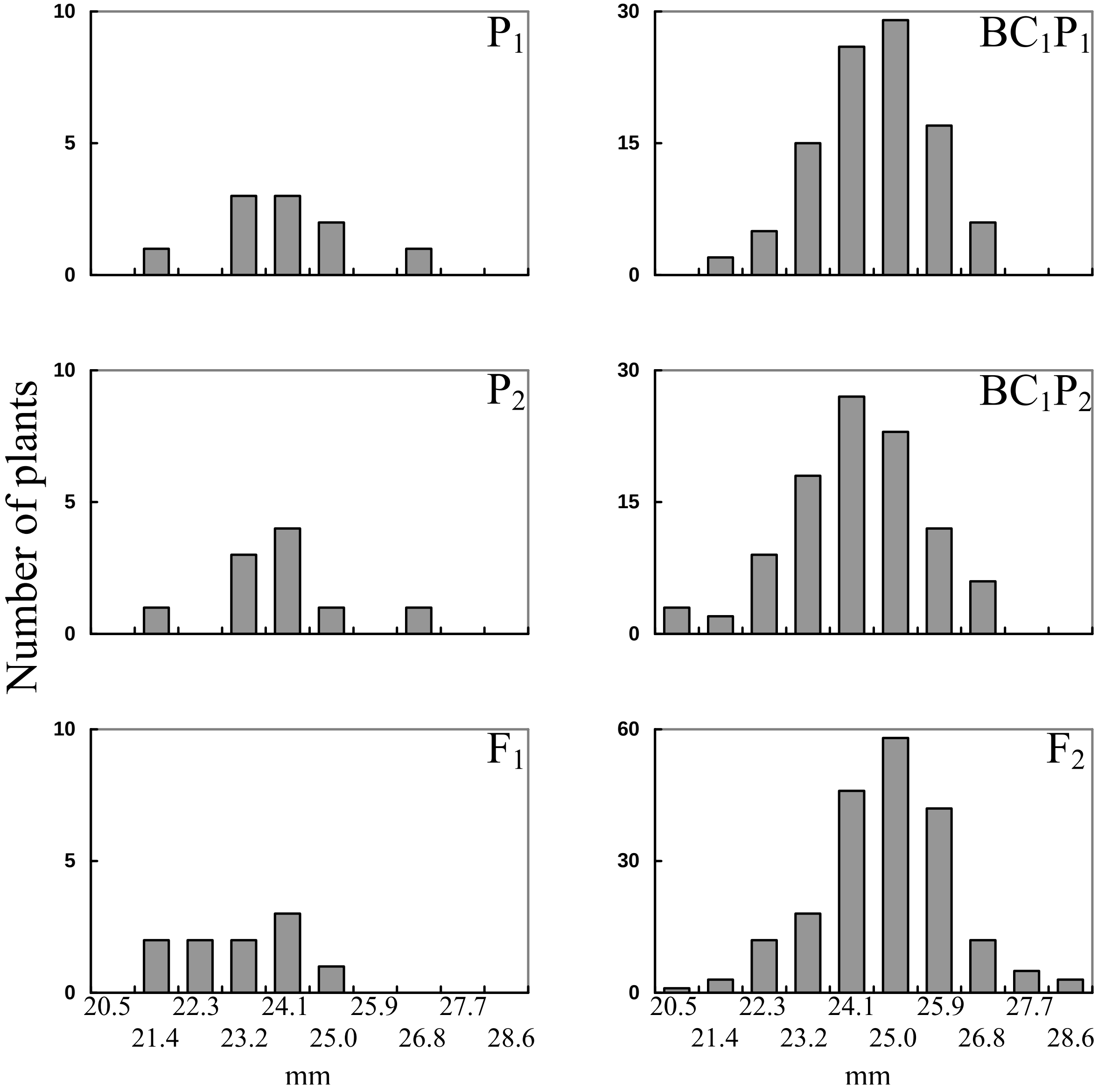

Fig. 30. Frequency distribution of FLn in the P$_1$, P$_2$, F$_1$, BC$_1$P$_1$, BC$_1$P$_2$, and F$_2$ generation for the near-long x near-long parental combination of Fibermax 832 (P$_1$) x TAM 94L-25 (P$_2$) in 2002.

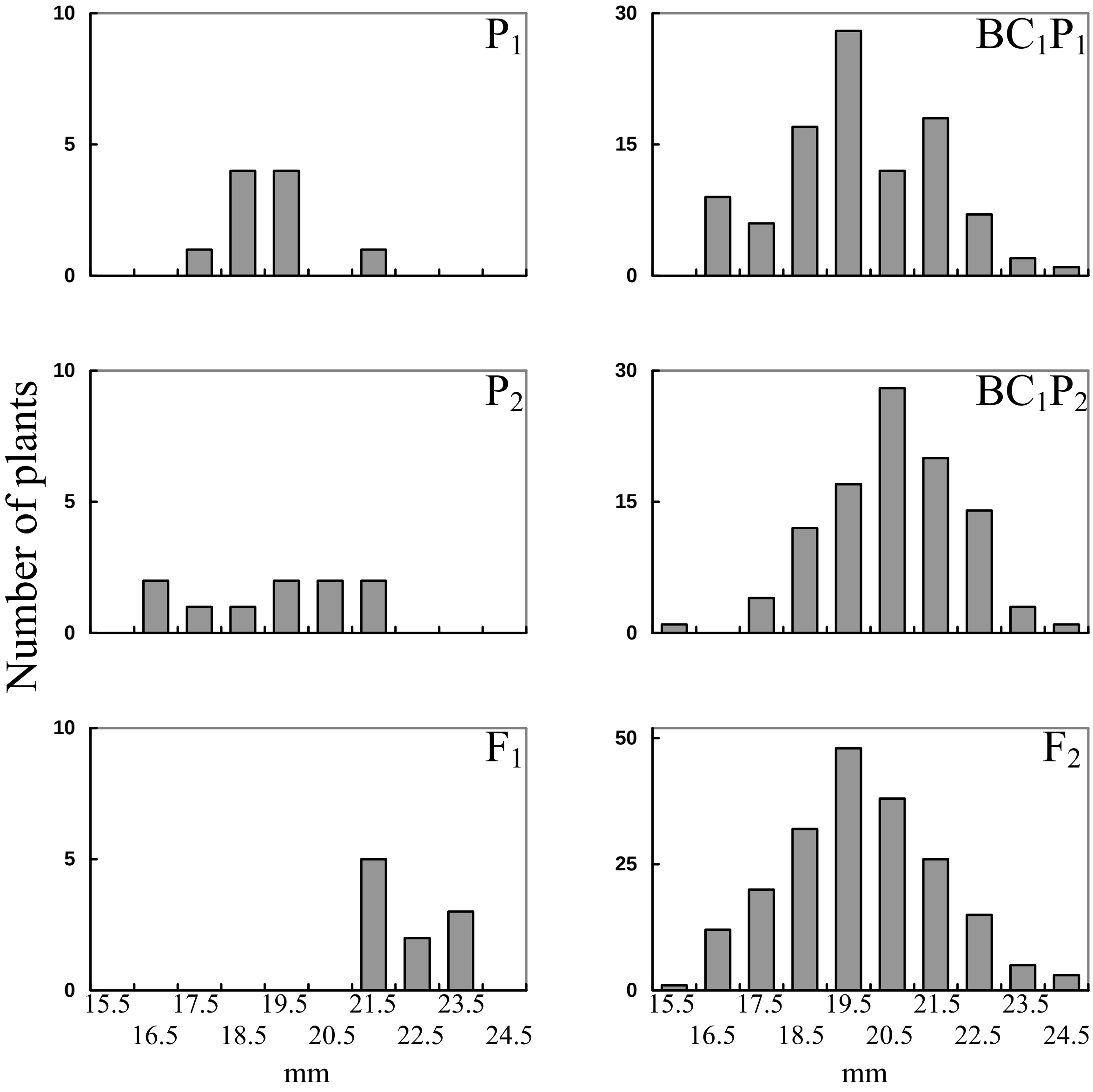

Fig. 31. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of TAM 94L-25 (P_1) x TTU 202 (P_2) in 2001.

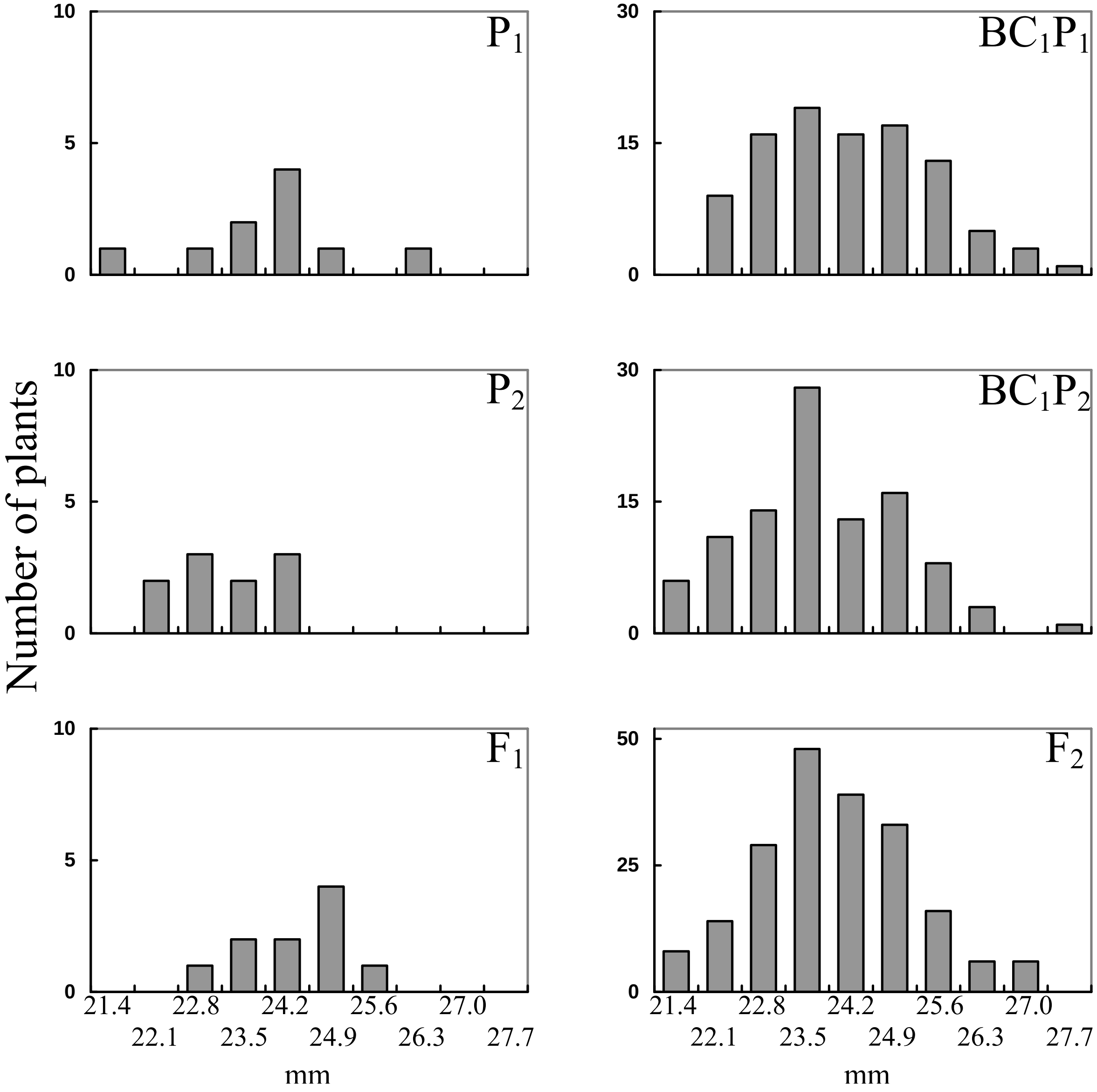

Fig. 32. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of TAM 94L-25 (P_1) x TTU 202 (P_2) in 2002.

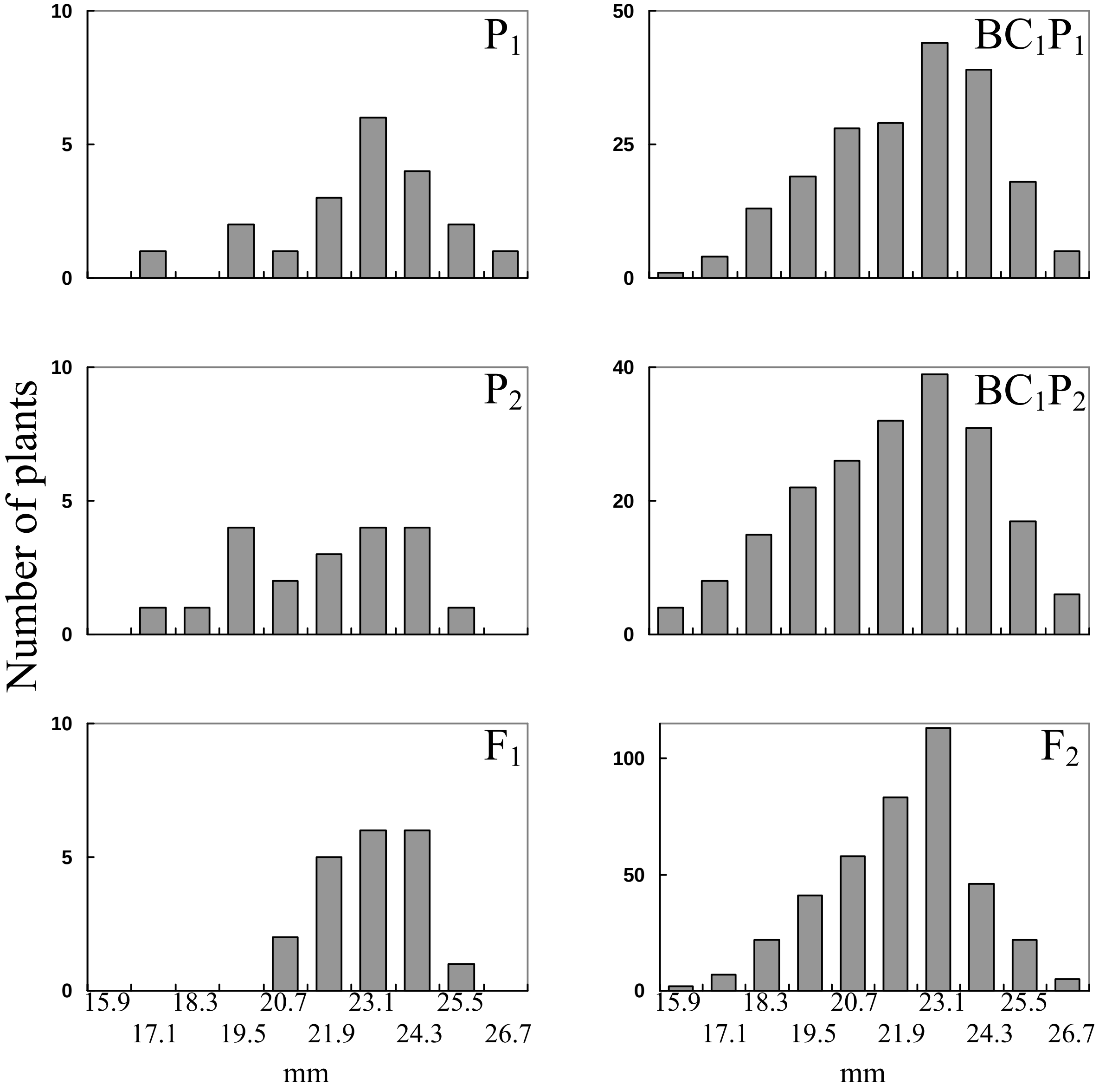

Fig. 33. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of Fibermax 832 (P_1) x Acala 1517-99 (P_2) across 2001 and 2002.

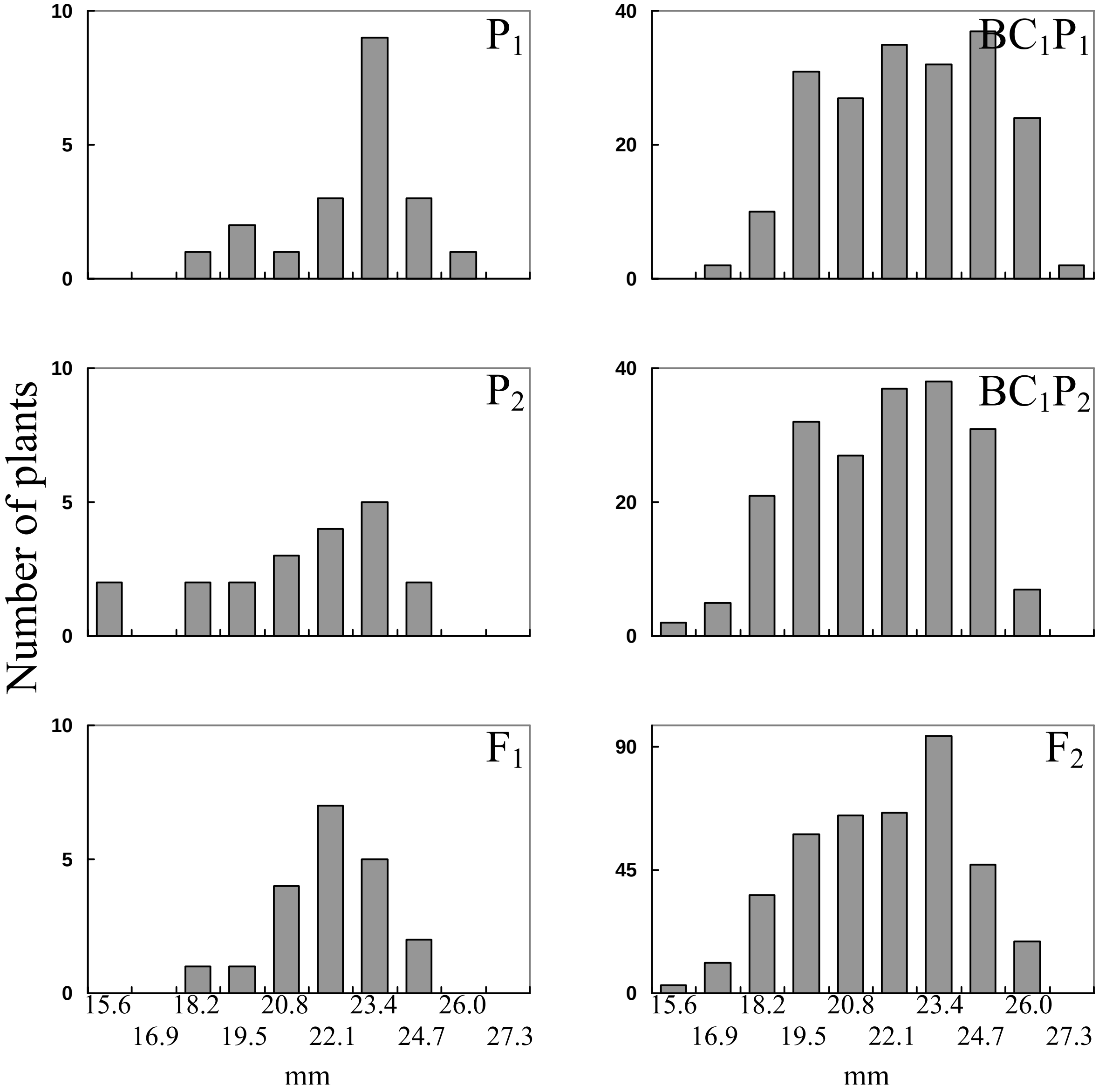

Fig. 34. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of Fibermax 832 (P_1) x TTU 202 (P_2) across 2001 and 2002.

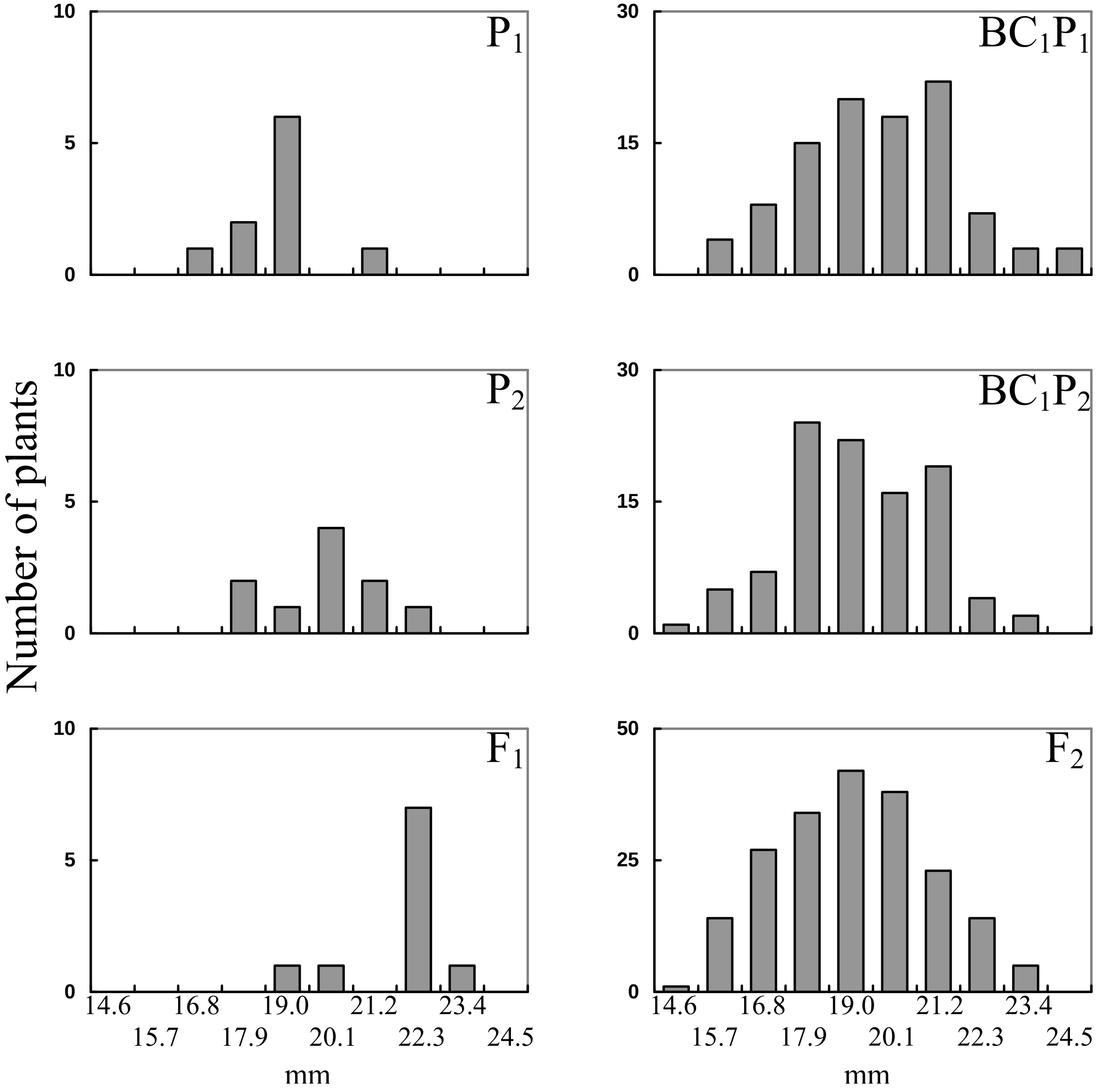

Fig. 35. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of TAM 94L-25 (P_1) x Acala 1517-99 (P_2) in 2001.

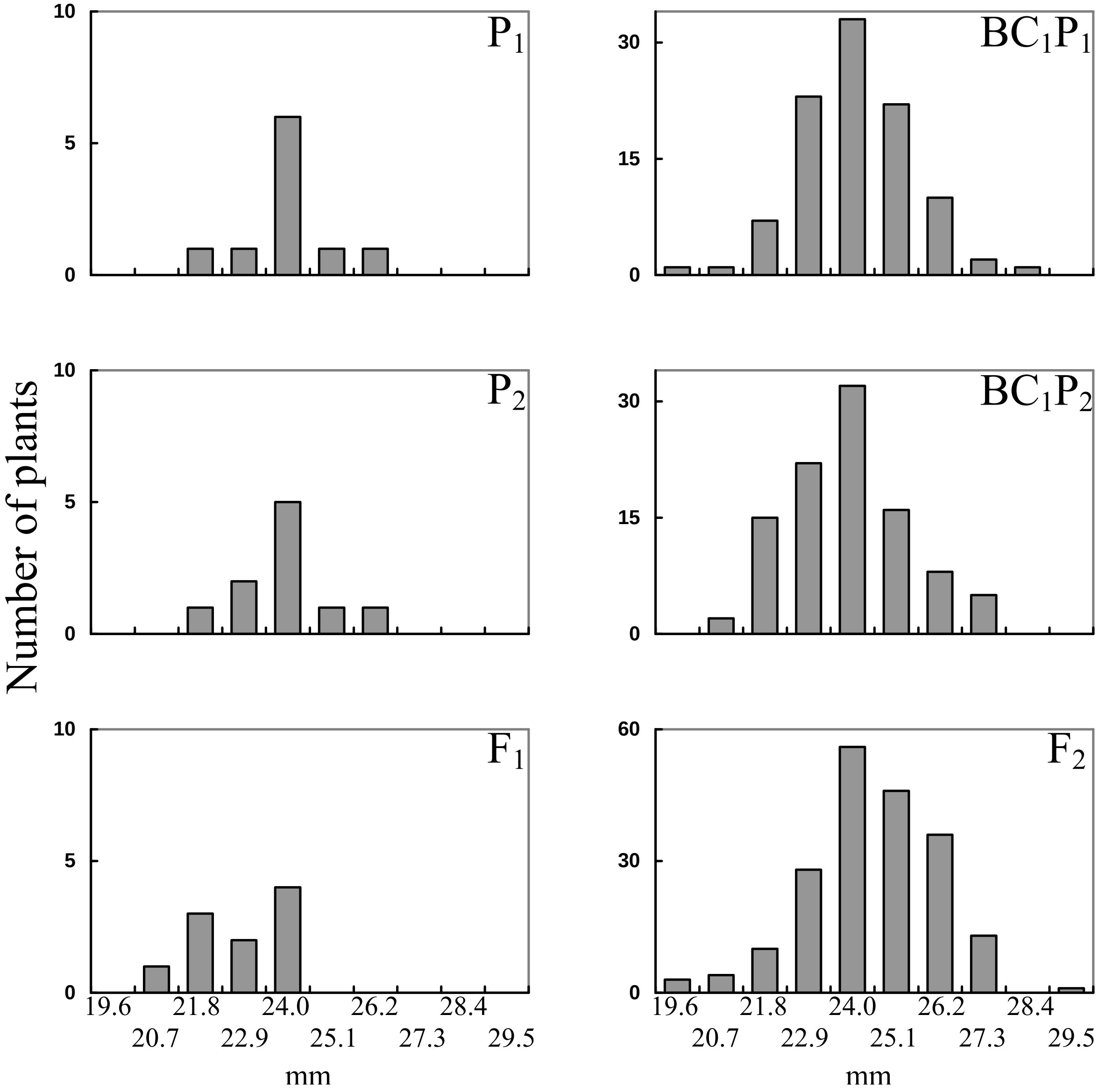

Fig. 36. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of TAM 94L-25 (P_1) x Acala 1517-99 (P_2) in 2002.

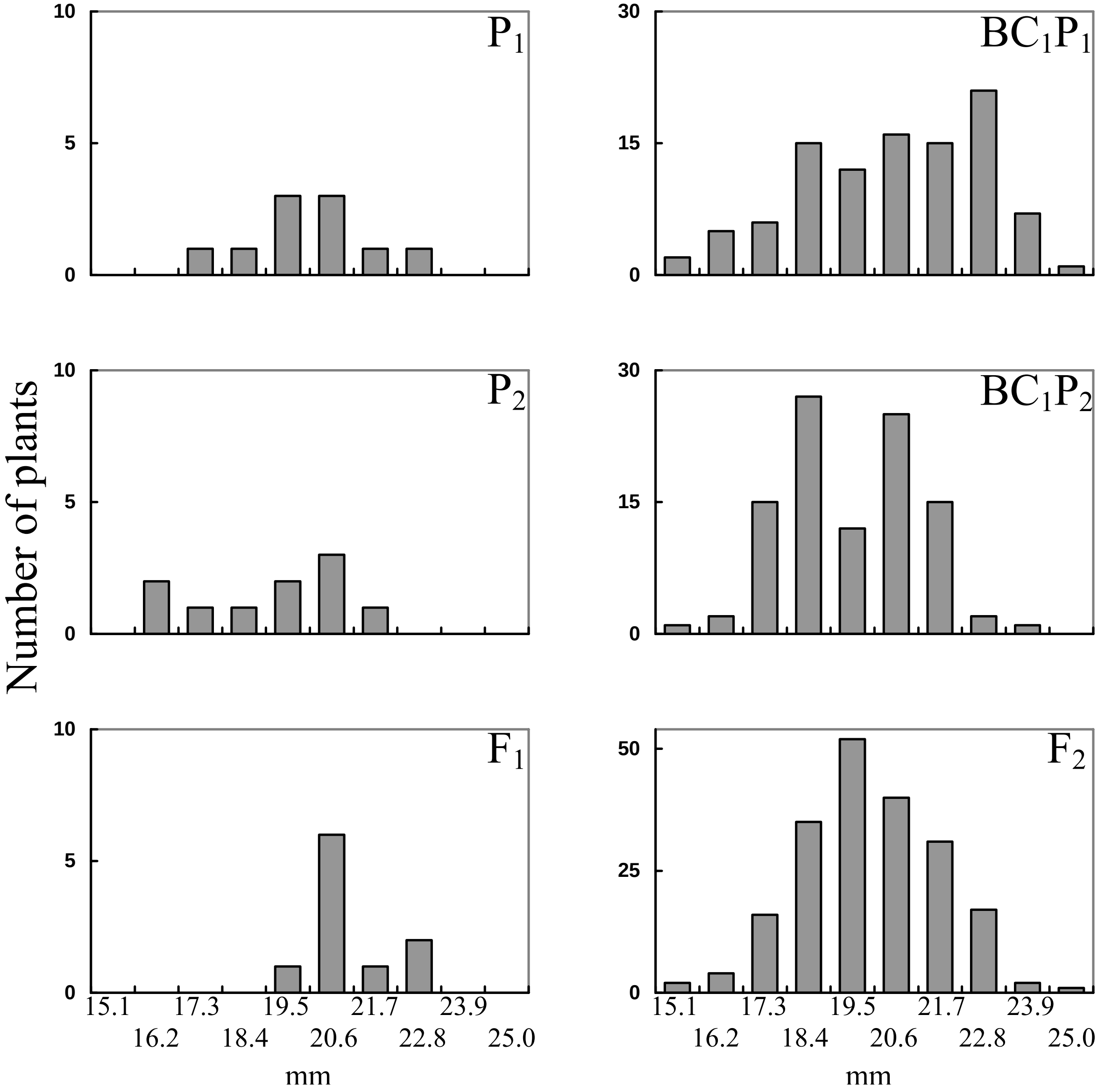

Fig. 37. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of Acala 1517-99 (P_1) x TTU 202 (P_2) in 2001.

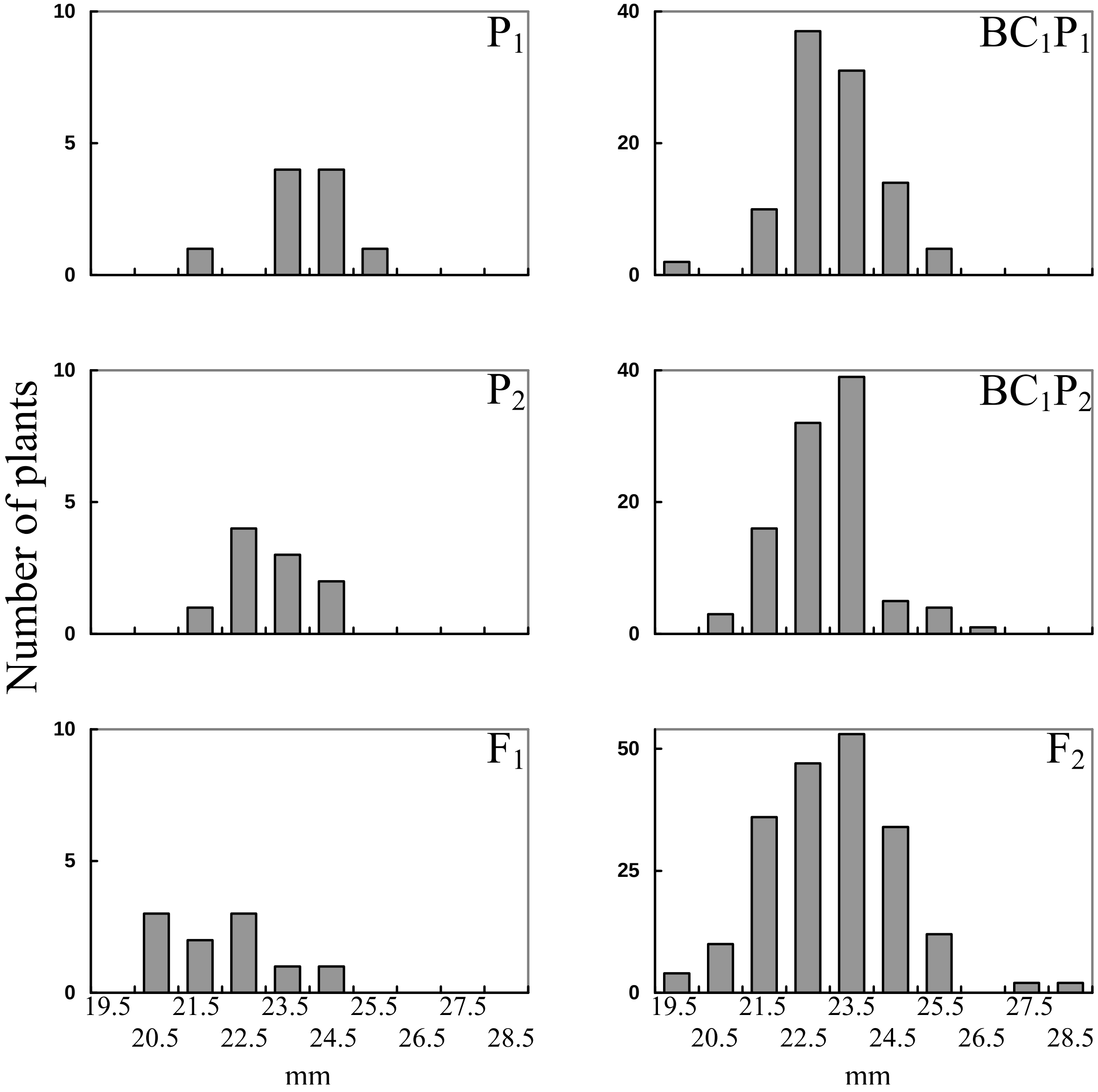

Fig. 38. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of Acala 1517-99 (P_1) x TTU 202 (P_2) in 2002.

