DIALLEL ANALYSIS AND HERITABILITY ESTIMATES OF FIBER TRAITS FOR ELS, *GOSSYPIUM HIRSUTUM* L., PROGENY

A Thesis

by

GREGORY LAWRENCE BERGER

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

MASTER OF SCIENCE

May 2009

Major Subject: Plant Breeding

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Approved by:

Chair of Committee,	Steve Hague
Committee Members,	C. Wayne Smith
	Hongbin Zhang
	Lori Hinze
Head of Department,	David Baltensperger

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ABSTRACT

Diallel Analysis and Heritability Estimates of Fiber Traits for ELS, *Gossypium hirsutum* L., Progeny.

(May 2009)

Gregory Lawrence Berger, B.S., Texas A&M University

Chair of Advisory Committee: Dr. Steve Hague

With a demand for high-quality cotton fiber in international markets, improvement of fiber quality in U.S. grown commercial cultivars is necessary. Smith, Hague, Thaxton, and Jones developed a group of experimental lines in 2008 that produced extra-long staple fiber (>35.6 mm). This study determined general combining ability (GCA), and specific combining ability (SCA) of four experimental ELS lines and four commercial cultivars utilizing biplot and conventional diallel analysis, determined performance of F_2 progeny, calculated broad-sense (H^2) heritability estimates for F_2 progeny, and verified the ability of selected parental combinations to produce variable segregating populations with variability of fiber traits. Initial crosses were made in 2007, with additional crosses being made in the field and in a greenhouse in 2008. F_1 progeny and parents were grown in a replicated trial near College Station, TX, in 2007 and 2008. F_2 progeny lines and parents were grown in replicated trials at two locations in 2008. Due to a significant GxY interaction for all F_1 fiber traits, data were reported by years. Experimental ELS lines showed positive GCA effects for fiber length, strength, and

length uniformity, while the majority of commercial lines showed negative effects. These findings suggest experimental ELS lines contain alleles for fiber length and strength not present in this particular set of commercial cultivars. Experimental ELS lines exhibited negative GCA effects for lint percent, which suggests further selection is needed for these lines to be commercially competitive. Performances of F_2 lines suggest differences in fiber traits are predominantly due to additive gene action. Furthermore, data suggests alleles for fiber length and strength is present in the experimental ELS lines not present in the commercial cultivars. F_2 progeny exhibited moderate heritability for all fiber traits. Sufficient variability exists within selected F_2 progeny to select for phenotypes exhibiting improved fiber quality over commercial cultivar potential with similar agronomic qualities of commercial cultivars. The ELS lines are a useful source of germplasm for plant breeders looking to improve fiber qualities in their programs.

DEDICATION

This thesis is dedicated to my parents, Larry and Patricia Berger, whose help, love, and guidance throughout the years has helped me to achieve all of my goals. Without their support, I would have not been able to be who I am today.

I would also like to dedicate this thesis to my fiancée, Bethany Hopkins, whose undying love and support have helped me throughout the past five years. Without you I would not be where I am today.

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I would also like to take this time to thank Nino Brown, Dawn Deno, fellow graduate students, and student workers at the Cotton Improvement Lab who have helped me to complete this project. Without their support and assistance, I would have never been able to complete this research.

Thanks to Cotton Incorporated and Texas Department of Agriculture for financial support. Without their funding, this project would not have been possible.

Finally, thanks to my mother and father for their encouragement and to my fiancée for her patience, love, and support.

ACRONYMS

AFIS - Advanced fiber information system

CCC – Commodity credit corporation

ELS – Extra long staple

GCA – General combining ability

GCAxY – General Combining ability x year interaction

GxE – Genotype x environment interaction

GxY – Genotype x year interaction

HVI – High volume instrumentation

LSD – Least significant difference

SCA – Specific combining ability

SCAxY – Specific combining ability x year interaction

UHM – Upper half mean

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CHAPTER I

INTRODUCTION

Improvement of fiber quality is necessary for American grown cotton to stay competitive in international markets. In 2007 U.S. cotton exports reached over 3.4 million bales (National Cotton Council, 2008). With high quality cotton fibers being produced in other countries, it is necessary for breeders in the United States to look for different methods of improving cultivars. In turn, advancements in quality of cotton grown by U.S. growers will keep us competitive in the world market. Breeders also should be aware of those cotton fiber qualities needed by textile mills to operate efficiently. Many plant breeding methods have been utilized to improve fiber quality in Upland type cotton cultivars, (*Gossypium hirsutum* L.), while maintaining or improving agronomic qualities. One such method has been diallel mating systems for identification of superior parental combinations of cotton cultivars that lead to the improvement of fiber quality. This research project uses such a method to explore the value of ELS upland cotton as parental material for cotton plant breeders.

This thesis follows the style of Crop Science.

Objectives

Objectives of this research project are to:

1. Utilize a diallel mating system involving four commercial cultivars, 'Deltapine 50' (PI 529566), 'Deltapine 491' (PI 618609), 'FiberMax 832' (PI 603955), and 'Tamcot CAMD-E' (PI 529633), and four experimental lines, Hil-A-106-8, Hil B-147-21, Hil B-182-39, and Hil C-155-22 to estimate general combining ability (GCA) and specific combining ability (SCA) for fiber properties resulting from F_1 progeny, and parents.
2. Bilpot analysis of diallel data.
3. Determine heritability (H^2) for fiber properties from the F_2 population at Weslaco, TX, and College Station, TX in 2008.
4. Determine variance within and among genotypes from F_2 populations from one year at two locations.

CHAPTER II

REVIEW OF LITERATURE

Fiber testing and environmental effect

Development of high volume instrumentation (HVI) and the advanced fiber information system (AFIS) provided the cotton industry an objective system of evaluating fiber properties. This technology allowed breeders to identify genotypes with superior fiber quality traits and the universal classification of cotton fibers for marketing purposes. HVI analysis of cotton fiber includes length, length uniformity, strength, micronaire, trash content, and color. AFIS provides information about the complete array of fiber length, diameter distribution, trash and nep content, and fineness and maturity measurements (Calhoun et. el., 1997).

Research into HVI systems began in the late 1960's (Ramey, 1999). HVI system research has been an ongoing process, and led to the Commodity Credit Corporation (CCC) mandating that fiber strength testing for loan purposes beginning with the 1991 crop (Ramey, 1999). This mandate was the first step towards today's USDA classification of cotton by HVI (Ramey, 1999).

Fiber length

The HVI system reports fiber length as the mean length of the longest one-half of fibers (upper half mean length) to the nearest one-hundredth of an inch (Anthony, 2000). For commercial upland cultivars, four classes were established as short (< 21.1 mm), medium (22.1 – 24.9 mm), medium-long (25.9 – 27.9 mm), and long (29.0 – 34.0 mm)

(Bradow and Davidonis, 2000). Length uniformity is the ratio of the mean length of fibers to the upper mean half and expressed as a percentage (Anthony, 2000).

Fiber length elongation takes place in about the first 20 days after bloom (Walhood and Addicott, 1968). During this time, both genetic and environmental factors greatly influence fiber length. According to Bradow and Davidonis (2000), it is important to understand the concepts and limitations of fiber length measuring methodology in order to separate the strong genetic component of fiber length from environmental components. Genetic improvement of fiber length may not be realized if the response of the new genotypes to the growth environment hinders the full realization of the increased genetic potential (Bradow and Davidonis, 2000). Environmental effects that interact with allelic actions of a genotype include temperature, water, light, and mineral nutrition (Bradow and Davidonis, 2000). High and low temperature and drought stress can substantially reduce fiber length and uniformity, especially when these conditions occur during fiber elongation (Ramey, 1999, Walhood and Addicott, 1968).

Hsieh (2000) states that fiber length, fineness, length distribution, and strength are the most important fiber quality factors for textile processing. Hsieh (2000) further states the importance of each fiber quality varies according to the type of yarn spinning method, such as ring, rotor, and air jet. Fiber length is important for both ring and rotor spinning (Bradow and Davidonis, 2000, Felker, 2001). Fibers shorter than the average length contribute to poorly spun yarns with excessive hairiness, low uniformity, and low strength (Hsieh, 2000). According to Felker (2001), a upper half mean (UHM) length of 35.0 mm is desired for optimal ring and air-jet spinning while a length of 34.0 mm is

desirable for open-end spinning. Traditionally low-quality cotton, which is traded at a discount, is purchased and mixed with higher-quality cottons to reach a desirable quality level at a lower cost (El Mogahzy, 2000). This procedure, however, limits utility of blended cotton. Newer technologies, such as air-jet spinning, require longer fibers than do older and slower technologies in order to produce acceptable 100 percent cotton yarns (El Mogahzy, 2000).

Fiber strength

The HVI system measures fiber strength by utilizing the tuft of fiber used for fiber length measurement (Anthony, 2000). Fiber strength is commonly reported as grams of force per tex (g/tex) and kilonewton meter per kilogram (kN m kg^{-1}) (Anthony, 2000). The process requires placing the tuft of fiber in two clamps spaced 3.2 mm, 1/8 inches, apart (Ramey, 1999). Force is applied until the point of failure (Ramey, 1999). The amount of force needed to break the beard is recorded (Ramey, 1999). Mass of the fibers is calculated based upon the amount of fiber in the beard in the space between clamps (Ramey, 1999). Tenacity, grams force per tex (g/tex), is calculated from the amount of force needed to break the estimated mass (Ramey, 1999). The strength measurement is the average of the beards from each side of the sample (Ramey, 1999). Strength values can be converted to kN m kg^{-1} by multiplying g/tex by 9.807. Strength for upland cotton cultivars ranges from 226 to 314 kN m kg^{-1} (Cotton Incorporated, 2008). Average fiber strength classes in kN m kg^{-1} are: very weak (226 and below), intermediate (235 to 245), average (255 to 284), strong (284 to 294) very strong (304 and above) (Ramey, 1999). For 2008, the CCC loan schedule reports premiums for

upland cultivars range from 289 to 319 kN m kg^{-1} and above (National Cotton Council, 2008). Strengths below 250 kN m kg^{-1} are subject to discounted rates while strengths ranging from 250 to 289 kN m kg^{-1} are neither subject to discounts nor premiums (National Cotton Council, 2008).

Secondary cell wall thickening begins approximately 20 days after bloom and continues for 20-30 days (Walhood and Addicott, 1968). During this period, daily deposition of cellulose occurs and fiber strength is determined (Walhood and Addicott, 1968). The strength of cotton fibers is attributed to the rigidity of cellulosic chains, the highly fibrillar and crystalline structure, and extensive intermolecular and intramolecular hydrogen bonding (Hsieh, 2000). According to Walhood and Addicott (1968), the manner of cellulose deposition is controlled genetically while the environment determines the thickness of each layer. In a review of literature, Bradow and Davidonis (2000) detail numerous studies conducted to determine genotypic and environmental effect on fiber strength. Although strength is largely a function of genotype, both environment and response of a genotype to its environment are important in the determination of fiber strength (Sasser and Shane, 1996). Yet the effects of GxE interactions for fiber strength are not as well described as those interactions that determine fiber length (Bradow and Davidonis, 2000).

Fiber strength is important to the production of quality yarns and directly related to the strength of the yarn. Production of medium to fine yarns on rotor spinning processes requires higher levels of strength than other spinning methods (El Mogahzy, 2000). Perkins, Ethridge, and Bagg (1984) described the relationship between fiber

strength and yarn strength as significant. Cotton fibers with high strength are less susceptible to damage from the rigorous cleaning treatments (Perkins, Ethridge, and Bagg, 1984). These treatments are often necessary for the removal of foreign material, and to obtain the degree of opened, or fiber-to-fiber separation necessary for processing raw cotton into yarn (Perkins, Ethridge, and Bragg, 1984).

Micronaire, maturity, and fineness

Micronaire is a measurement of fiber diameter, or fineness, and thickness of the secondary wall (Weber and Backe, 1994). It is measured by passing air compressed of a standard volume through a sample of standard weight and volume (Anthony, 2000). The volume of airflow through the sample is reported as simple micronaire units. Acceptable micronaire measurements range from 3.5 to 4.9 as determined by the 2008 CCC loan schedule (National Cotton Council, 2008). Premiums values fall between 3.7 and 4.2 (National Cotton Council, 2008). Values falling below 3.5 or above 4.9 this range are subject to severe discounts (National Cotton Council, 2008). Causes of aberrant micronaire are strongly dependent upon genotype and interactions with growing environment and harvest practices.

Fiber maturity is an important consideration for textile producers. Wakelyn et al. (2007) state that knowledge of the maturity of cotton fiber is needed to predict the ultimate quality of the product as related to dyeability and ease of processing. Immature fibers tend to dye unevenly which results in poor quality finished textile product (Wakelyn et al., 2007). Immature fibers also result in wastage because of spinning and weaving breaks and faults (Wakelyn et al., 2007).

Fiber fineness, which is a measure of fiber diameter, has been defined by many different parameters (Wakelyn et al., 2007). According to Wakelyn et al. (2007), of the possible fineness parameters, mass per unit of length is the measurement most frequently used by spinners. Knowledge of mass per unit of length allows for selection of fibers based on the minimum numbers of fibers required to spin a certain size yarn (Wakelyn et al., 2007). Fineness of the yarn is related directly to the fineness of the individual cotton fibers (Wakelyn et al., 2007).

Trash content and color

Non-fiber plant parts from cotton and weeds, seed coat fragments, neps, and motes are examples of trash contaminants. The size and amount of trash present in samples have a direct effect on how cotton is processed in the textile mills (Werber and Backe, 1994). Trash content is measured using a video-based trashmeter, which scans the surface of the fiber sample (Ramey, 1999). The percent area of the fiber sample that is darker than a pre-determined threshold is reported as the amount of trash per sample (Ramey, 1999). Measurements are reported as the percentage of sample surface covered by non-lint particles, ranging from 0.1 to a maximum of less than 5.0 (Anthony, 2000). The average trash meter reading for upland cultivars are: strict middling (0.1), middling (0.2), strict low middling (0.4), low middling (0.7), strict good ordinary (1.1), and good ordinary (1.5) (Anthony, 2000). Smaller trash particles are harder to remove from samples than larger particles, and cause unevenness and imperfections in the yarn (Werber and Backe, 1994). In addition, shape and composition of the trash particle can

affect processing. Among the worst types of contaminants include pieces of plastic shopping bags, grass leaves, and even human hair.

In the HVI system, the colorimeter is used to determine the color of samples (Ramey, 1999). The surface of a sample being measured is pressed against an instrument window, illuminated, and the amount of reflected light is measured (Ramey, 1999). HVI color determinations are reported in terms of grayness, measured as Rd, and yellowness, measured as +b (Anthony, 2000). Grayness, percent reflectance, which indicates the lightness or darkness of a sample, ranges in values from 48 to 82 (Anthony, 2000). Yellowness, which describes the amount of yellow coloration in the sample, ranges in values from 5.0 to 17.0 (Anthony, 2000).

Premiums and discounts for staple length, color and trash content determined by the CCC loan schedule are determined utilizing a base of staple length of 1 1/16 inches, strict low middling of 41, and reflectance of 4 (National Cotton Council, 2008).

Breeding tools

Diallel analysis

Use of diallel mating systems for the identification of improved traits in cotton and other crops is well documented (Al-Rawi and Kohel, 1969,1970; A. Topal et. al 2004; Basal and Turgut 2003; Cheatam et al. 2003; Griffing, 1956; Jensen, 1970; Marani, 1967; Ragsdale and Smith, 2007; and Verhalen and Murray, 1967). Diallel mating systems have been used in cotton studies to evaluate yield and agronomic characters, within-boll seed yield components, and various fiber properties and quality parameters (Al-Rawi, 1969, 1970; Basal and Turgut 2003; Ragsdale and Smith, 2007;

Verhalen and Murray, 1967). There are two types of designs designated as Design I (Nested Design), and Design II (Factorial Design) utilized in diallel mating systems (Fehr, 1991). In a nested design, each male plant is mated to an equal number of females, and a different number of female parents are used for each male. In the factorial design, each male plant is mated to each female, but male parents are not crossed to each other, and female plants are not crossed to each other. The experimental design determines which diallel design is used for the experiment. These types of diallel designs are used for the analysis of general combining ability (GCA), and specific combining ability (SCA) resulting from the crosses made utilizing parental lines. The GCA effects reflect the parent's genetic ability to influence all of its progeny for a specific trait, which is an expression of additive genetic effects (Griffing, 1956). Interpreting the GCA effect data allows for the selection of the parent that is the best general combiner. The SCA effects represent non-additive genetic effects such intra-allelic (dominance) or inter- allelic (epistasis) interactions, multiplicative gene action, which can be viewed as a departure from performance, can be predicted in simple additive models (Henderson, 1952, Griffing, 1956). The SCA effect data can determine parents that provide the best specific combination for a given trait. In cotton, these estimates identify the best general combiner for the parental lines, and the best specific combiner resulting from the crosses for fiber length, length uniformity, fiber strength, micronaire, and elongation. In crops such as cotton, general combining ability is more easily utilized than specific combing ability for a program that is selecting for a pure-line variety (Varhalen and Murray, 1967).

Issues arise when determining a method to analyze diallel-mating systems. Models proposed by Hayman (1954, 1958), Griffing (1956), and Gardener and Eberhart (1966) set forth guidelines for the analysis of general and specific combining abilities under different models and methods. A diallel crossing system is one in which a set of p inbred lines is selected and crosses among the lines are made giving rise to a maximum of p^2 combinations (Griffing 1956). Griffing (1956) stated that diallel crossing techniques might vary depending upon whether or not parental inbreds or reciprocal F_1's are included or not. From this, four possible experimental methods were devised. These experimental methods include: (1) parents, one set of F_1's and reciprocal $F_{1's}$ are included (all p^2 combinations); (2) parents and one set of F_1's are included but reciprocal F_1's are not ($1/2p(p+1)$ combinations); (3) one set of F_1's and reciprocals are included but not the parents (p (p-1) combinations); and (4) one set of F_1's but neither parents nor reciprocal F_1's is included ($1/2p(p$-1) combinations, each form using a different form of analyses (Griffing, 1956). Gardner and Eberhart (1966), suggested models similar to models proposed by Hayman (1954), and Griffing (1956).

Griffing (1956) states that it is necessary to distinguish between situations in which lines have be selected and cannot be distinguished as a random sample from any population (fixed effects), and situations in which parental line or experimental material are assumed to be a random sample from a population about which inferences are to be made (random effects). According to Griffing (1956) these assumptions need to be integrated with a more general set of assumptions, which are made about the elements in the mathematical model for a randomized-block design. To incorporate these

assumptions we must first be familiar with the assumptions that are to be considered with regard to the genotypic and block effects. These assumptions are 1) genotypic and block effects are constants, 2) genotypic effects are random variables and the block effects are constants, 3) genotypic effects are constants and block effects are random variables, and 4) genotypic and block effects are both random variables (Griffing, 1956). The first set of assumptions describes a model in which all effects, except the error, are regarded as constants, while the last set of assumptions describes a model in which all effects except μ are random variables (Griffing, 1956). These situations are referred to as model I (fixed effects), and model II (random effects) respectively (Griffing, 1956). Assumptions two and three are used to describe mixed models that are not pertinent to the analysis of this projects data set. Baker (1978) states that from a statistical point of view one of the key issues is determining whether a model with fixed or random genotypic effects is used. Both models I and II have unique estimation problems and different test of hypotheses regarding combining ability effects (Griffing, 1956).

The primary objective of Model I is to compare combining abilities of parents when parents are used as testers to determine the best combination for the trait of interest (Griffing, 1956). When estimating combining ability effects and computing appropriate standard errors, it is necessary to assume only that e_{ijkl} are normally and independently distributed with mean zero and variance σ_e^2 (Griffing, 1956). Since inferences are not made about individuals, but about the parameters in the parental population in model II; estimations are based upon the genetic and environmental components of the complex population variance (Griffing, 1956). In this case, it is assumed that the effects in the

model (except μ) are normally and independently distributed with mean zero and variance σ_θ^2, where θ = b, g, s, or r (Griffing, 1956). Griffing (1956) states that variance component estimates for any diallel cross method can be obtained by equating the observed to the expected mean squares in the analysis of variance. The standard errors for the variance components can be calculated from the variances of the appropriate mean squares (Griffing, 1956).

Interpretation of both general and specific combining effects and associated variances is dependent on a number of factors. These include the diallel method, assumptions regarding the experimental material, and the conditions imposed in the combining ability effects (Griffing, 1956). When model I is used, equations for estimating combining ability effects are dependent on the method, which will yield unbiased estimates of the effects only when specified constraints are imposed on the elements (Griffing, 1956). Inferences made in model II are dependent on the diallel method being used and on knowledge of the nature of the population from which the lines came from (Griffing, 1956).

Diallel computer programs

Computer programs with different methods have been developed for the analysis of diallel models and methods originally proposed by Griffing, and later Gardener and Eberhart (Burrow and. Coors, 1994, Zhang et al., 1997, 2005, Agronomix Software inc., 2007). The diallel analysis function featured in Agrobase Gen. II software is based on models described by Griffing (Agronomix Software inc., 2007). Using the linear analysis model with either random or fixed effects, Agrobase Gen. II can analyze all four

methods described by Griffing (Agronomix Software inc., 2007). Output from the analysis provides the user with Parent x Parent (PxP) table of means, ANOVA's for both fixed effects and combining abilities, table of general combining ability effects, matrix of specific combining ability effects, and a table of standard errors (Agronomix Software inc., 2007). The sources of variation G_i, and G_i-G_j standard error's can be used to calculate a Fischer's LSD in order to separate GCA's effects from zero, and determine if two GCA are different (Agronomix Software inc., 2007). While the sources of variation S_{ij}, S_{ij}-S_{ik}, and S_{ij}-S_{kl} can be used to calculate a Fischer's LSD to determine if SCA effects are different from zero, SCA with a common parent are different, and SCA without a common parent are different (Agronomix Software inc., 2007).

Biplot analysis

The use of biplot approach for analysis of diallel data has been well described (Yan and Hunt, 2002, Yan and Kang, 2003). According to Yan and Hunt (2002), the biplot approach of diallel analysis allows the visualization of: 1) the GCA effect of each parent; 2) the SCA effect of each parent (not cross); 3) the best crosses; 4) the best testers; 5) the heterotic groups; and genetic constitutions of parents with regard to the trait under investigation. The model proposed by Yan and Kang (2003) for biplot analysis of diallel data is as follows:

$$\hat{Y}_{ij} - \mu - \beta_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij}$$

where $\hat{Y}_{ij}$ expected value of the cross between entry i and tester j; μ is the grand mean; β_j is the main effect of tester j; g_{il} and e_{lj} are called the primary effects for entry i and tester j, and ε_{ij} is the residue not explained by the primary or secondary effects (Yan and Kang,

2003). Construction of biplot is based upon the plotting of g_{i1} against g_{i2} and e_{1j} against e_{2j} in a single scatter plot (Yan and Kang, 2003). Aside from the visualizations that biplots provide, the analysis explains the total variation, as a sum of PC1 and PC2, which in a conventional analysis, would otherwise be partitioned into the GCA effects of the parents and SCA effects of the crosses (Yan and Kang, 2003).

In the average tester coordinate (ATC) view, the smaller circle represents an average tester (Yan and Hunt, 2000). The average tester can be defined as the average PC1 and PC2 values of all testers (Yan and Kang, 2003). The ATC abscissa, or the average tester axis, is the line passing through the biplot origin and average tester, while the line passing through the origin and perpendicular to the ATC abscissa is called the ATC ordinate, or average tester ordinate (Yan and Kang, 2003). Given that GCA and SCA are orthogonal, biplots display both GCA and SCA, and the projections of the entries onto the ATC abscissa approximate their GCA effects, projections of the entries onto the ATC ordinate approximate their SCA effects (Yan and Hunt, 2000). The SCA of the entries represents the ability of any given tester to produce superior combinations with some, but not all of the testers (Yan and Kang, 2003). All interpretation of biplots follows the guidelines set forth by Yan and Hunt (2000), and Yan and Kang (2003).