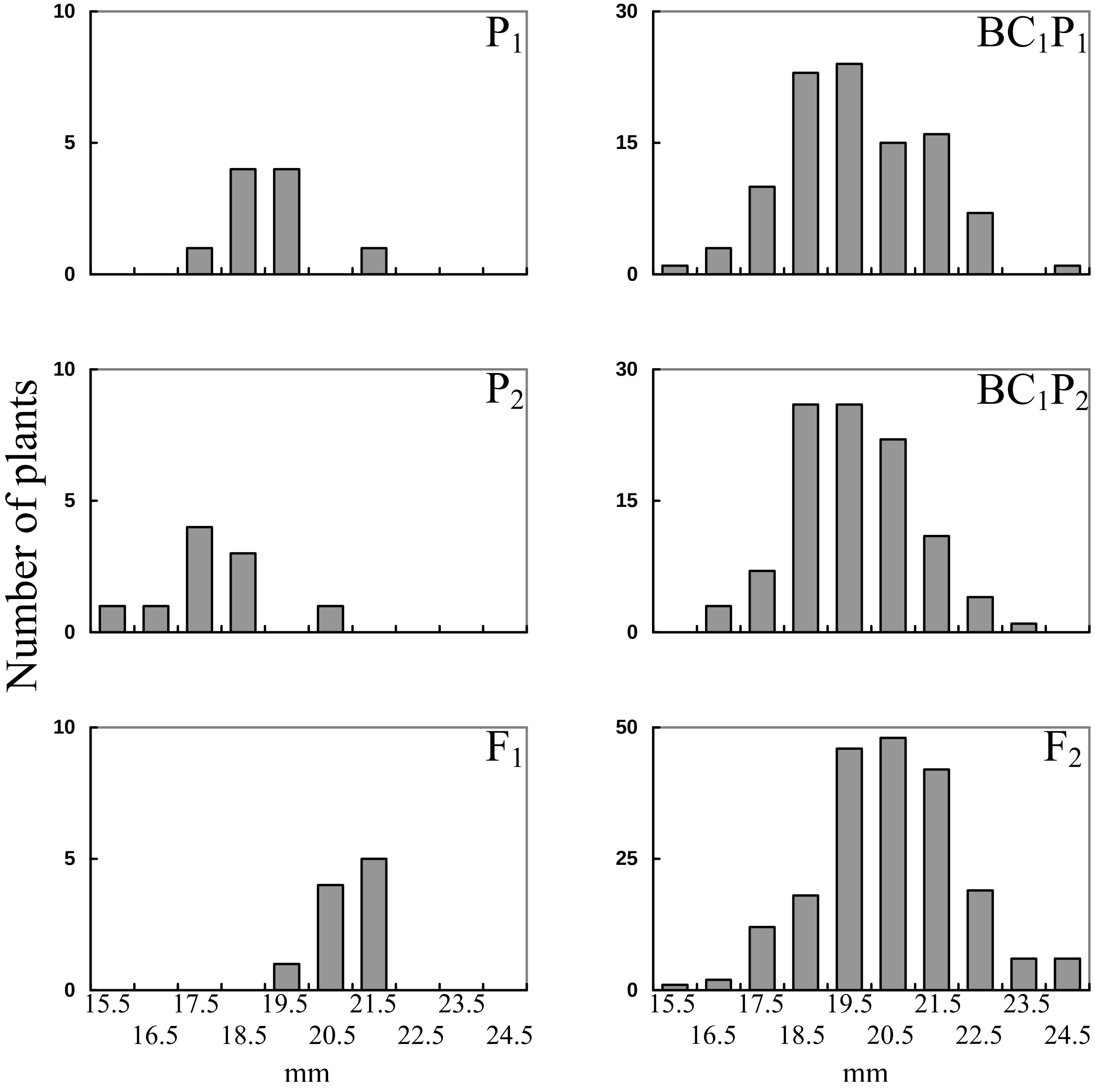

Fig. 39. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of TAM 94L-25 (P_1) x Tamcot CAMD-E (P_2) in 2001.

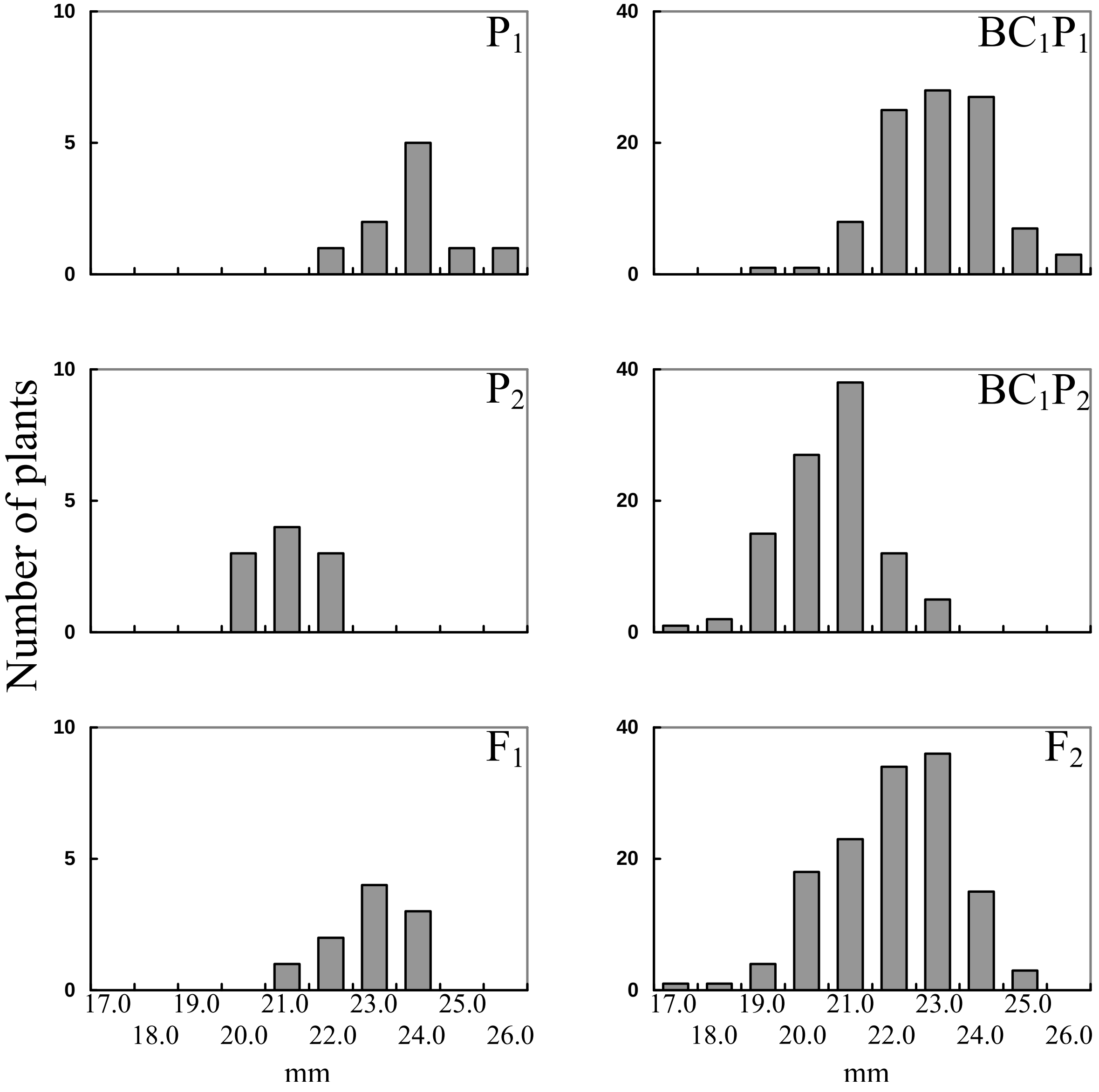

Fig. 40. Frequency distribution of FLn in the P$_1$, P$_2$, F$_1$, BC$_1$P$_1$, BC$_1$P$_2$, and F$_2$ generation for the near-long x short staple parental combination of TAM 94L-25 (P$_1$) x Tamcot CAMD-E (P$_2$) in 2002.

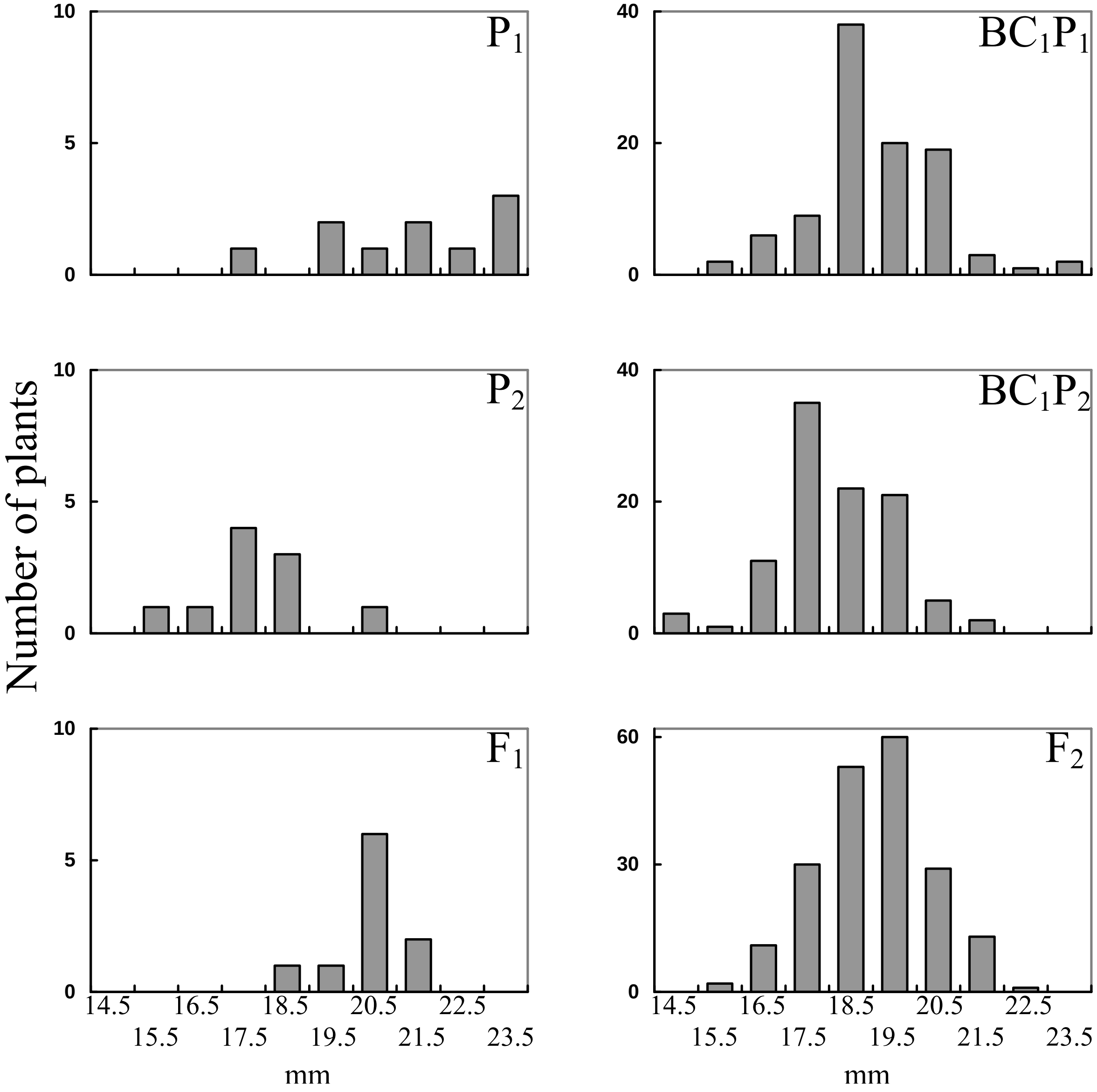

Fig. 41. Frequency distribution of FLn in the P$_1$, P$_2$, F$_1$, BC$_1$P$_1$, BC$_1$P$_2$, and F$_2$ generation for the near-long x short staple parental combination of Fibermax 832 (P$_1$) x Tamcot CAMD-E (P$_2$) in 2001.

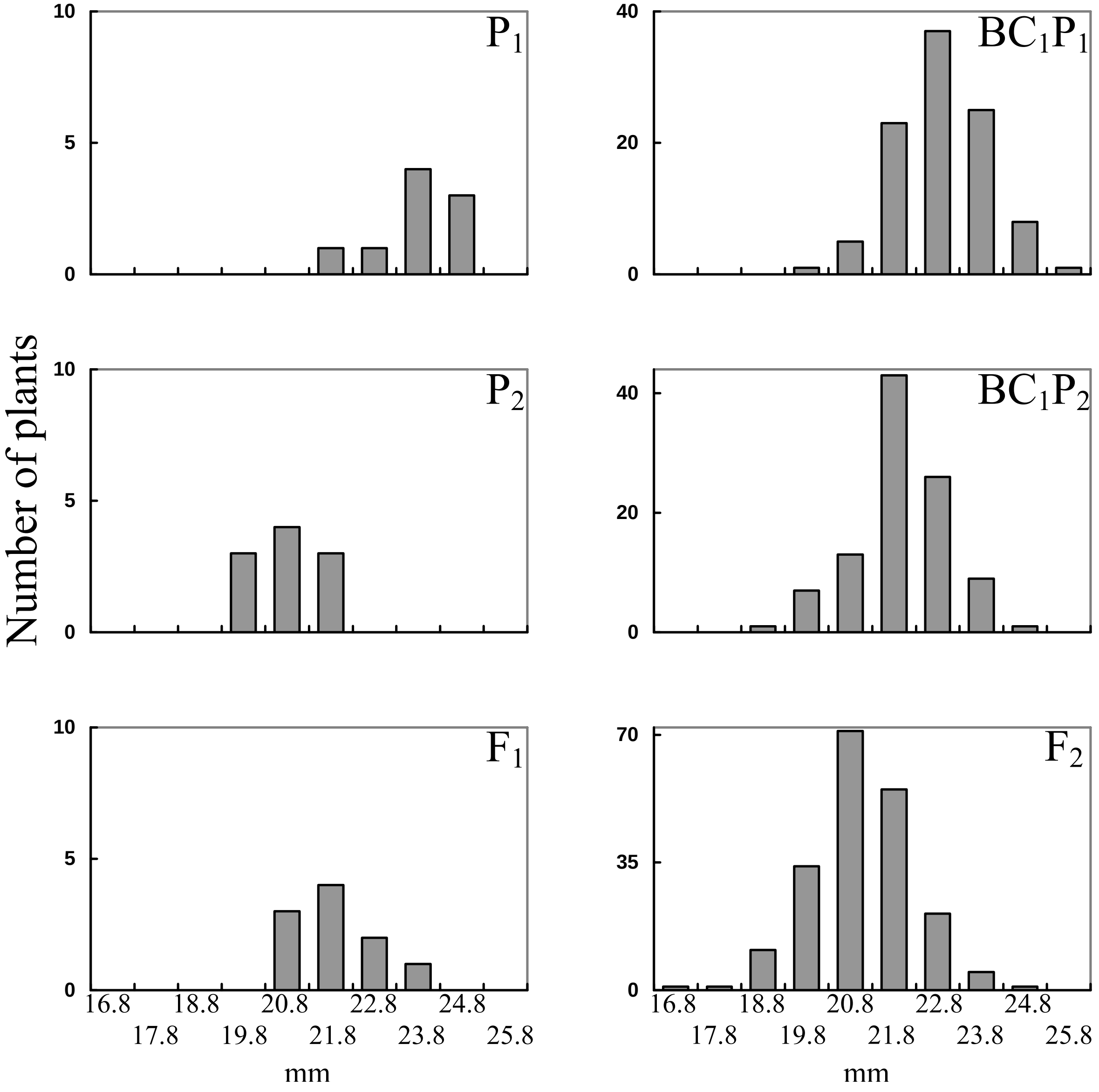

Fig. 42. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of Fibermax 832 (P_1) x Tamcot CAMD-E (P_2) in 2002.

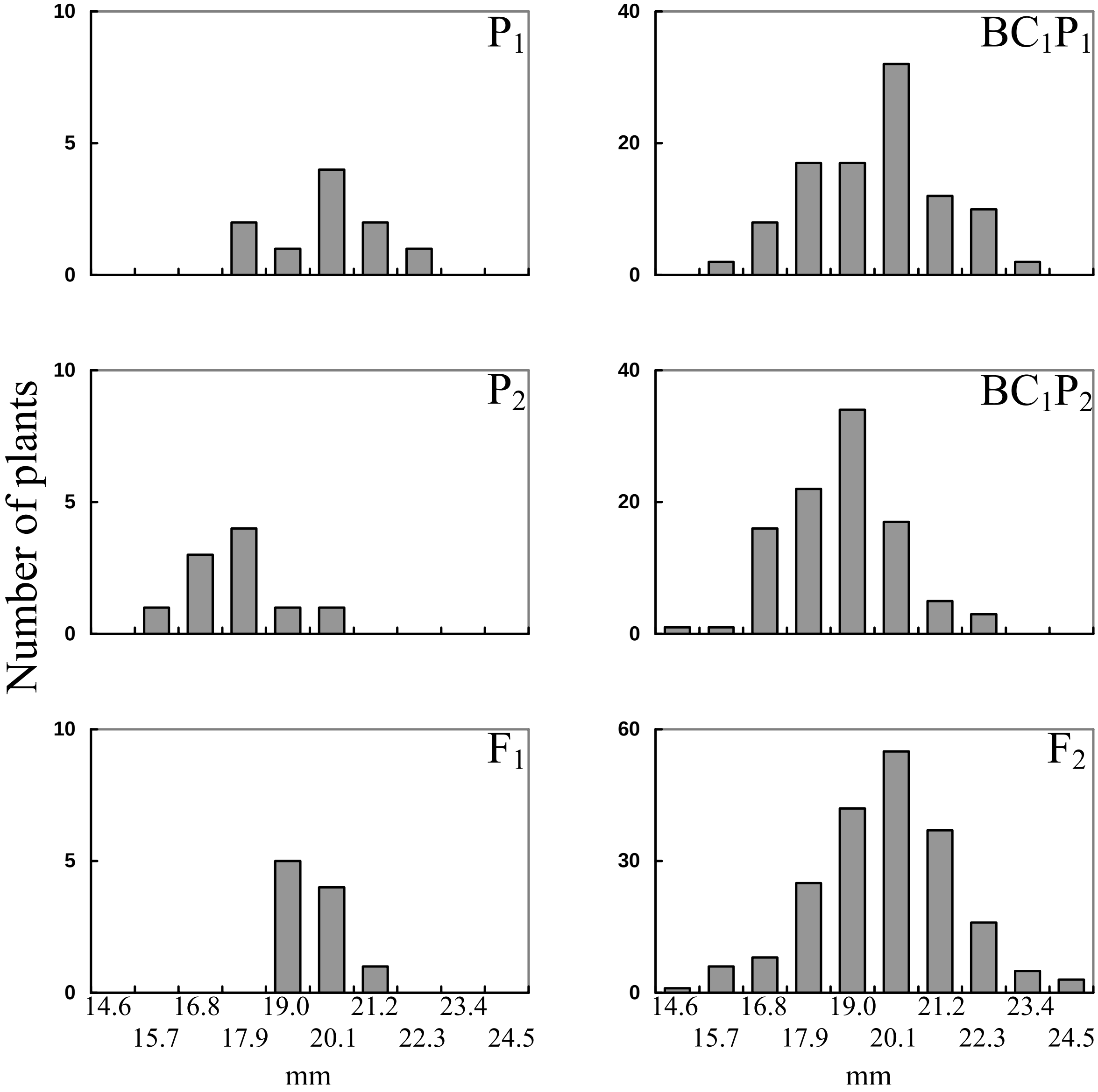

Fig. 43. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of Acala 1517-99 (P_1) x Tamcot CAMD-E (P_2) in 2001.

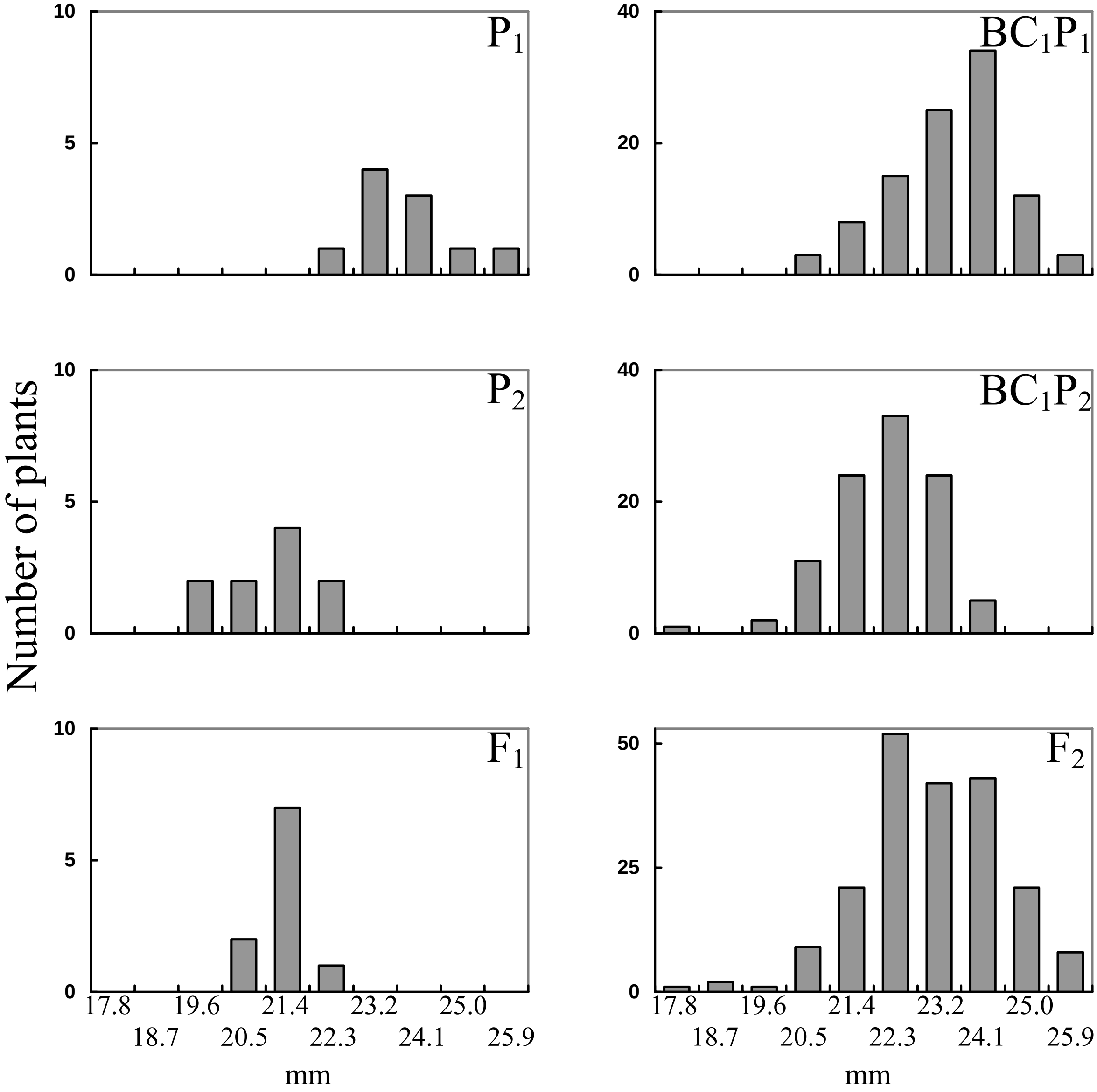

Fig. 44. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of Acala 1517-99 (P_1) x Tamcot CAMD-E (P_2) in 2002.

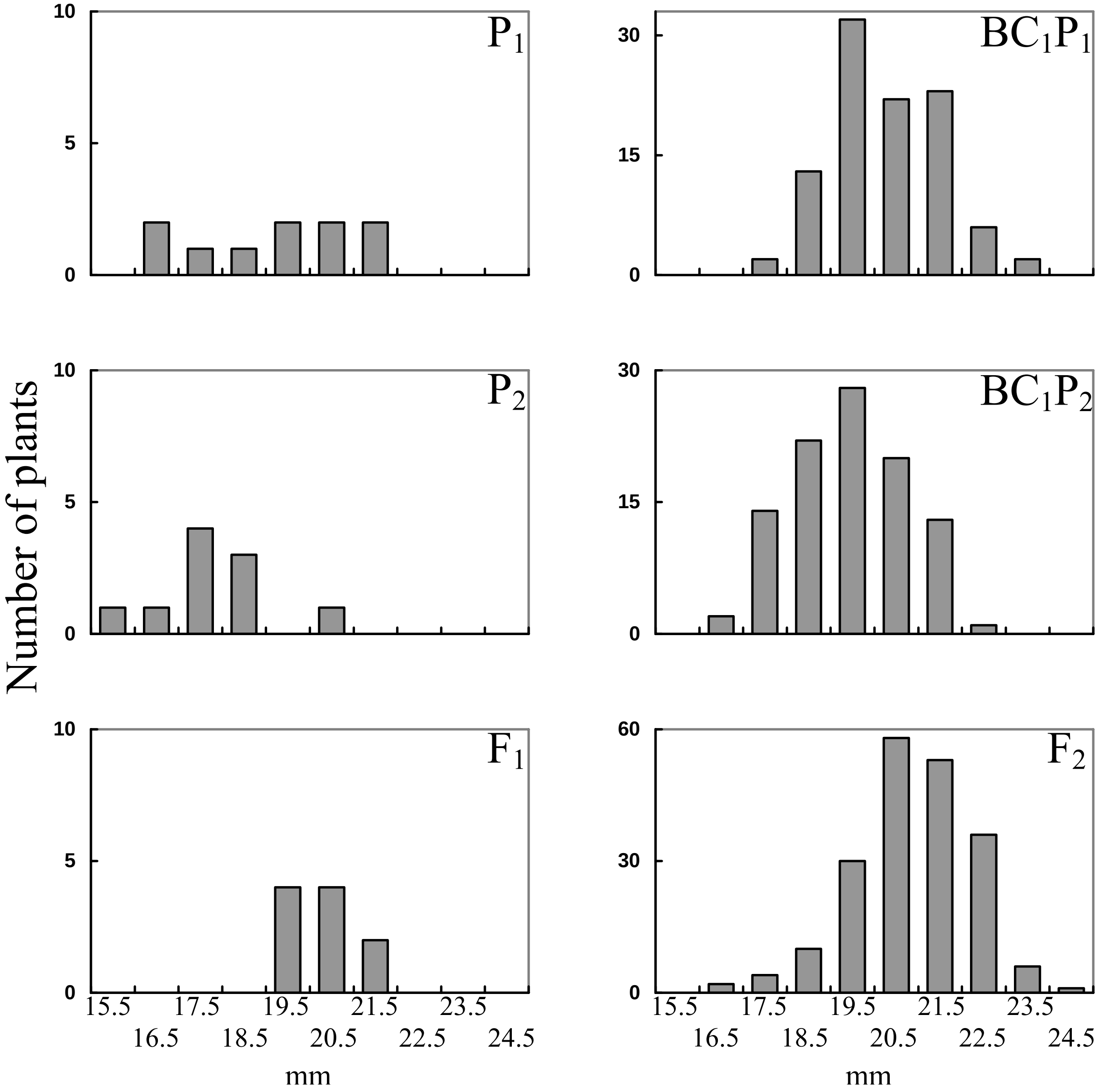

Fig. 45. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of TTU 202 (P_1) x Tamcot CAMD-E (P_2) in 2001.

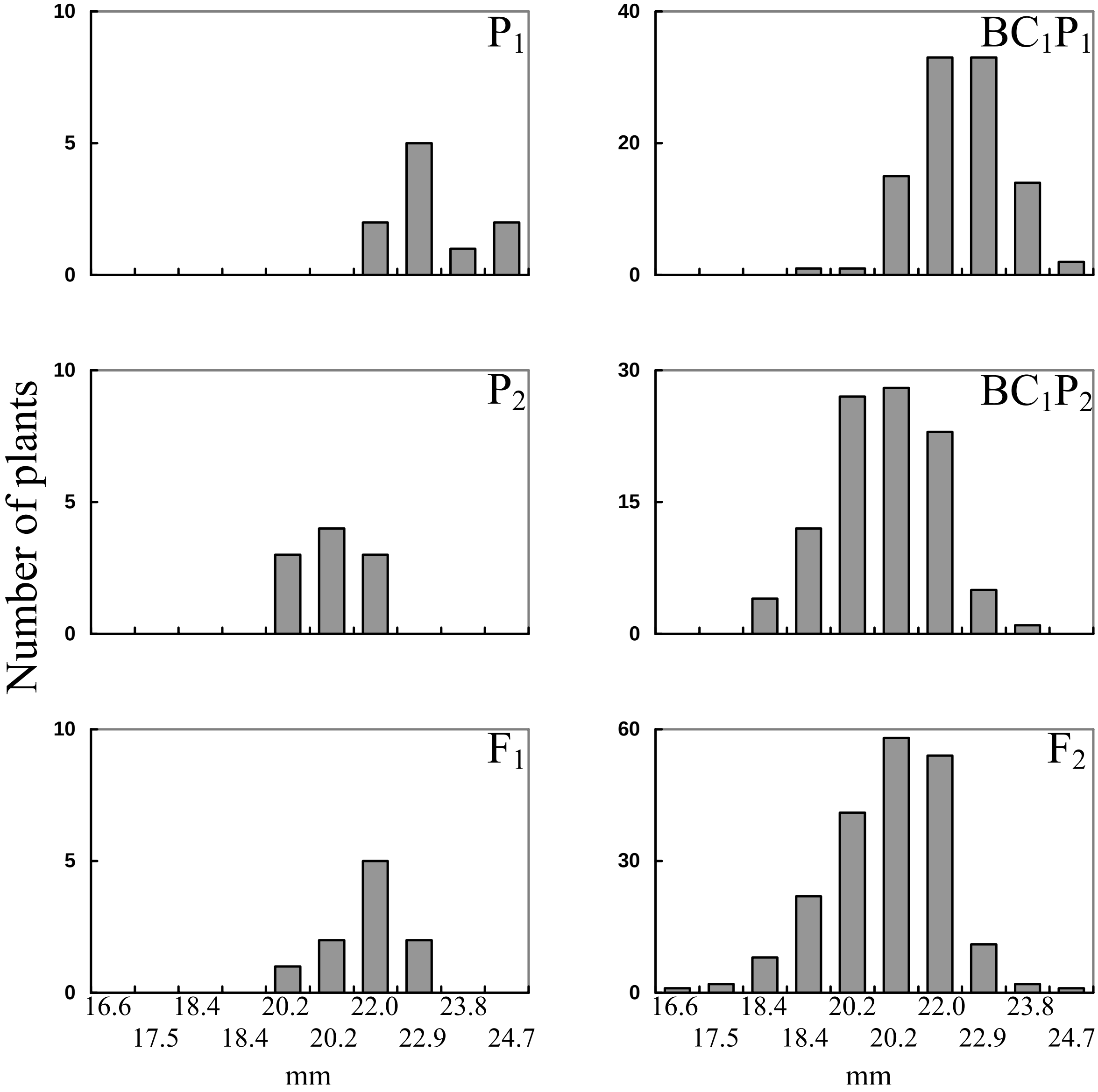

Fig. 46. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of TTU 202 (P_1) x Tamcot CAMD-E (P_2) in 2002.

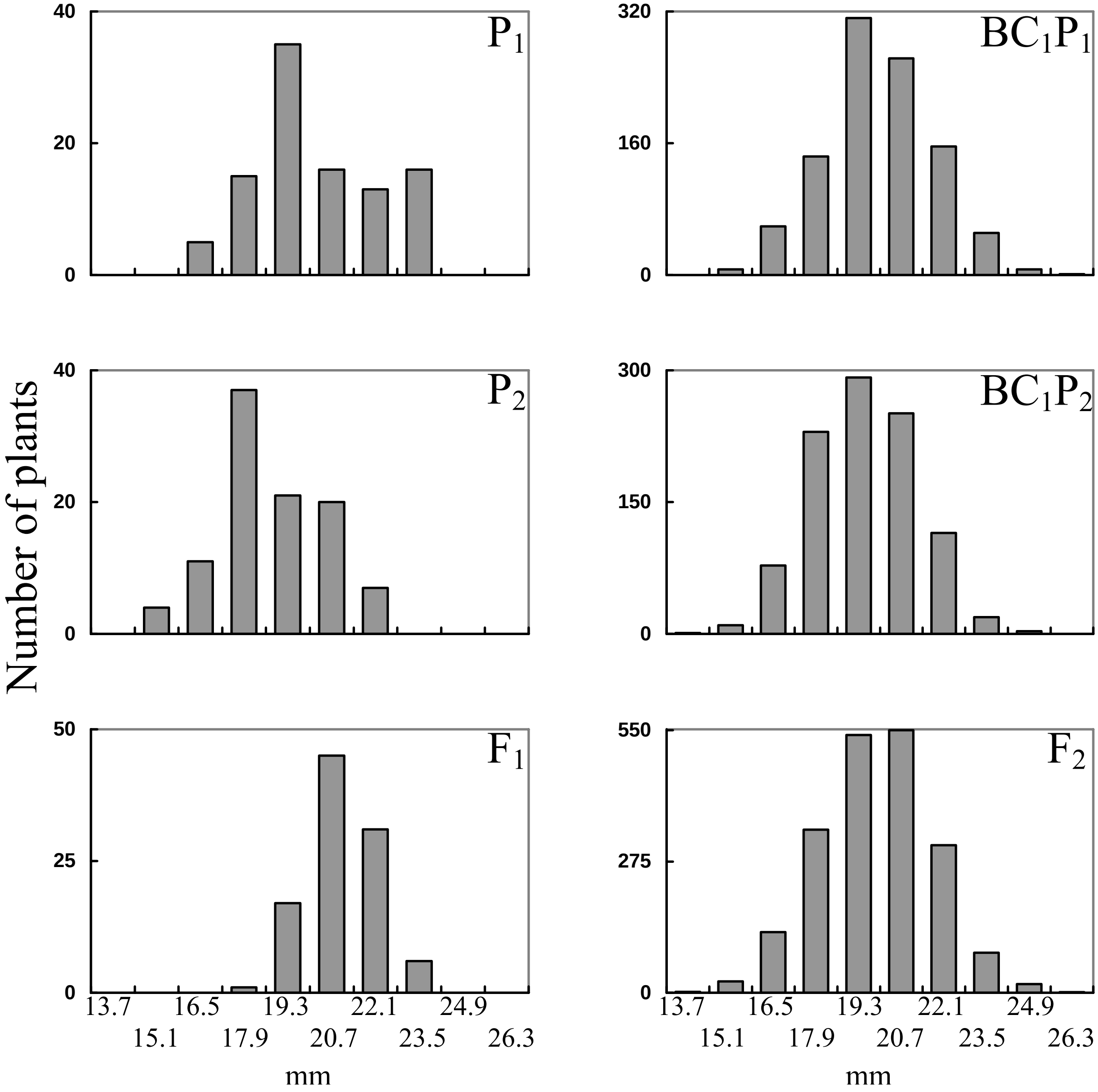

Fig. 47. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation among all parental combinations in 2001.

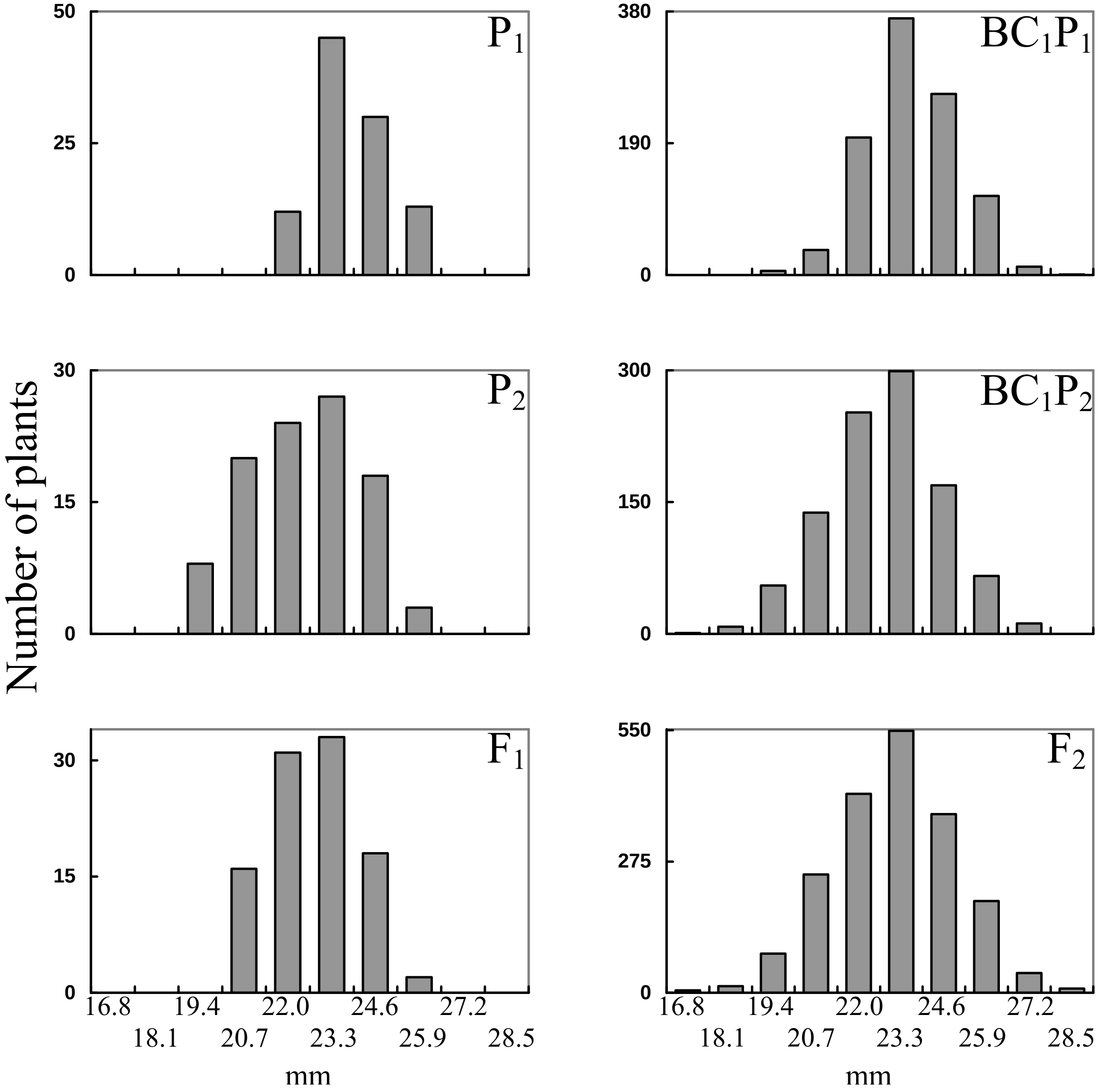

Fig. 48. Frequency distribution of FLn in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation among all parental combinations in 2002.