Heritability estimates

Heritability can be described in both the broad sense, and narrow sense (Dudley and Moll 1969, Falconer and Mackay 1996, Fehr 1991). Broad sense heritability (H^2) describes the ratio of total genetic variance to phenotypic variance σ^2_g/σ^2_{ph} (Dudley and Moll 1969, Fehr 1991). According to Fehr (1991), phenotypic variance can be

subdivided into components of variance attributable to factors that cause differences in the performance among individuals, which can be expressed as:

$$\sigma^2_{ph} = \sigma^2_e + \sigma^2_{ge} + \sigma^2_g.$$

The variance components σ^2_e,σ^2_{ge}, and σ^2_g are described as follows. Experimental error, or environmental variance (σ^2_e) is a measure of difference among phenotypes caused by the failure to treat each genotype exactly alike (Fehr, 1991). The term σ^2_{ge} is the sum of genotype x location (σ^2_{gl}), GxY (σ^2_{gy}), and GxY x location (σ^2_{gly}) interaction that represents the differences among phenotypes caused by GxE interaction (Fehr, 1991). Genotypic variance (σ^2_g) is the sum of the additive (σ^2_A), dominance (σ^2_D), and epistatic (σ^2_I) variance that expresses the variation caused by genetic differences among individuals (Fehr, 1991).

Broad-sense heritability (H^2) can also be calculated based on the variance of the F_2 combination (V_{F2}) and the variance of the parents used to create the combination (V_{P1}, and V_{P2}) as described by Acquaah (2007):

$$H^2 = [V_{F2} - ½(V_{P1} + V_{P2})]/V_{F2}$$

Narrow sense heritability (h^2) describes the ratio of additive genetic variance to phenotypic variance, and expressed as, σ^2_A/σ^2_{ph} (Dudley and Moll 1969, Fehr 1991). Calculation of narrow sense heritability requires an estimate of the additive genetic variance in a population obtained from the analysis of the diallel design used in the experiment (Fehr, 1991). The variance component method of heritability estimation is based on the variance components obtained from the analysis of variance of the diallel (Fehr, 1991). This method can be used to calculate heritability based upon a single plant,

a plot, or an entry mean basis (Fehr, 1991). Heritability based upon an entry mean basis is as follows:

$$h^2 = \sigma^2 / (\sigma^2_e/rt + \sigma^2_{ge}/t + \sigma^2_g)$$

Heritability estimates have been used extensively in plant breeding (Al-Rawi and Kohel 1970, Dudley and Moll 1969, Falconer and Mckay 1991, Fehr 1991, Henning and Townsend 2005, May 2000, Murray and Verhalen 1969, Nguyen and Sleper 1983, Ulloa 2006, Wilson and Wilson 1975). Broad-sense heritability estimates allow breeders to determine the proportion of total genotypic variance, which includes additive, dominance, and epistasis variance, to the phenotypic variance, while narrow-sense estimates allow breeders to determine the importance of additive genetic variance which is of particular importance to inbred cultivars like cotton (May, 2000, Fehr, 1991). Fehr (1991) states that narrow-sense heritability estimates are particularly important when breeders are predicting gain expected from selection for a character. Single-plant selections, frequently used in cotton breeding programs, may be effective for a trait with high heritability but ineffective for a trait with low heritability (Fehr, 1991).

In cotton, heritability estimates have been calculated for traits such as lint yield, crop maturity, and fiber traits like length, strength, elongation, and micronaire (Al-Rawi and Kohel 1970, May 2000 Murray and Verhalen 1969). In a review of heritability studies, May (2000) describes both narrow- and broad-sense heritability estimates for fiber length ranging from 0.10 to 1.00, fiber strength estimates ranging from 0.10 to 0.90, fiber elongation estimates ranging from 0.21 to 0.90, and micronaire estimates ranging from 0.08 to 0.87. Verhalen and Murray (1969) calculated narrow- and broad-

sense heritability estimates for lint yield, crop maturity, and fiber micronaire and strength. Heritability estimates for lint yield ranged from 0.00 to 0.75 for narrow-sense and 0.20 to 0.82 for broad-sense; crop maturity estimates ranging from 0.00 to 0.55 for narrow-sense, and 0.00 to 0.57 for broad-sense; fiber micronaire estimates ranging from 0.00 to 0.46 for narrow-sense, and 0.00 to 0.02 for broad-sense; and fiber strength estimates ranging from 0.00 to 0.19 for narrow-sense, and 0.10 to 0.24 for broad-sense (Murray and Verhalen 1969). Narrow-sense heritability estimates are particularly important in cotton breeding because traits such as fiber length, strength, elongation, and micronaire are greatly influenced by additive genetic variance (May, 2000).

CHAPTER III

MATERIALS AND METHODS

Diallel development

A diallel mating system was established utilizing four commercial cultivars, Deltapine 50, Deltapine 491, FiberMax 832, and Tamcot CAMD-E, and four experimental lines, Hil A-106-8, Hil B-147-21, Hil B-182-39, and Hil C-155-22. Initial hybridizations were made in a greenhouse in College Station, TX, in the spring of 2007 with additional cross-pollinations being made in the field near College Station, TX, during the summer of 2007. All possible cross-pollinations and reciprocal crosses were made. Bolls were hand harvested, and seed for individual combinations and individual reciprocal combinations were combined. All crosses were ginned on a laboratory-scale roller gin, and seed was collected. In an effort to generate additional seed, ten plants from each line were stumped and potted in the greenhouse in the fall of 2007. Boll samples were taken from all plants for verification of fiber related phenotype. Crosses were made on these plants in the greenhouse in the spring of 2008.

F_1 experimental method

The resulting F_1 progeny, parents, and reciprocals were hand planted in a complete randomized block design at the Texas A&M University research farm near College Station in 2007, and again in 2008. Soil at the research station is a Westwood silt loam. Agronomic practices were carried out based on recommendations for the area.

Fiber testing

A 50-boll sample was hand harvested from middle fruiting positions of plants in each plot in 2007, while a 25-boll sample was harvested in the same manner in 2008. Samples were ginned on laboratory-scale saw gins with no lint cleaning. Fiber samples were analyzed using the HVI system at the Fiber and Biopolymer Research Institute in Lubbock, TX. An additional 100 bolls were harvested from each plot for seed increase.

Analysis to determine combining ability

Analysis of the diallel for the general combining ability (GCA) and specific combining ability (SCA) for all traits were based on Model I, Method II proposed by Griffing (1956). Griffing (1956) proposed that in model I variety effects are fixed, and block effects are random. In method II, parents, one set of F_1's but not reciprocal F_1's are included [p (p+1)/2 combinations].

Various programs are available for diallel analysis (Zhang et al. 2005, Agronomix Software inc., 2007). Analyses of Griffing's model I, method II was conducted using the diallel analysis function in Agrobase Gen. II. The 2007 data set had sixteen missing entries out of 144 total entries, and in 2008 the data set had two missing entries out of 144 total entries. Trait values were predicted based upon the traits mean values to produce a balanced data set. Using Agrobase Gen. II, both GCA and SCA effects were determined. Fischer's Least Significant Difference LSD, p=0.05, were calculated based on standard errors provided by the diallel analysis function. Using the standard error of G_i, Fischer's LSD was calculated and used to separate significant GCA

effects from zero, while the standard error of S_{ij} is used to calculate Fischer's LSD to separate significant SCA effects from zero.

In order to determine if significant GxY, GCAxY, and SCAxY interactions were present for traits of interest; the diallel analysis of variance for combined F_1 data for 2007 and 2008 was conducted utilizing Diallel-SAS05 as described by Zhang et al. (2005). Missing data points for 2007 and 2008 were calculated based on trait mean values as previously described to produce a balanced data set. Mean squares from the combined analysis are provided in Table 1.

Biplot analysis was performed on F_1 data for 2007 and 2008 separately due to significant GxY interactions for most traits of interest (Table 1). All interpretations follow guidelines described by Yan and Kang (2003).

Heritability estimates

Broad-sense heritability estimates were computed for an F_2 population grown in Weslaco, TX, and College Station, TX in 2008. Due to a significant GxE interaction, data was separated by location for lint percent and fiber micronaire. A significant GxE interaction was not detected for all other traits so that data was pooled. These estimates show the amount of phenotypic variation due to differences between genotypes.

F_2 population performance and variance

The F_2 populations were grown at two locations in 2008. They were planted in a randomized complete block design at the Texas Agrilife Research Station near Weslaco, TX, and at the Texas A&M University research farm in College Station, TX. A 25-boll sample was harvested from the middle fruiting position of the plants in each plot. All

data were analyzed using a mixed ANOVA using SAS 9.1 (SAS Instituite, 2003) with means separated using Fischer's LSD. This allowed comparisons of variance for each genotype, and estimation of broad-sense heritability. Location means for traits were separated where a significant GxE interaction existed.

In an effort to compare variances within populations, four parents, Deltapine 50, Deltapine 491, Hil B-182-39, and Hil C-155-22, and six F_2 progeny, Deltapine 491/Deltapine 50, Deltapine 491/Hil B-182-39, Deltapine 491/Hil C-155-22, Deltapine 50/Hil B-182-39, Deltapine 50/Hil C-155-22, and Hil B-182-39/Hil C-155-22 were selected for analysis. Nine plants in each plot were individually harvested. Boll samples from each plant were ginned on a laboratory-scale saw gin without lint cleaning. Fiber samples were analyzed with HVI at the Fiber and Biopolymer Research Institute in Lubbock, TX. Fiber data for the entries was analyzed for mean, standard deviation, skewness, coefficient of variation, and variance using the PROC UNIVARIATE function in SAS 9.1 (SAS Institute, 2003).

CHAPTER IV

RESULTS AND DISCUSSION

Combining ability

Analysis of variance indicated significant effect of genotypes for all traits of interest, significant effect of years, and significant interaction of GxYs for all traits of interest except lint percent for the eight parental genotypes and respective 28 F_1 progeny (Table 1). The analysis indicates a significant GCA (p=0.01) for all six traits of interest and significant SCA effects (p=0.05) for all traits of interest except lint percent (Table 1). Interestingly, GCAxY interactions (p=0.05) were only noted for fiber micronaire and elongation (Table 1), which can be influenced by numerous environmental factors. This suggests that general combining ability among the parental lines was stable across years. Highly significant (p=0.01) SCAxYs interactions were noted for all traits of interest except lint percent. Furthermore, the data suggest that variation within the population could allow for the selection of these traits.

Table 1: Diallel analysis of variance for fiber traits of eight cotton (*Gossypium hirsutum* L.) genotypes and their F_1 progeny when grown in College Station, TX, in 2007 and 2008.

Sources	df	Lint Percent	Micronaire	Length	Strength	Uniformity	Elongation
Years (Y)	1	175.31	26.16**	357.11**	86147.09**	207.91**	505.09**
Year X Reps Error A	6	33.49	0.12**	8.88**	6.334.06**	13.18**	1.34**
Genotypes (G)	35	29.16**	0.40**	32.80**	3498.09**	7.77**	1.40**
GCA	7	57.10**	1.69**	151.04**	80.74**	29.21**	5.47**
SCA	28	1.67*	2.62**	3.24**	2.91**	2.41**	0.39**
G X Y – Error B	35	4.94**	0.06**	1.77*	347.56**	1.50*	0.17**
GCA X Y	7	2.52*	0.05*	1.38	107.80	1.06	0.22**
SCA X Y	28	2.07**	2.33**	1.83*	407.50	1.61**	0.15**
Error C	210	2.29	0.03	1.12	189.34	0.76	0.08

*, ** Significantly different from zero at p=0.05, and p=0.01 respectively.

Lint percent

Biplot analysis of lint percent shows that entries FiberMax 832, Deltapine 491, Deltapine 50, and Hil C-155-22 have positive GCA effects for lint percent in 2007 as they were on the positive end of the average tester coordinate (ATC) abscissa (Figure 1). While Tamcot CAMD-E, Hil B-182-39, Hil B-147-21, and Hil A-106-8 have negative GCA effects for lint percent (Figure 1). An entry positive GCA effect is an indication of its contribution to an increase in lint percent in its offspring. Deltapine 491, exhibited the highest GCA effect, while an experimental line Hil A-106-8, exhibited the lowest GCA effect (Figure 1). The relative ranking of entries based on GCA effects in are Deltapine 491 > FiberMax 832 > Deltapine 50 ≈ Hil C-155-22 > Hil B-182-39 ≈ Tamcot CAMD-E > Hil B-147-21 > Hil A-106-8 (Figure 1). When the rankings are compared with the GCA effects as analyzed by Agrobase Gen. II the ranking of effects are similar (Table 2). Furthermore, the biplot explained 92.9% (PC1 = 82.7% and PC2 = 10.2%) of the total variation that would be partitioned into GCA effects of the parents and SCA effects of the crosses in conventional analyses (Figure 1).