FLn on 3 of the 22 parental combinations x environments tested, those being TAM 94L-25 x TTU 202 in 2002 and Acala 1517-99 x TTU 202 in 2001 and 2002 (Table 14). TAM 94L-25 x TTU 202 was also fit by the three-parameter model for FLw (Table 9). In these combinations and environments, the variation among generation means for FLn was explained sufficiently by the simple additive-dominance model, indicating that epistasis was not involved in the inheritance of trait. The best approximation of additive and dominance effects can be obtained from the three-parameter, additive-dominance model because these effects are unbiased due to the absence of epistasis (Hayman, 1958). TAM 94L-25 x TTU 202 in 2002 and Acala 1517-99 x TTU 202 in 2001 and 2002 were the only near-long x near-long parental combinations to exhibit significant additive effects with values of 0.44, 1.02, and 0.34, respectively. Acala 1517-99 x TTU 202 in 2001 was the only near-long x near-long parental combinations to show significant dominance effects with a value of 1.63.

Results of the three-parameter model analysis indicated that non-allelic interactions were present in the other near-long x near-long parental combinations. Therefore, the six-parameter model was used to determine the type and magnitude of gene effects involved in the inheritance of FLn. All near-long x near-long parental combinations displayed significant additive x additive effects except for Fibermax 832 x Acala 1517-99 and Fibermax 832 x TTU 202 combined across years (Table 14). In 2001, Fibermax 832 x TAM 94L-25, TAM 94L-25 x TTU 202, and TAM 94L-25 x Acala 1517-99 had positive additive x additive estimates of 3.33, 1.55, and 1.90, respectively. In 2002, Fibermax 832 x TAM 94L-25 and TAM 94L-25 x Acala 1517-99

Table 14. Estimates of gene effects for FLn (per parental combination and across combinations) at College Station, TX in 2001 and 2002.

		Gene effects†					
Parental Combinations	Year	*m*	*a*	*d*	*aa*	*ad*	*dd*
Fibermax 832 x TAM 94L-25‡	2001	16.50**	1.41	5.93	3.33**	-2.47	-1.03
Fibermax 832 x TAM 94L-25‡	2002	26.05**	0.15	-2.84	-1.99**	0.42	0.76
TAM 94L-25 x TTU 202‡	2001	17.60**	-0.82	4.33	1.55*	-0.04	-0.22
TAM 94L-25 x TTU 202‡§	2002	23.36**	0.44*	1.04	-	-	-
Fibermax 832 x Acala 1517-99‡	2001/02	22.85**	0.20	-1.68	0.42	0.67	1.67
Fibermax 832 x TTU 202‡	2001/02	21.85**	0.66	1.86	0.97	-0.23	-1.97
TAM 94L-25 x Acala 1517-99‡	2001	17.53**	-0.65	1.36	1.90**	2.13	3.16
TAM 94L-25 x Acala 1517-99‡	2002	26.08**	-0.03	-3.38	-2.28**	1.03	0.07
Acala 1517-99 x TTU 202‡§	2001	19.20**	1.02**	1.63*	-	-	-
Acala 1517-99 x TTU 202‡§	2002	23.51**	0.34*	-1.07	-	-	-
TAM 94L-25 x Tamcot CAMD-E¶	2001	21.55**	0.47	-3.44	-3.34**	-1.08	2.59
TAM 94L-25 x Tamcot CAMD-E¶	2002	23.33**	1.53**	-4.96*	-0.78	1.94	4.57**
Fibermax 832 x Tamcot CAMD-E¶	2001	21.08**	2.03*	-7.52*	-1.73**	-2.25	6.85**
Fibermax 832 x Tamcot CAMD-E¶	2002	17.23**	1.55*	11.00**	5.33**	-1.27	-6.59**
Acala 1517-99 x Tamcot CAMD-E¶	2001	21.13**	0.92	-3.57	-2.47**	-0.10	1.79
Acala 1517-99 x Tamcot CAMD-E¶	2002	23.56**	1.46*	-0.20	-1.04*	-0.21	-1.92
TTU 202 x Tamcot CAMD-E¶	2001	23.44**	1.42**	-6.73**	-4.26**	-1.01	3.38*
TTU 202 x Tamcot CAMD-E¶	2002	19.43**	0.98	4.23*	2.60**	1.09	-2.30
Among all combinations	2001	19.82**	0.76**	-0.48	-0.86**	-0.41	1.35*
Among all combinations	2002	22.85**	0.59*	0.73	0.40	0.82	-1.29

*, ** Significant at the 0.05 and 0.01 probability level on the basis of *t* test with n – 1 =5 degrees of freedom, respectively.

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

‡ Near-long x near-long parental combination.

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

¶ Near-long x short staple parental combination.

had negative estimates of -1.99 and -2.28, respectively. The negative additive x additive estimate shows the genes pairs responsible for FLn are in dispersive form (Mather and Jinks, 1977). This means both parents contributed alleles for FLn among these near-long x near-long parental combinations. Among these combinations, additive effects accounted for a smaller portion of the observed variability than dominance effects. Reviewing all genetic effects, the dominance effects remained the largest, but significant additive x additive effects are probably the most important in determining FLn among the near-long x near-long parental combinations.

In the near-long x short staple parental combinations, the six-parameter model was necessary to determine the type and magnitude of gene effects involved in the inheritance of FLn (Table 14). In 2001 and 2002, additive effects were significant and positive for all near-long x short staple parental combinations except for TAM 94L-25 x Tamcot CAMD-E in 2001, Acala 1517-99 x Tamcot CAMD-E in 2001, and TTU 202 x Tamcot CAMD-E in 2002. Two parental combinations had different direction of response for dominance effects in 2002 than in 2001, indicating that dominance effects were contributed differently among the parents depending upon the environment. In 2001, dominance effects for Fibermax 832 x Tamcot CAMD-E were negative with a value of -7.52, and positive in 2002 with a value of 11.00. In 2001, dominance effects for TTU 202 x Tamcot CAMD-E were negative with a value of -6.53, yet positive in 2002 with an estimated value of 4.23. TAM 94L-25 x Tamcot CAMD-E and Acala 1517-99 x Tamcot CAMD-E exhibited negative dominance effect estimates in both years. Negative dominance effects resulted from alleles differing in the Tamcot CAMD-

E, while the positive dominance effect was contributed by the genes differing in the longer parent. Additive x additive gene effect estimates were significant in all near-long x short staple parental combinations except for TAM 94L-25 x Tamcot CAMD-E in 2002. In 2001, additive x additive effects were negative, suggesting both parents contributed alleles for FLn, while in 2002 additive x additive effect estimates were positive except for Acala 1517-99 x Tamcot CAMD-E which had an estimate of -1.04. No additive x dominance effect estimates were significant for FLn. In 2001, Fibermax 832 x Tamcot CAMD-E, and TTU 202 x Tamcot CAMD-E had significant dominance x dominance effects with estimated values of 6.85 and 3.38, respectively. In 2002, TAM 94L-25 x Tamcot CAMD-E had a dominance x dominance effect estimate of 4.57 while Fibermax 832 x Tamcot CAMD-E had an estimated value of -6.59. For TAM 94L-25 x Tamcot CAMD-E in 2002, Fibermax 832 x Tamcot CAMD-E in 2001, and TTU 202 x Tamcot CAMD-E in 2001, the dominance effects were negative while the dominance x dominance effects were positive. The contrasting direction of response between dominance and dominance x dominance gene effect estimates suggests negative duplicate epistasis (Kearsey and Pooni, 1996). The 2002 parental combination of Fibermax 832 x Tamcot CAMD-E had positive dominance and negative dominance x dominance gene effect estimates suggesting positive duplicate epistasis.

Generation means analysis indicated that genetic control for FLn among these near-long x short staple parental combinations is complex, even more so than FLw. Several effects significantly contributed to the inheritance of FLn. Except for one parental combination and environment, dominance effects accounted for a larger portion of the observed variability than additive effects. In comparing the relative magnitude of additive x additive to dominance x dominance effects, it depended on the parental combination and environment as to which one was greater. Among all combinations in 2001, additive, additive x additive, and dominance x dominance effects were significant with dominance x dominance being larger in magnitude. Among all combinations in 2002, only additive effects were significant.

Variance components and broad- and narrow-sense heritability estimates for FLn were calculated to determine the relative importance of the various determinants of the phenotype, the extent to which individuals' phenotypes are determined by their genotypes, and the extent to which phenotypes are determined by the alleles transmitted from the parents (Falconer and MacKay, 1996). Higher environmental variances were seen in 2001 than in 2002 (Table 15). In 2001, environmental variance among the four near-long x near-long parental combinations ranged from 1.41 to 1.82 with an average of 1.65, while the near-long x short staple parental combinations ranged from 0.79 to 1.85 with an average of 1.39. Environmental variance among the near-long x near-long combinations in 2002 ranged from 0.98 to 1.55 with an average of 1.31, while the near-long x short staple parental combinations in 2002 ranged from 0.64 to 1.05 with an average of 0.84. Additive variance was higher in 2002 than 2001, however, 85% of the sum in 2002 came from two near-long x near-long parental combinations, TAM 94L-25 x Acala 1517-99 and Acala 1517-99 x TTU 202. In 2001, the additive variance among the near-long x near-long parental combinations ranged from 0.00 to 1.25 with an average of 0.82, while the near-long x short staple combinations ranged from 0.00 to

Table 15. Variance components and broad (H^2) and narrow (h^2) sense heritability estimates for FLn for 10 parental combinations grown at College Station, TX in 2001 and 2002.

		Variance components†			Heritability estimates	
Parental Combinations	Year	σ^2_E	σ^2_A	σ^2_D	H^2	h^2
Fibermax 832 x TAM 94L-25‡	2001	1.76	1.06	0.67	0.50	0.30 ± 0.04
Fibermax 832 x TAM 94L-25‡	2002	1.55	0.57	-0.21	0.27	0.27 ± 0.04
TAM 94L-25 x TTU 202‡	2001	1.59	1.25	0.56	0.53	0.37 ± 0.03
TAM 94L-25 x TTU 202‡	2002	0.98	-0.33	0.62	0.39	0.00 ± 0.06
Fibermax 832 x Acala 1517-99‡	2001/02	3.51	-2.79	0.66	0.16	0.00 ± 0.07
Fibermax 832 x TTU 202‡	2001/02	4.05	0.00	1.43	0.26	0.00 ± 0.04
TAM 94L-25 x Acala 1517-99‡	2001	1.41	0.98	1.57	0.64	0.25 ± 0.04
TAM 94L-25 x Acala 1517-99‡	2002	1.37	1.33	0.03	0.50	0.49 ± 0.03
Acala 1517-99 x TTU 202‡	2001	1.82	-1.79	1.29	0.42	0.00 ± 0.08
Acala 1517-99 x TTU 202‡	2002	1.32	2.31	-1.30	0.64	0.64 ± 0.01
TAM 94L-25 x Tamcot CAMD-E§	2001	0.79	0.45	1.29	0.69	0.18 ± 0.04
TAM 94L-25 x Tamcot CAMD-E§	2002	1.05	1.20	-0.26	0.53	0.53 ± 0.03
Fibermax 832 x Tamcot CAMD-E§	2001	1.85	-0.42	-0.06	0.00	0.00 ± 0.06
Fibermax 832 x Tamcot CAMD- E§	2002	0.99	0.56	-0.14	0.36	0.36 ± 0.03
Acala 1517-99 x Tamcot CAMD-E§	2001	1.26	1.66	0.20	0.60	0.53 ± 0.03
Acala 1517-99 x Tamcot CAMD-E§	2002	0.64	1.47	-0.09	0.69	0.69 ± 0.02
TTU 202 x Tamcot CAMD-E§	2001	1.67	0.36	-0.21	0.18	0.18 ± 0.04
TTU 202 x Tamcot CAMD-E§	2002	0.66	0.67	0.12	0.55	0.46 ± 0.03
Among all combinations	2001	2.37	0.57	0.43	0.30	0.17 ± 0.00
Among all combinations	2002	1.84	2.00	-0.37	0.52	0.52 ± 0.00

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

‡ Near-long x near-long parental combination.

§ Near-long x short staple parental combination.

1.66 with an average of 0.62. In 2002, the additive variance among the near-long x near-long parental combinations ranged from 0.00 to 2.31 with an average of 1.05, while the near-long x short staple parental combinations ranged from 0.56 to 1.47 with an average of 0.98. Dominance variance was higher in 2001 than in 2002. In 2001, the dominance variance among the near-long x near-long parental combinations ranged from 0.56 to 1.57 with an average of 1.02, while the near-long x short staple combinations ranged from 0.00 to 1.29 with an average of 0.37. In 2002, the dominance variance among the near-long x near-long combinations ranged from 0.00 to 0.62 with an average of 0.16, while the near-long x short staple parental combinations ranged from 0.00 to 0.12 with an average of 0.04. Among all combinations in 2001, the environmental, additive, and dominance variance was 2.37, 0.57, and 0.43, respectively. Among all combinations in 2002, the environmental, additive, and dominance variance was 1.84, 2.00, and 0.00, respectively.

Among the near-long x near-long parental combinations, broad-sense heritability (H^2) averaged 0.52 in 2001, slightly higher than the 0.45 estimate in 2002, even though the environmental variance was higher in 2001 (Table 15). In general, higher broad-sense heritability estimates were attained in 2001 because of higher genetic variances. Narrow-sense heritability estimates (h^2) were higher in 2002 than 2001, averaging 0.35 and 0.23, respectively. However, the 2002 narrow-sense heritability average is slightly skewed because of the 0.64 estimated attained in the Acala 1517-99 x Tamcot CAMD-E parental combination. Fibermax 832 x Acala 1517-99 and Fibermax 832 x TTU 202 were the two parental combinations in which the ANOVA indicated no significant generation x environment interaction and, thus, the data of 2001 and 2002 were pooled together. The lower heritability estimates for these three parental combinations is due to the generation x environment interaction being accounted for in the total phenotypic variance. Fibermax 832 x Acala1517-99 had a low genetic variance due to the absence of any additive variance and in conjunction with a high environmental variance had low broad- and zero narrow-sense heritability estimates. Fibermax 832 x TTU 202 had a low additive variance which correlated into minuscule narrow-sense heritability estimates of 0.00. Within the Fibermax 832 x TAM 94L-25 parental combination, the total genetic variance was higher in 2001 and corresponded to a higher broad-sense heritability estimate. Narrow-sense heritability estimates in 2001 and 2002 were 0.30 and 0.27, respectively. Within the TAM 94L-25 x TTU 202 parental combination, higher total genetic variance was attained in 2001 and translate into a higher broad-sense heritability estimate. No additive variance was displayed in 2002. Within the TAM 94L-25 x Acala 1517-99 parental combination, the total genetic variance was higher in 2001, however the higher additive variance in 2002 led to an increased narrow-sense heritability estimate of 0.49, compared to the narrow-sense heritability estimate of 0.25 in 2001. The Acala 1517-99 x TTU 202 parental combination had zero additive variance in 2001, but the highest additive variance in 2002 with an estimate of 2.31 which corresponded into a narrow-sense heritability estimate of 0.64.

Among the near-long x short staple parental combinations, broad-sense heritability averaged 0.37 and 0.53 in 2001 and 2002, respectively (Table 15). The higher broad-sense heritability estimates attained in 2002 are attributed to either greater total genetic variance or a lower environmental variance, or a combination of the two. Only TAM 94L-25 x Tamcot CAMD-E had higher broad-sense heritability estimate in 2001 due to greater genetic and lower environmental variances. Narrow-sense heritability averaged 0.22 and 0.53 in 2001 and 2002, respectively. The higher narrow-sense heritability estimates in 2002 are due to greater additive variance and zero or little dominance variance, except for Acala 1517-99 x Tamcot CAMD-E, which is due to less environmental variance. Among all combinations in 2001, the broad- and narrow-sense heritability estimates were 0.30 and 0.17. Among all combinations in 2002, the broad- and narrow-sense heritability estimates were 0.47 and 0.52.

Estimates of additive effects could be small due to a high degree of dispersion of alleles increasing FLn between parents. This might explain why additive genetic components of variance varied greatly and a definitive relationship between additive effects and additive genetic variance could not be detected. The negative estimates of dominance variance seen for this trait could have been due to sampling error and/or the fact that basic generations are inefficient when used for determining dominance variance.

Summary and conclusions

Cotton is a natural product with lint characteristics determined by environmental and genetic factors. There is limited information available about the native fiber length distribution (i.e., on the seed), however it is believe that cotton possesses a normal fiber length distribution (probably is highly heritable) when bolls are hand picked cautiously and ginned carefully with a razor, tweezer, and aid of a microscope. Whatever the genetic determination of length distribution, the mechanical operations in harvesting, ginning, and textile manufacturing alter the distribution by breaking longer fibers into shorter ones (Anthony and Griffin, 2001a; Anthony and Griffin, 2001b; Robert et al., 2000). These successive stages of mechanical handling and processing incrementally but unavoidably inflict some fractures upon fibers being processed.

The degree of fiber breakage is dependent primarily upon fiber length, maturity, strength, and elongation. Longer fibers allow for a greater chance of tension forces being held at both ends, so they therefore have a higher probability of breakage than shorter fibers. Length distributions are also influenced by fiber maturity, and maturity is directly related to growing conditions. Immature fibers have underdeveloped, weak, thin secondary walls that are prone to break during mechanical processes. Fully mature fibers are less likely to be damaged or broken. The load, a specimen of a single fiber or a bundle of fibers in its axial direction, at which the specimen breaks provides a measure of fiber strength. Fiber elongation, the increase in length of fiber during tensile loading, is important in determining the processing propensity of fibers and the mechanical behavior of yarn. Two cottons with the same strength, but with different elongations will behave differently under mechanical stresses.

The environment influenced the magnitude of FLn in 2001 and 2002. The mean responses of the generations indicated that plants had longer fibers by number in 2002 than in 2001. The climatological conditions of the two years were normal in terms of temperature and rainfall. However, rainfall events at physiological maturity during 2001 extended the harvesting period and thus weathering of fibers might have shortened the mean fiber length (Hequet, 2004). Significant generation x environment interactions were detected in all parental combinations. No distinct relationship between genotypic means and gene effects could be detected. In 2001, all near-long x near-long F_1 hybrids had an FLn mean similar to or greater than the longest parent suggesting dominance or overdominance, however, the generation means analysis does not substantiate this conclusion. In 2002, some near-long x near-long F_1 means were similar to or shorter than the shorter parent.

Frequency distributions of individual plant values revealed that segregating populations followed a normal distribution, implying that FLn is quantitatively inherited. A higher percent of transgressive segregation appeared in the BC_1P_1 than in other segregating populations. However, most breeders will attempt to select superior individual plants among the F_2 population and continue selecting throughout subsequent generations with the goal of looking for transgressive segregants among a population of inbred lines derived from the selfing of an F_1 hybrid. The presence of transgressive segregation in the segregating populations of these near-long x near-long combinations suggests that the parental material chosen herein for this study contained different length alleles for FLn, thus suggesting that breeders could make further improvements for upland cotton fiber length among these near-long staple parental genotypes, but only if the appropriate breeding method is implemented. Cotton already has a narrow genetic base (Van Esbroeck et al., 1999) and limited progress in cultivar improvement has been made in recent years because closely-related parents have been used to make successful cultivars (Meredith, 1991; Meredith et al., 1997). Even though transgressive segregation was present in this study, it was at a low frequency thus, requiring large populations for detection. Most breeding programs use a pedigree method, in which seeds are harvested separately from each F_2 to produce F_3 families and continue to keep each F_2 pedigree distinct throughout successive generations. However, if any of the seeds are bulked between the F_2 to F_4 generation so that it is not possible to identify which seeds are derived from individual F_2 plants, considerable loss of already limited variability may occur.

All parental combinations were analyzed by individual environments for FLn. For most parental combinations, analyses of genetic effects indicated that a simple additive-dominance model did not account for most of the genetic variation for FLn. Therefore, a six-parameter model fit the generation means indicating that epistatic effects were present and suggested that inheritance is complex such that multiple alleles interacted to affect upland cotton fiber length. Among the near-long x near-long parental combinations, additive x additive gene effects were predominate, of which a few had negative estimates suggesting both parents contributed alleles for FLn. Among the near-long x short staple parental combinations, significant gene effects were numerous. Both additive and additive x additive gene effects were abundant in the expression of FLn, however the presence and magnitude of dominance and dominance x dominance gene effects can not be ignored. For the parental combinations that were controlled by additive gene action, simple selection in early segregating generations would be successful. Whereas for those parental combinations controlled by non-additive gene action, selection in later generations could prove to be more effective.

Several explanations of the inconsistent gene effects in this study can be proposed. First, parents used in this study were from vastly different genetic backgrounds. The dispersion of alleles in the parents, complete or partial, affects the magnitude and composition of the additive component. The mean and dominance components of the parents remain independent of gene dispersion. Two loci having an inter-allelic interaction will change the F_2 mean, the magnitude and direction of additive x additive and additive x dominance effects, and the magnitude and direction of the variances (Kearsey and Pooni, 1996). Higher order interactions, such as trigenic interactions, may be needed with enough generations to adequately understand the inheritance of cotton fiber length.

The environmental variance for FLn was high, contradicting May (1999) who concluded that extensive environmental replication is not necessary to evaluate and select breeding material on the basis of fiber length parameters. Among the near-long x near-long parental combinations, genetic control for FLn contained additive and non-additive genetic variance, as to which portion was greater depended upon the parental combination and environment. Among the near-long x short staple parental combinations the predominant portion was additive. Numerous studies in the past concluded that additive variance within upland cotton genotypes tended to be more prominent than non-additive variance (Miller and Marani, 1963; Ramey and Miller, 1966; Lee et al., 1967; Al-Rawi and Kohel, 1969; Al-Rawi and Kohel, 1970; Meredith and Bridge, 1972; Quisenberry 1975; Green and Culp, 1990; Tang et al., 1993), however, a few experiments have found non-additive variance to be more important

(Verhalen and Murray, 1969; Baker and Verhalen, 1973; May and Green, 1994; Cheatham et al., 2003).

The moderate broad-sense heritability estimates found in this study suggest that improvement for FLn can be realized through breeding if some of the genetic variation is additive in nature. Moderate to relatively high values for broad and narrow-sense heritability ($H^2 > 0.50$ and $h^2 > 0.50$) for fiber length parameters, 2.5% span length and UHM length, have been reported previously (May, 1999; May and Jividen, 1999; Herring et al., 2004). Depending upon the parental combination and environment, the sometimes moderate to high values for narrow-sense heritability found in this study suggest that conventional pedigree and early generation selection methods should be effective for initial improvements in FLn in cotton. However, low narrow-sense heritability estimates were more often the norm, suggesting that inheritance is complex and progress will be difficult.

Gene effects and variances for FLn were inherited quite differently in specific environments and specific parental combinations suggesting environmentally specific mechanisms for FLn. This type of interaction would make selection of fiber length and superior genotypes that are adapted to wide geographic areas much more difficult. This would explain why improvement of fiber length in upland cotton has been slow, even though many genetic studies have indicated that fiber length is moderately to highly heritable. Cotton fiber length is a complex trait, and improved fiber length is the result of many different loci. These results show that both the adequacy of certain modes of inheritance as well as the importance and significance of gene effects were dependent upon the particular parental combination and environment, stressing the importance of the appropriate selection of both parents and environment for the success of a cotton breeding program.

CHAPTER VII

AFIS Uqlw GENERATION MEANS ANALYSIS

Results and discussion

The parental, F_1, F_2, and backcross generations differed ($P \leq 0.01$) in Uqlw, a length by weight measurement, for all parental combinations (Table 16). The ANOVA also revealed a significant generation x environment interaction in four parental combinations, Fibermax 832 x TAM 94L-25, TAM 94L-25 x TTU 202,TAM 94L-25 x Acala 1517-99, and TAM 94L-25 x Tamcot CAMD-E. The data from the six other parental combinations, Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, Acala 1517-99 x TTU 202, Fibermax 832 x Tamcot CAMD-E, Acala 1517-99 x Tamcot CAMD-E, and TTU 202 x Tamcot CAMD-E, and among all combinations were pooled over years. The lack of a significant effect of genotype x environment in these parental combinations for Uqlw supports the premise that there is a strong genetic basis for fiber length (May, 1999).

Uqlw means from P_1 and P_2 were different ($P \leq 0.05$) in each parental combination except for Fibermax 832 x TAM 94L-25 in 2002 and Acala 1517-99 x TTU 202 combined across years (Table 17). Generally, F_1 hybrids had an Uqlw similar to the longest parent or intermediate of the parental genotypes. However, the F_1 hybrids of Fibermax 832 x TAM 94L-25 in 2002, TAM 94L-25 x TTU 202 in 2001 and 2002, and TAM 94L-25 x Acala 1517-99 in 2001 and 2002, exhibited an Uqlw mean greater than the longest parent, thus demonstrating heterosis. Depending upon the parental combination and environment, F_2 means were either similar to the longest parent or

Table 16. Mean squares for Uqlw measured on P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 (per parental combination and among all combinations) at College Station, TX in 2001 and 2002.

A.

		Parental Combinations †					
Source	df	832 x L-25	L-25 x 202	832 x 1517	832 x 202	L-25 x 1517	1517 x 202
Environment (E)	1	40.95**	29.47**	12.73**	27.03**	43.32**	21.21**
Reps/E	6	0.51	0.28	0.45	0.22	0.47	0.44
Generation (Gn)	5	2.85**	6.46**	7.03**	5.12**	7.45**	1.01*
Gn x E	5	0.90*	0.74**	0.08	0.21	1.11**	0.16
Error	30	0.34	0.21	0.40	0.32	0.29	0.39

B.

		Parental Combinations‡				
Source	df	L-25 x CD-E	832 x CD-E	1517 x CD-E	202 x CD-E	Among
Environment (E)	1	13.82**	31.55**	26.45**	8.49**	24.40**
Reps/E	6	0.54	0.24	0.17	0.14	0.04
Generation (Gn)	5	31.22**	35.67**	14.09**	17.51**	8.60**
Gn x E	5	0.65**	0.63	0.06	0.62	0.06
Error	30	0.19	0.28	0.24	0.27	0.05

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

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

Table 17. Means of P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 for Uqlw (mm) per parental combination and across combinations at College Station, TX in 2001 and 2002. First parent listed is P_1, second parent is P_2.

A.

	Parental Combinations†								
	832 x L-25		L-25 x 202		832 x 1517	832 x 202	L-25 x 1517		1517 x 202
Gen.‡	2001	2002	2001	2002	2001/02	2001/02	2001	2002	2001/02
P_1	34.0 ab§	34.9 bc	32.6 b	34.3 b	34.4 a	34.4 a	32.6 bc	34.3 cd	32.1 b
P_2	32.6 c	34.3 c	31.7 c	33.2 c	32.1 c	32.4 c	31.4 d	32.7 e	32.4 ab
F_1	34.6 a	35.9 a	34.9 a	35.3 a	34.3 a	34.4 a	34.3 a	35.2 ab	33.0 a
F_2	32.9 bc	35.7 a	32.9 b	34.9 ab	33.3 b	33.5 b	31.9 cd	34.7 bc	32.6 ab
BC_1P_1	33.5 abc	35.6 ab	33.3 b	35.5 a	34.3 a	34.2 a	33.0 b	35.5 a	32.7 ab
BC_1P_2	33.7 abc	35.9 a	32.9 b	34.5 b	33.1 b	33.3 b	31.7 cd	33.9 d	33.0 a

B.

	Parental Combinations¶					
	L-25 x CD-E		832 x CD-E	1517 x CD-E	202 x CD-E	Among
Gen.	2001	2002	2001/02	2001/02	2001/02	2001/02
P_1	32.6 a	34.3 a	34.3 a	32.1 a	32.4 a	33.5 a
P_2	27.8 d	29.1 d	28.5 f	28.5 e	28.5 e	30.9 d
F_1	32.6 a	33.9 a	32.2 c	31.1 cd	31.6 bc	33.5 a
F_2	31.9 b	32.4 b	31.4 d	31.5 bc	31.1 c	32.7 b
BC_1P_1	32.7 a	34.1 a	33.0 b	31.9 ab	32.0 ab	33.5 a
BC_1P_2	30.7 c	31.0 c	30.2 e	30.8 d	29.9 d	32.2 c

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ Gen., generation; 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 K = 100 (approximates p = 0.05) according to Waller-Duncan LSD.

¶ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

intermediate. In 2002, the F_2 mean of Fibermax 832 x TAM 94L-25, the two parents with the longest fiber length in this study, exhibited an Uqlw greater than the longest parent, thus demonstrating heterosis once again. In most parental combinations, the mean values of the backcrosses were shifted toward the values observed for the recurrent parent. However, the BC_1P_1 means were not different from the BC_1P_2 means in the near-long x near-long parental combinations of Fibermax 832 x TAM 94L-25 in 2001 and 2002, TAM 94L-25 x TTU 202 in 2001, and Acala 1517-99 x TTU 202 combined across years.

As with FLw and FLn, the parental combinations were divided into two categories, near-long x near-long and near-long x short staple parental combinations. For each parental combination, P_1 was assigned accordingly to the parent with the longest FLw. The near-long x near-long parental combinations consisted of Fibermax 832 x TAM 94L-25, TAM 94L-25 x TTU 202, Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, TAM 94L-25 x Acala 1517-99, and Acala 1517-99 x TTU 202. The near-long x short staple parental combinations were Fibermax 832, TAM 94L-25, Acala 1517-99, and TTU 202 crosses with Tamcot CAMD-E.

Uqlw frequency distributions of each parental combination were constructed to visually gain a more comprehensive understanding into the generation means and to determine transgressive segregation (Figs. 49-63). For each figure the y-axis is the number of plants, and the x-axis is Uqlw in mm divided into 10 length classes. The classes within each figure are the same for the non-segregating and segregating populations. However, the overall range and class size does change from figure to figure.

Examination of the frequency distribution of individual plant values of each parental combination indicated that the segregating populations followed a normal distribution, suggesting that Uqlw is quantitatively inherited. Transgressive segregation, individual F_2 or backcross plant observations with values exceeding the longest parent or F_1 observation (Kearsey and Pooni, 1996), were visible in both near-long x near-long and near-long x short staple parental combinations. At least two segregating populations in all near-long x near-long parental combinations exhibited transgressive segregation. Averaging the percent of plants exhibiting transgressive segregation for each segregating population among the near-long x near-long combinations, the BC_1P_1 had the highest transgressive segregation at 7.3%, followed by the F_2 at 5.5%, and the BC_1P_2 at 3.2%. Within individual combinations, TAM 94L-25 x TTU 202, 2002, had the highest percentage of transgressive segregation among the BC_1P_1 and F_2 populations, 25.0 and 15.0%, respectively (Fig. 52). Also, TAM 94L-25 x Acala 1517-99, 2002, had a high percentage of transgressive segregation among the BC_1P_1 and F_2 populations, 23.0 and 14.5%, respectively (Fig. 56). In 2002, Fibermax 832 x TAM 94L-25, the longest staple length parents in the study, had the highest percent of transgressive segregation among the BC_1P_2 at 13.0% (Fig. 50). Also, this parental combination and environment had 10.5% transgressive segregation in the F_2 population (Fig. 50). It is interesting to note that a high percentage of transgressive segregation for Uqlw was observed in Fibermax 832 x TAM 94L-25 parental combination in 2002. This suggests that the two longest

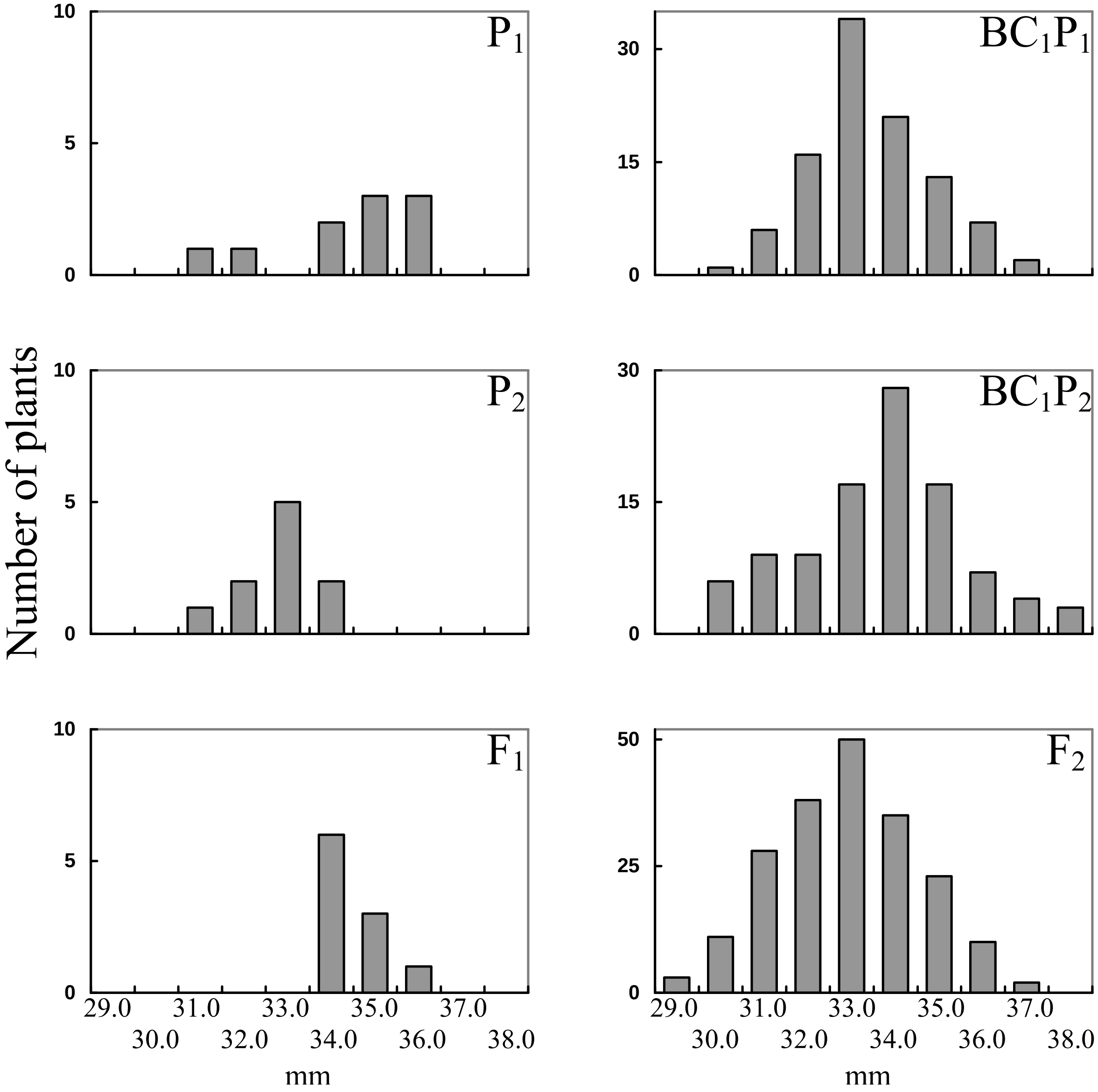

Fig. 49. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of Fibermax 832 (P_1) x TAM 94L-25 (P_2) in 2001.

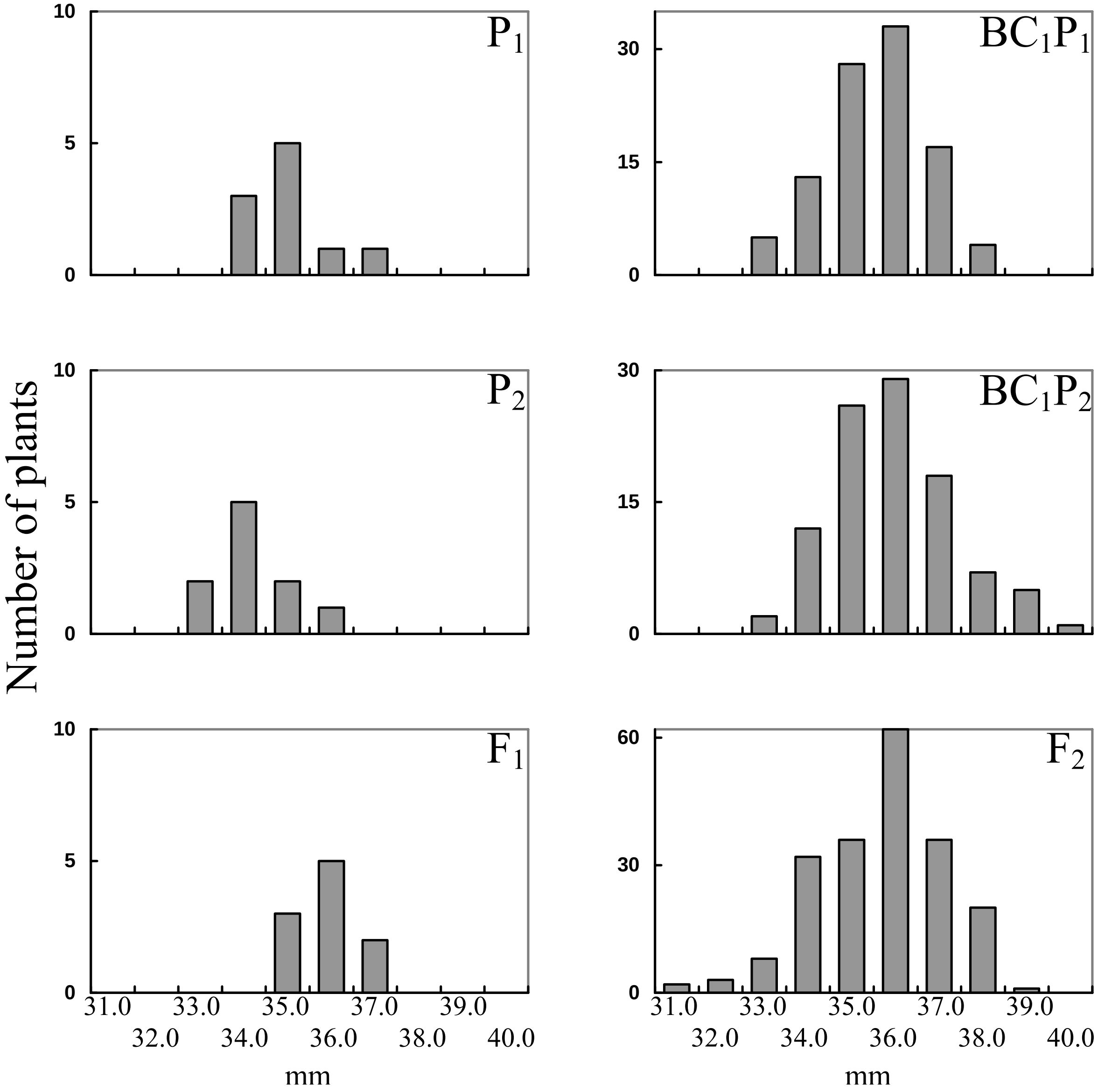

Fig. 50. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of Fibermax 832 (P_1) x TAM 94L-25 (P_2) in 2002.

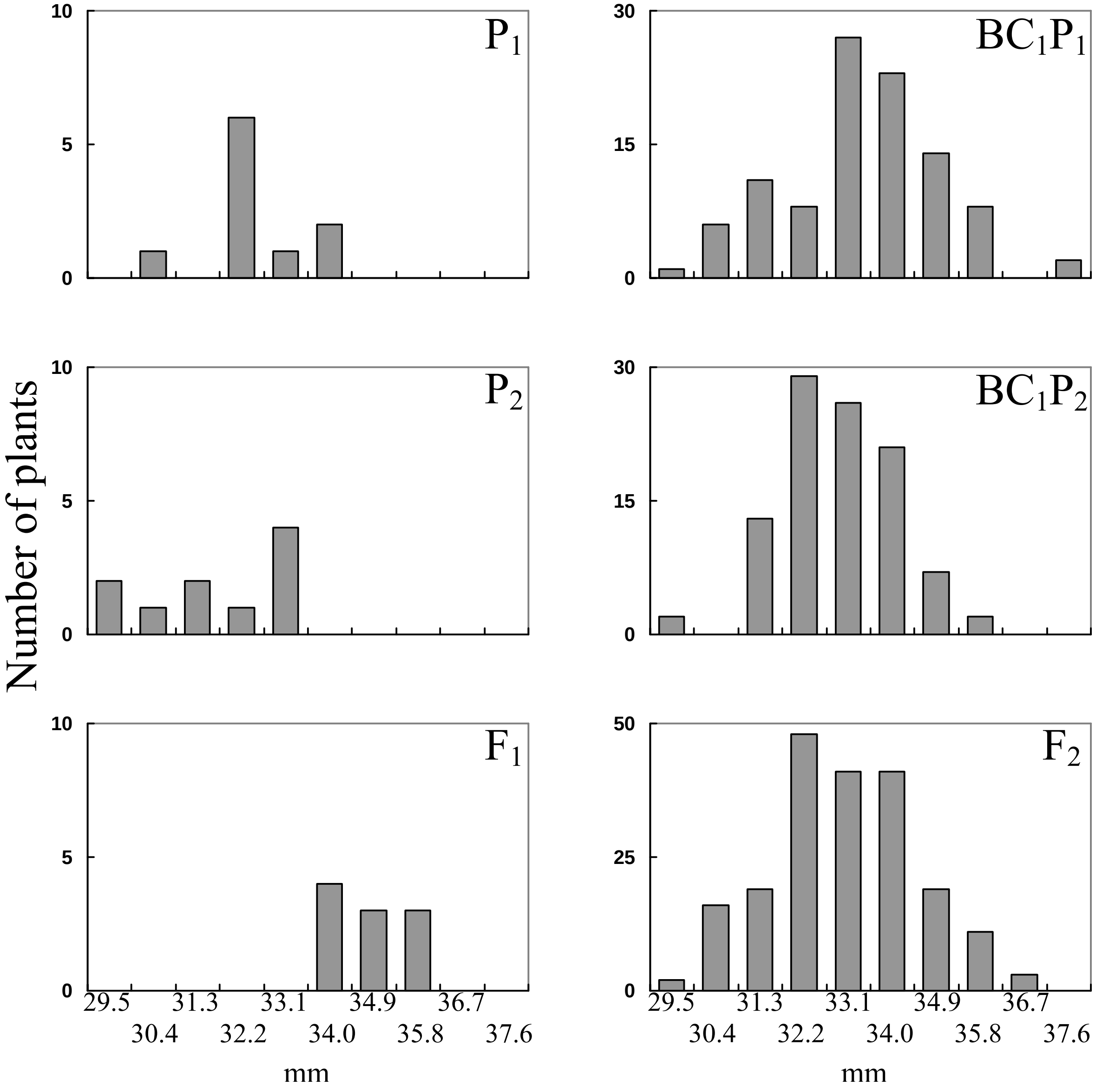

Fig. 51. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of TAM 94L-25 (P_1) x TTU 202 (P_2) in 2001.

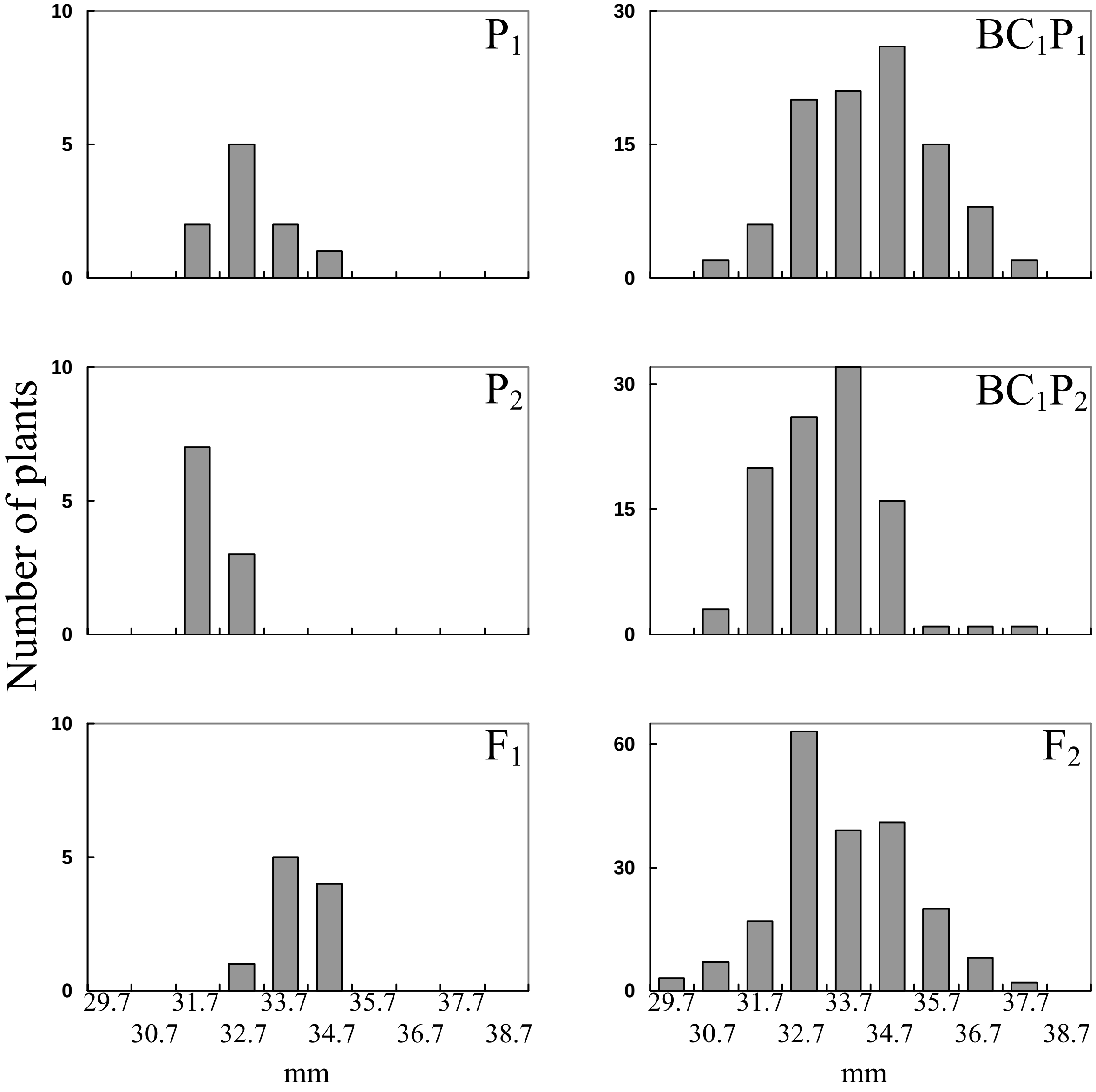

Fig. 52. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of TAM 94L-25 (P_1) x TTU 202 (P_2) in 2002.

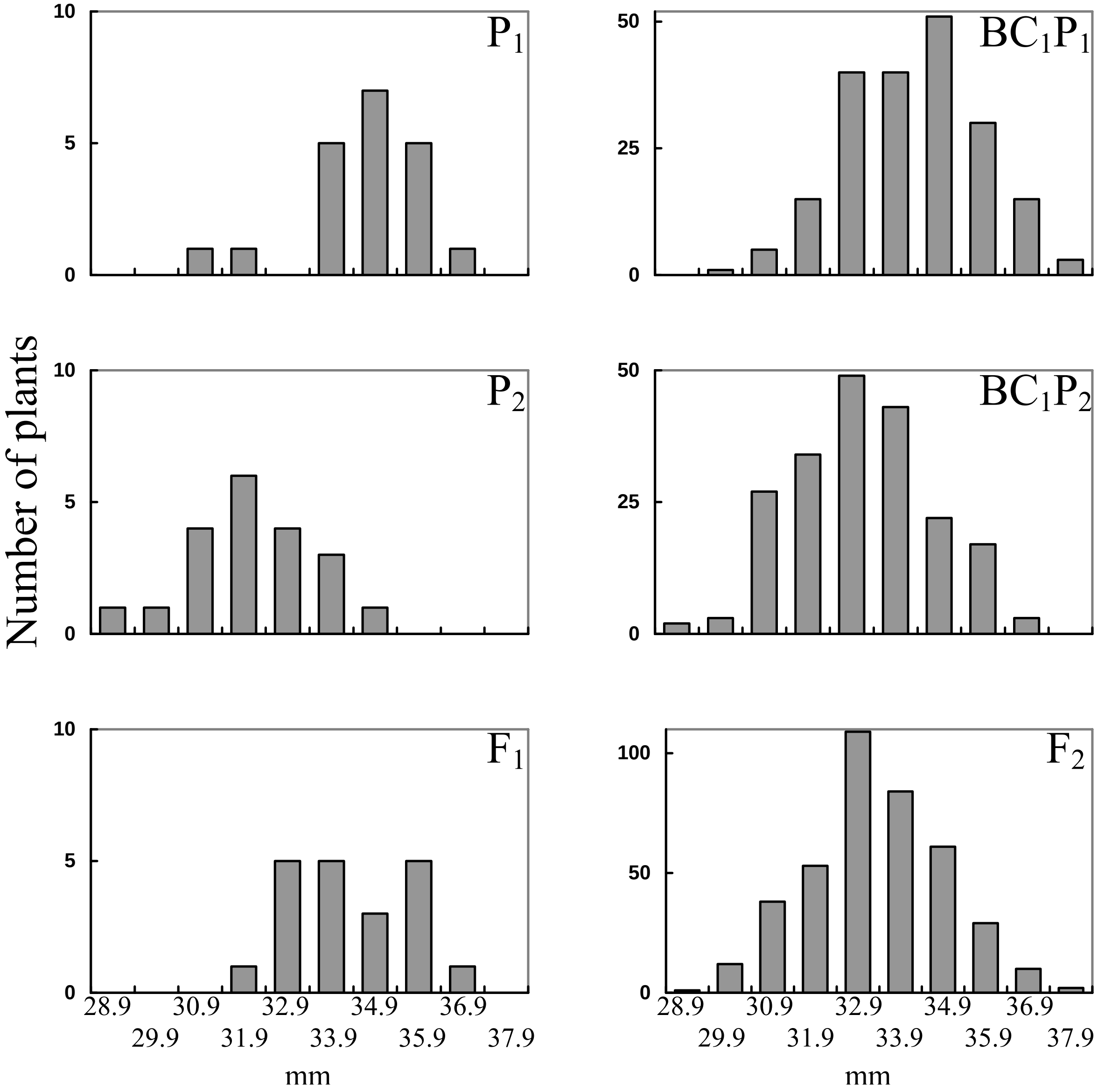

Fig. 53. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of Fibermax 832 (P_1) x Acala 1517-99 (P_2) across 2001 and 2002.

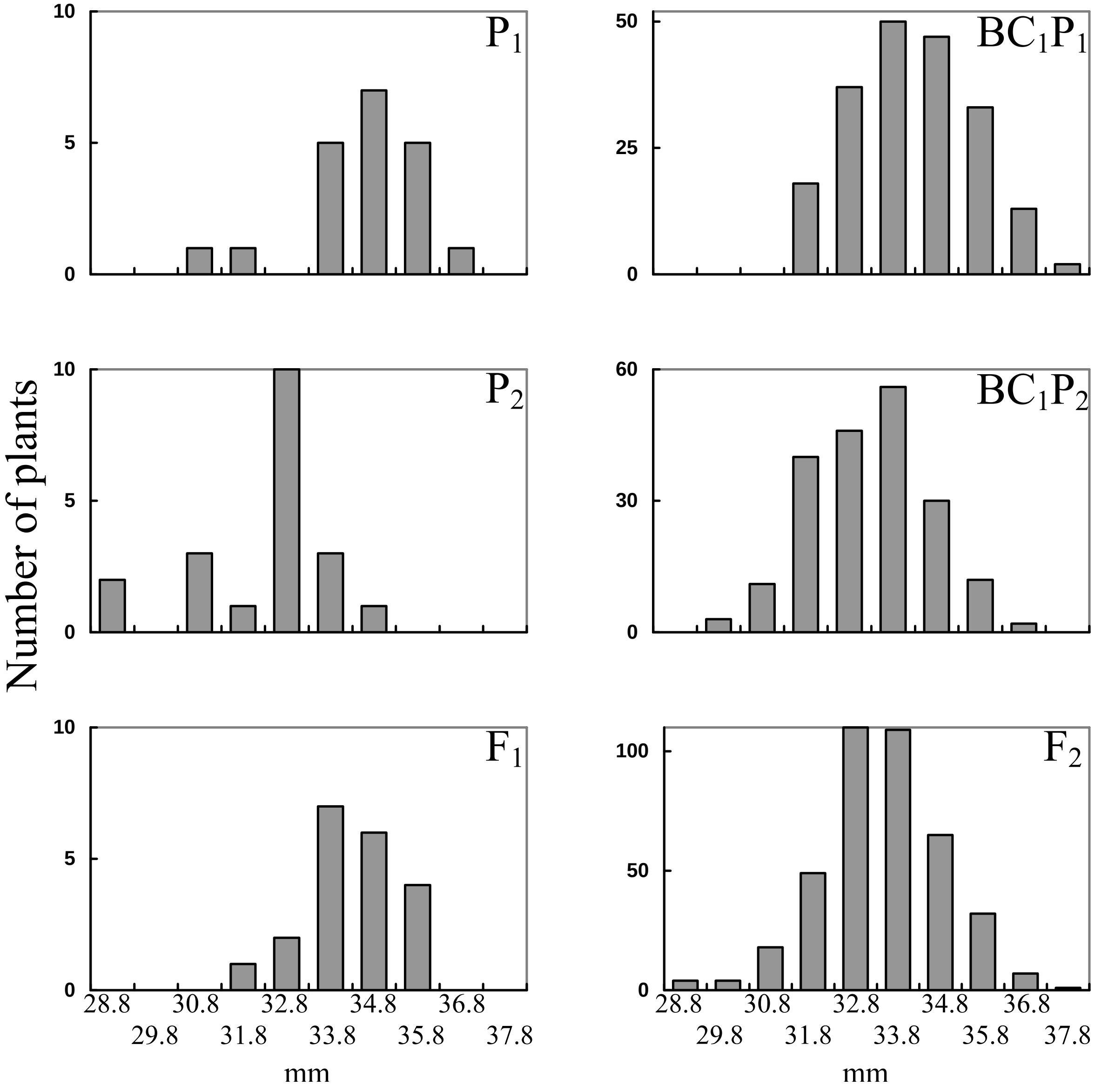

Fig. 54. Frequency distribution of Uqlw in the P$_1$, P$_2$, F$_1$, BC$_1$P$_1$, BC$_1$P$_2$, and F$_2$ generation for the near-long x near-long parental combination of Fibermax 832 (P$_1$) x TTU 202 (P$_2$) across 2001 and 2002.

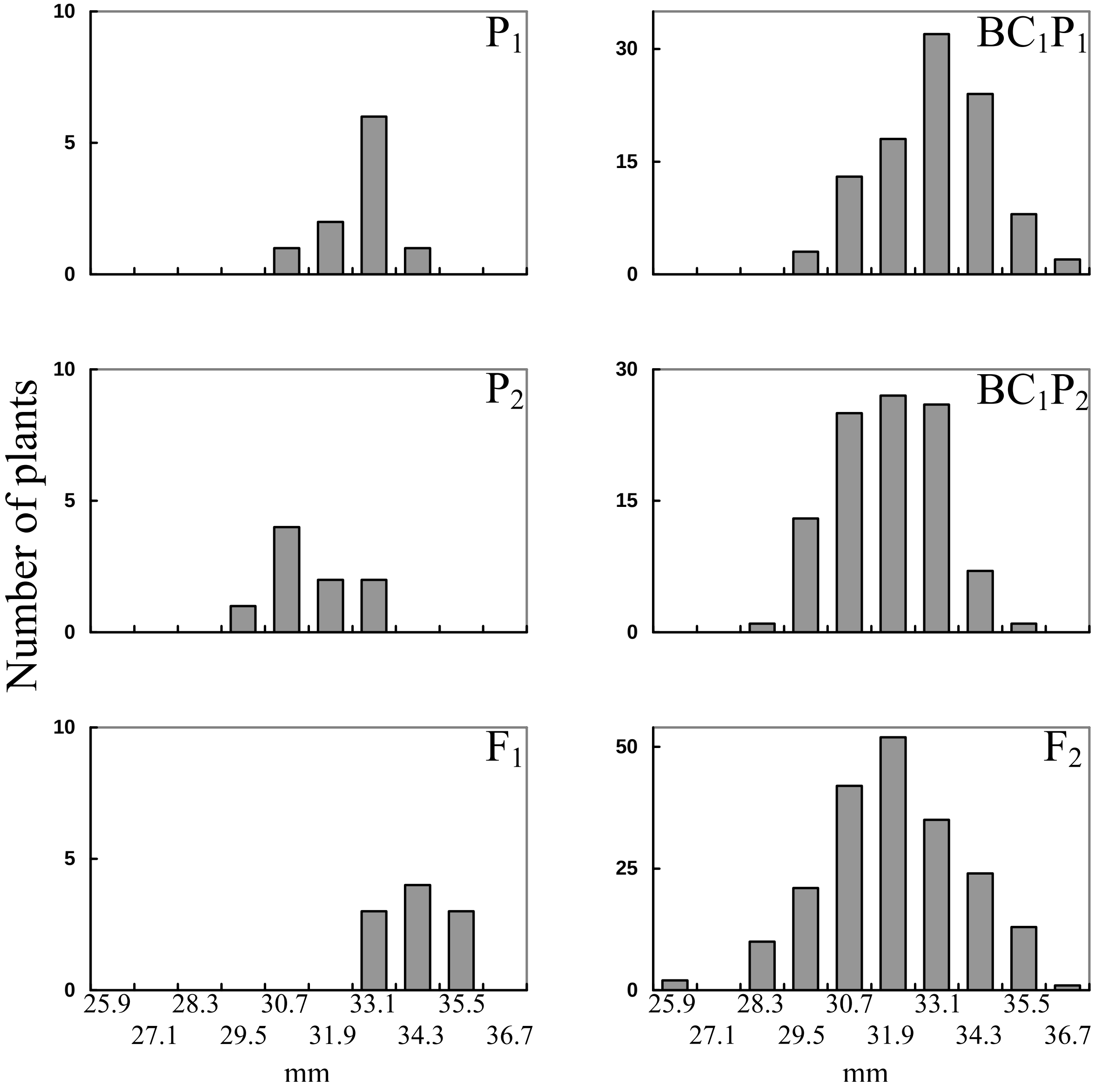

Fig. 55. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of TAM 94L-25 (P_1) x Acala 1517-99 (P_2) in 2001.

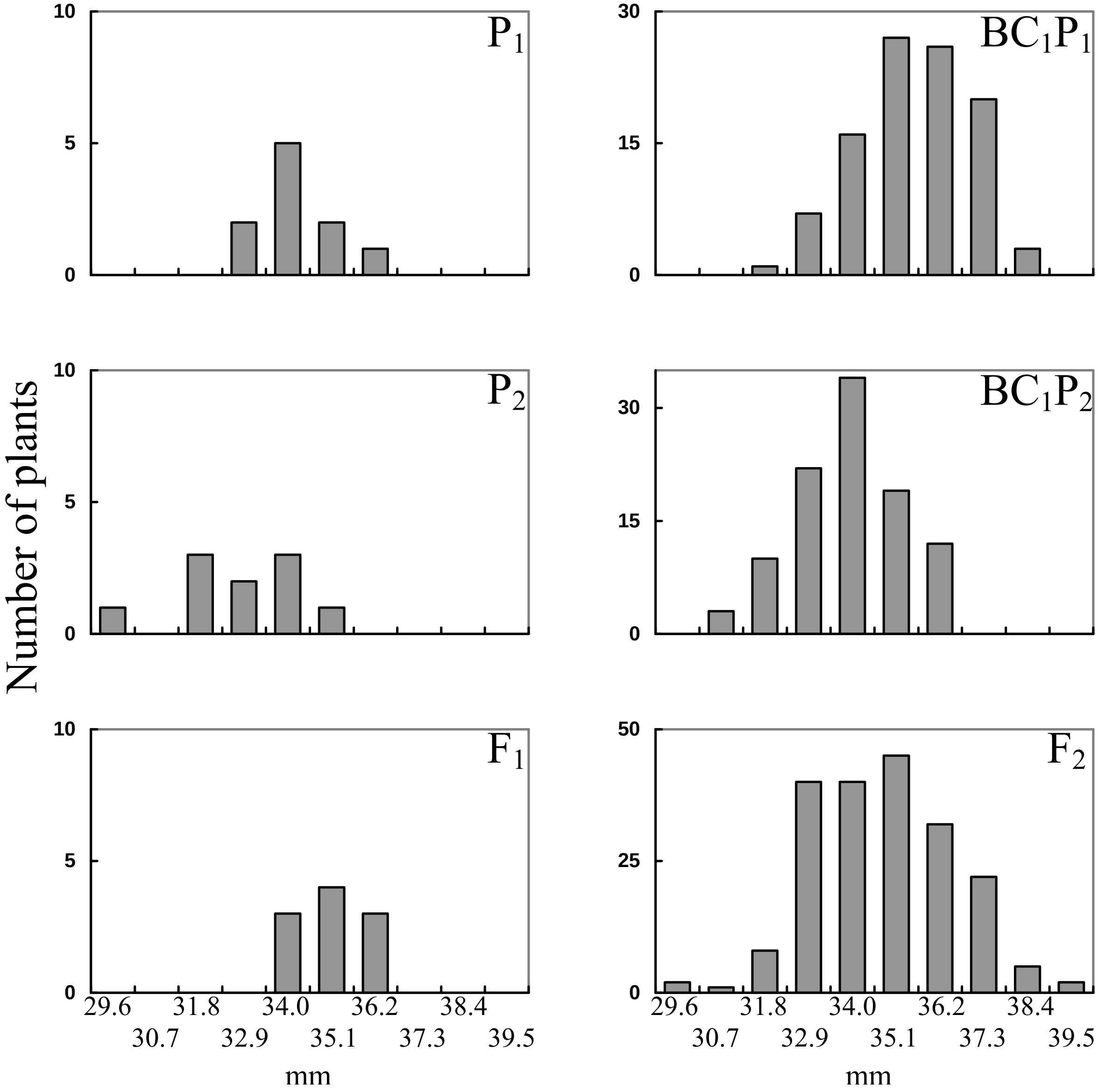

Fig. 56. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of TAM 94L-25 (P_1) x Acala 1517-99 (P_2) in 2002.

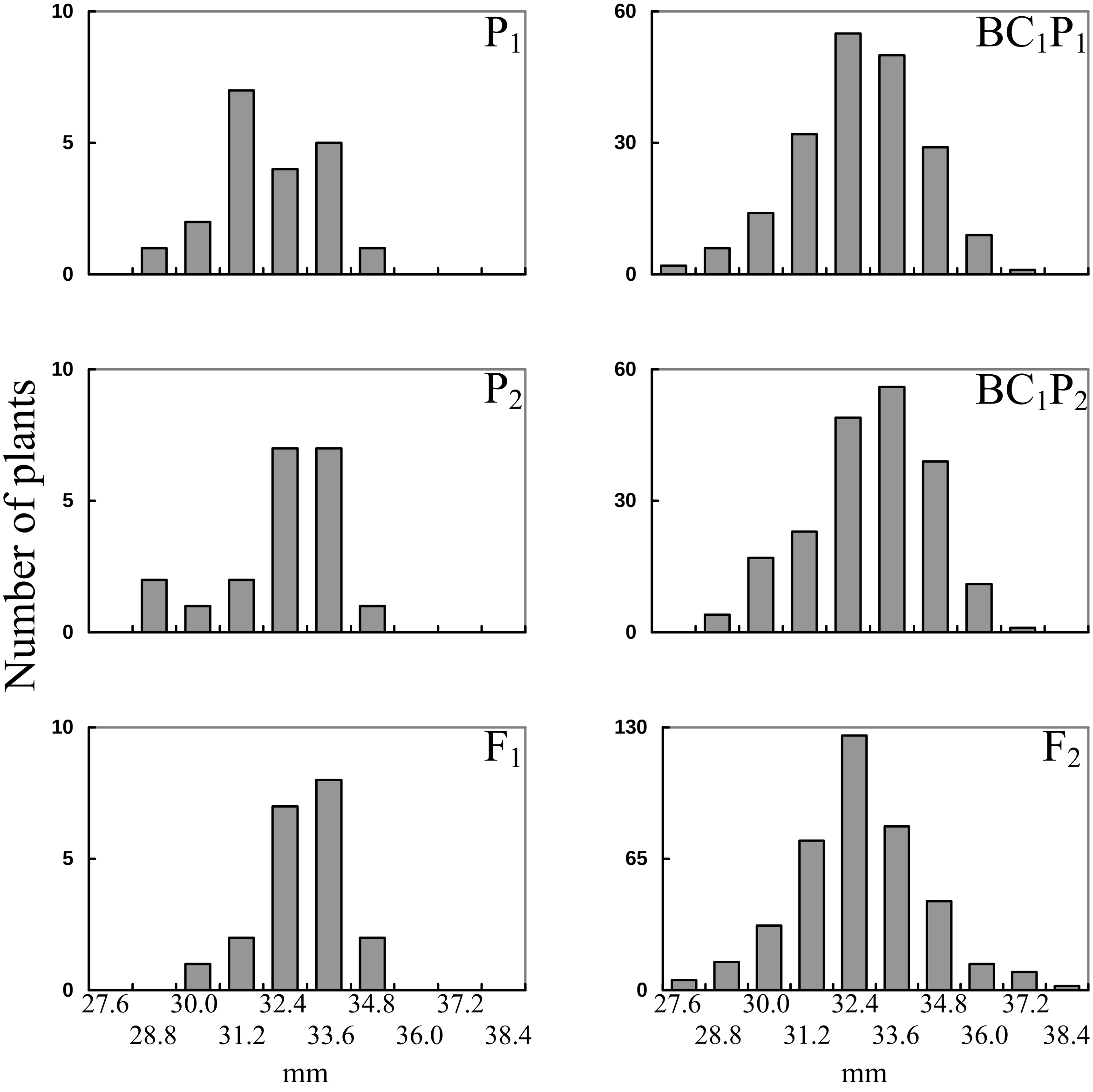

Fig. 57. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x near-long parental combination of Acala 1517-99 (P_1) x TTU 202 (P_2) across 2001 and 2002.

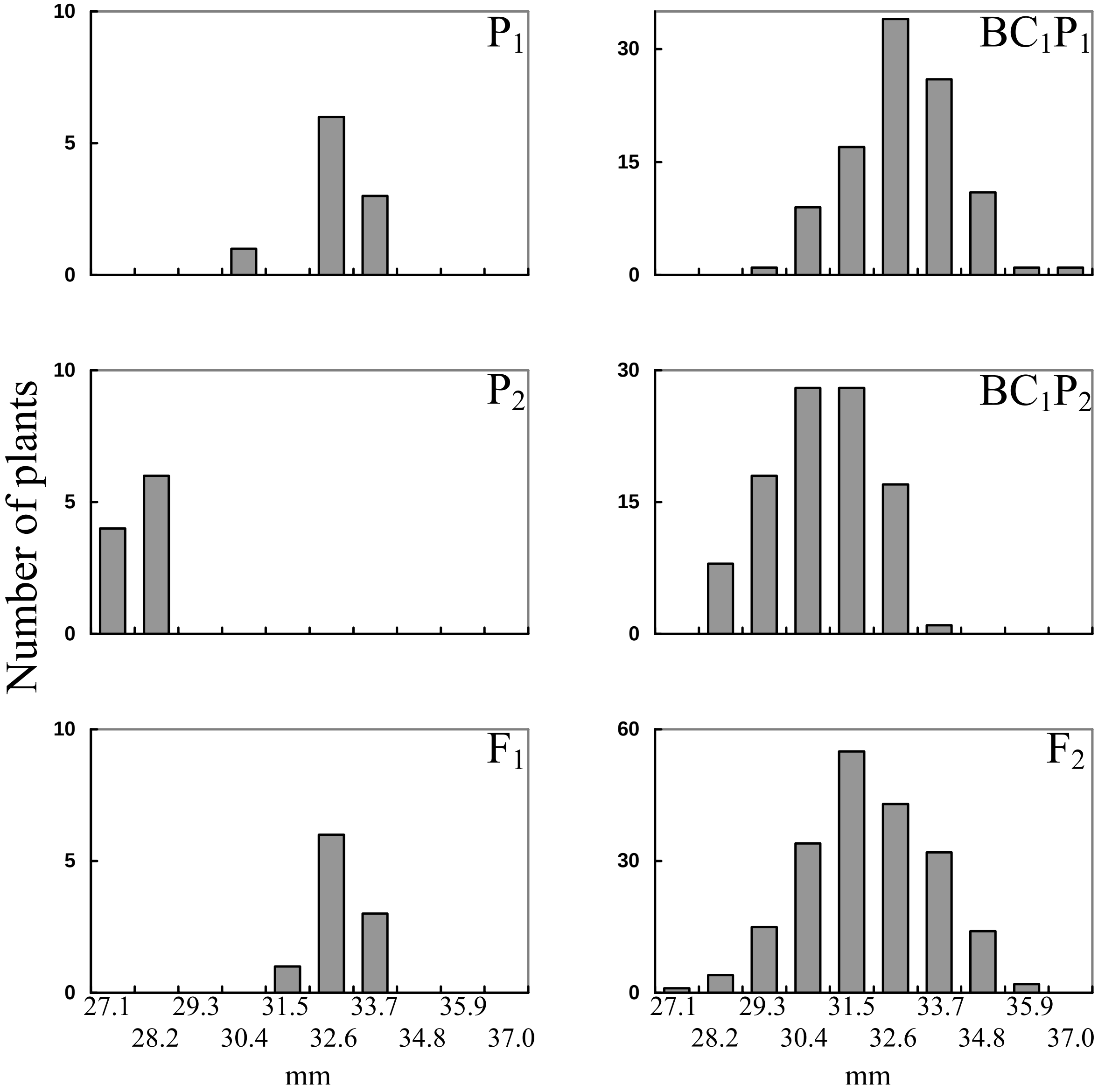

Fig. 58. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of TAM 94L-25 (P_1) x Tamcot CAMD-E (P_2) in 2001.