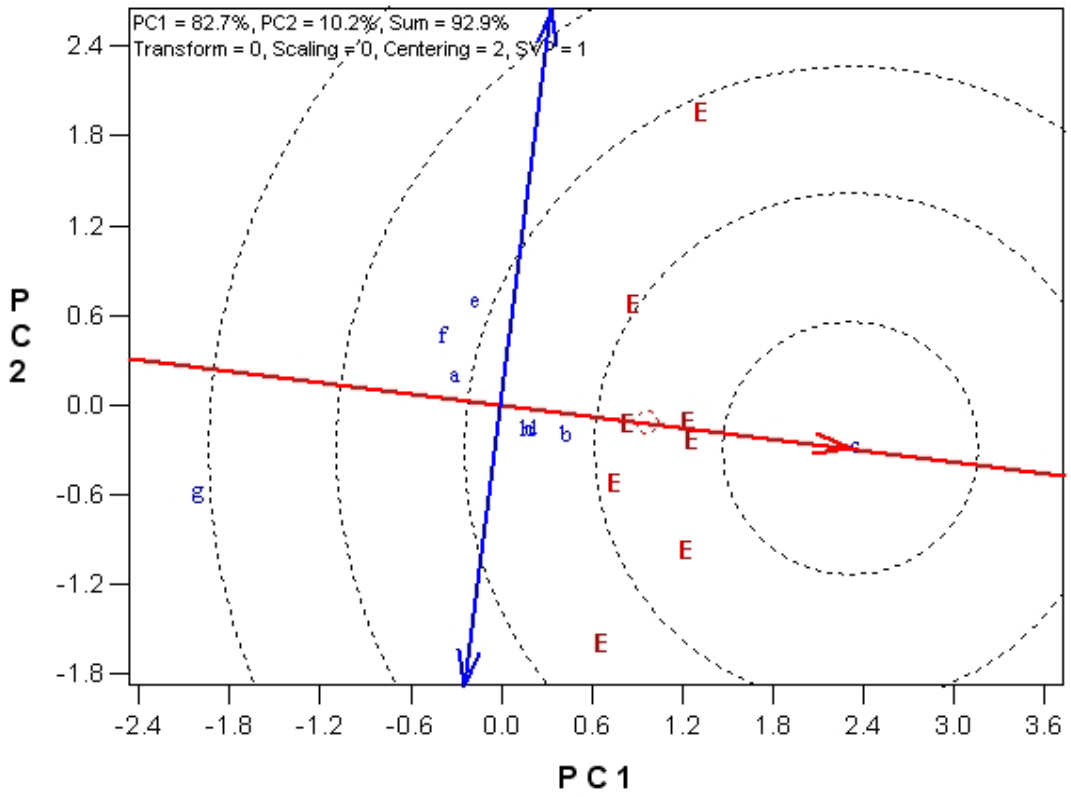

Figure 1: Biplot showing average tester coordinate view, based on diallel data for lint percent in 2007. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

In 2008, entries Tamcot CAMD-E, FiberMax 832, and Deltapine 491 exhibited positive GCA effects while entries Deltapine 50, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 exhibited the negative GCA effects for lint percent (Figure 2). Similar to the 2007 analysis, Deltapine 491, exhibited the highest GCA effect, while Hil A-106-8, exhibited the lowest GCA effect (Figure 2). The relative ranking of entries based on GCA effects are Deltapine 491 > Tamcot CAMD-E > FiberMax 832 > Deltapine 50 > Hil C-155-22 > Hil B-182-39 > Hil B-147-21 > Hil C-155-22 (Figure 2). The same results are observed in the table of means provided by the Agrobase analysis (Table 2). The biplot explained 90.4% (PC1 = 79.7% and PC2 = 20.7%) of the total variation that would be partitioned into GCA effects of the parents and SCA effects of crosses in conventional analyses (Figure 2).

Significant GxY and GCAxY interactions (p=0.05) were observed for lint percent (Table 1). Mean values for 2008 were lower than 2007, which led to a change in ranking of values between years (Table 2). This change in ranking directly contributed to the GxY interaction. The change in mean values between years also contributed to the change in GCA effects and their significance, which contributed to GCAxY interaction (Table 2). Highly significant differences (p=0.01) among genotypes and among GCA effects for lint percent suggest sufficient variation within this population for selection of this trait (Table 1).

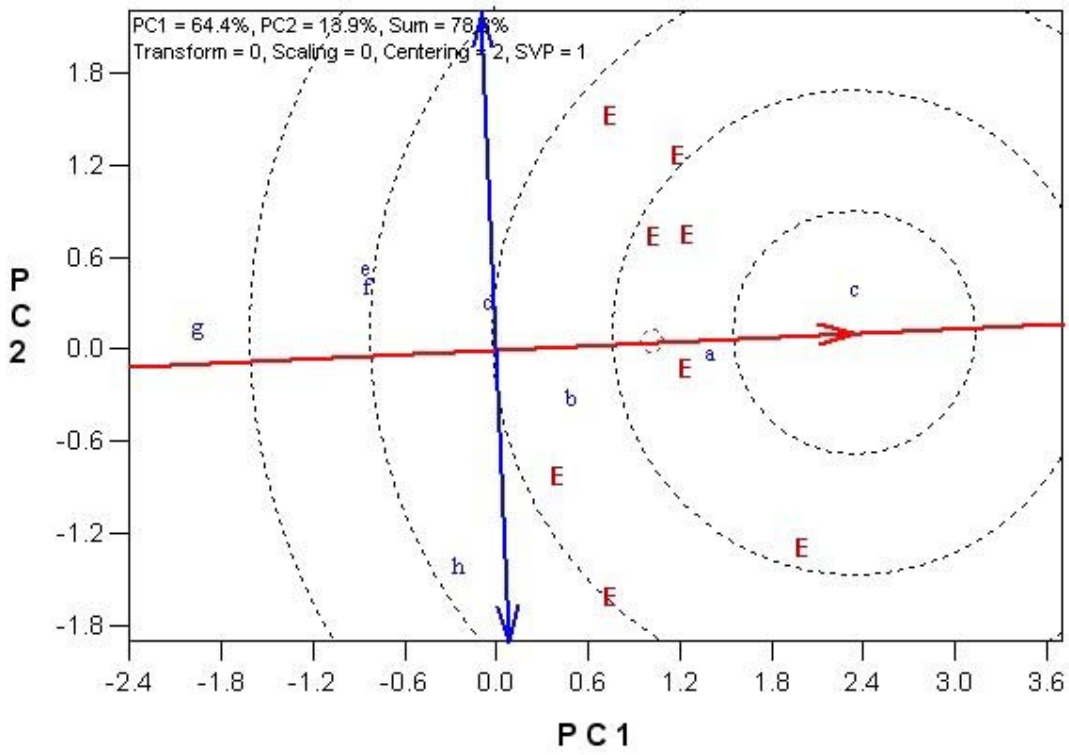

Figure 2: Biplot showing average tester coordinate view, based on diallel data for lint percent in 2008. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Table 2: Table of means, GCA effects, and SCA effects from diallel analysis of lint percent for eight cotton (Gossypium hirsutum L.) genotypes and 28 F_1 progeny in 2007 and 2008.

	Lint Percent			
	2007		2008	
Parent	Mean -%-	GCA	Mean -%-	GCA
Tamcot CAMD-E	36.5	-0.275	36.1	1.123**
FiberMax 832	37.8	0.453**	35.7	0.474
Deltapine 491	42.1	2.400**	38.3	2.311**
Deltapine 50	36.1	0.118	33.8	-0.101
Hil B-182-39	35.1	-0.408*	34.7	-0.731**
Hil B-147-21	35.9	-0.373*	33.5	-0.759**
Hil A-106-8	31.1	-2.070**	30.3	-2.151**
Hil C-155-22	36.4	0.155	35.9	-0.166
LSD (0.05)		0.314		0.543
Combinations	Mean -%-	SCA	Mean -%-	SCA
Tamcot CAMD-E/FiberMax 832	36.8	-0.080	37.8	1.132
Tamcot CAMD-E/Deltapine 491	38.3	-0.578	37.4	-1.031
Tamcot CAMD-E/Deltapine 50	36.1	-0.420	36.6	0.532
Tamcot CAMD-E/Hil B-182-39	35.9	-0.145	34.1	-1.363
Tamcot CAMD-E/Hil B-147-21	36.1	0.070	35.9	0.464
Tamcot CAMD-E/Hil A-106-8	34.8	0.442	34.1	0.107
Tamcot CAMD-E/Hil C-155-22	36.7	0.067	38.4	2.447**
FiberMax 832/Deltapine 491	39.8	0.195	37.9	0.094
FiberMax 832/Deltapine 50	37.7	0.452	36.2	0.807
FiberMax 832/Hil B-182-39	36.7	-0.073	35.2	0.387
FiberMax 832/Hil B-147-21	36.3	-0.458	32.9	-1.861*
FiberMax 832/Hil A-106-8	34.6	-0.460	33.4	0.007
FiberMax 832/Hil C-155-22	37.3	-0.010	35.4	0.022
Deltapine 491/Deltapine 50	39.9	0.655	37.1	-0.131
Deltapine 491/Hil B-182-39	38.4	-0.320	37.2	0.574
Deltapine 491/Hil B-147-21	37.9	-0.805	37.0	0.427
Deltapine 491/Hil A-106-8	37.3	0.242	36.3	1.069
Deltapine 491/Hil C-155-22	38.6	-0.633	38.8	1.634
Deltapine 50/Hil B-182-39	36.9	0.487	35.9	1.687*
Deltapine 50/Hil B-147-21	36.4	-0.073	35.0	0.789
Deltapine 50/Hil A-106-8	34.8	0.225	32.3	-0.518
Deltapine 50/Hil C-155-22	37.4	0.400	33.6	-1.948*
Hil B-182-39/Hil B-147-21	35.5	-0.423	33.2	-0.331
Hil B-182-39/Hil A-106-8	36.1	1.875**	30.8	-1.338
Hil B-182-39/Hil C-155-22	36.6	0.175	32.2	-1.948*
Hil B-147-21/Hil A-106-8	34.9	0.615	34.8	2.689**
Hil B-147-21/Hil C-155-22	37.7	1.240*	31.9	-1.128
Hil A-106-8/Hil C-155-22	34.7	-0.063	31.6	2.323**
CV (%)	3.17		7.20	
LSD (0.05)	1.36	0.964	2.59	1.663
Grand Mean	36.7		35.0	

*,** Significantly different at 0.05, and 0.01 respectively

Determining the best tester for lint percent can be accomplished by interpreting the biplot in Figure 3. An ideal tester must be both highly discriminating and representative of all testers (Yan and Hunt, 2002). Furthermore, based on the guidelines set forth by Yan and Kang (2003), FiberMax 832 is the best tester for 2007 in the data set because it lies closest to the ATC axis, and is the most discriminating. Although Deltapine 50 is similar to FiberMax 832, the length of its vector is shorter than that of FiberMax 832 causing it to be less discriminating (Figure 3). Hil B-182-39 is the poorest tester for lint percent as it falls furthest from the ideal center of the concentric circles (Figure 3). In 2008, FiberMax 832 was determined to be the best tester for lint percent (Figure 4) based on its vector length and proximity to the ideal tester center. Deltapine 491, was once again determined to be the poorest tester for lint percent (Figure 4). It is considered to be the poorest tester as it falls furthest from the ideal tester center.