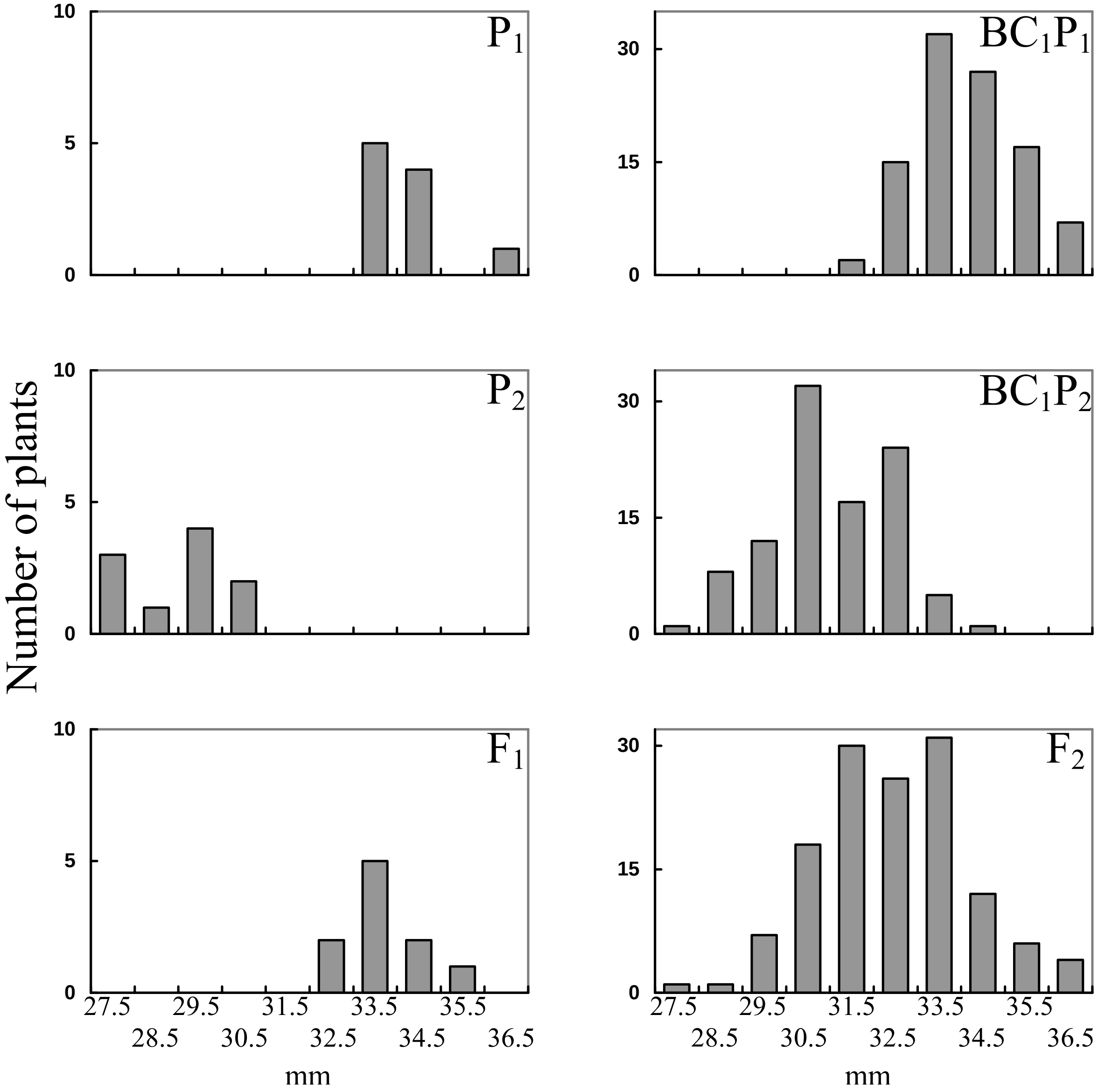

Fig. 59. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of TAM 94L-25 (P_1) x Tamcot CAMD-E (P_2) in 2002.

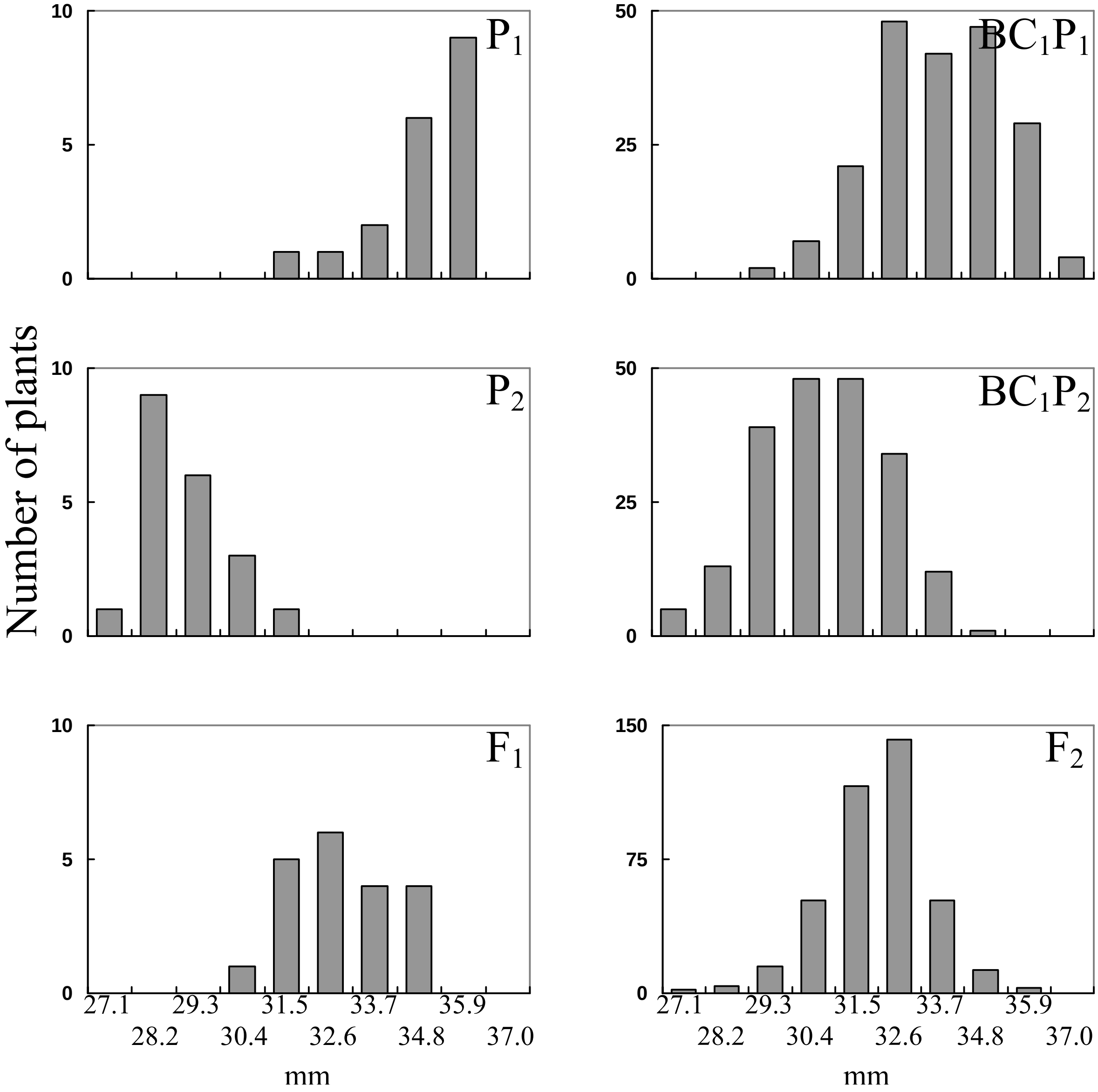

Fig. 60. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of Fibermax 832 (P_1) x Tamcot CAMD-E (P_2) across 2001 and 2002.

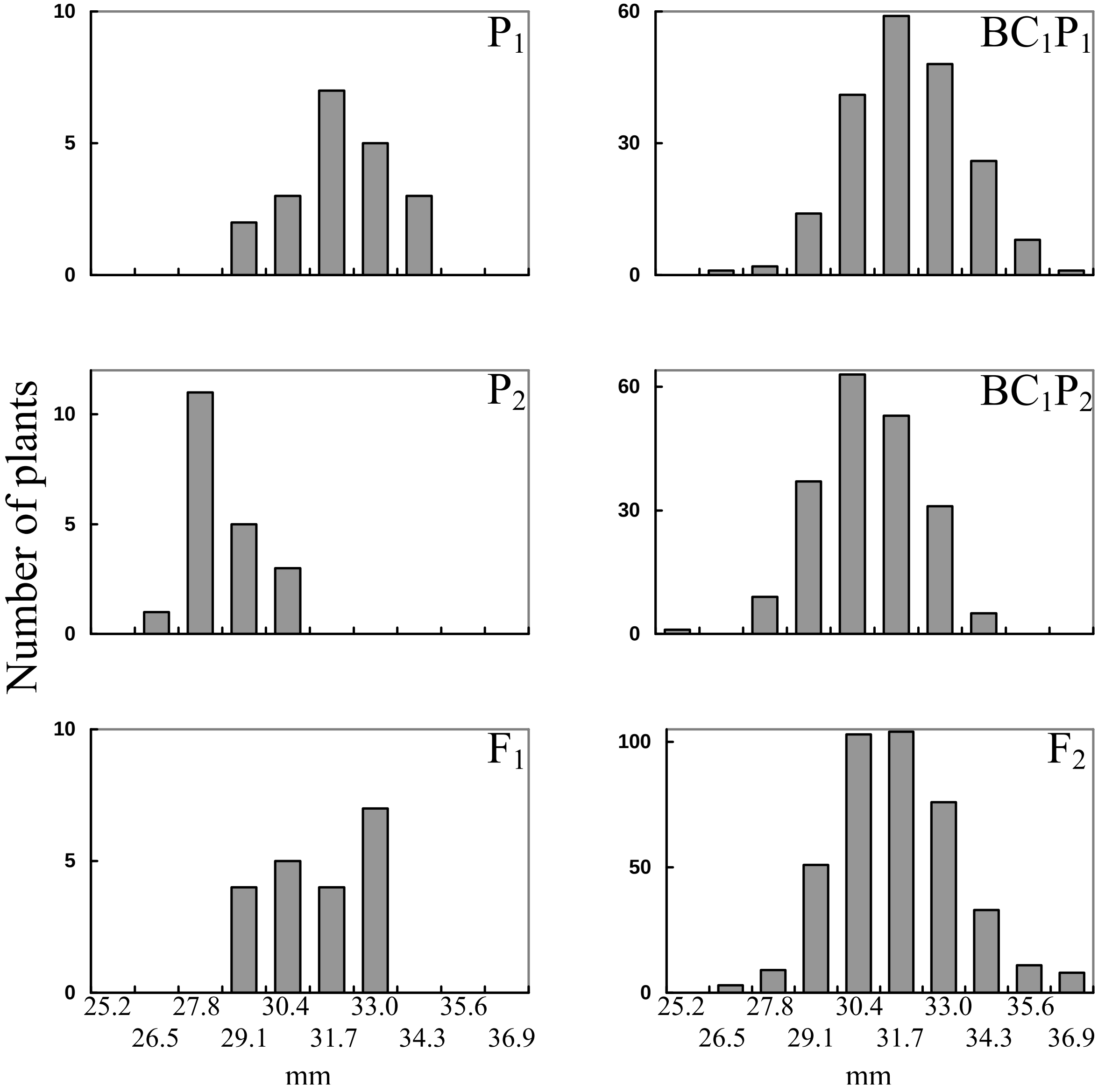

Fig. 61. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of Acala 1517-99 (P_1) x Tamcot CAMD-E (P_2) across 2001 and 2002.

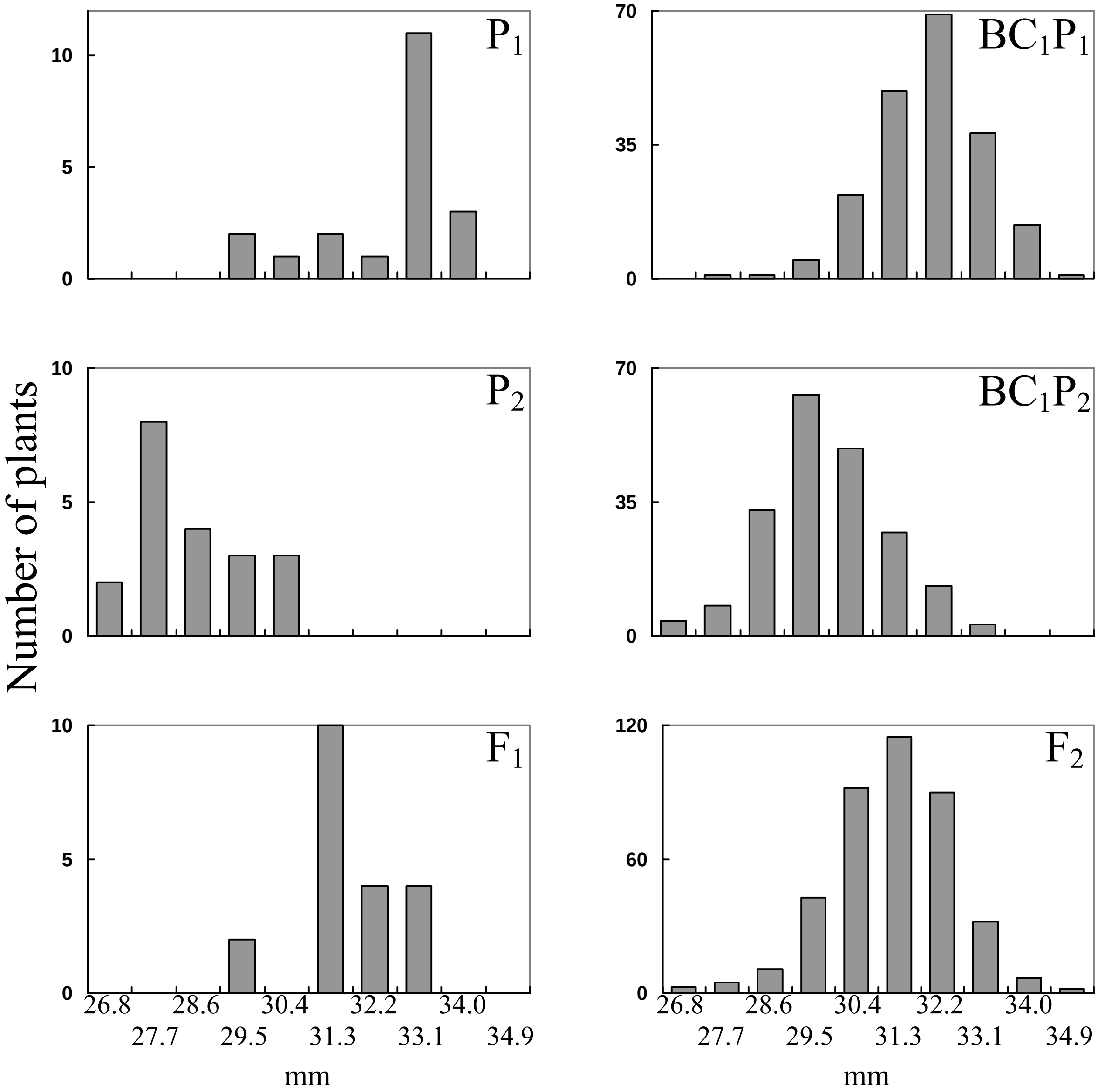

Fig. 62. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation for the near-long x short staple parental combination of TTU 202 (P_1) x Tamcot CAMD-E (P_2) across 2001 and 2002.

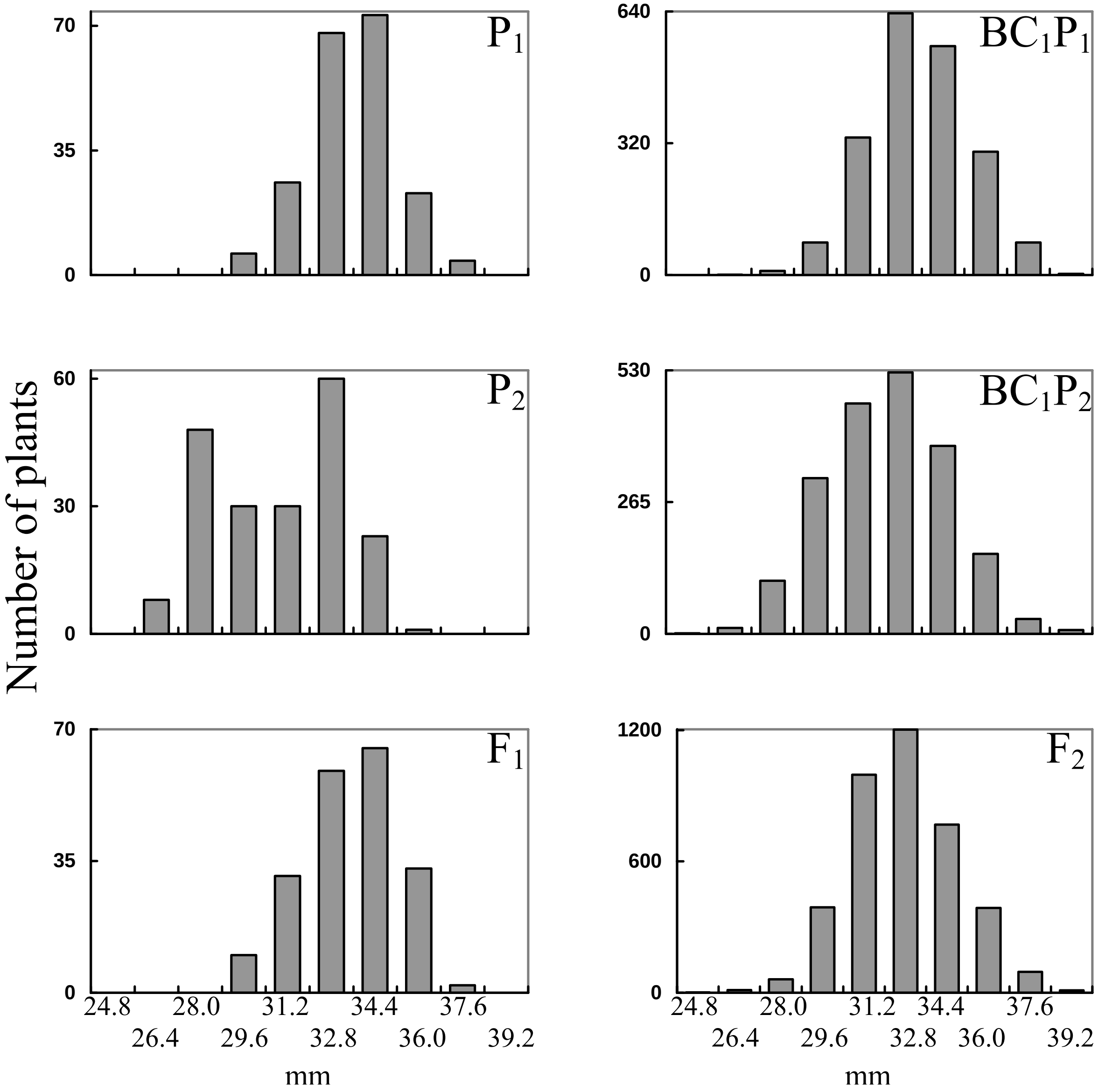

Fig. 63. Frequency distribution of Uqlw in the P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 generation among all parental combinations in 2001 and 2002.

genotypes in this study have different alleles for Uqlw and that further improvement of fiber length is possible.

Fewer transgressive segregates appeared among the near-long x short staple parental combinations, and none appeared in the backcrosses to Tamcot CAMD-E (Figs. 58-62). In 2001, TAM 94L-25 x Tamcot CAMD-E had the highest percentage of BC_1P_1 and F_2 transgressive segregation, 13.0 and 8.0%, respectively (Fig. 58). Other near-long x short staple parental combinations either displayed no or a very low percentage of transgressive segregation.

Generation mean analyses tested three- and six-parameter models for the best fit to explain genetic control of Uqlw in various upland parental combinations. Effects were first estimated with the three-parameter model and accepted if $P \geq 0.05$. The three-parameter model did not satisfactorily explain the genetic differences of Uqlw for any of the parental combinations, indicating that epistasis was present (Table 18). Therefore, the six-parameter model was fit to determine the type and magnitude of gene effects involved in the inheritance of Uqlw. Fibermax 832 x Acala 1517-99 was the only near-long x near-long parental combination to display additive effects with an estimate of 1.15. Dominance effects were exhibited in the parental combinations of Fibermax 832 x TAM 94L-25 in 2002, TAM 94L-25 x TTU 202 in 2002, and Fibermax 832 x Acala 1517-99 combined across years.

Among the non-allelic interactions and near-long x near-long parental combinations, additive x additive, additive x dominance, and dominance x dominance gene effect estimates were significant for Uqlw. This is unlike FLw and FLn, which had

Table 18. Estimates of gene effects for Uqlw (per parental combination and among all combinations) at College Station, TX in 2001 and 2002.

		Gene effects†					
Parental Combinations	Year	*m*	*a*	*d*	*aa*	*ad*	*dd*
Fibermax 832 x TAM 94L-25‡	2001	31.10**	0.99	3.75	2.66**	-2.39*	-0.33
Fibermax 832 x TAM 94L-25‡	2002	33.80**	0.61	5.54**	0.41	-1.91*	-3.56**
TAM 94L-25 x TTU 202‡	2001	31.57**	0.23	2.31	0.52	0.44	0.82
TAM 94L-25 x TTU 202‡	2002	32.95**	0.13	5.65**	0.50	1.80*	-3.53*
Fibermax 832 x Acala 1517-99‡	2001/02	31.77**	1.15*	4.33*	1.73**	0.44	-2.50
Fibermax 832 x TTU 202‡	2001/02	33.14**	0.77	-0.85	0.80*	0.46	3.30**
TAM 94L-25 x Acala 1517-99‡	2001	30.01**	0.57	3.45	1.90**	1.34	0.62
TAM 94L-25 x Acala 1517-99‡	2002	33.41**	0.36	3.63	-0.04	2.66	-2.05
Acala 1517-99 x TTU 202‡	2001/02	31.09**	-0.37	2.49	1.70**	0.09	0.65
TAM 94L-25 x Tamcot CAMD-E§	2001	30.81**	2.30**	2.12	-0.60	-0.74	0.01
TAM 94L-25 x Tamcot CAMD-E§	2002	31.04 **	2.36**	2.72	0.43	1.52	0.28
Fibermax 832 x Tamcot CAMD-E§	2001/02	30.01**	3.28**	3.81*	1.31**	-0.67	-2.01
Acala 1517-99 x Tamcot CAMD-E§	2001/02	30.51**	2.18**	2.71	-0.35	-1.97	-2.17
TTU 202 x Tamcot CAMD-E§	2001/02	31.22**	2.54**	-0.99	-0.60	-0.78	1.60
Among all combinations	2001/02	31.03**	1.71**	2.92**	0.80**	-0.66*	0.51

*, ** Significant at the 0.05 and 0.01 probability level on the basis of *t* test with n – 1 =5 degrees of freedom, respectively.

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

‡ Near-long x near-long parental combination.

§ Near-long x short staple parental combination.

only significant additive x additive gene effect estimates. Additive x additive effects were significant in Fibermax 832 x TAM 94L-25 in 2001, Fibermax 832 x Acala 1517-99 combined across years, Fibermax 832 x TTU 202, TAM 94L-25 x Acala 1517-99 in 2001, and Acala 1517-99 x TTU 202 with estimated values of 2.66, 1.73, 0.80, 1.90, and 1.70, respectively (Table 18). Additive x dominance effects were negative for Fibermax 832 x TAM 94L-25 in 2001 and 2002 with values of -2.39 and -1.91, while TAM 94L-25 x TTU 202 in 2002 had a positive additive x dominance estimate of 1.80. Dominance x dominance effects were significant in Fibermax 832 x TAM 94L-25 in 2002, TAM 94 L-25 x TTU 202 in 2002, and Fibermax 832 x TTU 202 with estimated values of -3.56, -3.53, and 3.30. In 2002, the dominance effects for Fibermax 832 x TAM 94L-25 and TAM 94L-25 x TTU 202 were positive while the dominance x dominance effects were negative. This contrasting direction of response suggests positive duplicate epistasis (Kearsey and Pooni, 1996). Uqlw was the only AFIS measurement to have positive duplicate epistasis among a near-long x near-long combination. Among the near-long x near-long parental combinations, additive effects accounted for a smaller portion of the observed variability than dominance effects. In comparing the relative magnitude of additive x additive to dominance x dominance effects, it depended on the parental combination and environment as to which one was greater. Overall, dominance and non-allelic interaction effects were the most important in determining Uqlw among near-long x near-long parental combinations.

For all near-long x short staple parental combinations, additive gene effect estimates were significant and positive. Fibermax 832 x Tamcot CAMD-E combined across years was the only parental combination to exhibit dominance and additive x additive gene effects with estimates of 3.81 and 1.31, respectively (Table 18). No additive x dominance or dominance x dominance effects were significant among these near-long x short staple parental combinations.

Generation means analysis indicated that genetic control for Uqlw among near-long x short staple parental combinations was not as complex as other AFIS fiber length measurements, FLw and FLn. Additive effects for Uqlw accounted for a larger portion of the observed variability when compared to FLw and FLn and were sometimes larger in magnitude than dominance effects. Additive effects were significant more often than dominance effects because of the generation means analysis produced larger standard errors, although primarily among near-long x short staple parental combinations, for dominance than for additive effects (data not shown). In comparing the relative magnitude of additive x additive to dominance x dominance, it depended on the parental combination and environment as to which one was greater. Overall, additive effects appear to be a more important factor in Uqlw among near-long x short staple parental combinations. The genetic data among all combinations had significant additive, dominance, additive x additive, and additive x dominance effects with dominance effects being the largest in magnitude.

Variance components and broad- and narrow-sense heritability estimates for Uqlw were calculated to determine the relative importance of the various determinants of the phenotype, the extent to which individuals' phenotypes are determined by their genotypes, and the extent to which phenotypes are determined by the alleles transmitted from the parents (Falconer and MacKay, 1996). Environmental variance among the nine near-long x near-long parental combinations ranged from 0.51 to 1.75 with an average of 1.17, while the five near-long x short staple parental combinations ranged from 0.43 to 1.16 with an average of 0.95 (Table 19). The additive variance among the near-long x near-long parental combinations ranged from 0.17 to 2.55 with an average of 1.02, while the near-long x short staple parental combinations ranged from 0.00 to 2.58 with an average of 1.31. The dominance variance among the near-long x near-long parental combinations ranged from 0.00 to 1.53 with an average of 0.55, while the near-long x short staple parental combinations ranged from 0.00 to 0.49 with an average of 0.17. Among all combinations, the environmental, additive, and dominance variance was 3.60, 0.00, and 0.72, respectively.

Among the near-long x near-long parental combinations in 2001 and 2002, broad- (H^2) and narrow-sense (h^2) heritability estimates averaged 0.56 and 0.33, respectively (Table 19). Fibermax 832 x TAM 94L-25 had the same broad-sense heritability estimate of 0.63 in 2001 and 2002, although a higher additive variance value in 2002 corresponded to a higher narrow-sense heritability estimate. In 2002, TAM 94L-25 x TTU 202 had a larger genetic and additive variance. This in conjunction with a lower environmental variance led to higher broad- and narrow-sense heritability estimates in 2002 than in 2001. In 2001, TAM 94L-25 x Acala 1517-99 had the highest total genetic variance among the near-long x near-long parental combinations. In 2001 and 2002, TAM 94L-25 x Acala 1517-99 had high narrow-sense heritability estimates of 0.71 and 0.68, respectively. Among the near-long x near-long parental combinations,

Table 19. Variance components and broad (H^2) and narrow (h^2) sense heritability estimates for Uqlw for 10 parental combinations grown at College Station, TX in 2001 and 2002.

		Variance components†			Heritability estimates	
Parental Combinations	Year	σ^2_E	σ^2_A	σ^2_D	H^2	h^2
Fibermax 832 x TAM 94L-25‡	2001	1.00	0.19	1.53	0.63	0.07 ± 0.05
Fibermax 832 x TAM 94L-25‡	2002	0.78	1.03	0.31	0.63	0.48 ± 0.03
TAM 94L-25 x TTU 202‡	2001	1.03	0.17	0.95	0.52	0.08 ± 0.04
TAM 94L-25 x TTU 202‡	2002	0.51	0.63	1.09	0.77	0.28 ± 0.04
Fibermax 832 x Acala 1517-99‡	2001/02	1.75	0.30	0.64	0.35	0.11 ± 0.04
Fibermax 832 x TTU 202‡	2001/02	1.55	0.35	0.17	0.25	0.17 ± 0.03
TAM 94L-25 x Acala 1517-99‡	2001	0.94	2.55	0.10	0.74	0.71 ± 0.02
TAM 94L-25 x Acala 1517-99‡	2002	1.20	2.50	-0.58	0.68	0.68 ± 0.02
Acala 1517-99 x TTU 202‡	2001/02	1.75	1.45	0.20	0.49	0.43 ± 0.03
TAM 94L-25 x Tamcot CAMD-E§	2001	0.43	1.70	0.49	0.83	0.65 ± 0.02
TAM 94L-25 x Tamcot CAMD-E§	2002	0.95	2.58	-0.67	0.73	0.73 ± 0.02
Fibermax 832 x Tamcot CAMD-E§	2001/02	1.51	-1.47	0.27	0.15	0.00 ± 0.08
Acala 1517-99 x Tamcot CAMD-E§	2001/02	1.67	1.73	0.07	0.52	0.50 ± 0.02
TTU 202 x Tamcot CAMD-E§	2001/02	1.22	0.53	-0.13	0.30	0.30 ± 0.03
Among all combinations	2001/02	3.60	-0.11	0.72	0.14	0.00 ± 0.00

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

‡ Near-long x near-long parental combination.

§ Near-long x short staple parental combination.

Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, and Acala 1517-99 x TTU 202 were the parental combinations in which the ANOVA indicated no significant generation x environment interaction and thus, the data of 2001 and 2002 were pooled. The heritability estimates for these parental combinations account for the generation x environment interaction in the total phenotypic variance. Among these three parental combinations, Acala 1517-99 x TTU 202 had the highest total genetic and additive variance, which corresponded into higher broad- and narrow-sense heritability estimates.

Among the near-long x short staple parental combinations, broad- and narrow-sense heritability estimates averaged 0.51 and 0.44, respectively (Table 19). In 2001, TAM 94L-25 x Tamcot CAMD-E, with a lower environment variance, had a higher broad-sense heritability estimate, despite a lower total genetic variance. However in 2002, TAM 94L-25 x Tamcot CAMD-E had a higher narrow-sense heritability estimate. Fibermax 832 x Tamcot CAMD-E combined across years had zero additive variance and a low broad-sense heritability estimate. Acala 1517-99 x Tamcot CAMD-E and TTU 202 x Tamcot CAMD-E combined over years had broad- and narrow-sense heritability estimates of 0.52, 0.50, 0.30, and 0.30 respectively. Among all combinations, the broad and narrow-sense heritability estimates were 0.14 and 0.00, respectively.

Estimates of additive effects could be small due to a high degree of dispersion of alleles increasing Uqlw between parents. This might explain why the additive genetic components of variance varied and a definitive relationship between additive effects and additive genetic variance could not be detected. The negative estimates of dominance variance seen in this study could have been due to sampling error and/or the fact that basic generations are inefficient when used for determining dominance variance.

Summary and conclusions

Cotton is a natural product with lint characteristics determined by environmental and genetic factors. There is limited information available about the native fiber length distribution (i.e., on the seed), however it is believe that cotton possesses a normal fiber length distribution (probably is highly heritable) when bolls are hand picked cautiously and ginned carefully with a razor, tweezer, and aid of a microscope. Whatever the genetic determination of length distribution, the mechanical operations in harvesting, ginning, and textile manufacturing alter the distribution by breaking longer fibers into shorter ones (Anthony and Griffin, 2001a; Anthony and Griffin, 2001b; Robert et al., 2000). These successive stages of mechanical handling and processing incrementally but unavoidably inflict some fractures upon fibers being processed.

The degree of fiber breakage is dependent primarily upon fiber length, maturity, strength, and elongation. Longer fibers allow for a greater chance of tension forces being held at both ends, so they therefore have a higher probability of breakage than shorter fibers. Length distributions are also influenced by fiber maturity, and maturity is directly related to growing conditions. Immature fibers have underdeveloped, weak, thin secondary walls that are prone to break during mechanical processes. Fully mature fibers are less likely to be damaged or broken. The load, a specimen of a single fiber or a bundle of fibers in its axial direction, at which the specimen breaks provides a measure of fiber strength. Fiber elongation, the increase in length of fiber during tensile loading, is important in determining the processing propensity of fibers and the mechanical behavior of yarn. Two cottons with the same strength, but with different elongations will behave differently under mechanical stresses.

The environment influenced the magnitude of Uqlw in 2001 and 2002, but not to the extent seen with FLw and FLn. Fewer significant generation x environment interactions were detected among the parental combinations. The climatological conditions of the two years were normal in terms of temperature and rainfall. However, rainfall events at physiological maturity during 2001 extended the harvesting period and thus weathering of the fiber might have shortened the mean fiber length. All near-long x near-long F_1 hybrids had an Uqlw mean similar to or greater than the longest parent suggesting dominance or overdominance, and the generation means analysis adequately validate this conclusion.

Frequency distributions of individual plant values revealed that the segregating populations followed a normal distribution, implying that Uqlw is quantitatively inherited. A higher percent of transgressive segregation appeared in the BC_1P_1 than in other segregating populations. However, most breeders will attempt to select superior individual plants among the F_2 population and continue selecting throughout subsequent generations with the goal of looking for transgressive segregants among a population of inbred lines derived from the selfing of an F_1 hybrid. The presence of transgressive segregation in the segregating populations of these near-long x near-long combinations suggests that the parental material chosen for this study contained different length alleles for Uqlw, thus suggesting that breeders could make further improvements for upland cotton fiber length among these near-long staple parental genotypes, but only if the appropriate breeding method is implemented. Cotton already has a narrow genetic base (Van Esbroeck et al., 1999) and limited progress in cultivar improvement has been made in recent years because closely-related parents have been used to make successful cultivars (Meredith, 1991; Meredith et al., 1997). Even though transgressive segregation was present in this study, it was at a low frequency thus requiring large populations and suggesting incremental improvement will or should be expected. Most breeding programs use a pedigree method, in which seeds are harvested separately from each F_2 to produce F_3 families and continue to keep each F_2 pedigree distinct throughout successive generations. However, if any of the seeds are bulked between the F_2 to F_4 generation so that it is not possible to identify which seeds are derived from individual F_2 plants, considerable loss of already limited variability may be made.

Half of the parental combinations for Uqlw were analyzed by individual environments and the other five with combined years. Except for one parental combination, analyses of genetic effects indicated that a simple additive-dominance model did not account for most of the genetic variation for Uqlw. Therefore, a six-parameter model fit the generation means indicating that epistatic effects were present and suggested that inheritance is complex such that multiple alleles interacted to affect upland cotton Uqlw. Among the near-long x near-long parental combinations, few allelic and non-allelic gene effects were detected. This minimal number possibly indicates a high degree of dispersion of alleles increasing Uqlw between parents. Among the near-long x short staple parental combinations, significant gene effects were numerous. Additive effects were present in all parental combinations and additive x additive effects were identified in most. While additive and additive x additive effects were abundant in the expression of Uqlw, the magnitude of some dominance and dominance x dominance effects can not be ignored. For the parental combinations that were controlled by additive gene action, simple selection in early segregating generations would be successful. Whereas for those parental combinations controlled by non-additive gene action, selection in later generations could prove to be more effective.

Several explanations of the inconsistent gene effects in this study can be proposed. First, parents used in this study were from vastly different genetic backgrounds. The dispersion of alleles in the parents, complete or partial, affects the magnitude and composition of the additive component. The mean and dominance components of the parents remain independent of gene dispersion. Two loci having an inter-allelic interaction will change the F_2 mean, the magnitude and direction of additive x additive and additive x dominance effects, and the magnitude and direction of the variances (Kearsey and Pooni, 1996). Higher order interactions, such as trigenic interactions, may be needed with enough generations to adequately understand the inheritance of cotton fiber length.

The environmental variance for Uqlw was moderate to high, contradicting May (1999) who concluded that extensive environmental replication is not necessary to evaluate and select breeding material on the basis of fiber length parameters. Among the near-long x near-long parental combinations, genetic control for Uqlw contained additive and non-additive genetic variance, but the greater portion was additive. Among the near-long x short staple parental combinations the predominant genetic variance was additive. Numerous studies in the past concluded that additive variance within upland cotton genotypes tended to be more prominent than non-additive variance (Miller and Marani, 1963; Ramey and Miller, 1966; Lee et al., 1967; Al-Rawi and Kohel, 1969; Al-Rawi and Kohel, 1970; Meredith and Bridge, 1972; Quisenberry 1975; Green and Culp, 1990; Tang et al., 1993). However, a few experiments have found non-additive variance to be more important (Verhalen and Murray, 1969; Baker and Verhalen, 1973; May and Green, 1994; Cheatham et al., 2003).

The moderate to high broad-sense heritability estimates found in this study suggest that improvement for Uqlw can be realized through breeding if some of the genetic variation is additive in nature. Moderate to relatively high values for broad and narrow-sense heritability ($H^2 > 0.50$ and $h^2 > 0.50$) for fiber length parameters, 2.5% span length and UHM length, have been reported previously (May, 1999; May and Jividen, 1999; Herring et al., 2004). Depending upon the parental combination and environment, the sometimes moderate to high values for narrow-sense heritability found in this study suggest that conventional pedigree and early generation selection methods should be effective for initial improvements in Uqlw in cotton. However, among near-long x near-long parental combinations narrow-sense heritability estimates were more often low, suggesting that the inheritance is complex and progress will be difficult.