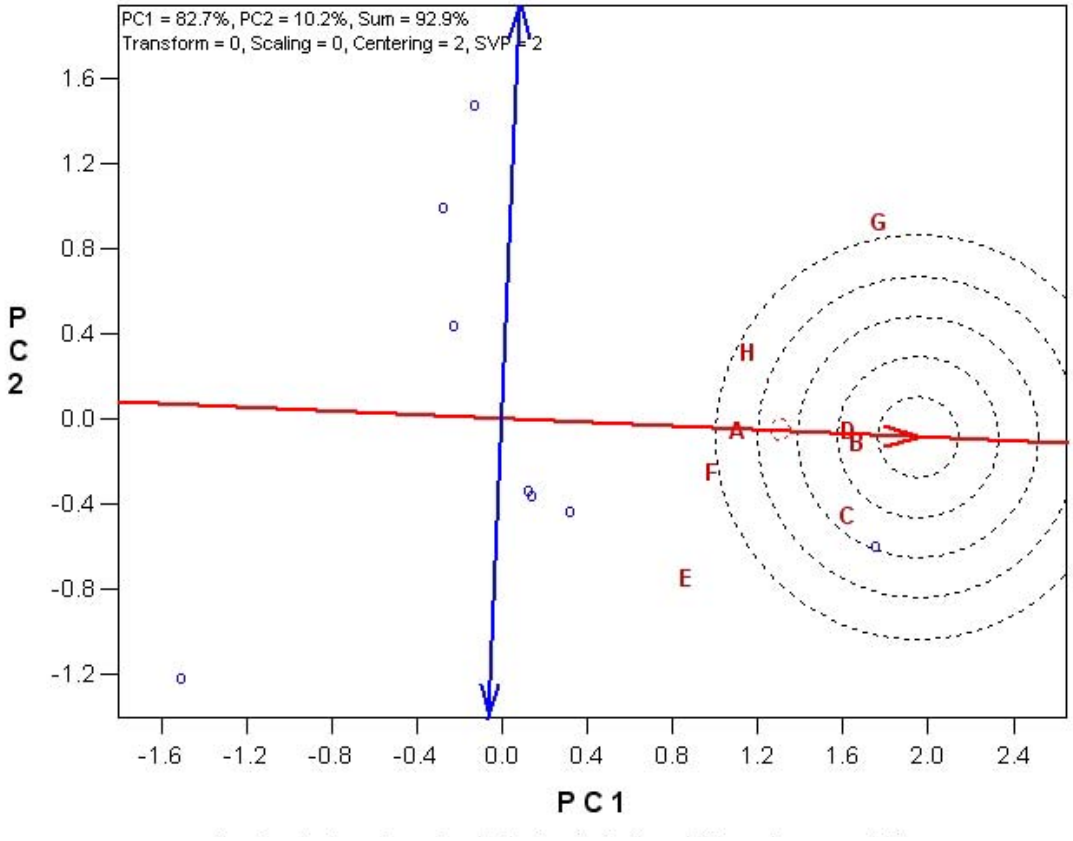

Figure 3: Biplot showing the evaluation of parents as ideal tester for lint percent in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

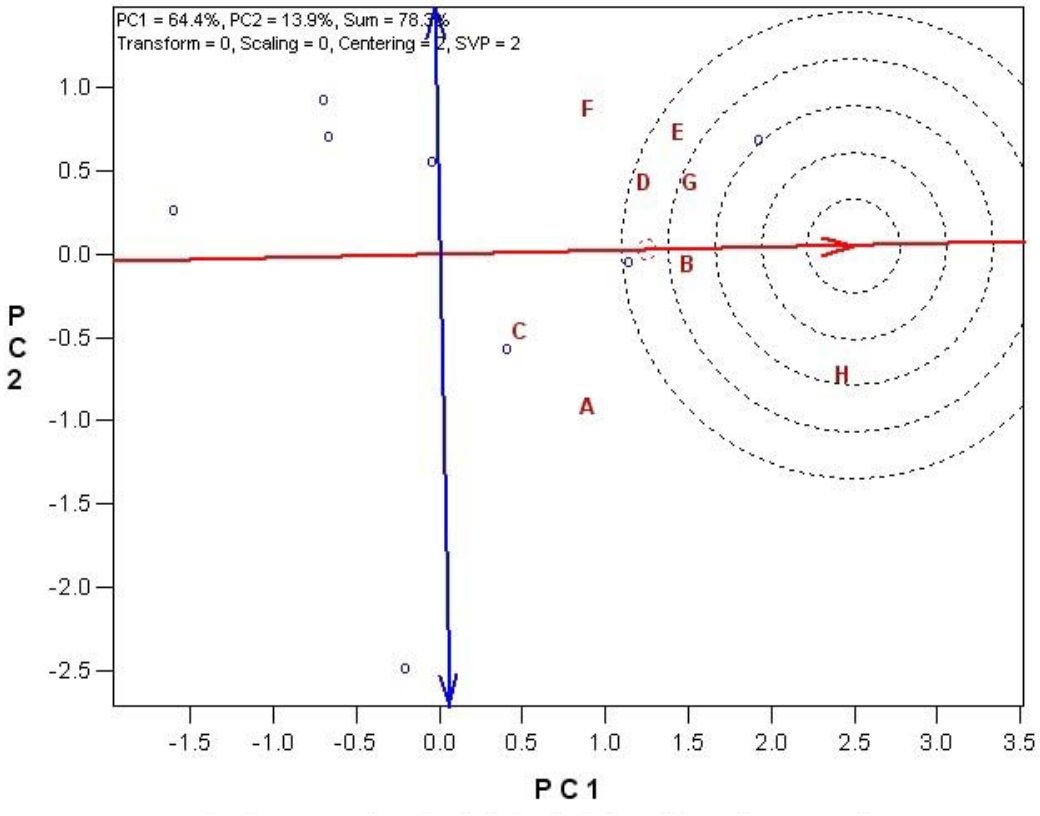

Figure 4: Biplot showing the evaluation of parents as ideal tester for lint percent in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

The polygon view of the biplot for lint percent (Figure 5) provides us with three sectors formed by Deltapine 491, Hil B-182-39, and Hil A-106-8. All testers fall into the Deltapine 491 sector, while none fall into the Hil B-182-39 sector or the Hil A-106-8 sector suggesting these entries were not the best mating partners with any genotypes. Based on this data, Deltapine 491 is the best mating partner with all genotypes for lint percent. This is reflected in the table of means constructed from the diallel analysis in Agrobase Gen. II (Table 2). Deltapine 491 had the highest overall mean of all parents tested, and also exhibited the highest GCA, which was significantly different from zero at p=0.01 (Table 2). However, since Deltapine 491 fell into its own sector, it provides us with the best combination among all crosses involving Deltapine 491 (Figure 5). Furthermore, heterosis defined as the performance greater than the best parent, between Deltapine 491 and any other parent is not possible (Figure 5). This is consistent with the table of means for lint percent provided by the Agrobase Gen. II analysis (Table 2). Deltapine 491 exhibited the highest mean for lint percent at 42.1%, which is significantly different at p=0.05 when compared with all parents and combinations. Thus, the Agrobase Gen. II and biplot analysis produced similar results. This is consistent with the interpretation provided by Yan and Kang (2003). Overall, entry Hil A-106-8 and tester Hil A-106-8 were located furthest from each other on the biplot suggesting that Hil A-106-8 is the poorest combiner for lint percent (Figure 5). This is reflected in the table of means for lint percent, as Hil A-106-8, exhibited the lowest mean for lint percent at 31.1% when compared to both parents and combinations (Table 2).

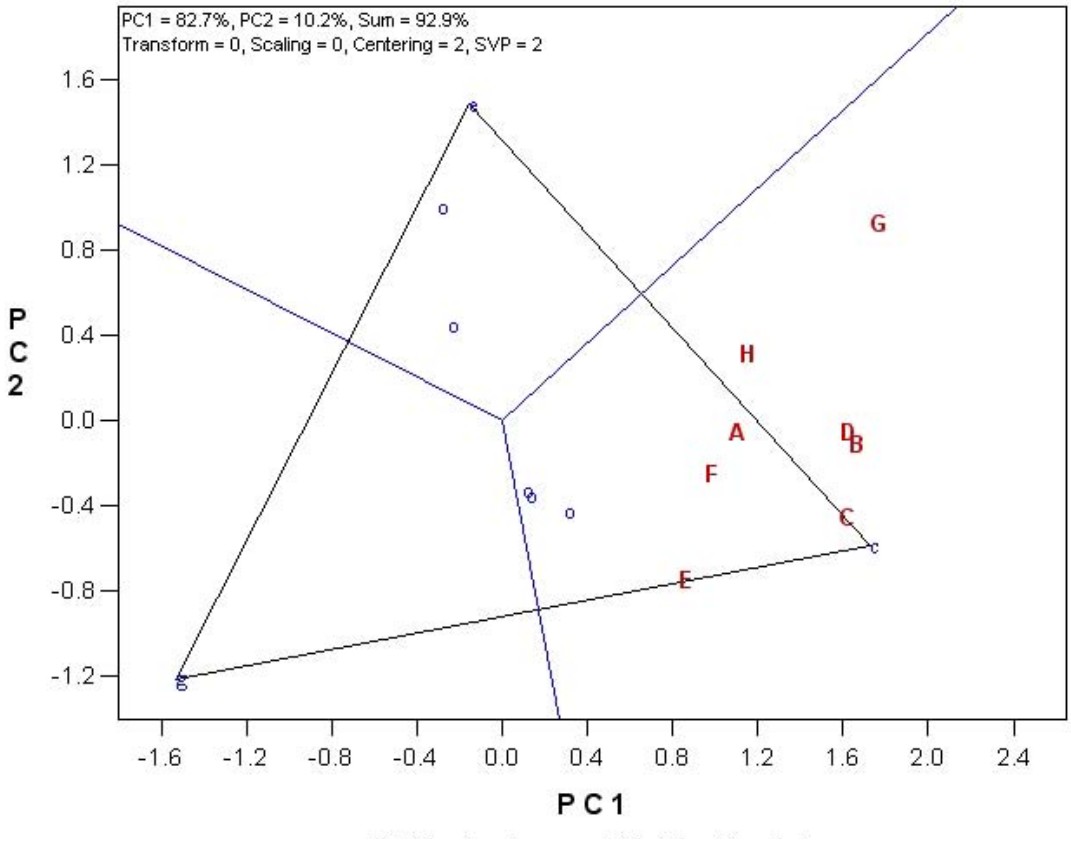

Figure 5: Biplot showing polygon view of three parents for lint percent in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

The polygon view of the biplot for lint percent from 2008 (Figure 5) provides us with four sectors. Entries Deltapine 491, Hil B-182-39, Hil A-106-8, and Hil C-155-22 form these sectors. No testers fell into Hil B-182-39 or Hil A-106-8 sectors suggesting these entries were not the best mating partners with some or all of the testers (Figure 6). Tamcot CAMD-E and Deltapine 491 fell into the Hil C-155-22 sector, while testers FiberMax 832, Deltapine 50, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 fell into the Deltapine 491 sector (Figure 6). Since neither sector contained its own tester, we can conclude that all combinations involving entries Deltapine 491 and Hil C-155-22 must be heterotic (Figure 6). Furthermore, since Deltapine 491 fell into Hil C-155-22 sector, and Hil C-155-22 fell into Deltapine 491 sector, we can predict that the combination Deltapine 491/Hil C-155-22 is the best among all combinations involving Deltapine 491, and Hil C-155-22 (Figure 6). This is consistent with the data from the Agrobase analysis (Table 2) for lint percent. The combination Deltapine 491/Hil C-155-22 provides us with the highest mean lint percent at 38.8% (Table 2). Although this mean is numerically higher than all values for combinations involving Deltapine 491, it is not significantly different from them at $p=0.05$ (Table 2). Overall, entry Hil A-106-8 and tester Hil A-106-8 were located furthest from each other on the biplot (Figure 6) suggesting that Hil A-106-8 is the poorest combiner for lint percent. This is reflected in the table of means for lint percent, as Hil A-106-8, exhibited the lowest mean for lint percent at 30.3% when compared to both parents and progeny (Table 2).

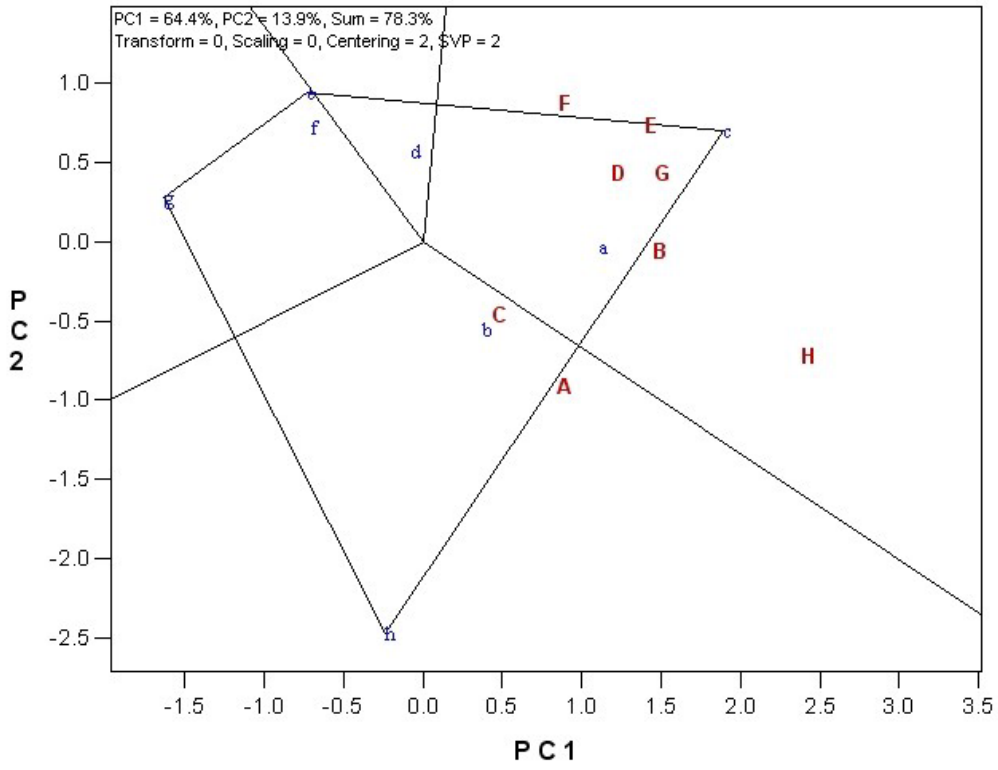

Figure 6: Biplot showing polygon view of four parents for lint percent in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Fiber micronaire

All fiber samples had micronaire means that fell within the non-discount range as defined by the 2008 CCC Loan Schedule (National Cotton Council, 2008). Biplot analysis of micronaire showed that Deltapine 50, and Deltapine 491 have positive GCA effects, and entries Tamcot CAMD-E, FiberMax 832, Hil B-182-39, Hil B-147-21, Hil A-10-68, and Hil C-155-22 have negative GCA effects (Figure 7). The biplot explained 77.4% (PC1=61.5%, and PC2=15.9%) of the total variation that would be partitioned into GCA effects of the parents and SCA effects of the crosses in conventional analyses. Deltapine 50, exhibited the highest GCA effect, while Tamcot CAMD-E, exhibited the lowest GCA effect. The relative ranking for GCA effects is Deltapine 50 > Deltapine 491 > Hil C-155-22 > FiberMax 832 > Hil B-182-39 > Hil A-106-8 > Hil B-147-21 > Tamcot CAMD-E. When compared to the diallel analysis performed in Agrobase Gen. II (Table 3), the biplot analysis returned similar results with the exception of ranking the effect Hil A-106-8 > Hil B-147-21 > Hil B-182-39 instead of the ranking Hil B-182-39 > Hil A-106-8 > Hil B-147-21 provided by the biplot analysis. Hil A-106-8 and Hil B-182-39 are located in a similar location on the ATC abscissa, while Hil B-147-21 is located further from the ATC abscissa (Figure 7). According to Table 2, Hil A-106-8 exhibited a GCA effect of –0.084, Hil B-147-21 exhibited a GCA effect of –0.094, and Hil B-182-39 exhibited a GCA effect of –0.099. GCA effects for entries Hil B-182-39, Hil B-147-21, and Hil A-106-8 GCA effects were significantly different from zero at p=0.01 based on the LSD calculated from table of standard errors provided by Agrobase Gen. II (Table 3).

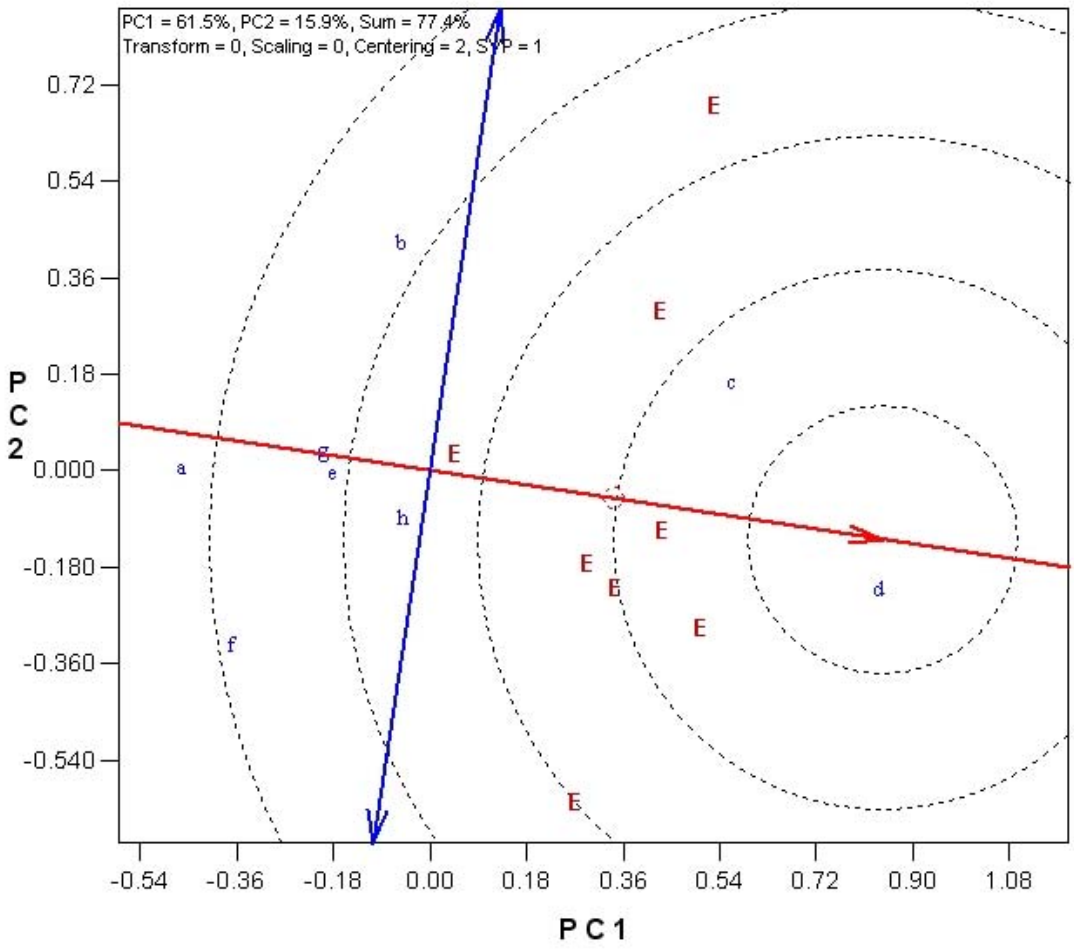

Figure 7: Biplot showing average tester coordinate view, based on diallel data for fiber micronaire in 2007. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Table 3: Table of means, GCA effects, and SCA effects from diallel analysis of fiber micronaire for eight cotton (Gossypium hirsutum L.) genotypes and 28 F_1 progeny in 2007 and 2008.

	Micronaire			
	2007		2008	
Parent	Mean -units-	GCA	Mean -units-	GCA
Tamcot CAMD-E	4.1	-0.129**	4.5	-0.076**
FiberMax 832	4.2	-0.029	4.9	0.019
Deltapine 491	4.5	0.189**	5.1	0.121**
Deltapine 50	4.7	0.271**	5.3	0.306**
Hil B-182-39	3.9	-0.099**	4.7	-0.131**
Hil B-147-21	4.1	-0.094**	4.6	-0.041
Hil A-106-8	3.9	-0.084**	4.9	-0.109**
Hil C-155-22	4.1	-0.026	4.7	-0.089**
LSD (0.05)		0.045		0.051
Combinations	Mean -units-	SCA	Mean -units-	SCA
Tamcot CAMD-E/FiberMax 832	3.9	-0.094	4.9	0.203*
Tamcot CAMD-E/Deltapine 491	4.1	-0.136	4.9	0.051
Tamcot CAMD-E/Deltapine 50	4.0	-0.269**	4.9	-0.109
Tamcot CAMD-E/Hil B-182-39	3.9	-0.024	4.3	-0.222**
Tamcot CAMD-E/Hil B-147-21	3.9	-0.054	4.7	0.088
Tamcot CAMD-E/Hil A-106-8	4.1	0.186**	4.7	0.081
Tamcot CAMD-E/Hil C-155-22	4.0	-0.021	4.7	0.111
FiberMax 832/Deltapine 491	4.6	0.314**	4.7	-0.169*
FiberMax 832/Deltapine 50	4.3	-0.144*	5.1	-0.004
FiberMax 832/Hil B-182-39	4.0	-0.049	4.6	-0.041
FiberMax 832/Hil B-147-21	3.9	-0.129	4.6	-0.157
FiberMax 832/Hil A-106-8	4.1	0.061	4.7	0.036
FiberMax 832/Hil C-155-22	4.0	-0.071	4.7	-0.034
Deltapine 491/Deltapine 50	4.7	0.089	5.3	0.068
Deltapine 491/Hil B-182-39	4.2	-0.016	4.6	-0.169
Deltapine 491/Hil B-147-21	4.2	-0.046	4.9	0.041
Deltapine 491/Hil A-106-8	4.2	-0.056	4.9	0.108
Deltapine 491/Hil C-155-22	4.2	-0.089	4.8	-0.037
Deltapine 50/Hil B-182-39	4.6	0.276**	5.1	0.171*
Deltapine 50/Hil B-147-21	4.3	-0.029	5.1	0.081
Deltapine 50/Hil A-106-8	4.4	0.061	5.0	0.023
Deltapine 50/Hil C-155-22	4.5	0.104	5.0	0.003
Hil B-182-39/Hil B-147-21	4.0	0.041	4.6	0.018
Hil B-182-39/Hil A-106-8	3.8	-0.169*	4.4	-0.114
Hil B-182-39/Hil C-155-22	4.1	0.049	4.5	-0.059
Hil B-147-21/Hil A-106-8	4.1	0.101	4.7	0.071
Hil B-147-21/Hil C-155-22	4.0	-0.056	4.7	0.051
Hil A-106-8/Hil C-155-22	4.1	0.033	4.4	-0.182*
CV (%)	3.73		3.65	
LSD (0.05)	0.18	0.139	0.20	0.156
Grand Mean	4.15		4.75	

*,** Significantly different at 0.05, and 0.01 respectively

High micronaire values were ascertained (Table 3) in 2008 as some values entered the discount range as defined by the 2008 CCC Loan Schedule (National Cotton Council, 2008). A highly significant GxY interaction (p=0.01) and significant GCAxY interaction (p=0.05) was noted for micronaire (Table 1). As previously noted, aberrant micronaire values can be directly related to a genotypes performance and its interaction in a growing environment. Biplot analysis of micronaire for 2008 showed entries FiberMax 832, Deltapine 491 and Deltapine 50 exhibiting positive GCA effects, while entries Tamcot CAMD-E, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 exhibited negative GCA effects (Figure 8). The rankings based upon the biplot analysis are Deltapine 50 > Deltapine 491 > FiberMax 832 > Hil B-147-21 > Tamcot CAMD-E > Hil A-106-8 > Hil C-155-22 > Hil B-182-39 (Figure 8). The biplot explained 76.9% (PC1=65.3%, and PC2=11.6%) of the total variation that would be partitioned into GCA effects of the parents and SCA effects of the crosses in conventional analyses. Similar to 2007, Deltapine 50, exhibited the highest GCA effect (Figure 8). However, in 2008 Hil B-182-39 exhibited the lowest GCA effect (Figure 8). Results are similar when compared to the analysis performed in Agrobase (Table 3) with the exception of the ranking of Hil A-106-8, and Hil C-155-22. All GCA effects, excluding FiberMax 832 and Hil B-147-21, were significantly different from zero at p=0.01 (Table 3). The biplot analysis ranks Hil A-106-8 > Hil C-155-22 while the Agrobase Gen. II analysis ranks the entries Hil C-155-22 > Hil A-106-*8*. Hil A-106-8, exhibited a negative GCA effect of -0.109, while Hil C-155-22, exhibited a negative GCA effect of -0.089 (Table 3).