Gene effects and variances for Uqlw were inherited quite differently in specific environments and parental combinations suggesting environmentally specific mechanisms for Uqlw. This type of interaction would make selection of fiber length and superior genotypes that are adapted to wide geographic areas much more difficult. This would explain why improvement of fiber length in upland cotton has been so slow, even though many genetic studies have indicated that fiber length is moderately to highly heritable. Cotton fiber length is a complex trait, and improved fiber length may be the result of many different loci. These results show that both the adequacy of certain modes of inheritance as well as the importance and significance of gene effects were dependent upon the particular parental combination and environment, stressing the importance of the appropriate selection of both parents and environment for the success of a cotton breeding program.

CHAPTER VIII

AFIS FLw DISTRIBUTION DIALLEL

Efforts were made in this study to find practical and effective applications of the distribution data provided by the AFIS. FLw was the trait selected to be analyzed by various distribution statistical parameters. Cross entropy is a method to measure how good a distribution approximates another distribution, with a value of 0 being a perfect match. Scientific quandary with this procedure surrounds the proposition of what shall serve as the ideal cotton fiber length distribution. No published material exists identifying the optimal length distribution. Questions arise as should the distribution be artificially fabricated, what genotype, how many samples or environments shall be appropriate. In the current study, two genotypes grown in a single environment and one genotype grown in two environments were examined as possible cross entropy check candidates. The raw AFIS FLw distribution data containing the 40 length classes of the three checks are graphed in Figure 64. Additional fiber length data for the three checks are provided in Table 20.

Results and discussion

Parents differed ($P \leq 0.05$) in cross entropy values among the three different checks evaluated (Table 21). Analysis of variance indicated a significant parent x environment interaction for CEA and CEB, but not CEC. Genotypic rank varied depending upon the distribution used as the check, however, CEA and CEB more closely resembled each other in magnitude and rank than CEC to either CEA or CEB (Table 22). For CEA and CEB, large magnitude differences existed between 2001 and 2002. The

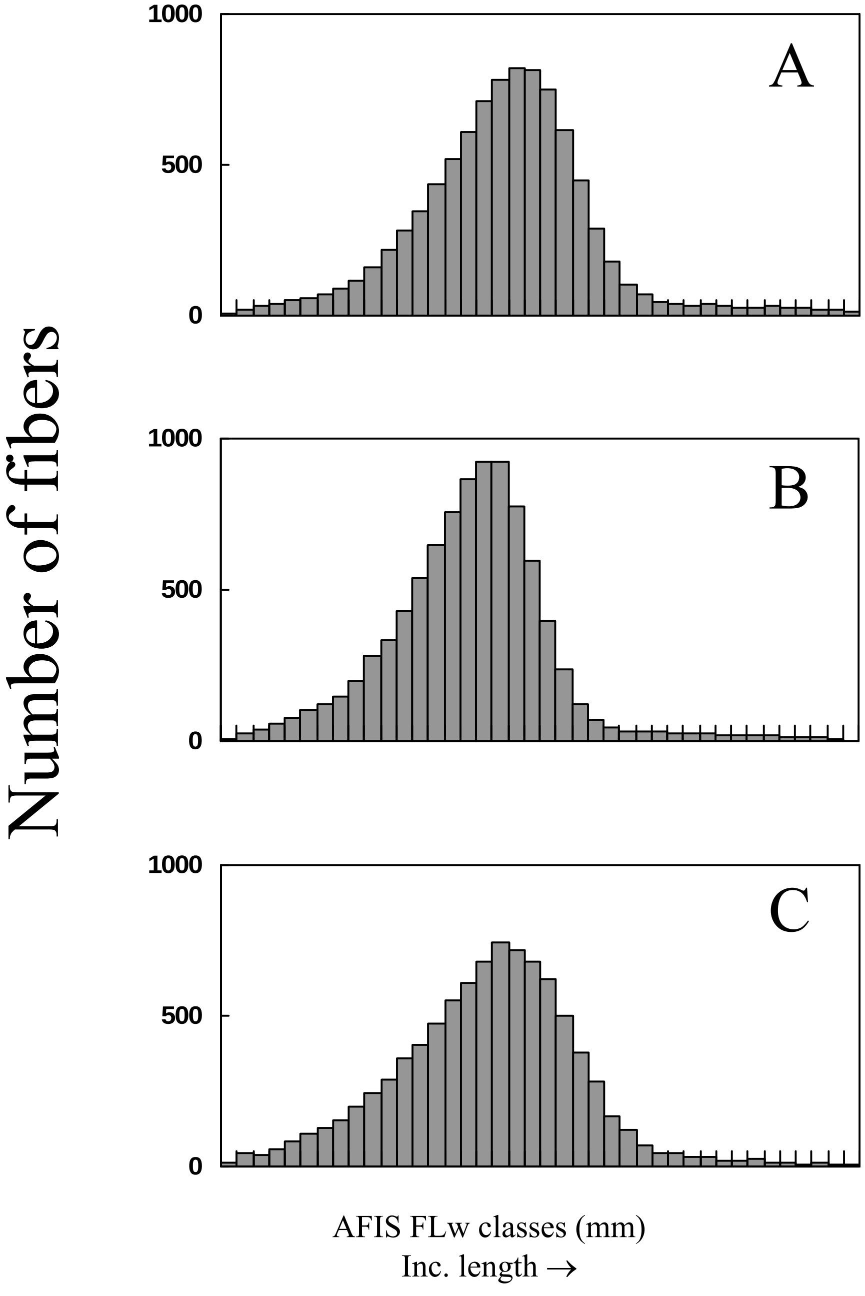

Fig. 64. Raw FLw distribution for (A) CEA, Cross entropy distribution data of Acala 1517-99 hand harvested plants averaged across 2002 as the check, (B) CEB, Cross entropy distribution data of Tamcot CAMD-E hand harvested plants averaged across 2002 as the check, and (C) CEC, Cross entropy distribution data of Acala 1517-99 combined over 2 environments and machine harvested at two locations as the check.

Table 20. Raw AFIS data for three cross entropy checks.†

Check‡	FLw	FLn	Uqlw	SFCw	SFCn	IFC	Fine	MR
	-------------- mm	-------------		-------------- %	---------------			
CEA	1.11	0.94	1.29	4.13	15.32	4.3	176	0.99
CEB	0.98	0.83	1.14	6.40	18.99	4.5	189	0.97
CEC	1.05	0.83	1.26	6.99	23.75	6.7	163	0.93

† FLw, mean fiber length by weight; FLn, mean fiber length by number; Uqlw, upper quartile length by weight; SFCw, short fiber content by weight; SFCn, short fiber content by number; IFC, immature fiber content; Fine, fineness; MR, maturity ratio.

‡ CEA, Cross entropy distribution data of Acala 1517-99 hand harvested plants averaged across 2002 as the check; CEB, Cross entropy distribution data of Tamcot CAMD-E hand harvested plants averaged across 2002 as the check; CEC, Cross entropy distribution data of Acala 1517-99 combined over 2 environments and machine harvested at two locations as the check;

Table 21. Combined analyses of variance of diallel crosses among five upland cotton genotypes for FLw distribution data measurements at College Station, TX in 2001 and 2002.†

		Mean squares				
Source	Df	CEA	CEB	CEC	FLwKurt	FLwSkew
Environment (E)	1	378.15**	488.40**	34.43**	3.29**	6.84**
Reps/E	6	3.22	2.84	1.61	0.08	0.31
Genotypes (G)	14	60.39	53.25	15.63	1.37**	19.97**
Parents (P)	4	115.34*	109.71*	9.99*	2.80**	29.86*
P vs. F_1	1	16.16	14.71	143.44	2.10	34.26
F_1	9	40.89**	32.43**	3.93	0.66**	13.99**
GCA	4	86.01*	67.25*	7.34	1.39**	30.40**
SCA	5	4.79	4.58	1.20	0.08	0.87
G x E	14	38.38**	37.89**	6.79**	0.33**	1.86**
P x E	4	16.63**	12.08**	1.31	0.17*	2.68**
P vs. F_1 x E	1	246.32**	200.87**	3.68	3.16**	10.66**
F_1 x E	9	7.17	4.58	1.57	0.09	0.52
GCA x E	4	9.39*	5.68	1.42	0.07	0.65
SCA x E	5	5.39	3.70	1.69	0.11	0.41
Error	84	3.82	4.18	1.46	0.06	0.57
Mean		868.25	749.93	467.65	1.00	0.00
CV, %		22.51	27.26	25.88	24.72	8963.75

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

† CEA, Cross entropy distribution data of Acala 1517-99 hand harvested plants averaged across 2002 as the check; CEB, Cross entropy distribution data of Tamcot CAMD-E hand harvested plants averaged across 2002 as the check; CEC, Cross entropy distribution data of Acala 1517-99 combined over 2 environments and machine harvested at two locations as the check; FLwKurt, mean fiber length by weight kurtosis; FLwSkew, mean fiber length by weight skewness.

Table 22. Means of five upland parental genotypes for FLw distribution measurements evaluated near College Station, TX in 2001 and 2002.†

Genotype	CEA		CEB		CEC	FLwKurt		FLwSkew	
	2001	2002	2001	2002	2001/02	2001	2002	2001	2002
TAM 94L-25	2300 c‡	596 bc	2252 c	465 bc	736 b	0.02 c	1.26 b	-0.05 a	0.07 a
TTU 202	1419 b	801 d	1294 b	552 c	531 ab	0.60 b	1.26 b	0.01 a	-0.08 a
Fibermax 832	1175 ab	621 cd	1062 ab	495 c	479 a	0.56 b	1.03 b	-0.07 a	-0.09 a
Tamcot CAMD-E	918 ab	424 ab	724 ab	275 a	702 b	1.74 a	2.42 a	0.28 c	0.42 b
Acala 1517-99	689 a	258 a	567 a	309 a	663 ab	1.03 b	1.93 a	0.12 b	0.30 b

† CEA, Cross entropy distribution data of Acala 1517-99 hand harvested plants averaged across 2002 as the check; CEB, Cross entropy distribution data of Tamcot CAMD-E hand harvested plants averaged across 2002 as the check; CEC, Cross entropy distribution data of Acala 1517-99 combined over 2 environments and machine harvested at two locations as the check; FLwKurt, mean fiber length by weight kurtosis; FLwSkew, mean fiber length by weight skewness.

‡ Means within a column followed by the same letter are not different at K = 100 (approximates p = 0.05) according to Waller-Duncan LSD at K = 100 (approximates p = 0.05) according to Waller-Duncan LSD.

data for CEC was combined over the two years. In 2001, CEA and CEB had the same genotypic rank and subtle differences in 2002. For CEA and CEB in 2001, Acala 1517-99 had the lowest cross entropy values but not different from Tamcot CAMD-E or Fibermax 832. TTU 202 followed and then TAM 94L-25 had the highest CEA and CEB values of 2300 and 2252, respectively. In 2002, Acala 1517-99 once again had the lowest CEA value but not different from Tamcot CAMD-E, followed by TAM 94L-25 and Fibermax 832 which were similar to each other with TAM94L-25 being equivalent to Tamcot CAMD-E and Fibermax 832 being similar to TTU 202 with the highest CEA value of 801. For CEB in 2002, Tamcot CAMD-E had the lowest value although not different from Acala 1517-99. Of note, the average of the Tamcot CAMD-E plants from 2002 was used to attain the CEB distribution. TAM 94L-25 had the next lowest value at 465 but was not different from Fibermax 832 and TTU 202 with values of 495 and 552, respectively. The range of CEC values over 2001 and 2002 were minimal compared to CEA and CEB. Fibermax 832 had the lowest CEC value of 479 but was only different from Tamcot CAMD-E and TAM 94L-25.

Parents differed ($P \leq 0.05$) in FLwKurt (Table 21), with significant parent x environment interactions detected. In 2001 and 2002, Tamcot CAMD-E had the highest FLwKurt values of 1.74 and 2.42, respectively, however, the value in 2002 was not different from Acala 1517-99 value at 1.93 (Table 22). In 2001, Acala 1517-99, TTU 202, and Fibermax 832 had similar FLwKurt values of 1.03, 0.60, and 0.56, respectively. TAM 94L-25 had the lowest FLwKurt value of 0.02. In 2002, TAM 94L-25, TTU 202, and Fibermax 832 had equivalent values of 1.26, 1.26, and 1.03, respectively.

Parents differed ($P \leq 0.05$) in FLwSkew (Table 21). Significant parent x environment interactions were detected for FLwSkew, due to changes in magnitude and not changes in genotypic rank. In 2001, TTU 202 had a distribution closest to zero with a value of 0.01, but was not different from Fibermax 832 and TAM 94L-25, which had negative FLwSkew values of -0.07 and -0.05, respectively (Table 22). Acala 1517-99 followed with a FLwSkew value of 0.12 and Tamcot CAMD-E had a distribution farthest from normal with a FLwSkew value of 0.28. In 2002, TAM 94L-25, TTU 202, and Fibermax 832 once again had equivalent FLwSkew values of 0.07, -0.08, and -0.09, respectively. Acala 1517-99 and Tamcot CAMD-E had distributions farthest from normal with FLwSkew values of 0.30 and 0.42.

GCA effects were observed ($P \leq 0.05$) for all FLw distribution data measurements except CEC (Table 21). The ANOVA revealed a significant GCA x environment interaction for CEA. The preponderance of GCA effects suggest that progeny performance for FLw distribution data measurements can be well predicted from GCA alone (93.5%, 92.5%, 93.6%, and 96.5% of total F_1 sums of squares were attributable to GCA for CEA, CEB, FLwKurt, and FLwSkew respectively). For CEB and CEC, Tamcot CAMD-E had the lowest negative GCA effects for improving distributions to resemble the check, i.e., lowering the cross entropy value (Table 23). It had GCA effects of -213 and -82, respectively. TAM 94L-25, a near-long parental genotype, had the highest positive significant GCA effects for impairing the shape of the distribution for CEB with a value of 231. TTU 202, Fibermax 832, and Acala 1517-99 had no significant GCA effects on the cross entropy values. Tamcot CAMD-E and

TAM 94L-25 had again contrasting GCA effect for FLwKurt. Tamcot CAMD-E had a GCA effect of 0.32 which contributed to peaking the distribution and attaining more fibers in a narrower length range, whereas TAM 94L-25 had a GCA effect of -0.32. This effect would impair and flatten the distribution, increasing the range in which the fibers were amassed. Tamcot CAMD-E and TAM 94L-25 both had FLwSkew GCA effects in which they moved the distribution away from normal, although in opposite directions. The positive GCA effect of Tamcot CAMD-E, 0.17, moved the distribution to the left and had a long right tail and TAM 94L-25 had a negative GCA effect of -0.13, moving the distribution to the right and having a long left tail.

Crosses differed ($P \leq 0.05$) for all FLw distribution data measurements except CEC (Table 21), however the ANOVA showed no significant SCA effects. However, Fibermax 832 x Acala 1517-99 and Acala 1517-99 x Tamcot CAMD-E did have contrasting SCA effects for FLwSkew with estimates of -0.044 and 0.040 (Table 24). The test for average heterosis yielded no differences between the parents and crosses. All crosses x environment and SCA x environment effects were not significant.

As with the parental genotypes, CEA and CEB closely resembled each other in magnitude and had subtle changes in genotypic rank among the parental combinations (Table 25). Compared with CEA and CEB, CEC not only differed with a lower magnitude, but had acute differences in discriminating the parental combinations. For CEA, Acala 1517-99 x Tamcot CAMD-E and Fibermax 832 x Tamcot CAMD-E had the lowest cross entropy values of 503 and 636, respectively, while Acala 1517-99 x Tamcot CAMD-E, TTU 202 x Tamcot CAMD-E, and Fibermax 832 x Tamcot CAMD-E had the

Table 23. Estimates of general combining ability (GCA) effects of five upland parents for FLw distribution measurements evaluated near College Station, TX in 2001 and 2002. †

Genotype	CEA		CEB	CEC	FLwKurt	FLwSkew
	2001	2002				
TAM 94L-25	361	151	231**	48	-0.32**	-0.13**
TTU 202	3	43	-12	-2	0.06	-0.03
Fibermax 832	47	108	78	54	-0.13	-0.04
Tamcot CAMD-E	-298	-184	-213**	-82*	0.32**	0.17**
Acala 1517-99	-113	-118	-85	-17	0.07	0.03
LSD (0.05) $(g_i - g_j)$	368	220	105	52	0.12	0.04

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

† CEA, Cross entropy distribution data of Acala 1517-99 hand harvested plants averaged across 2002 as the check; CEB, Cross entropy distribution data of Tamcot CAMD-E hand harvested plants averaged across 2002 as the check; CEC, Cross entropy distribution data of Acala 1517-99 combined over 2 environments and machine harvested at two locations as the check; FLwKurt, mean fiber length by weight kurtosis; FLwSkew, mean fiber length by weight skewness.

Table 24. Estimates of specific combining ability (SCA) effects of 10 upland F_1 crosses for FLw distribution measurements evaluated near College Station, TX in 2001 and 2002. †

F_1 cross‡	CEA	CEB	CEC	FLwKurt	FLwSkew
832 x L-25	105	92	41	-0.02	0.023
L-25 x 202	-92	-86	28	0.13	-0.002
L-25 x 1517	-4	3	-27	-0.06	-0.004
832 x 202	4	37	-41	-0.11	0.019
L-25 x CD-E	-9	-9	-42	-0.04	-0.016
1517 x 202	53	26	3	-0.02	0.009
832 x 1517	-66	-72	-3	0.10	-0.044*
202 x CD-E	35	23	11	0.01	-0.026
832 x CD-E	-42	-56	4	0.04	0.002
1517 x CD-E	17	43	27	-0.01	0.040*
LSD (0.05) ($s_{ij} - s_{ik}$)	214	178	120	0.30	0.059
LSD (0.05) ($s_{ij} - s_{kl}$)	152	126	85	0.22	0.042

* Significant at the 0.05 probability level.

† CEA, Cross entropy distribution data of Acala 1517-99 hand harvested plants averaged across 2002 as the check; CEB, Cross entropy distribution data of Tamcot CAMD-E hand harvested plants averaged across 2002 as the check; CEC, Cross entropy distribution data of Acala 1517-99 combined over 2 environments and machine harvested at two locations as the check; FLwKurt, mean fiber length by weight kurtosis; FLwSkew, mean fiber length by weight skewness.

‡ 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 832 x 202, Fibermax 832 x TTU 202; L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 1517 x 202, Acala 1517-99 x TTU 202; 832 x 1517, Fibermax 832 x Acala 1517-99; 202 x CD-E, TTU 202 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E.

Table 25. Means of F_1 crosses for FLw distribution measurements evaluated near College Station, TX in 2001 and 2002. †

F_1 cross‡	CEA	CEB	CEC	FLwKurt	FLwSkew
832 x L-25	1280 h§	1126 g	533 e	0.43 g	-0.18 f
L-25 x 202	1029 g	859 ef	464 de	0.77 def	-0.20 f
L-25 x 1517	980 fg	875 f	394 bcd	0.59 fg	-0.14 ef
832 x 202	946 efg	828 ef	401 de	0.72 ef	-0.09 de
L-25 x CD-E	848 def	734 de	314 a	0.86 cde	-0.01 c
1517 x 202	803 cde	655 cd	373 abc	1.01 bc	-0.03 cd
832 x 1517	738 bcd	647 bcd	424 cd	0.95 bcd	-0.09 de
202 x CD-E	659 bc	523 ab	317 a	1.30 a	0.08 b
832 x CD-E	636 ab	535 abc	366 abc	1.14 ab	0.10 b
1517 x CD-E	503 a	471 a	318 ab	1.28 a	0.21 a

† CEA, Cross entropy distribution data of Acala 1517-99 hand harvested plants averaged across 2002 as the check; CEB, Cross entropy distribution data of Tamcot CAMD-E hand harvested plants averaged across 2002 as the check; CEC, Cross entropy distribution data of Acala 1517-99 combined over 2 environments and machine harvested at two locations as the check; FLwKurt, mean fiber length by weight kurtosis; FLwSkew, mean fiber length by weight skewness.

‡ 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 832 x 202, Fibermax 832 x TTU 202; L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 1517 x 202, Acala 1517-99 x TTU 202; 832 x 1517, Fibermax 832 x Acala 1517-99; 202 x CD-E, TTU 202 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E.

§ Means within a column followed by the same letter are not different at K = 100 (approximates p = 0.05) according to Waller-Duncan LSD.

lowest CEB values of 471, 523, and 535, respectively. For CEC, any parental combination with Tamcot CAMD-E, including TAM 94L-25, and Acala 1517-99 x TTU 202 had the lower cross entropy values. On the contrary, all three cross entropy checks showed Fibermax 832 x TAM 94L-25 as having the highest values of 1280, 1126, and 533 for CEA, CEB, and CEC respectively, suggesting this parental combination had the least ideal FLw distribution. TAM 94L-25 x TTU 202 also exhibited a CEC value similar to Fibermax 832 x TAM 94L-25. Although no significant CEA GCA effects for TAM 94L-25 were exhibited because the data were analyzed for individual years because of a GCA x environment interaction, F_1 means of all near-long parental combinations containing TAM 94L-25 when the data were combined showed higher CEA values (Table 23). Also, when the data were combined all parental combinations with Tamcot CAMD-E, except with TAM 94L-25, exhibited lower CEA values. The GCA effects and F_1 means for CEB and CEC do corroborate with each other.

The GCA effects and F_1 means for FLwKurt and FLwSkew also appear to proceed with each other, as F_1 means of parental combinations containing Tamcot CAMD-E, except with TAM 94L-25, increased the kurtosis or skewness values and those containing TAM 94L-25 decreased the values (Table 25). By decreasing the values, TAM 94L-25 is flattening the distribution and skewing it to the right. TAM 94L-25 x Tamcot CAMD-E had a FLwSkew value of -0.01, two extremes combining to form an almost perfect normal distribution suggest additive gene action. The additive effect of this combination is also seen with FLwKurt.

Significant variation was found in all FLw distribution data, i.e., CEA, CEB, CEC, FLwKurt, and FLwSkew, for all sources of variation measured (Table 21). GCA x environment for CEA was significant among these F_1 while it was non-significant for all other distribution measurements. When parents and F_1 were combined, they did not differ in CEA, CEB, or CEC, but significant variation was found for FLwKurt and FLwSkew. CEC did not detect the same trend of significance as CEA and CEB. Of concern is the extremely high CV for FLwSkew, 8964, which makes this measurement useless. The standardized distribution shape of CEA and CEB were similar to each other with a cross entropy value of 174 (data not shown). CEC having a slightly wider distribution corresponded into higher cross entropy values of 549 and 550 (data not shown) when compared to CEA and CEB, respectively. Even though this distribution is less than ideal, it is a more representative sample of commercial production practices and takes into account two environments and mechanical harvest. All FLw distribution measurements, CEA, CEB, CEC, FLwKurt, and FLwSkew were associated ($P < 0.01$) with each other (Table 26). As expected, CEA and CEB were highly correlated. FLwKurt had a poor negative correlation with CEA and CEB, however, it offers a promising description of the shape of a fiber length distribution. FLwSkew had a high negative correlation with CEA and CEB, suggesting that undesirable length distributions are associated with longer staple genotypes.

Table 26. Pearson's correlation coefficient among FLw distribution data among non-segregating and segregation population grown at College Station, TX in 2001 and 2002.†

	CEB	CEC	FLwKurt	FLwSkew
CEA	0.98‡	0.48	-0.18	-0.80
	<0.01§	<0.01	<0.01	<0.01
CEB		0.50	-0.10	-0.79
		<0.01	<0.01	<0.01
CEC			0.20	0.01
			<0.01	<0.01
FLwKurt				0.47
				<0.01

† CEA, Cross entropy distribution data of Acala 1517-99 hand harvested plants averaged across 2002 as the check; CEB, Cross entropy distribution data of Tamcot CAMD-E hand harvested plants averaged across 2002 as the check; CEC, Cross entropy distribution data of Acala 1517-99 combined over 2 environments and machine harvested at two locations as the check; FLwKurt, mean fiber length by weight kurtosis; FLwSkew, mean fiber length by weight skewness.

‡ Pearson correlation coefficient.

§ Probability of a larger *r* value.

Summary and conclusions

Successful breeding approaches are a direct consequence of the gene action prevalent in the breeding population under consideration. The relative importance of additive vs. non-additive effects for FLw distribution measurements in diallel crosses is an indication of the type of gene action (Baker, 1978). GCA estimates additive genetic effects. The GCA effects reflect performance of parental lines in combination with all other lines, so the parents with the highest GCA effects should have the greatest impact on trait improvement. The diallel reported herein has demonstrated that there is sufficient genetic variation among these parents for FLw distribution measurements to facilitate improvement though selection. The ANOVA revealed GCA effects for all FLw distribution measurements, except CEC (Table 21). GCA effects and F_1 means containing Tamcot CAMD-E, except when crossed with TAM 94L-25, exhibited lower cross entropy values and higher peaked distribution curves that were skewed to the left. Also, GCA effects and F_1 means containing TAM 94L-25, except with the Tamcot CAMD-E combination, showed higher cross entropy values and flattened distribution curves that were skewed to the right.

In the opinion of the author, of the three cross entropy checks evaluated, CEA is the preferred standard although no significant GCA effects were detected. It has a peaked distribution, large number of fibers uniform in length, and a lower percentage of short fibers than CEB. FLwKurt and FLwSkew are also potential measurements that could be use to discriminate fiber length distributions, but only upon further testing and experiments, especially since FLwSkew appears to be extremely variable as indicated by a percent CV of 8964 in this study.

Knowledge of the type of genetic action controlling fiber length distribution in upland cotton genotypes would allow a breeder to choose effective parents for developing segregating populations. Our results show considerable variation in GCA effects among the parental genotypes. This study is the first to conclude that additive genetic effects for FLw distribution measurements tend to be more prominent within upland cotton genotypes than non-additive genetic effects. Numerous other diallel studies, although studying cotton fiber length only and not its distribution characteristics, have concluded additive effects to be dominant (Miller and Marani, 1963; Lee et al., 1967; Al-Rawi and Kohel, 1969; Al-Rawi and Kohel, 1970; Meredith and Bridge, 1972; Green and Culp, 1990; Tang et al., 1993).

SCA reflects dominant gene effects. SCA effects represent the deviation of hybrid performance from that expected from the GCA effects of each parent. SCA effects can identify the best hybrid combination, but they also can identify complementary alleles for trait performance (Kearsey and Pooni, 1996). The ANOVA revealed no SCA effects, however two parental combinations for FLwSkew were significant.

The genetic interpretation of a diallel with a reduced number of parental inbreds, such as this one, can be biased by the lack of independent distribution of genes in the parental lines (Baker, 1978). Therefore, combining abilities reported here could be biased by the correlation of gene frequencies and should be interpreted with caution.

Despite these limitations, this diallel is useful for determining which of these upland parents has the most desirable GCA expression of distribution data measurements.

To enhance our research efforts, we need to determined which AFIS measurements and which fiber properties could aid in the selection and advancement of superior fiber quality genotypes. Also, the massive quantity AFIS data generated needs to be refined and organized into a user-friendly spreadsheet. The AFIS data currently produced includes a considerable amount of trivial information. Slow and time-consuming macros were widely depended upon in this project to arrange the fiber characteristics accumulated. A software program is needed to take the electronic information and generate only the relevant data and statistics.

Cotton is a natural product with lint characteristics determined by environmental and genetic factors. There is limited information available about the native fiber length distribution (i.e., on the seed), however it is believe that cotton possesses a normal fiber length distribution (probably is highly heritable) when bolls are hand picked cautiously and ginned carefully with a razor, tweezer, and aid of a microscope. Whatever the genetic determination of length distribution, the mechanical operations in harvesting, ginning, and textile manufacturing alter the distribution by breaking longer fibers into shorter ones (Anthony and Griffin, 2001a; Anthony and Griffin, 2001b; Robert et al., 2000). These successive stages of mechanical handling and processing incrementally but unavoidably inflict some fractures upon fibers being processed.

The degree of fiber breakage is dependent primarily upon fiber length, maturity, strength, and elongation. Longer fibers allow for a greater chance of tension forces being held at both ends, so they therefore have a higher probability of breakage than shorter fibers. Length distributions are also influenced by fiber maturity, and maturity is directly related to growing conditions. Immature fibers have underdeveloped, weak, thin secondary walls that are prone to break during mechanical processes. Fully mature fibers are less likely to be damaged or broken. The load, a specimen of a single fiber or a bundle of fibers in its axial direction, at which the specimen breaks provides a measure of fiber strength. Fiber elongation, the increase in length of fiber during tensile loading, is important in determining the processing propensity of fibers and the mechanical behavior of yarn. Two cottons with the same strength, but with different elongations will behave differently under mechanical stresses.

With this knowledge, two genotypes with the same native fiber length distribution could differ vastly after mechanical processing stages. A parametric model incorporating these other fiber quality characteristics needs to be developed to gain a more comprehensive understanding on alterations to the fiber length distribution.

Questions to be addressed while selecting genotypes with preferred length distributions involve how to harvest and gin lint samples. Individual plant selections in segregating populations would be hand harvested, and if every cracked or open boll is harvested, this would include mature and immature fibers. Subsequent advance yield and quality trails may be harvested by a plot picker or stripper, or a fifty to hundred boll sample may be harvested by hand. If the true genetic potential was to be studied, hand harvesting would be the only method possible. Selections and advancement within a breeding program could be done if the same harvesting machine is used for each test, and if maintenance was the same across all trial locations. As for ginning, true genetic potential, once again, could only be maintained if hand ginned. Saw or roller ginning would have to be done on the same gin or on gins that perform the same according to ginning standards. Frequent checks must be done to control for variation among gins. Selection, advancement, and release of genotypes or germplasm with an ideal length distribution within a breeding program could be successful. Problems across breeding programs would occur, especially in the private industry that compares advance cotton fiber quality data from breeders that used different harvestors and gins. By studying the true genetic potential, hopefully the influence of other fiber characteristics on length distributions could be more easily determined.

Precautions were taken in this study to limit the variability for fiber breakage as all samples were hand picked from the middle fruiting zone, ginned on the same roller gin with the same personal, and analyzed with the same technician and AFIS machine.

Cotton is not only competing against itself in terms of fiber quality but against man-made fibers which continue to expand market share because their distribution and other traits are not limited by natural variation. Improving the length distribution, regardless of the staple length, will enable improved spinning performance and product quality. Developing genotypes with an optimal fiber length distribution and high mean length should be a priority and selection criteria of breeding programs across the Cotton Belt. Currently, most cotton programs are focused on breeding for longer fibers alone because the current premium and discount schedule rewards this type of cotton. Long UHM length genotypes with an undesirable length distribution reward the producers but presents challenges to spinners who are concerned with the fiber quality impact on costly disruptions in yarn-spinning processes and when significant defects appear in yarn and finished fabrics. The U.S. already exports over two-thirds of our product to oversees mills, and foreign competition, in the production and processing of cotton, is advancing and presents a serious threat to the long-term survival of the U.S. cotton industry. Therefore, despite only small financial incentives offered by fiber markets to produce the highest quality cotton, we must enhance the value of U.S. fiber through research and breeding.

CHAPTER IX

AFIS FLw DISTRIBUTION GENERATION MEANS ANALYSIS

Results and discussion

A generation means analysis is a simple but useful technique for estimating gene effects for a polygenic trait, such as the fiber length distribution of cotton. The greatest merit of a generation means analysis lies in the ability to estimate epistatic gene effects, interaction of alleles at different loci, such as additive x additive, additive x dominance, and dominance x dominance effects. Besides gene effects, breeders would also like to know how much variation in a crop is genetic and to what extent this variation is heritable because efficiency of selection depends mainly on additive genetic variance, influence of the environment, and interaction between genotype and environment. No literature currently exists regarding the inheritance of the distribution of cotton fiber length. Therefore, information about the gene effects and the available genetic variability, estimates of the variance components, and broad- and narrow-sense heritability estimates were calculated for FLw distribution data measurements.

CEA

From the distribution diallel analysis, it was determined that CEA possessed a more ideal distribution shape and adequately discriminated the parental genotypes. CEA was selected as the check for a generations means analysis of fiber length distribution as determined by cross entropy. The parental, F_1, F_2, and backcross generations differed ($P \leq 0.01$) in CEA for all parental combinations except Fibermax 832 x TTU 202 (Table 27). The ANOVA also revealed a significant generation x environment interaction in all parental combinations except Fibermax 832 x Acala 1517-99. The parental combinations indicated that some generations reacted differently to each environment, suggesting that selection and evaluation should be conducted within a given environment if reliable knowledge of CEA is to be obtained.

CEA means from P_1 and P_2 were different ($P \leq 0.05$) for most parental combinations, however there were six combinations and years in which P_1 and P_2 did not differ (Table 28). A lower cross entropy value was preferred because the sample's distribution more closely resembled the check. As to which parent had the lower CEA value, it depended upon the parental combination and sometimes the year.

In 2001, F_1 hybrids had distribution shapes better or similar to the parent with the lower CEA value. In 2002, F_1 hybrids had distribution shapes worse or similar to the parent with the higher CEA value. Fibermax 832 x Tamcot CAMD-E in 2001 and TTU 202 x Tamcot CAMD-E in 2001 had CEA F_1 hybrid means lower than the lowest parent. In 2001 and 2002, F_2 means followed no established pattern. The mean values of the backcrosses were not different ($P \leq 0.05$) for eight parental combinations and years. For the parental combinations in which the mean values of the backcrosses were different, CEA values were shifted toward the values observed for the recurrent parent only if the parents also differed.

The parental combinations were divided into two categories, near-long x near-long and near-long x short staple parental combinations. For each parental combination, P_1 was assigned accordingly to the parent with the longest FLw in 2002. The near-long x near-long parental combinations consisted of Fibermax 832 x TAM 94L-25, TAM

Table 27. Mean squares for CEA of AFIS FLw distribution data measured on P_1, P_2, F_1, F_2, BC_1P_1, and BC_2P_2 (per parental combination and among all combinations) at College Station, TX in 2001 and 2002.

A.

		Parental Combinations†					
Source	df	832 x L-25	L-25 x 202	832 x 1517	832 x 202	L-25 x 1517	1517 x 202
Environment (E)	1	12231.97**	10494.61**	2954.99**	6091.14**	10813.35**	3952.84**
Reps/E	6	64.93	14.61	45.28	31.49	35.41	43.60
Generation (Gn)	5	394.82**	465.43**	203.57**	118.98	1011.07**	547.39**
Gn x E	5	576.89**	459.34**	43.50	255.66**	560.80**	253.60**
Error	30	31.35	48.78	33.37	51.26	27.48	55.86

B.

		Parental Combinations‡				
Source	df	L-25 x CD-E	832 x CD-E	1517 x CD-E	202 x CD-E	Among
Environment (E)	1	6086.47**	2919.60**	2579.72**	1103.79**	5326.96**
Reps/E	6	6.63	37.43	14.65	39.56	2.73
Generation (Gn)	5	889.96**	260.57**	84.00**	268.62**	98.72**
Gn x E	5	595.46**	327.71**	76.22*	127.11**	144.40**
Error	30	40.21	22.62	22.89	21.78	9.05

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

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

Table 28. Means of P_1, P_2, F_1, F_2, BC_1, and BC_2 for CEA (per parental combination and among all combinations) at College Station, TX in 2001 and 2002. First parent listed is P_1, second parent is P_2.

A.

	Parental Combinations†										
	832 x L-25		L-25 x 202		832 x 1517	832 x 202		L-25 x 1517		1517 x 202	
Gen.‡	2001	2002	2001	2002	2001/02	2001	2002	2001	2002	2001	2002
P_1	1175 a§	621 a	2300 c	596 a	898 b	1175 ab	621 a	2300 d	596 c	689 a	258 a
P_2	2300 c	596 a	1419 a	801 ab	474 a	1419 abc	801 ab	689 a	258 a	1419 bc	800 c
F_1	1402 ab	1159 c	1224 a	835 bc	738 b	10003 a	888 b	1112 b	847 d	783 a	822 c
F_2	2095 c	690 a	1836 b	986 bc	751 b	1660 c	646 a	1758 c	529 bc	1305 bc	521 b
BC_1P_1	1726 b	675 a	2334 c	1049 c	921 b	1505 bc	580 a	1920 c	852 d	1087 ab	443 b
BC_1P_2	2062 c	962 b	1757 b	992 bc	754 b	1738 c	689 ab	1425 b	427 b	1705 c	700 c

B.