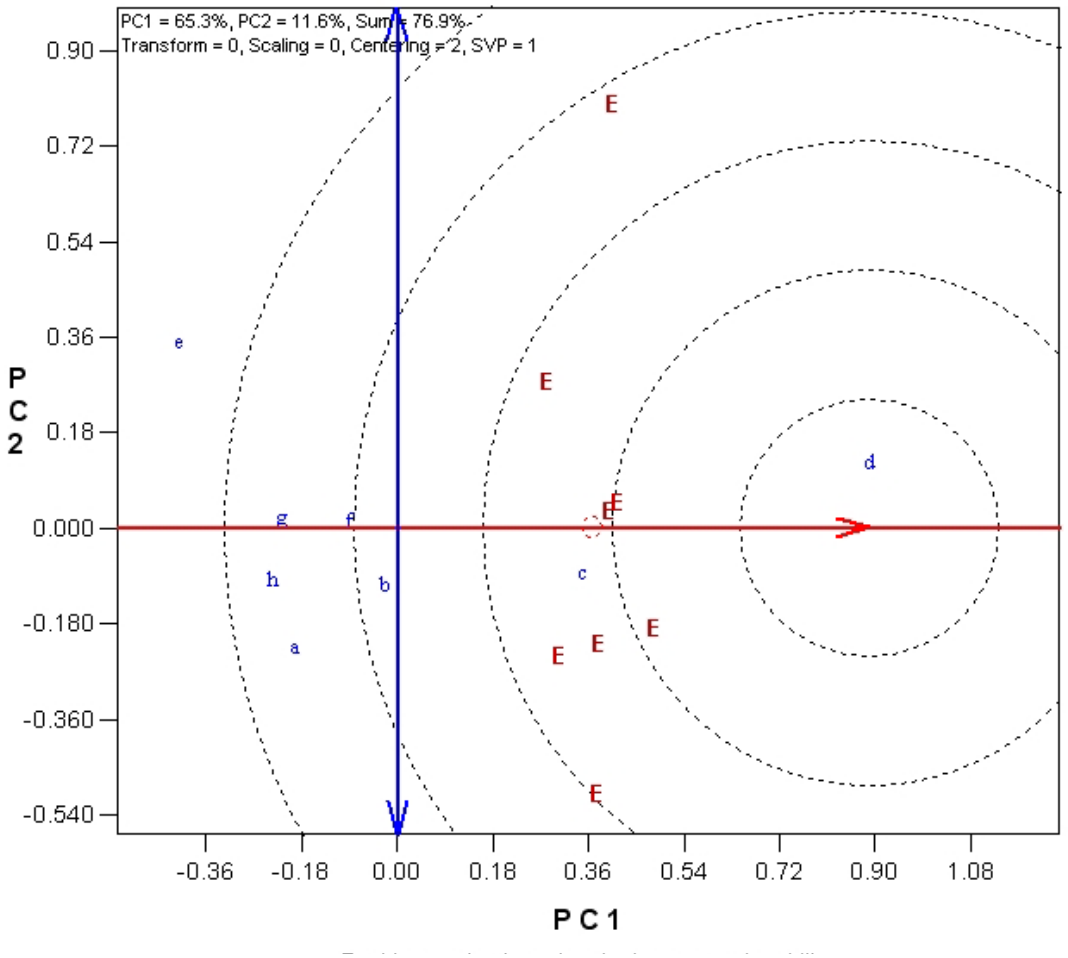

Figure 8: Biplot showing average tester coordinate view, based on diallel data for fiber micronaire in 2008. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

In order to determine the cause of the GCAxY interaction for micronaire, relative rankings provided by the Agrobase analysis were compared against each other and the GCA effect from 2007 and 2008 (Table 3). Relative rankings for 2007 were Deltapine 50 > Deltapine 491 > Hil C-155-22 > FiberMax 832 > Hil B-182-39 > Hil A-106-8 > Hil B-147-21 > Tamcot CAMD-E, while in 2008 rankings were Deltapine 50 > Deltapine 491 > FiberMax 832 > Hil B-147-21 > Tamcot CAMD-E > Hil A-106-8 > Hil C-155-22 > Hil B-182-39 (Table 3). Rankings of all entries except, Deltapine 491 and Deltapine 50, differed between years (Table 3). In both 2007 and 2008, both entries Deltapine 491 and Deltapine 50 exhibited positive GCA effects and the same rankings between years (Table 3). In 2008, FiberMax 832, exhibited a positive GCA effect of 0.019 which was not significantly different from zero at p=0.05, while in 2007 it exhibited a negative GCA effect of -0.029 which was not significantly different from zero at p=0.05 (Table 3). All other entries exhibited negative GCA effects during both years (Table 3). However, the significance differed between years (Table 3). Redistribution of rankings and significance of GCA effects from zero, as well as environmental conditions between years, contributed to the GCAxY and GxY interactions.

Based on the proximity of Deltapine 50 to the ATC abscissa and its vector length, we can determine it is the best tester for micronaire (Figure 9). Even though Hil B-182-39 is more discriminating than Deltapine 50, its distance from the ATC axis makes it a less desirable tester (Figure 9). Clearly, Tamcot CAMD-E, is considered the poorest tester in the data set (Figure 9). Although, it is near the ATC axis, it vector is the shortest and the least discriminating of all testers (Figure 9). Thus, Tamcot CAMD-E is the furthest from the ideal tester center making it the poorest tester (Figure 9).

Based on the proximity Hil A-106-8 to the ATC abscissa and its vector length, we can determine it is the best tester for micronaire in 2008 (Figure 10). Deltapine 50 is considered to be the poorest tester because of its proximity to the ATC abscissa and the length of its vector (Figure 10). A significant GxY interaction was present for micronaire (Table 1). The effect of this can be seen in the biplot analysis as Deltapine 50 was considered the best tester in 2007 and the worst tester for micronaire in 2008 (Figure 9, 10).

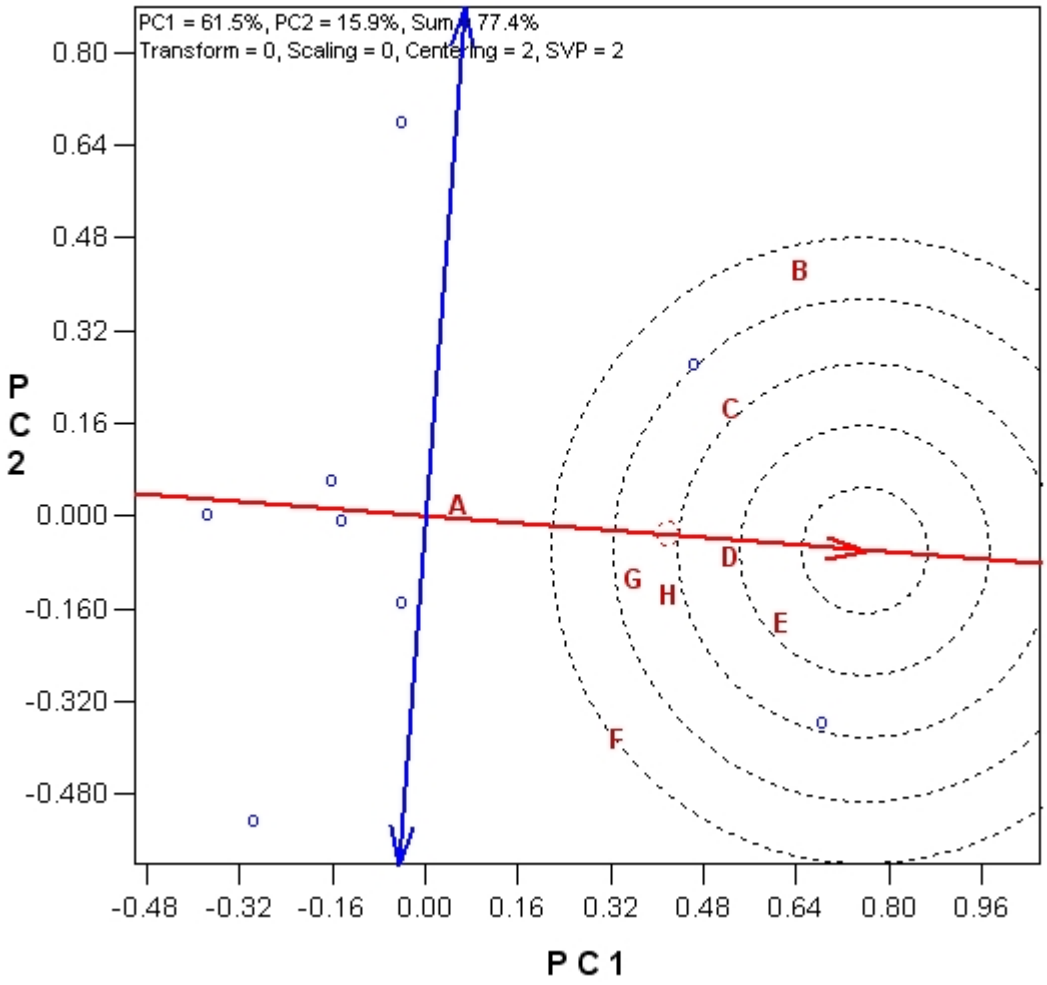

Figure 9: Biplot showing the evaluation of parents as ideal tester for fiber micronaire in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

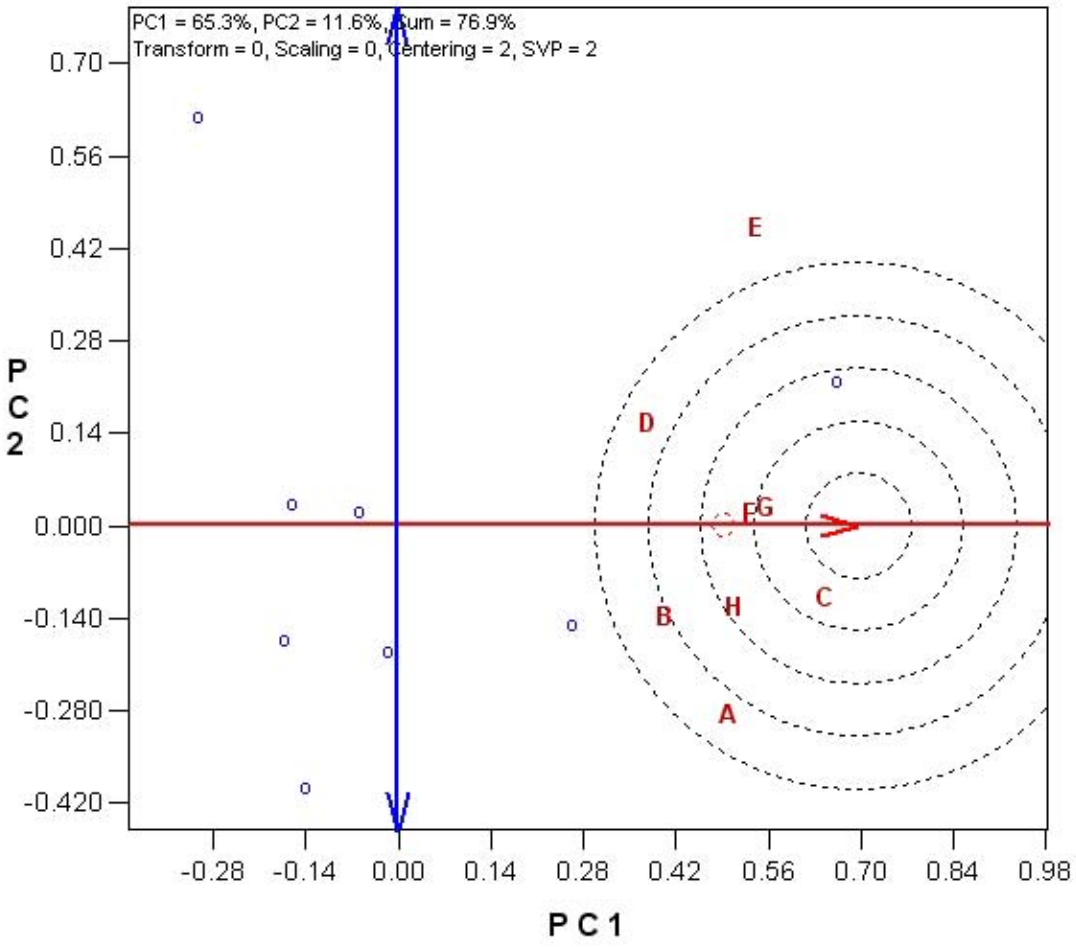

Figure 10: Biplot showing the evaluation of parents as ideal tester for fiber micronaire in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