	Parental Combinations¶									
	L-25 x CD-E		832 x CD-E		1517 x CD-E		202 x CD-E		Among	
Gen.	2001	2002	2001	2002	2001	2002	2001	2002	2001	2002
P_1	2300 b	596 ab	1175 b	621 b	689 a	258 a	1419 c	801 c	1440 c	559 ab
P_2	918 a	424 a	918 b	424 a	918 bc	424 b	918 ab	424 a	1161 b	521 a
F_1	1020 a	677 bc	528 a	745 b	560 a	446 b	672 a	646 bc	919 a	761 d
F_2	1294 a	871 cd	1151 b	725 b	865 abc	387 ab	789 a	760 c	1371 bc	666 cd
BC_1P_1	2005 b	1010 d	1622 c	611 b	1055 c	355 ab	1146 b	699 bc	1563 c	689 cd
BC_1P_2	1107 a	793 bcd	1129 b	437 a	991 bc	426 b	763 a	557 ab	1377 bc	640 bc

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ Gen., generation; 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 K = 100 (approximates p = 0.05) according to Waller-Duncan LSD.

¶ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

94L-25 x TTU 202, Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, TAM 94L-25 x Acala 1517-99, and Acala 1517-99 x TTU 202. The near-long x short staple parental combinations were Fibermax 832, TAM 94L-25, Acala 1517-99, and TTU 202 crosses with Tamcot CAMD-E.

Generation mean analyses tested three- and six-parameter models for the best fit to explain genetic control of CEA in various upland parental combinations. Effects were first estimated with the three-parameter model and accepted if $P \geq 0.05$. In 2002, the three-parameter model satisfactorily explained the genetic differences for CEA in Acala 1517-99 x Tamcot CAMD-E (Table 29). In this combination and environment, the variation among generation means was explained sufficiently by the simple additive-dominance model, indicating that epistasis was not involved in the inheritance of the trait. The best approximation of additive and dominance effects can be obtained from the three-parameter additive-dominance model because these effects are unbiased due to the absence of epistasis (Hayman, 1958).

In the near-long x near-long parental combinations for CEA, TAM 94L-25 x TTU 202 in 2001, Fibermax 832 x Acala 1517-99 combined across years, and TAM 94L-25 x Acala 1517-99 in 2001 had positive additive effects (Table 29). Dominance effects were positive for the parental combinations of Fibermax 832 x TAM 94L-25 in 2002, TAM 94L-25 x TTU 202 in 2001 and 2002, and TAM 94L-25 x Acala 1517-99 in 2002. A negative dominance effect was exhibited in Fibermax 832 x Acala 1517-99 combined across years.

Table 29. Estimates of gene effects for CEA of AFIS FLw distribution data (per crossing combination and among all combinations) at College Station, TX in 2001 and 2002.

		Gene effects†					
Parental Combinations	Year	*m*	*a*	*d*	*aa*	*ad*	*dd*
Fibermax 832 x TAM 94L-25‡	2001	2801**	-314	-1365	-856**	-48	-58
Fibermax 832 x TAM 94L-25‡	2002	115	-7	1325*	491**	-626*	-391
TAM 94L-25 x TTU 202‡	2001	1091**	447*	2716**	816**	311	-2470**
TAM 94L-25 x TTU 202‡	2002	574**	-56	1675**	93	251	-1684**
Fibermax 832 x Acala 1517-99‡	2001/02	1001**	645**	-1121**	-150	-731**	756**
Fibermax 832 x TTU 202‡	2001	1661**	131*	507	-160	-713**	-1085*
Fibermax 832 x TTU 202‡	2002	771**	-72	-707	-95	-110	903**
TAM 94L-25 x Acala 1517-99‡	2001	1893**	824**	147	-445	-605	-829
TAM 94L-25 x Acala 1517-99‡	2002	-95	205	1447**	501**	417	-508
Acala 1517-99 x TTU 202‡	2001	992**	-334	1260	-23	-922	-1310
Acala 1517-99 x TTU 202‡	2002	260	-259	349	201	-22	302
TAM 94L-25 x Tamcot CAMD-E§	2001	564	605*	2382*	1104**	694	-1902**
TAM 94L-25 x Tamcot CAMD-E§	2002	307	120	1754**	177	136	-1364**
Fibermax 832 x Tamcot CAMD-E§	2001	361	246	2991**	929**	487	-2879**
Fibermax 832 x Tamcot CAMD- E§	2002	1264**	110*	-1751**	-771**	112	1281**
Acala 1517-99 x Tamcot CAMD-E§	2001	208	-211	2512**	657**	473	-2476**
Acala 1517-99 x Tamcot CAMD-E§¶	2002	286**	-81**	190**	-	-	-
TTU 202 x Tamcot CAMD-E§	2001	571**	152	720	646**	463	-580
TTU 202 x Tamcot CAMD-E§	2002	1140**	174*	-984*	-586**	5	356
Among all combinations	2001	896**	486**	1261**	678**	-461**	-1361**
Among all combinations	2002	478**	16	376**	-189	52	-236**

*, ** Significant at the 0.05 and 0.01 probability level on the basis of *t* test with n – 1 =5 degrees of freedom, respectively.

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

‡ Near-long x near-long parental combination.

§ Near-long x short staple parental combination

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

Among the non-allelic interactions, a negative additive x additive gene effect estimate was attained in Fibermax 832 x TAM 94L-25 in 2001, suggesting both parents contributed alleles for CEA. Positive additive x additive effects were obtained in Fibermax 832 x TAM 94L-25 in 2002, TAM 94L-25 x TTU 202 in 2001, and TAM 94L-25 x Acala 1517-99 in 2002. Negative additive x dominance effects were demonstrated in Fibermax 832 x TAM 94L-25 in 2002 Fibermax 832 x Acala 1517-99 combined across years, and Fibermax 832 x TTU 202 in 2001. A positive dominance x dominance effect was attained in Fibermax 832 x Acala 1517-99 combined across years and Fibermax 832 x TTU 202 in 2002. Negative dominance x dominance effects were obtained in TAM 94L-25 x TTU 202 in 2001 and 2002. For the parental combination TAM 94L-25 x TTU 202 in 2001 and 2002, the dominance effects were positive while the dominance x dominance effects were negative. The contrasting direction of response between dominance and dominance x dominance gene effect estimates suggests positive duplicate epistasis (Kearsey and Pooni, 1996). For Fibermax 832 x Acala 1517-99 combined across years, the dominance effect was negative while the dominance x dominance effect was positive, suggesting negative duplicate epistasis. Among the near-long x near-long parental combinations, additive effects accounted for a notable smaller portion of the observed variability than dominance effects. In general, dominance x dominance effects were larger than additive x additive. In reviewing all genetic effects, dominance and dominance x dominance effects are probably the most important in determining CEA among the near-long x near-long parental combinations.

In the near-long x short staple parental combinations, the results of the three-parameter model analysis indicated that epistasis was present in all but one combination. Additive effects were positive for TAM 94L-25 x Tamcot CAMD-E in 2001, Fibermax 832 x Tamcot CAMD-E in 2002, and TTU 202 x Tamcot CAMD-E in 2002 (Table 29). In 2002, a negative additive effect was attained in Acala 1517-99 x Tamcot CAMD-E. All parental combinations displayed dominance effects except for TTU 202 x Tamcot CAMD-E in 2001. Positive dominance effects were attained in TAM 94L-25 x Tamcot CAMD-E in 2001 and 2002, Fibermax 832 x Tamcot CAMD-E in 2001, and Acala 1517-99 x Tamcot CAMD-E in 2001 and 2002. In 2002, negative dominance effects were obtained in Fibermax 832 x Tamcot CAMD-E and TTU 202 x Tamcot CAMD-E. This indicates that the F_1 mean was lower than the mid-parent value and that there existed a directional dominance of alleles with decreasing effect that exerted their influence in P_1, rather than in P_2, the parent with the lower CEA value. Significant additive x additive effects were attained in all near-long x short staple parental combinations except TAM 94L-25 x Tamcot CAMD-E in 2002. Positive additive x additive estimates were obtained in TAM 94L-25 x Tamcot CAMD-E in 2001, Fibermax 832 x Tamcot CAMD-E in 2001, Acala 1517-99 x Tamcot CAMD-E in 2001, and TTU 202 x Tamcot CAMD-E in 2001, while in 2002 negative estimates were attained in Fibermax 832 x Tamcot CAMD-E and TTU 202 x Tamcot CAMD-E. No additive x dominance effects were demonstrated. All near-long x short staple parental combinations displayed dominance x dominance effects except for TTU 202 x Tamcot CAMD-E. TAM 94L-25 x Tamcot CAM-E in 2001 and 2002, Fibermax 832 x Tamcot

CAMD-E in 2001, and Acala 1517-99 x Tamcot CAMD-E in 2001 had negative dominance x dominance effects while Fibermax 832 x Tamcot CAMD-E in 2002 showed a positive dominance x dominance effect. For TAM 94L-25 x Tamcot CAMD-E in 2001 and 2002, Fibermax 832 x Tamcot CAMD-E in 2001, and Acala 1517-99 x Tamcot CAMD-E in 2001, the dominance effect was positive while the dominance x dominance effect was negative, suggesting positive duplicate epistasis. In 2002, the dominance estimate of Fibermax 832 x Tamcot CAMD-E was negative while the dominance x dominance estimate was positive. The contrasting direction of response among the dominance and dominance x dominance effects suggest negative duplicate epistasis (Kearsey and Pooni, 1996).

Generation means analysis indicated that genetic control for CEA among near-long x short staple parental combinations was as dependent upon dominance or dominance x dominance gene action as was the near-long x near-long parental combinations. All dominance effects were larger in magnitude than additive effects and significant more often. Among the non-allelic interactions, dominance x dominance effects accounted for a larger portion of the observed variability than additive x additive. Among all combinations in 2001, all gene effects for CEA were significant (Table 29). Among all combinations in 2002, dominance and dominance x dominance effects were significant.

Variance components and broad- and narrow-sense heritability estimates for CEA were calculated to determine the relative importance of the various determinants of the phenotype, the extent to which individuals' phenotypes are determined by their genotypes, and the extent to which phenotypes are determined by the alleles transmitted from the parents (Falconer and MacKay, 1996). For all parental combinations, higher environmental variances were seen in 2001 than in 2002 (Table 30). In 2001, environmental variance among the 5 near-long x near-long parental combinations ranged from 1243 to 1493 with an average of 1384, while the 4 near-long x short staple parental combinations ranged from 1144 to 1530 with an average of 1311. Environmental variance among the near-long x near-long combinations in 2002 ranged from 429 to 1120 with an average of 766, while the near-long x short staple parental combinations in 2002 ranged from 337 to 723 with an average of 436. Among the near-long x near-long parental combinations, Fibermax 832 x TAM 94L-25 and TAM 94L-25 x Acala 1517-99 had the highest and lowest environmental variance for each year, respectively. Among the near-long x short staple parental combinations, Fibermax 832 x Tamcot CAMD-E had the lowest environmental variance in 2001, yet the highest in 2002.

Additive variance was higher in 2001 for the near-long x near-long parental combinations, however, in the near-long x short staple parental combinations a higher additive variance was attained in 2002 (Table 30). In 2001, the additive variance among the near-long x near-long parental combinations ranged from 0 to 3378 with an average of 1635, while the near-long x short staple combinations ranged from 0 to 249 with an average of 70. In 2002, the additive variance among the near-long x near-long parental combinations ranged from 0 to 362 with an average of 175, while the near-long x short staple parental combinations ranged from 272 to 1588 with an average of 924. Five

Table 30. Variance components and broad (H^2) and narrow (h^2) sense heritability estimates for CEA of AFIS FLw for 10 parental combinations grown at College Station, TX in 2001 and 2002.

		Variance components†			Heritability estimates	
Parental Combinations	Year	σ^2_E	σ^2_A	σ^2_D	H^2	h^2
Fibermax 832 x TAM 94L-25‡	2001	1493	3378	880	0.74	0.58 ± 0.03
Fibermax 832 x TAM 94L-25‡	2002	1120	-277	-231	0.00	0.00 ± 0.08
TAM 94L-25 x TTU 202‡	2001	1423	1830	1601	0.71	0.38 ± 0.03
TAM 94L-25 x TTU 202‡	2002	679	-132	328	0.33	0.00 ± 0.06
Fibermax 832 x Acala 1517-99‡	2001/02	1062	-1665	1507	0.59	0.00 ± 0.05
Fibermax 832 x TTU 202‡	2001	1402	1492	1372	0.67	0.35 ± 0.04
Fibermax 832 x TTU 202‡	2002	660	362	-150	0.35	0.35 ± 0.03
TAM 94L-25 x Acala 1517-99‡	2001	1243	1477	2599	0.77	0.28 ± 0.04
TAM 94L-25 x Acala 1517-99‡	2002	429	305	117	0.50	0.36 ± 0.04
Acala 1517-99 x TTU 202‡	2001	1357	-1240	3698	0.73	0.00 ± 0.06
Acala 1517-99 x TTU 202‡	2002	942	207	-161	0.18	0.18 ± 0.04
TAM 94L-25 x Tamcot CAMD-E§	2001	1354	249	1515	0.57	0.08 ± 0.04
TAM 94L-25 x Tamcot CAMD-E§	2002	337	495	594	0.76	0.35 ± 0.04
Fibermax 832 x Tamcot CAMD-E§	2001	1144	-782	1412	0.55	0.00 ± 0.07
Fibermax 832 x Tamcot CAMD- E§	2002	723	1588	-934	0.69	0.69 ± 0.01
Acala 1517-99 x Tamcot CAMD-E§	2001	1216	29	1788	0.60	0.01 ± 0.04
Acala 1517-99 x Tamcot CAMD-E§	2002	342	272	-89	0.44	0.44 ± 0.03
TTU 202 x Tamcot CAMD-E§	2001	1530	-150	97	0.06	0.00 ± 0.05
TTU 202 x Tamcot CAMD-E§	2002	342	1343	-359	0.80	0.80 ± 0.01
Among all combinations	2001	2989	812	1886	0.47	0.14 ± 0.00
Among all combinations	2002	877	109	292	0.31	0.09 ± 0.00

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

‡ Near-long x near-long parental combination.

§ Near-long x short staple parental combination.

parental combinations did not show any additive variance in one year, only for it to be present in the other.

In 2001, the dominance variance among the near-long x near-long parental combinations ranged from 880 to 3698 with an average of 2087, while the near-long x short staple combinations ranged from 97 to 1788 with an average of 1203 (Table 30). In 2002, the dominance variance among the near-long x near-long combinations with three zero values ranged from 0 to 328 with an average of 89, while TAM 94L-25 x Tamcot CAMD-E was the only near-long x short staple parental combination to have a positive dominance variance of 594. Six of the nine parental combinations demonstrated dominance variance in 2001, but none in 2002. Fibermax 832 x Acala 1517-99 combined across years had zero additive variance and a dominance variance estimate of 1507. Among all combinations in 2001, the environmental, additive, and dominance variance was 2989, 812, and 1886, respectively. Among all combinations in 2002, the environmental, additive, and dominance variance was 877, 109, and 292, respectively.

Among the near-long x near-long parental combinations, broad-sense heritability (H^2) averaged 0.72 in 2001, higher than the 0.27 estimate in 2002 (Table 30). Despite higher environmental variance in 2001, higher broad-sense heritability estimates were attained due to a higher total genetic variance. Narrow-sense heritability estimates (h^2) were low in 2001 and 2002, averaging 0.32 and 0.18, respectively. Fibermax 832 x Acala 1517-99 combined across years had broad- and narrow-sense heritability estimates of 0.59 and 0.00, respectively.

Among the near-long x short staple parental combinations, broad-sense heritability averaged 0.45 and 0.67 in 2001 and 2002, respectively (Table 30). Higher broad-sense heritability estimates were generally attained in the year with a lower environmental variance, however, Acala 1517-99 x Tamcot CAMD-E had a higher estimate in 2002 because of a greater total genetic variance. Narrow-sense heritability averaged 0.02 and 0.57 in 2001 and 2002, respectively. Higher narrow-sense heritability estimates were obtained in the year with smaller environmental and greater additive variance. Among all combinations in 2001, the broad- and narrow-sense heritability estimates were 0.47 and 0.14. Among all combinations in 2002, the broad- and narrow-sense heritability estimates were 0.31 and 0.09.

FLw kurtosis

The parental, F_1, F_2, and backcross generations differed ($P \leq 0.01$) in Uqlw, a length by weight measurement, for all parental combinations except Fibermax 832 x TTU 202 (Table 31). The ANOVA also indicated a significant generation x environment interaction for all parental combinations except Fibermax 832 x Acala 1517-99, thus this parental combination was pooled over years. The other parental combinations indicated that some generations reacted differently to each environment, suggesting that selection and evaluation should be conducted within environment if reliable knowledge of FLw kurtosis is to be obtained.

FLw kurtosis means from P_1 and P_2 were different ($P \leq 0.05$) in each parental combination except Fibermax 832 x TAM 94L-25 in 2002, TAM 94L-25 x TTU 202 in 2002, and Fibermax 832 x TTU 202 in 2001 and 2002 (Table 32). For the majority of the parental combinations, P_2, parent with the shorter AFIS FLw for most combinations, had the higher FLw kurtosis measurement. TAM 94L-25 had a FLw kurtosis value of 0.02 in 2001 and 1.26 in 2002, so in combination with Fibermax 832 it switched from the low parent to the high parent from 2001 to 2002, respectively. Acala 1517-99, representing P_1 in combination with TTU 202, had a higher FLw kurtosis value than P_2 when averaged over years.

In 2001, no established pattern of F_1 hybrids could be identified as means fluctuated from being similar to low parent, intermediate, and similar to high parent (Table 32). In 2002, all parental F_1 hybrid combinations had FLw kurtosis means either lower than both parents or similar to the low parent. No F_1 hybrid had an FLw kurtosis mean greater than the highest parent. In general, F_2 means were similar to the shorter parent. In most parental combinations, the mean values of the backcrosses were different and shifted toward the values observed for the recurrent parent. Since P_2 had a higher FLw kurtosis value in most parental combinations, BC_1P_2 values were higher than BC_1P_1. However, the BC_1P_2 means were not different from BC_1P_1 means in the parental combinations of Fibermax 832 x TAM 94L-25 in 2001 and 2002, TAM 94L-25 x TTU 202 in 2002, Fibermax 832 x TTU 202 in 2001 and 2002, Acala 1517-99 x TTU 202 in 2001, and Acala 1517-99 x Tamcot CAMD-E in 2001 and 2002.

The parental combinations were divided into two categories, near-long x near-long and near-long x short staple parental combinations. For each parental combination, P_1 was assigned accordingly to the parent with the longest FLw. The near-long x near-long parental combinations consisted of Fibermax 832 x TAM 94L-25, TAM 94L-25 x

Table 31. Mean squares for FLw kurtosis from the distribution data measured on P_1, P_2, F_1, F_2, BC_1P_1, and BC_2P_2 (per parental combination and among all combinations) at College Station, TX in 2001 and 2002.

A.

		Parental Combinations†					
Source	df	832 x L-25	L-25 x 202	832 x 1517	832 x 202	L-25 x 1517	1517 x 202
Environment (E)	1	58.89**	59.13**	39.00**	34.20**	77.90**	43.65**
Reps/E	6	0.33	0.19	0.35	0.38	0.35	0.30
Generation (Gn)	5	1.80**	2.77**	5.19**	0.53	10.37**	4.55**
Gn x E	5	2.39**	1.61**	0.75	2.54**	3.13**	2.28**
Error	30	0.23	0.29	0.57	0.48	0.18	0.47

B.

		Parental Combinations‡				
Source	df	L-25 x CD-E	832 x CD-E	1517 x CD-E	202 x CD-E	Among
Environment (E)	1	39.10**	23.54**	46.95**	15.84**	42.13**
Reps/E	6	0.81	0.30	0.53	1.02	0.10
Generation (Gn)	5	24.39**	21.02**	6.54**	13.14**	4.50**
Gn x E	5	2.79**	2.44*	2.20*	1.44*	1.31**
Error	30	0.53	0.72	0.77	0.56	0.13

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

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

Table 32. Means of P_1, P_2, F_1, F_2, BC_1P_1, and BC_2P_2 for FLw kurtosis (per parental combination and among all combinations) at College Station, TX in 2001 and 2002. First parent listed is P_1, second parent is P_2.

A.

	Parental Combinations†										
	832 x L-25		L-25 x 202		832 x 1517	832 x 202		L-25 x 1517		1517 x 202	
Gen.‡	2001	2002	2001	2002	2001/02	2001	2002	2001	2002	2001	2002
P_1	0.56 a§	1.03 a	0.02 c	1.26 a	0.80 c	0.56 ab	1.03 a	0.02 e	1.26 b	1.03 a	1.93 a
P_2	0.02 d	1.26 a	0.60 a	1.26 a	1.48 a	0.60 ab	1.26 a	1.03 a	1.93 a	0.60 b	1.26 bc
F_1	0.32 b	0.55 c	0.55 a	0.98 ab	0.95 bc	0.81 a	0.65 b	0.54 b	0.63 e	1.04 a	0.98 c
F_2	0.13 cd	0.99 ab	0.31 b	0.90 b	1.10 b	0.37 b	1.10 a	0.40 c	1.37 bc	0.69 ab	1.44 b
BC_1P_1	0.23 bc	0.98 ab	0.00 c	0.74 b	0.82 c	0.34 b	1.11 a	0.20 d	0.89 d	0.79 ab	1.48 b
BC_1P_2	0.05 cd	0.71 bc	0.40 ab	0.95 b	1.14 b	0.38 b	1.10 a	0.58 b	1.54 b	0.43 b	1.11 c

B.

	Parental Combinations¶									
	L-25 x CD-E		832 x CD-E		1517 x CD-E		202 x CD-E		Among	
Gen.	2001	2002	2001	2002	2001	2002	2001	2002	2001	2002
P_1	0.02 c	1.26 bc	0.56 d	1.03 c	1.03 b	1.93 b	0.60 d	1.26 c	0.50 c	1.30 b
P_2	1.74 a	2.42 a	1.74 a	2.42 a	1.74 a	2.42 a	1.74 a	2.42 a	1.08 a	1.86 a
F_1	0.75 b	0.97 cd	1.23 b	1.05 c	1.29 ab	1.28 c	1.27 bc	1.32 c	0.85 b	0.96 d
F_2	0.82 b	1.19 bc	0.77 cd	1.06 c	1.19 b	1.84 b	1.37 ab	1.48 c	0.69 b	1.27 bc
BC_1P_1	0.24 c	0.86 d	0.40 d	1.04 c	0.92 b	1.82 b	0.97 cd	1.39 c	0.46 c	1.14 c
BC_1P_2	0.98 b	1.28 b	1.07 bc	1.83 b	1.08 b	1.71 b	1.56 ab	1.82 b	0.73 b	1.35 b

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ Gen., generation; 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 K = 100 (approximates p = 0.05) according to Waller-Duncan LSD.

¶ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

TTU 202, Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, TAM 94L-25 x Acala 1517-99, and Acala 1517-99 x TTU 202. The near-long x short staple parental combinations were Fibermax 832, TAM 94L-25, Acala 1517-99, and TTU 202 crosses with Tamcot CAMD-E.

Generation mean analyses tested three- and six-parameter models for the best fit to explain genetic control of FLw kurtosis in various upland parental combinations. Effects were first estimated with the three-parameter model and accepted if $P \geq 0.05$. The three-parameter model did not satisfactorily explained the genetic differences for FLw kurtosis of any parental combination. Therefore, the six-parameter model was used to determine the type and magnitude of gene effects involved in the inheritance of FLw kurtosis.

In the near-long x near-long parental combinations for FLw kurtosis, TAM 94L-25 x TTU 202 in 2001, Fibermax 832 x Acala 1517-99 combined across years, and TAM 94L-25 x Acala 1517-99 in 2001 had negative additive effects, reemphasizing that P_2 had a higher FLw kurtosis mean than P_1 (Table 33). Fibermax 832 x TAM 94L-25 in 2001 and Acala 1517-99 x TTU 202 in 2002 had positive additive effects of 0.31 and 0.31, respectively. Dominance effects were negative for the parental combinations of Fibermax 832 x TAM 94L-25 in 2002, TAM 94L-25 x TTU 202 in 2001, Fibermax 832 x TTU 202 in 2001, and Acala 1517-99 x TTU 202 in 2001 and 2002. The negative dominance effect indicates that the F_1 mean was lower than the mid-parent value and that there existed a directional dominance of alleles with decreasing effect that exerted their influence in the long staple genotype, P_1, rather than in P_2, the genotype with higher

Table 33. Estimates of gene effects for FLw kurtosis from the distribution data (per crossing combination and among all combinations) at College Station, TX in 2001 and 2002.

		Gene effects†					
Parental Combinations	Year	*m*	*a*	*d*	*aa*	*ad*	*dd*
Fibermax 832 x TAM 94L-25‡	2001	0.13	0.31*	-0.35	0.14	-0.24	0.58
Fibermax 832 x TAM 94L-25‡	2002	1.87**	0.10	-2.21**	-0.49**	0.35	0.85
TAM 94L-25 x TTU 202‡	2001	0.82**	-0.40**	-1.80**	-0.42**	0.02	1.53**
TAM 94L-25 x TTU 202‡	2002	1.38**	0.00	-1.54	-0.18	-0.40	1.11
Fibermax 832 x Acala 1517-99‡	2001/02	1.21**	-0.68**	0.40	-0.09	0.44**	-0.70
Fibermax 832 x TTU 202‡	2001	0.73**	-0.15	-1.44*	-0.03	0.20	1.38*
Fibermax 832 x TTU 202‡	2002	1.32**	0.11	-0.25	0.10	-0.20	-0.43
TAM 94L-25 x Acala 1517-99‡	2001	0.58**	-0.53**	-0.67	0.01	0.32	0.58
TAM 94L-25 x Acala 1517-99‡	2002	2.27**	-0.32	-1.83	-0.76**	-0.59	0.14
Acala 1517-99 x TTU 202‡	2001	1.35**	0.10	-2.35**	-0.38	0.51	2.00*
Acala 1517-99 x TTU 202‡	2002	2.12**	0.31**	-1.55*	-0.56*	0.11	0.31
TAM 94L-25 x Tamcot CAMD-E§	2001	1.68**	-0.74*	-2.49*	-0.94**	-0.03	1.51*
TAM 94L-25 x Tamcot CAMD-E§	2002	2.44**	-0.55	-3.52**	-0.71**	0.15	2.06**
Fibermax 832 x Tamcot CAMD-E§	2001	1.28**	-0.45	-1.99	-0.25	-0.37	1.97
Fibermax 832 x Tamcot CAMD- E§	2002	0.35	-0.42	2.19*	1.48**	-0.75	-1.54
Acala 1517-99 x Tamcot CAMD-E§	2001	1.97**	-0.20	-2.56*	-0.71**	0.11	1.94
Acala 1517-99 x Tamcot CAMD-E§	2002	2.37**	-0.18	-1.23	-0.31	0.58	0.32
TTU 202 x Tamcot CAMD-E§	2001	1.58**	-0.36	-0.44	-0.48*	-0.47	0.01
TTU 202 x Tamcot CAMD-E§	2002	1.21**	-0.52*	0.90	0.54**	0.18	-0.77
Among all combinations	2001	0.81**	-0.16**	-0.74**	-0.50**	-0.08	0.48**
Among all combinations	2002	1.55**	0.05	-1.05**	-0.08	-0.43**	0.58**

*, ** Significant at the 0.05 and 0.01 probability level on the basis of *t* test with n – 1 =5 degrees of freedom, respectively.

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

‡ Near-long x near-long parental combination.

§ Near-long x short staple parental combination.

FLw kurtosis value. Negative additive x additive gene effect estimates were attained among Fibermax 832 x TAM 94L-25 in 2002, TAM 94L-25 x TTU 202 in 2001, TAM 94L-25 x Acala 1517-99 in 2002, and Acala 1517-99 x TTU 202 in 2002, suggesting both parents contributed alleles for FLw kurtosis. Fibermax 832 x Acala 1517-99 exhibited a positive additive x dominance effect. Positive dominance x dominance effects were attained in TAM 94L-25 x TTU 202 in 2001, Fibermax 832 x TTU 202 in 2001, and Acala 1517-99 x TTU 202 in 2001. For the 2001 parental combinations of TAM 94L-25 x TTU 202, Fibermax 832 x TTU 202, and Acala 1517-99 x TTU 202, the dominance effect was negative while the dominance x dominance effect was positive. The contrasting direction of response between dominance and dominance x dominance gene effect estimates suggests negative duplicate epistasis (Kearsey and Pooni, 1996). Among the near-long x near-long parental combinations, additive effects accounted for a smaller portion of the observed variability than dominance effects. Significant dominant effects were at least four times greater than additive. In general, dominance x dominance effects were larger than additive x additive, however, additive x additive effects were significant more frequently.

In the near-long x short staple parental combinations, the results of the three-parameter model analysis indicated that epistasis was present. Additive effects were negative for TAM 94L-25 x Tamcot CAMD-E in 2001 and TTU 202 x Tamcot CAMD-E in 2002 (Table 33). The negative additive effect once again only signifies that P_2 had a higher FLw kurtosis mean than P_1. TAM 94L-25 x Tamcot CAMD-E in 2001 and 2002 and Acala 1517-99 x Tamcot CAMD-E in 2001 had negative dominance effects.

Fibermax 832 x Tamcot CAMD-E in 2002 had positive dominance effects. Significant additive x additive effects were attained in all near-long x short staple parental combinations except Fibermax 832 x Tamcot CAMD-E in 2001 and Acala 1517-99 x Tamcot CAMD-E in 2002. Negative additive x additive estimates were obtained in TAM 94L-25 x Tamcot CAMD-E in 2001 and 2002, Acala 1517-99 x Tamcot CAMD-E in 2001, and TTU 202 x Tamcot CAMD-E in 2001, while positive estimates were attained in Fibermax 832 x Tamcot CAMD-E in 2002 and TTU 202 x Tamcot CAMD-E in 2002. No additive x dominance effects were demonstrated. TAM 94L-25 x Tamcot CAMD-E in 2001 and 2002 was the only near-long x short staple parental combination to display dominance x dominance effects. In 2001 and 2002, the dominance estimate of TAM 94L-25 x Tamcot CAMD-E was negative while the dominance x dominance estimates were positive. The contrasting direction of response among the dominance and dominance x dominance effects suggests negative duplicate epistasis (Kearsey and Pooni, 1996).

Generation means analysis indicated that genetic control for FLw kurtosis among near-long x short staple parental combinations was as complex as among near-long x near-long parental combinations. All dominance effects were larger in magnitude than additive effects. Among the non-allelic interactions, in general, dominance x dominance effects accounted for a larger portion of the observed variability than additive x additive, however, additive x additive effects were significant more often because the generation means analysis produced larger standard errors for dominance x dominance than for additive x additive effects (data not shown). Among all combinations in 2001, additive, dominance, additive x additive, and dominance x dominance effects were significant (Table 33). Among all combinations in 2002, dominance, additive x dominance, and dominance x dominance effects were significant.

Variance components and broad- and narrow-sense heritability estimates for FLw kurtosis were calculated to determine the relative importance of the various determinants of the phenotype, the extent to which individuals' phenotypes are determined by their genotypes, and the extent to which phenotypes are determined by the alleles transmitted from the parents (Falconer and MacKay, 1996). For the 10 near-long x near-long parental combinations, higher environmental variances were seen in 2002 than in 2001, however, among the 8 near-long x short staple parental combinations higher environmental variances were noted in 2001 (Table 34). In 2001, environmental variance among near-long x near-long parental combinations ranged from 0.11 to 1.41 with an average of 0.58, while the near-long x short staple parental combinations ranged from 1.64 to 2.66 with an average of 2.19. Environmental variance among the near-long x near-long combinations in 2002 ranged from 0.12 to 1.21 with an average of 0.83, while the near-long x short staple parental combinations in 2002 ranged from 1.55 to 2.02 with an average of 1.74. Additive variances were higher in 2001 than 2002, except for TAM 94L-25 x Acala 1517-99 and Acala 1517-99 x TTU 202. In 2001, the additive variance among the near-long x near-long parental combinations ranged from 0.21 to 1.42 with an average of 0.78, while the near-long x short staple combinations ranged from 0.00 to 2.42 with an average of 1.32. In 2002, the additive variance among the near-long x near-long parental combinations ranged from 0.08 to 2.29 with an average of

Table 34. Variance components and broad (H^2) and narrow (h^2) sense heritability estimates for FLw kurtosis for 10 parental combinations grown at College Station, TX in 2001 and 2002.

		Variance components†			Heritability estimates	
Parental Combinations	Year	σ^2_E	σ^2_A	σ^2_D	H^2	h^2
Fibermax 832 x TAM 94L-25‡	2001	0.39	1.42	-0.24	0.79	0.79 ± 0.01
Fibermax 832 x TAM 94L-25‡	2002	1.21	0.94	-0.30	0.44	0.44 ± 0.03
TAM 94L-25 x TTU 202‡	2001	0.36	1.27	0.31	0.81	0.65 ± 0.03
TAM 94L-25 x TTU 202‡	2002	1.05	0.98	-0.20	0.48	0.48 ± 0.03
Fibermax 832 x Acala 1517-99‡	2001/02	0.19	0.21	0.02	0.54	0.50 ± 0.02
Fibermax 832 x TTU 202‡	2001	1.41	0.41	-0.46	0.23	0.23 ± 0.04
Fibermax 832 x TTU 202‡	2002	0.99	0.08	0.65	0.43	0.05 ± 0.05
TAM 94L-25 x Acala 1517-99‡	2001	0.65	0.59	0.58	0.64	0.32 ± 0.04
TAM 94L-25 x Acala 1517-99‡	2002	0.77	2.29	0.24	0.77	0.70 ± 0.02
Acala 1517-99 x TTU 202‡	2001	0.11	0.21	0.07	0.71	0.54 ± 0.03
Acala 1517-99 x TTU 202‡	2002	0.12	0.28	0.01	0.71	0.68 ± 0.02
TAM 94L-25 x Tamcot CAMD-E§	2001	1.64	1.52	-0.51	0.48	0.48 ± 0.03
TAM 94L-25 x Tamcot CAMD-E§	2002	1.73	0.77	0.37	0.40	0.27 ± 0.05
Fibermax 832 x Tamcot CAMD-E§	2001	2.06	-0.10	-0.47	0.00	0.00 ± 0.07
Fibermax 832 x Tamcot CAMD- E§	2002	2.02	-1.13	-0.17	0.00	0.00 ± 0.11
Acala 1517-99 x Tamcot CAMD-E§	2001	2.66	2.42	-1.28	0.48	0.48 ± 0.02
Acala 1517-99 x Tamcot CAMD-E§	2002	1.64	3.76	0.06	0.70	0.69 ± 0.02
TTU 202 x Tamcot CAMD-E§	2001	2.41	1.32	0.29	0.35	0.38 ± 0.04
TTU 202 x Tamcot CAMD-E§	2002	1.55	1.75	-0.23	0.53	0.53 ± 0.03
Among all combinations	2001	2.87	1.43	-0.33	0.33	0.33 ± 0.00
Among all combinations	2002	2.57	0.76	0.39	0.31	0.20 ± 0.00

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

‡ Near-long x near-long parental combination.

§ Near-long x short staple parental combination.

0.91, while the near-long x short staple parental combinations ranged from 0.00 to 3.76 with an average of 1.57. In 2001, the dominance variance among the near-long x near-long parental combinations ranged from 0.00 to 0.58 with an average of 0.19, while the near-long x short staple combinations ranged from 0.00 to 0.29 with an average of 0.07. In 2002, the dominance variance among the near-long x near-long combinations ranged from 0.00 to 0.65 with an average of 0.18, while the near-long x short staple parental combinations ranged from 0.00 to 0.37 with an average of 0.11. Among all combinations in 2001, the environmental, additive, and dominance variance was 2.87, 1.43, and 0.00, respectively. Among all combinations in 2002, the environmental, additive, and dominance variance was 2.57, 0.76, and 0.39, respectively.

Among the near-long x near-long parental combinations, broad-sense heritability of FLw kurtosis (H^2) averaged 0.64 in 2001, slightly higher than the 0.57 estimate in 2002 (Table 34). Generally, higher broad-sense heritability estimates were attained in the year with the lower environmental variance. In 2002, a higher broad-sense heritability estimate was attained in TAM 94L-25 x Acala 1517-99 because of a larger total genetic variance. Narrow-sense heritability estimates (h^2) were similar in 2001 and 2002, averaging 0.51 and 0.47, respectively. The broad- and narrow-sense heritability estimates of FLw kurtosis in Fibermax 832 x Acala 1517-99 combined across years were 0.54 and 0.50, respectively.

Among the near-long x short staple parental combinations, broad-sense heritability averaged 0.33 and 0.41 in 2001 and 2002, respectively (Table 34). Higher broad-sense heritability estimates were attained in the year with a lower environmental variance and greater total genetic variance. Narrow-sense heritability averaged 0.33 and 0.37 in 2001 and 2002, respectively. Higher narrow-sense heritability estimates were obtained in the year with smaller environmental and greater additive variance. Of interest is the Fibermax 832 x Tamcot CAMD-E parental combination exhibiting zero additive and dominance variance in 2001 and 2002.

Among all combinations in 2001, the broad- and narrow-sense heritability estimates were 0.33 and 0.33, respectively. Among all combinations in 2002, the broad- and narrow-sense heritability estimates were 0.31 and 0.20, respectively.

FLw skewness

FLw skewness differed ($P \leq 0.05$) across environments for the parental combinations of Fibermax 832 x TAM 94L-25, TAM 94L-25 x TTU 202, Fibermax 832 x TTU 202, TAM 94L-25 x Acala 1517-99, Acala 1517-99 x Tamcot CAMD-E, and among all combinations (Table 35). The ANOVA indicated that generations of all parental combinations differed ($P \leq 0.05$) in FLw skewness, except for Fibermax 832 x TTU 202. The ANOVA also revealed a significant generation x environment interaction in all parental combinations except Fibermax 832 x TTU 202, thus this parental combination was pooled over years. The other parental combinations indicated that some generations reacted differently to each environment, suggesting that selection and evaluation should be conducted within environment if reliable knowledge of FLw skewness is to be obtained.

FLw skewness means from P_1 and P_2 were different ($P \leq 0.05$) in each parental combination except Fibermax 832 x TAM 94L-25 in 2001 and 2002, TAM 94L-25 x

TTU 202 in 2001 and 2002, Fibermax 832 x TTU 202 combined across years, and Acala 1517-99 x Tamcot CAMD-E in 2002 (Table 36). For the majority of the parental combinations, P_2, the parent with the shorter AFIS FLw for most combinations, had the higher FLw skewness measurement. Acala 1517-99, representing P_1 in combination with TTU 202, had a higher FLw skewness value than P_2 in 2001 and 2002.

In general, F_1 hybrids means were either lower than both parents or similar to the low parent (Table 36). No F_1 hybrid had an FLw skewness mean greater than the highest parent. No trend was observed in the F_2 means. All parental combinations and years in which P_1 did not differ from P_2, translated into BC_1P_1 not altering from BC_1P_2. In addition, BC_1P_1 of Acala 1517-99 x TTU 202 in 2001 and Acala 1517-99 x Tamcot CAMD-E did not contrast with BC_1P_2. For all other parental combinations, the mean values of the backcrosses were different and shifted toward the values observed for the recurrent parent. Since P_2 had a higher FLw skewness value in these parental combinations, BC_1P_2 values were higher than BC_1P_1.

The parental combinations were divided into two categories, near-long x near-long and near-long x short staple parental combinations. For each parental combination, P_1 was assigned accordingly to the parent with the longest FLw in 2002. The near-long x near-long parental combinations consisted of Fibermax 832 x TAM 94L-25, TAM 94L-25 x TTU 202, Fibermax 832 x Acala 1517-99, Fibermax 832 x TTU 202, TAM 94L-25 x Acala 1517-99, and Acala 1517-99 x TTU 202. The near-long x short staple parental combinations were Fibermax 832, TAM 94L-25, Acala 1517-99, and TTU 202 crosses with Tamcot CAMD-E.

Table 35. Mean squares for FLw skewness from the distribution data measured on P_1, P_2, F_1, F_2, BC_1P_1, and BC_2P_2 (per parental combination and among all combinations) at College Station, TX in 2001 and 2002.

A.

		Parental Combinations†					
Source	df	832 x L-25	L-25 x 202	832 x 1517	832 x 202	L-25 x 1517	1517 x 202
Environment (E)	1	157.42**	112.90**	1.23	69.81**	21.72**	9.23
Reps/E	6	2.21	2.64	4.21	2.04	4.67	3.78
Generation (Gn)	5	16.97**	28.34**	105.76**	7.00	135.12**	79.39**
Gn x E	5	11.29**	13.79**	14.45**	1.86	31.46**	23.52**
Error	30	2.17	1.60	3.00	3.58	2.09	3.23

B.

		Parental Combinations‡				
Source	df	L-25 x CD-E	832 x CD-E	1517 x CD-E	202 x CD-E	Among
Environment (E)	1	0.18	17.87	68.83**	1.22	12.68**
Reps/E	6	8.31	6.36	4.66	2.22	0.80
Generation (Gn)	5	209.98**	193.72**	25.60**	160.45**	44.62**
Gn x E	5	12.76*	23.66**	16.86*	15.58*	6.80**
Error	30	3.85	4.56	6.32	5.82	0.80

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

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

Table 36. Means of P_1, P_2, F_1, F_2, BC_1P_1, and BC_2P_2 for FLw skewness (per parental combination and among all combinations) at College Station, TX in 2001 and 2002. First parent listed is P_1, second parent is P_2.

A.

	Parental Combinations†										
	832 x L-25		L-25 x 202		832 x 1517		832 x 202	L-25 x 1517		1517 x 202	
Gen.‡	2001	2002	2001	2002	2001	2002	2001/02	2001	2002	2001	2002
P_1	-0.07 bc§	-0.09 ab	-0.05 ab	-0.07 a	-0.07 b	-0.09 c	-0.08 ab	-0.05 cd	-0.07 c	0.12 a	0.30 a
P_2	-0.05 b	-0.07 a	0.01 a	-0.08 a	0.12 a	0.30 a	-0.04 ab	0.12 a	0.30 a	0.01 b	-0.08 c
F_1	-0.12 c	-0.25 d	-0.21 c	-0.20 b	-0.06 b	-0.12 c	-0.09 b	-0.11 d	-0.18 d	0.02 b	-0.09 c
F_2	0.03 a	-0.16 bc	-0.08 b	-0.20 b	0.04 a	0.02 b	-0.01 a	0.07 ab	-0.03 c	0.10 a	0.08 b
BC_1P_1	-0.02 ab	-0.15 abc	-0.02 ab	-0.24 b	-0.06 b	-0.08 c	-0.05 ab	0.01 bc	-0.20 d	0.14 a	0.12 b
BC_1P_2	-0.03 ab	-0.22 cd	-0.05 ab	-0.19 b	0.04 a	0.05 b	-0.03 ab	0.10 a	0.07 b	0.07 ab	-0.05 c

B.

	Parental Combinations¶									
	L-25 x CD-E		832 x CD-E		1517 x CD-E		202 x CD-E		Among	
Gen.	2001	2002	2001	2002	2001	2002	2001	2002	2001	2002
P_1	-0.05 d	-0.07 cd	-0.07 d	-0.09 c	0.12 c	0.30 ab	0.01 c	-0.08 d	-0.02 d	-0.01 cd
P_2	0.28 a	0.42 a	0.28 a	0.42 a	0.28 a	0.42 a	0.28 a	0.42 a	0.13 a	0.20 a
F_1	0.02 c	-0.04 cd	0.19 b	0.01 c	0.25 ab	0.16 b	0.13 b	0.03 cd	0.01 cd	-0.08 e
F_2	0.03 c	0.02 c	0.19 b	0.14 b	0.19 abc	0.26 b	0.14 b	0.10 bc	0.07 b	0.02 bc
BC_1P_1	-0.03 d	-0.12 d	0.08 c	-0.02 c	0.16 bc	0.25 b	0.03 c	0.03 cd	0.03 c	-0.05 de
BC_1P_2	0.14 b	0.15 b	0.26 ab	0.25 b	0.19 abc	0.26 b	0.22 a	0.24 b	0.09 b	0.05 b

† 832 x L-25, Fibermax 832 x TAM 94L-25; L-25 x 202, TAM 94L-25 x TTU 202; 832 x 1517, Fibermax 832 x TTU 202; L-25 x 1517, TAM 94L-25 x Acala 1517-99; 1517 x 202, Acala 1517-99 x TTU 202.

‡ Gen., generation; 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 K = 100 (approximates p = 0.05) according to Waller-Duncan LSD.

¶ L-25 x CD-E, TAM 94L-25 x Tamcot CAMD-E; 832 x CD-E, Fibermax 832 x Tamcot CAMD-E; 1517 x CD-E, Acala 1517-99 x Tamcot CAMD-E; 202 x CD-E, TTU 202 x Tamcot CD-E; Among, Among all combinations.

Generation mean analyses tested three- and six-parameter models for the best fit to explain genetic control of FLw skewness in various upland parental combinations. Effects were first estimated with the three-parameter model and accepted if $P \geq 0.05$. The three-parameter model satisfactorily explained the genetic differences for FLw skewness in Fibermax 832 x Acala 1517-99 (Table 37). In this combination and environment, the variation among generation means was explained by the simple additive-dominance model, indicating that epistasis was not involved in the inheritance of the trait. The best approximation of additive and dominance effects can be obtained from the three-parameter additive-dominance model because these effects are unbiased due to the absence of epistasis (Hayman, 1958). For the remaining parental combinations, the six-parameter model was used to determine the type and magnitude of gene effects involved in the inheritance of FLw skewness.

In the near-long x near-long parental combinations for FLw skewness, Fibermax 832 x Acala 1517-99 in 2001 and 2002, 2002 being fit with the three-parameter model, and TAM 94L-25 x Acala 1517-99 in 2001 had negative additive effects, reemphasizing that P_2 had a higher FLw skewness mean than P_1 (Table 37). Dominance effects were negative for the parental combinations of Fibermax 832 x TAM 94L-25 in 2002 and TAM 94L-25 x TTU 202 in 2002. The negative dominance effect of Fibermax 832 x TAM 94L-25 and TAM 94L-25 x TTU 202 coincides with the F_1 means in relationship to their respective parents. While TAM 94L-25 x TTU 202 in 2002 had a negative dominance effect of -0.54, it had a positive effect of 0.53 in 2001. Negative additive x additive gene effect estimates were attained among Fibermax 832 x TAM 94L-25 in

Table 37. Estimates of gene effects for FLw skewness from the distribution data (per crossing combination and among all combinations) at College Station, TX in 2001 and 2002.

Parental Combinations	Year	Gene effects†					
		m	*a*	*d*	*aa*	*ad*	*dd*
Fibermax 832 x TAM 94L-25‡	2001	0.07	-0.02	0.01	-0.17**	0.02	-0.19
Fibermax 832 x TAM 94L-25‡	2002	0.04	-0.03	-0.49*	-0.12*	0.20*	0.18
TAM 94L-25 x TTU 202‡	2001	-0.21**	-0.03	0.53**	0.18**	0.12*	-0.53**
TAM 94L-25 x TTU 202‡	2002	-0.03	0.01	-0.54**	-0.03	-0.14	0.38*
Fibermax 832 x Acala 1517-99‡	2001	0.18**	-0.13**	-0.36	-0.21**	0.06	0.17
Fibermax 832 x Acala 1517-99‡§	2002	0.11*	-0.16**	-0.20	-	-	-
Fibermax 832 x TTU 202‡	2001/02	0.02	-0.05	0.10	-0.09**	0.08	-0.33**
TAM 94L-25 x Acala 1517-99‡	2001	0.07	-0.08**	0.18	-0.06	-0.03	-0.37**
TAM 94L-25 x Acala 1517-99‡	2002	0.22	-0.18	-0.61	-0.11	-0.19	0.21
Acala 1517-99 x TTU 202‡	2001	0.05	0.04	0.25	0.02	0.06	-0.29*
Acala 1517-99 x TTU 202‡	2002	0.32**	0.18	-0.46	-0.21**	-0.04	-0.03
TAM 94L-25 x Tamcot CAMD-E¶	2001	0.01	-0.14**	0.09	0.08	-0.06	-0.08
TAM 94L-25 x Tamcot CAMD-E¶	2002	0.27**	-0.35**	-0.73**	0.02	0.14*	0.41**
Fibermax 832 x Tamcot CAMD-E¶	2001	0.11*	-0.17**	0.22	-0.05	-0.03	-0.12
Fibermax 832 x Tamcot CAMD- E¶	2002	0.41**	-0.37**	-0.68**	-0.13**	0.18	0.30
Acala 1517-99 x Tamcot CAMD-E¶	2001	0.24**	-0.06	-0.21	-0.07	0.08	0.26
Acala 1517-99 x Tamcot CAMD-E¶	2002	0.48**	-0.17	0.61	-0.01	0.37	0.31
TTU 202 x Tamcot CAMD-E¶	2001	0.15**	-0.12**	-0.00	-0.06	-0.16*	-0.03
TTU 202 x Tamcot CAMD-E¶	2002	0.14	-0.36**	-0.07	0.14*	0.29**	-0.03
Among all combinations	2001	-0.03	-0.00	0.35**	-0.04*	-0.15**	-0.30**
Among all combinations	2002	0.26**	-0.21**	-0.68**	-0.10**	0.21**	0.27**

*, ** Significant at the 0.05 and 0.01 probability level on the basis of *t* test with n – 1 =5 degrees of freedom, respectively.

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

‡ Near-long x near-long parental combination.

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

¶ Near-long x short staple parental combination.

2001 and 2002, Fibermax 832 x Acala 1517-99 in 2001, Fibermax 832 x TTU 202 combined across years, and Acala 1517-99 x TTU 202 in 2002, suggesting both parents contributed alleles for FLw skewness. In 2001, a positive additive x additive effect was obtained in TAM 94L-25 x TTU 202 parental combination. Fibermax 832 x TAM 94L-25 in 2002 and TAM 94L-25 x TTU 202 in 2001 demonstrated additive x dominance effects. Negative dominance x dominance effects were attained in TAM 94L-25 x TTU 202 in 2001, Fibermax 832 x TTU 202 combined across years, TAM 94L-25 x Acala 1517-99 in 2001, and Acala 1517-99 x TTU 202 in 2001, while a positive effect was obtained in TAM 94L-25 x TTU in 2002. For TAM 94L-25 x TTU 202 in 2002, the dominance effect was negative while the dominance x dominance effect was positive. The contrasting direction of response between dominance and dominance x dominance gene effect estimates suggests negative duplicate epistasis (Kearsey and Pooni, 1996). The 2001 parental combination of TAM 94L-25 x TTU 202 had positive dominance and negative dominance x dominance gene effect estimates suggesting positive duplicate epistasis. Among the near-long x near-long parental combinations, additive effects accounted for a smaller portion of the observed variability than dominance effects. In general, dominance x dominance effects were larger than additive x additive, however, additive x additive effects were significant more frequently.

In the near-long x short staple parental combinations, the results of the three-parameter model analysis indicated that epistasis was present. In 2001 and 2002, additive effects were significant and negative for all parental combinations except Acala 1517-99 x Tamcot CAMD-E in 2001 and 2002 (Table 37). The negative additive effect once again only signifies that P_2 had a higher mean than P_1. TAM 94L-25 x Tamcot CAMD-E in 2002 and Fibermax 832 x Tamcot CAMD-E in 2002 had negative dominance effects with estimates of -0.73 and -0.68, respectively. A negative additive x additive effect was attained in Fibermax 832 x Tamcot CAMD-E in 2002, while a positive additive x additive effect was obtained in TTU 202 x Tamcot CAMD-E in 2002. TAM 94L-25 x Tamcot CAMD-E in 2002 and TTU 202 x Tamcot CAMD-E in 2002 had positive additive x dominance effects, while TTU 202 x Tamcot CAMD-E in 2001 had a negative additive x dominance effect. TAM 94L-25 x Tamcot CAMD-E in 2002 was the only near-long x short staple parental combination to display a dominance x dominance effect. Its negative dominance effect of -0.73 and positive dominance x dominance effect of 0.41, suggest negative duplicate epistasis (Kearsey and Pooni, 1996).

Generation means analysis indicated that genetic control for FLw skewness among near-long x short staple parental combinations was not as complex as among near-long x near-long parental combinations. Dominance effects were twice the magnitude of additive effects when significant, however, additive effects were significant more often because the generation means analysis produced smaller standard errors for additive than for dominance effects (data not shown). Among the non-allelic interactions, in general, dominance x dominance effects accounted for a larger portion of the observed variability than additive x additive, however, additive effects were significant more often. Among all combinations in 2001, dominance, additive x additive, additive x dominance, and dominance x dominance effects were significant (Table 37). Among all combinations in 2002, all gene effects were significant.

Variance components and broad- and narrow-sense heritability estimates for FLw skewness were calculated to determine the relative importance of the various determinants of the phenotype, the extent to which individuals' phenotypes are determined by their genotypes, and the extent to which phenotypes are determined by the alleles transmitted from the parents (Falconer and MacKay, 1996). For the 10 near-long x near-long parental combinations analyzed by individual years and 8 near-long x short staple, higher environmental variances were seen in 2002 than in 2001 (Table 38). In 2001, environmental variance among near-long x near-long parental combinations ranged from 0.50 to 1.04 with an average of 0.81, while the near-long x short staple parental combinations ranged from 0.63 to 1.18 with an average of 1.01. Environmental variance among the near-long x near-long combinations in 2002 ranged from 0.89 to 2.00 with an average of 1.41, while the near-long x short staple parental combinations in 2002 ranged from 1.81 to 2.64 with an average of 2.14. Except for the Fibermax 832 x Tamcot CAMD-E parental combination, additive variance was higher in 2002 than 2001. In 2001, the additive variance among the near-long x near-long parental combinations ranged from 0.00 to 0.64 with an average of 0.28, while the near-long x short staple combinations ranged from 0.04 to 0.81 with an average of 0.34. In 2002, the additive variance among the near-long x near-long parental combinations ranged from 0.58 to 2.49 with an average of 1.63, while the near-long x short staple parental combinations ranged from 0.00 to 3.86 with an average of 1.83. In 2001, the dominance variance

Table 38. Variance components and broad (H^2) and narrow (h^2) sense heritability estimates for FLw skewness for 10 parental combinations grown at College Station, TX in 2001 and 2002.

		Variance components†			Heritability estimates	
Parental Combinations	Year	σ^2_E	σ^2_A	σ^2_D	H^2	h^2
Fibermax 832 x TAM 94L-25‡	2001	0.74	-0.16	0.80	0.52	0.00 ± 0.06
Fibermax 832 x TAM 94L-25‡	2002	1.07	0.78	-0.10	0.42	0.42 ± 0.03
TAM 94L-25 x TTU 202‡	2001	0.74	0.38	0.62	0.57	0.22 ± 0.04
TAM 94L-25 x TTU 202‡	2002	0.89	0.58	0.68	0.43	0.37 ± 0.03
Fibermax 832 x Acala 1517-99‡	2001	1.01	0.64	0.63	0.56	0.28 ± 0.04
Fibermax 832 x Acala 1517-99‡	2002	1.50	2.43	-0.38	0.62	0.62 ± 0.03
Fibermax 832 x TTU 202‡	2001/02	1.42	-0.25	-0.06	0.00	0.00 ± 0.05
TAM 94L-25 x Acala 1517-99‡	2001	0.50	0.36	0.99	0.73	0.19 ± 0.04
TAM 94L-25 x Acala 1517-99‡	2002	1.59	1.86	0.00	0.54	0.54 ± 0.03
Acala 1517-99 x TTU 202‡	2001	1.04	-0.21	0.84	0.45	0.00 ± 0.05
Acala 1517-99 x TTU 202‡	2002	2.00	2.49	-0.16	0.55	0.55 ± 0.03
TAM 94L-25 x Tamcot CAMD-E§	2001	0.63	0.42	0.36	0.55	0.30 ± 0.04
TAM 94L-25 x Tamcot CAMD-E§	2002	1.88	1.75	-1.22	0.48	0.48 ± 0.03
Fibermax 832 x Tamcot CAMD-E§	2001	1.08	0.04	0.11	0.13	0.03 ± 0.05
Fibermax 832 x Tamcot CAMD- E§	2002	2.23	-0.81	-0.73	0.00	0.00 ± 0.10
Acala 1517-99 x Tamcot CAMD-E§	2001	1.18	0.81	-0.07	0.39	0.39 ± 0.03
Acala 1517-99 x Tamcot CAMD-E§	2002	2.64	3.86	-0.65	0.55	0.55 ± 0.02
TTU 202 x Tamcot CAMD-E§	2001	1.16	0.08	0.58	0.36	0.04 ± 0.05
TTU 202 x Tamcot CAMD-E§	2002	1.81	1.70	-0.72	0.48	0.48 ± 0.03
Among all combinations	2001	2.34	-0.05	-0.03	0.00	0.00 ± 0.01
Among all combinations	2002	4.21	0.09	0.33	0.09	0.02 ± 0.01

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

‡ Near-long x near-long parental combination.

§ Near-long x short staple parental combination.

among the near-long x near-long parental combinations ranged from 0.62 to 0.99 with an average of 0.78, while the near-long x short staple combinations ranged from 0.00 to 0.58 with an average of 0.265. In 2002, only TAM 94L-25 x TTU 202, among all parental combinations, attained a non-zero dominance variance of 0.68. Among all combinations in 2001, the environmental, additive, and dominance variance was 2.34, 0.00, and 0.00, respectively. Among all combinations in 2002, the environmental, additive, and dominance variance was 4.21, 0.09, and 0.33, respectively.

Among the near-long x near-long parental combinations, broad-sense heritability (H^2) averaged 0.57 in 2001, slightly higher than the 0.51 estimate in 2002 (Table 38). Generally, higher broad-sense heritability estimates were attained in 2001 because of the lower environmental variance. In 2002, a higher broad-sense heritability estimate was attained in Fibermax 832 x Acala 1517-99 and Acala 1517-99 x TTU 202 because of a larger total genetic variance. Narrow-sense heritability estimates (h^2) were lower in 2001 than 2002, averaging 0.14 and 0.50, respectively. For the one near-long parental combinations combined over years, Fibermax 832 x TTU 202 had no total genetic variance resulting in 0.00 broad- and narrow-sense heritability estimates.

Among the near-long x short staple parental combinations, broad-sense heritability averaged 0.36 and 0.38 in 2001 and 2002, respectively (Table 38). Higher broad-sense heritability estimates were attained in the year with a lower environmental variance or a greater total genetic variance. Narrow-sense heritability averaged 0.19 and 0.38 in 2001 and 2002, respectively. Higher narrow-sense heritability estimates were obtained in the year with greater additive variance. Of interest is the Fibermax 832 x

Tamcot CAMD-E parental combination having low and zero additive and dominance variance in 2001 and 2002, respectively.

Among all combinations in 2001, the broad- and narrow-sense heritability estimates were 0.00 and 0.00. Among all combinations in 2002, the broad- and narrow-sense heritability estimates were 0.09 and 0.02.

Summary and conclusions

Cotton is a natural product with lint characteristics determined by environmental and genetic factors. There is limited information available about the native fiber length distribution (i.e., on the seed), however it is believe that cotton possesses a normal fiber length distribution (probably is highly heritable) when bolls are hand picked cautiously and ginned carefully with a razor, tweezer, and aid of a microscope. Whatever the genetic determination of length distribution, the mechanical operations in harvesting, ginning, and textile manufacturing alter the distribution by breaking longer fibers into shorter ones (Anthony and Griffin, 2001a; Anthony and Griffin, 2001b; Robert et al., 2000). These successive stages of mechanical handling and processing incrementally but unavoidably inflict some fractures upon fibers being processed.

The degree of fiber breakage is dependent primarily upon fiber length, maturity, strength, and elongation. Longer fibers allow for a greater chance of tension forces being held at both ends, so they therefore have a higher probability of breakage than shorter fibers. Length distributions are also influenced by fiber maturity, and maturity is directly related to growing conditions. Immature fibers have underdeveloped, weak, thin secondary walls that are prone to break during mechanical processes. Fully mature fibers are less likely to be damaged or broken. The load, a specimen of a single fiber or a bundle of fibers in its axial direction, at which the specimen breaks provides a measure of fiber strength. Fiber elongation, the increase in length of fiber during tensile loading, is important in determining the processing propensity of fibers and the mechanical behavior of yarn. Two cottons with the same strength, but with different elongations will behave differently under mechanical stresses.

The environment influenced the magnitude of CEA and FLw kurtosis in 2001 and 2002, however, AFIS FLw skewness was less affect by the environmental of production. The mean responses of the generations indicated that samples had better fiber length distributions in 2002 than in 2001. Besides the environment, the distribution check for CEA came from Acala 1517-99 samples in 2002, which may have contributed to the better distribution shapes. In most parental combinations, significant generation x environment interactions were detected for CEA, FLw kurtosis, and FLw skewness, therefore parental combinations were analyzed within individual environments. The climatological conditions of the two years were normal in terms of temperature and rainfall. However, rainfall events at physiological maturity during 2001 extended the harvesting period and thus weathering of the fiber might have shortened the mean fiber length and increased the percentage of short fibers after processing (Hequet, 2004).

For most parental combinations, analyses of genetic effects indicated that a simple additive-dominance model did not account for most of the genetic variation for the three distribution data traits. Therefore, a six-parameter model fit the generation means indicating that epistatic effects were present and suggested that inheritance is complex such that multiple alleles interacted to affect the upland cotton fiber length distribution. Among the near-long x near-long parental combinations, dominance and dominance x dominance gene effects were larger in magnitude than additive or additive x additive. However, significant additive, dominance, additive x additive, and dominance x dominance gene effects were predominantly displayed among the three distribution traits. Among the near-long x short staple parental combinations, the prevalent gene effect varied depending upon the distribution trait. For CEA, all dominance effects were larger in magnitude than additive and significant more often. Among the non-allelic interactions for CEA, dominance x dominance effects accounted for a larger portion of the observed variability than additive x additive. For FLw kurtosis, all dominance effects were once again larger in magnitude than additive effects, and among the non-allelic interactions, in general, dominance x dominance effects accounted for a larger portion of the observed variability than additive x additive. However, additive x additive effects were significant more often because the generation means analysis produced larger standard errors for dominance x dominance than for additive x additive effects. For FLw skewness, negative additive gene effects were predominant.

For the parental combinations where distributions traits were controlled by additive gene action, simple selection in early segregating generations would be successful, while for those parental combinations exhibiting distribution traits controlled by non-additive gene action, selection in later generations could prove to be more effective. These results show that both the adequacy of certain modes of inheritance as well as the importance and significance of gene effects were dependent upon the particular parental combination and environment, stressing the importance of the appropriate selection of both parents and environment for the success of a cotton breeding program.

Several explanations of the inconsistent gene effects across populations in this study can be proposed. First, parents used in this study were from of vastly different genetic backgrounds. The dispersion of alleles in the parents, complete or partial, affects the magnitude and composition of the additive component. This might explain why additive genetic component of variance varied greatly and a definitive relationship between additive effects and additive genetic variance could not be detected. The mean and dominance components of the parents remain independent of gene dispersion. The dominance variance could be small due to its bi-directional nature and sometimes negative. The negative estimates of dominance variance seen in this study could have been due to sampling error and/or the fact that basic generations are inefficient when used for determining dominance variance. Two loci having an inter-allelic interaction will change the F_2 mean, the magnitude and direction of additive x additive and additive x dominance effects, and the magnitude and direction of the variances (Kearsey and Pooni, 1996). Higher order interactions, such as trigenic interactions, may be needed with enough generations to adequately understand the inheritance of cotton fiber length distributions.

Gene effects and variances for the three distribution traits were inherited quite differently in specific environments and specific parental combinations, suggesting environmentally specific mechanisms for fiber length distributions. The environmental variance affected the heritability estimates for the three distribution traits, indicating that extensive environmental replication is necessary to evaluate and select breeding material on the basis of fiber length parameters. For CEA and FLw skewness, as to whether additive or non-additive variance was the greater portion of genetic control depended upon the parental combination and year. For FLw kurtosis, additive variance was the predominant genetic factor among all parental combinations, regardless of the year.

The moderate to high broad-sense heritability estimates found in this study suggest that improvement for AFIS FLw distribution data can be realized through breeding if some of the genetic variation is additive in nature. Depending upon the parental combination and environment, the moderate values for narrow-sense heritability suggest that conventional pedigree and early generation selection methods should be effective for initial improvements in AFIS FLw distribution data in cotton. However, narrow-sense heritability estimates for CEA and FLw skewness were low, suggesting that the inheritance is complex and progress will be difficult.

Distributions of cotton fiber length are difficult to study. In addition to the natural variability of cotton fiber length, fiber weathering and mechanical handling and processing will further distort the native length and length distribution. Sound statistical procedures to analyze the distribution data are lacking. In this study, cross entropy, kurtosis, and skewness were evaluated as possible distribution measurements. In the opinion of the author, kurtosis offers the most potential until an ideal length distribution for cross entropy is agreed upon by plant breeders and the textile industry. Kurtosis is a measure of whether the distribution data are peaked or flat relative to a normal distribution. Positive kurtosis indicates a relatively peaked distribution with a large number of uniform fibers in a narrow length range. Calculating kurtosis was easier and less time-consuming than calculating cross entropy values. From the diallel data kurtosis separated the parents and in this study discriminated the different generations. Additive variance for FLw kurtosis was positive among all near-long x near-long parental combinations, unlike CEA and FLw skewness. Broad- and narrow-sense heritability estimates were moderate to high depending upon the parental combination and environment, suggesting that improvements can be realized. While kurtosis does not give us any indication of the mean length or percent of short fibers, it could be used in conjunction with these and other fiber quality measurements to select genotypes with superior fiber quality traits which in turn potentially would spin higher quality yarns.

CHAPTER X

SUMMARY AND CONCLUSIONS

Fiber length and length distribution measurements from four elite NLS upland genotypes, with diverse programmatic origins, and one short staple genotype were evaluated by diallel and generation means analyses. The fiber length diallel reported herein demonstrated that there is sufficient genetic variation among the parents for HVI and AFIS fiber length measurements to facilitate improvement through selection, but not for the percentage of short fibers. While Fibermax 832 exhibited the longest fibers for all length measurements, TAM 94L-25 had the highest GCA effects for UHM, FLw, FLn, and Uqlw, thus would be the best parent to be used in parental combinations to improve fiber length. When comparing the HVI UHM with AFIS fiber length measurements of Uqlw, FLw, and FLn, Uqlw most closely followed the UHM length mean separation order and magnitude of difference among the parents. FLw attained the same rank as UHM, but magnitude differed slightly more.

In the generation means analysis for FLw and FLn, parental combinations were analyzed generally within individual environments due to significant G x E. For Uqlw, more parental combinations were analyzed across environments. For FLw, FLn, and Uqlw, analyses of genetic effects indicated generally that a simple additive-dominance model did not account for most of the genetic variation. Therefore, generation means fit a six-parameter model indicating that epistatic effects were present and suggested that inheritance is complex such that multiple alleles interacted to affect upland cotton fiber length.

Examination of the frequency distributions of individual plant values of each parental combination indicated that the segregating populations followed a normal distribution, suggesting that FLw, FLn, and Uqlw were quantitatively inherited. Transgressive segregation was visible in near-long x near-long and near-long x short staple parental combinations. A higher percent of transgressive segregation appeared in the BC_1P_1 generation than in other segregating populations for all three AFIS length measurements. The segregating populations in this study had a higher percentage of transgressive segregates for Uqlw and the lowest percentage for FLn. The presence of transgressive segregation in the segregating populations of these near-long x near-long combinations, although at a low frequency, suggests that the parental material chosen for this study contained different length alleles, thus suggesting that breeders could make further improvements for upland cotton fiber length among these near-long staple parental genotypes if the appropriate breeding method was implemented and large enough populations were grown.

Among the near-long x near-long parental combinations, few significant gene effects were detected for FLw and Uqlw, possibly indicating a high degree of dispersion of alleles increasing among parents fiber length as measured by these measurements. Significant additive x additive effects for FLn were displayed. Dominance effects generally were larger in magnitude than additive effects, contradicting the results of the fiber length diallel. In comparing the relative magnitude of additive x additive to dominance x dominance effects, it depended on the parental combination and environment as to which one was greater.

Among the near-long x short staple parental combinations, significant gene effects were numerous. Additive gene effects for FLw and Uqlw were significant for all parental combinations, and in five of the eight parental combinations and environments were significant for FLn. Significance of additive x additive effects for FLw and FLn were numerous. In addition, several significant dominance and dominance x dominance effects were detected among these parents for FLn, suggesting that the genetic control of this measurement is the most complex.

The environmental variance for all three measurements was moderate to high. Among the near-long x near-long parental combinations, genetic control for all three AFIS measurements contained additive and non-additive genetic variance, but the greater portion was primarily non-additive for FLw, dependant upon the parental combination and environment for FLn, and generally additive for Uqlw. Among the near-long x short staple parental combinations, the predominant portion was additive for FLw, FLn, and Uqlw.

The combining ability and mode of gene action and inheritance of three distribution statistical parameters, cross entropy, kurtosis, and skewness, were evaluated. Significant variation for FLw distribution data measurements can be detected within the five parental genotypes. The diallel analysis demonstrated that there was sufficient genetic variation in these measurements to facilitate trait improvement through selection. Environmental interactions indicate that multiple years and environments will be necessary to breed for improved length distributions. The parents, within this study, with the greatest potential to improve fiber length distributions were Tamcot CAMD-E, the short staple genotype, followed by Acala 1517-99. The parent with the least potential to improve fiber length distributions was TAM 94L-25, the parent with the most potential to increase fiber length. Currently, most cotton programs are focused on breeding for longer fibers alone because the current premium and discount schedule rewards this type of cotton. However, long UHM length genotypes with an undesirable length distribution reward the producers but present challenges to spinners. Spinners are concerned with the fiber quality impact on costly disruptions in yarn-spinning processes and with the presence of significant defects in yarn and finished fabrics.

In the generation means analysis for FLw distribution measurements, parental combinations generally were analyzed within individual environments. For CEA, FLwKurt, and FLwSkew, analyses of genetic effects indicated that a simple additive-dominance model would not account for most of the genetic variation. Therefore, generation means fit a six-parameter model indicating that epistatic effects were present and suggested that inheritance is complex such that multiple alleles interacted to affect upland cotton fiber length distribution. Among the near-long x near-long parental combinations, dominance and dominance x dominance gene effects were larger in magnitude than additive or additive x additive. However, significant additive, dominance, additive x additive, and dominance x dominance gene effects were predominantly displayed among the three distribution measurements. Among the near-long x short staple parental combinations, the prevalent gene effect varied depending upon the distribution measurement.

Environmental variance was high for the three distribution measurements, once again indicating that extensive environmental replication is necessary to evaluate and select breeding material on the basis of fiber length parameters.

The moderate broad-sense heritability estimates found in this study for fiber length and length distribution measurements suggest that improvement can be realized if some of the genetic variation was additive in nature. Depending upon the parental combination and environment, the sometimes moderate to high values for narrow-sense heritability found in this study suggest that conventional pedigree and early generation selection methods should be effective for initial improvements in cotton. However, most of the narrow-sense heritability estimates in this study for fiber length and length distribution were low, suggesting that the inheritance is complex and that selection of individual plants in an F_2 population will not be as simple as indicated by the broad-sense heritability estimate.

Gene effects and variances for the three AFIS fiber length and distribution measurements were inherited quite differently in specific environments and specific parental combinations, suggesting environmentally specific mechanisms for fiber length and its distribution. The results showed that both the adequacy of certain modes of inheritance as well as the importance and significance of gene effects were dependent upon the particular parental combination and environment, stressing the importance of the appropriate selection of both parents and environment for the success of a cotton breeding program.

Further research with fiber length distribution needs to occur. A software program is needed to remove the trivial distribution information and to generate only the relevant data and statistics. An area for further study is what will serve as the ideal cotton fiber length distribution. No published material exists identifying this optimal length distribution. Important questions such as, should the distribution be artificially fabricated? How many samples or environments will be appropriate? CEA and FlwKurt could be potential measurements used to discriminate fiber length distributions of different genotypes, but only upon further testing and substantiation with future experimental data collection.

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APPENDIX

ACRONYMS

AFIS –	Advance fiber information system
CCC –	Commodity credit corporation
CEA -	Cross entropy distribution data of Acala 1517-99 hand harvested plants averaged across 2002 as the check
CEB –	Cross entropy distribution data of Tamcot CAMD-E hand harvested plants averaged across 2002 as the check
CEC –	Cross entropy distribution data of Acala 1517-99 combined over 2 environments and machine harvested at two locations as the check
CP –	Coefficient of parentage
FLn –	Mean fiber length by number (AFIS)
FLw –	Mean fiber length by weight (AFIS)
FLwKurt –	Mean fiber length by weight kurtosis
FLwSkew –	Mean fiber length by weight skewness
GCA –	General combining ability
GxE –	Genotype x environment interaction
HVI –	High volume instrumentation
ML –	Mean length
NLS –	Near-long staple
SCA –	Specific combining ability
SFC –	Short fiber content
SFCn –	Short fiber content by number (AFIS)
SFCw –	Short fiber content by weight (AFIS)

UHM – Upper-half mean fiber length (HVI)

UQL – Upper-quartile length

Uqlw – Upper-quartile length by weight (AFIS)

USDA – United States Department of Agriculture

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