The polygon view of the biplot for micronaire (Figure 11) provides us with five sectors. Tamcot CAMD-E, FiberMax 832, Deltapine 491, Deltapine 50, and Hil B-147-21 form these sectors (Figure 11). No testers fell into Tamcot CAMD-E, Deltapine 491, or Hil B-147-21 sectors suggesting these entries produced the poorest combinations with some or all of the testers (Figure 11). The Deltapine 491 sector only contained FiberMax 832, suggesting that Deltapine 491 was the best mating partner with FiberMax 832. This is consistent with the data provided by the table of means (Table 3). The combination of FiberMax 832/Deltapine 491, provided a mean of 4.6, which is the highest for any cross involving FiberMax 832 as a parent. Furthermore, this suggests that there is heterosis between parent's Deltapine 491 and FiberMax 832, as no other tester fell within the Deltapine 491 sector (Figure 11). All other testers, Tamcot CAMD-E, Deltapine 491, Deltapine 50, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 fell into Deltapine 50's sector (Figure 11). This suggests that Deltapine 50 is the best mating partner for all of these testers. Since the tester Deltapine 50, fell into the Deltapine 50 sector, we can conclude that the pureline Deltapine 50 performs better than all combinations involving Deltapine 50. Furthermore, heterosis between Deltapine 50 and any other testers is not possible. This is confirmed in the table of means for micronaire (Table 3).

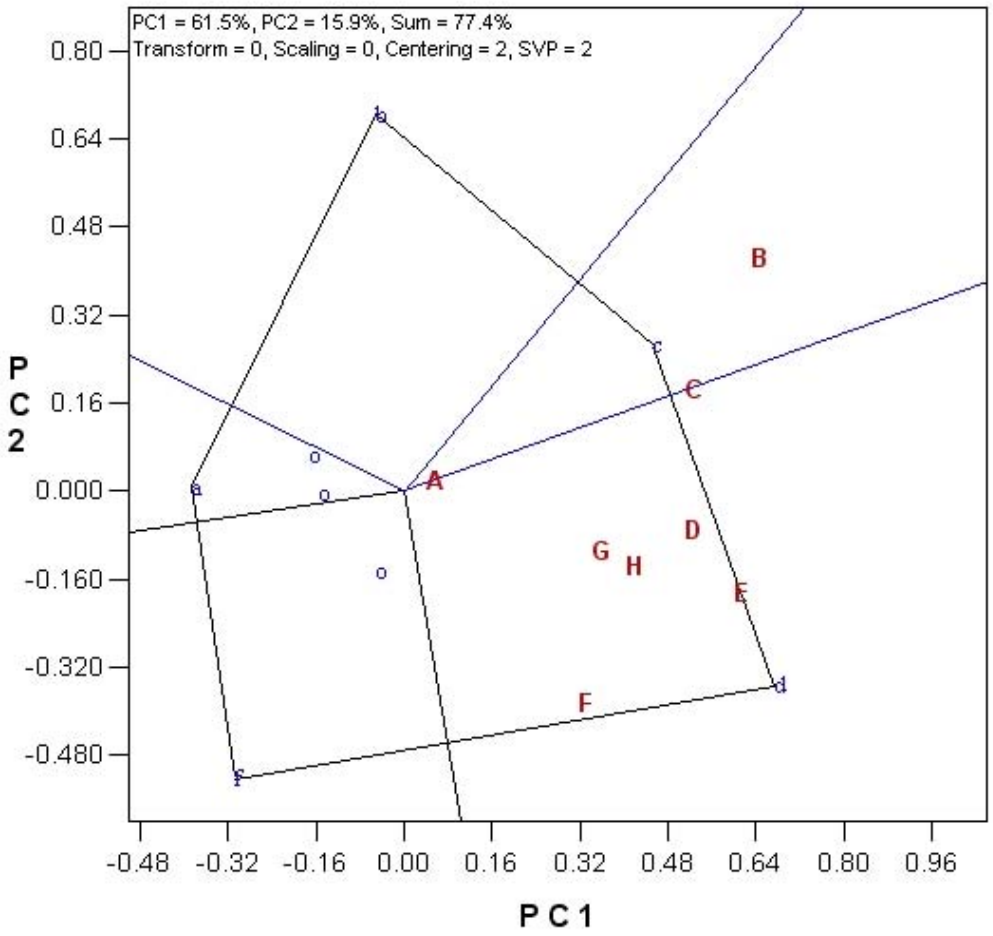

Figure 11: Biplot showing polygon view of five parents for fiber micronaire in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

The pureline Deltapine 50, was significantly different from all parents at p=0.05 (Table 3). When comparing the pureline Deltapine 50 among all combinations involving Deltapine 50 in the table of means for fiber micronaire (Table 3), we can conclude that the pureline is not significantly different from Deltapine 50/Hil B-182-39 at p=0.05. Although the biplot suggests the pureline Deltapine 50 will perform the best among all combinations within the Deltapine 50 sector, its performance is not significantly different from Deltapine 50/Hil B-182-39 (Table 3). Overall, Hil A-106-8 and tester Hil A-106-8 were located furthest from each other on the biplot (Figure 11) suggesting that Hil A-106-8 provided the poorest combination for micronaire. This is reflected in the table of means for lint percent, as Hil A-106-8 exhibited the lowest mean for micronaire at 3.9 (Table 3). However, Hil B-182-39 did not form a sector on the polygon view for micronaire (Figure 11). Yet, it still exhibited a mean value of 3.9 suggesting that Hil B-182-39 is equally as poor of a tester for micronaire as Hil A-106-8 (Table 3).

The polygon view of the biplot for fiber micronaire for 2008 provides us with four sectors (Figure 12). Entries Tamcot CAMD-E, Deltapine 491, Deltapine 50, and Hil B-182-39 form these sectors (Figure 12). No testers fell in the sectors of Tamcot CAMD-E or Hil B-182-39 suggesting these entries produced the poorest combinations with some or all of the testers (Figure 12). The Deltapine 491 sector contained testers Tamcot CAMD-E, FiberMax 832, Deltapine 491, and Hil C-155-22; while the Deltapine 50 sector contained testers Deltapine 50, Hil B-182-39, Hil B-147-21, and Hil C-155-22 (Figure 12). Since the Deltapine 491 sector contained the Deltapine 491 tester, and the Deltapine 50 sector contained the Deltapine 50 tester; we can conclude that pureline Deltapine 491 and pureline Deltapine 50 are the best among all combinations involving Deltapine 491 or Deltapine 50. Furthermore, this suggests that heterosis between Deltapine 491 or Deltapine 50 and any other testers is not possible. This prediction is confirmed by the table of means for micronaire provided by the Agrobase analysis (Table 3). The purline Deltapine 491 provides a mean value of 5.1, and pureline Deltapine 50 provides a mean value of 5.3 (Table 3). No combinations involving Deltapine 491 or Deltapine 50 exceed the mean values of the parent at $p=0.05$ (Table 3). This confirms that heterosis between Deltapine 491 and Deltapine 50 and any other tester is not present (Table 3). Overall Hil B-182-39 fell furthest from tester Hil B-182-39 on the biplot suggesting that the parental combination Hil B-182-39 is the poorest tester for fiber micronaire (Figure 12).

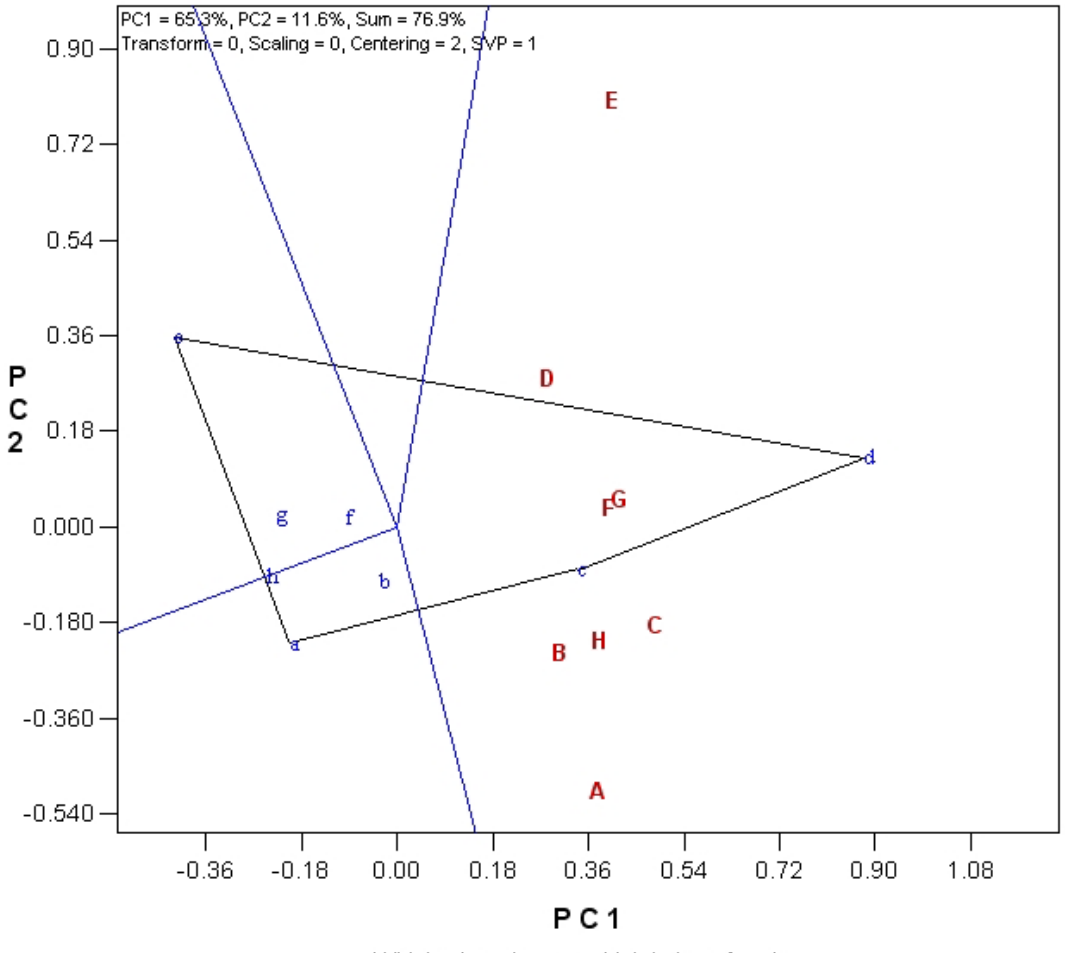

Figure 12: Biplot showing polygon view of four parents for fiber micronaire in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Fiber length uniformity

All values for fiber length uniformity were in the non-discount range as defined by the 2008 CCC Loan Schedule (National Cotton Council, 2008). Biplot analysis for fiber length uniformity (%) showed FiberMax 832, Hil B-147-21, Hil B-182-39, Hil A-06-8, and Hil C-155-22 had positive GCA effects; and Tamcot CAMD-E, Deltapine 491, and Deltapine 50 exhibited negative GCA effects (Figure 13). Hil A-106-8 exhibited the highest GCA effect, while Tamcot CAMD-E exhibited the lowest GCA effect. Both effects were significantly different than zero at p=0.01 (Table 4). The relative rankings based on the biplot analysis are Hil A-106-8 > Hil C-155-22 > Hil B-182-39 > Hil B-147-21 > FiberMax 832 > Deltapine 50 > Deltapine 491 > Tamcot CAMD-E (Figure 13). These rankings are similar to the results produced by the Agrobase analysis (Table 4). Furthermore, the biplot explained 83.9% (PC1= 63.1% and PC2= 20.8%) of the total variation partitioned into GCA effects of parents and SCA effects of progeny in conventional analyses.

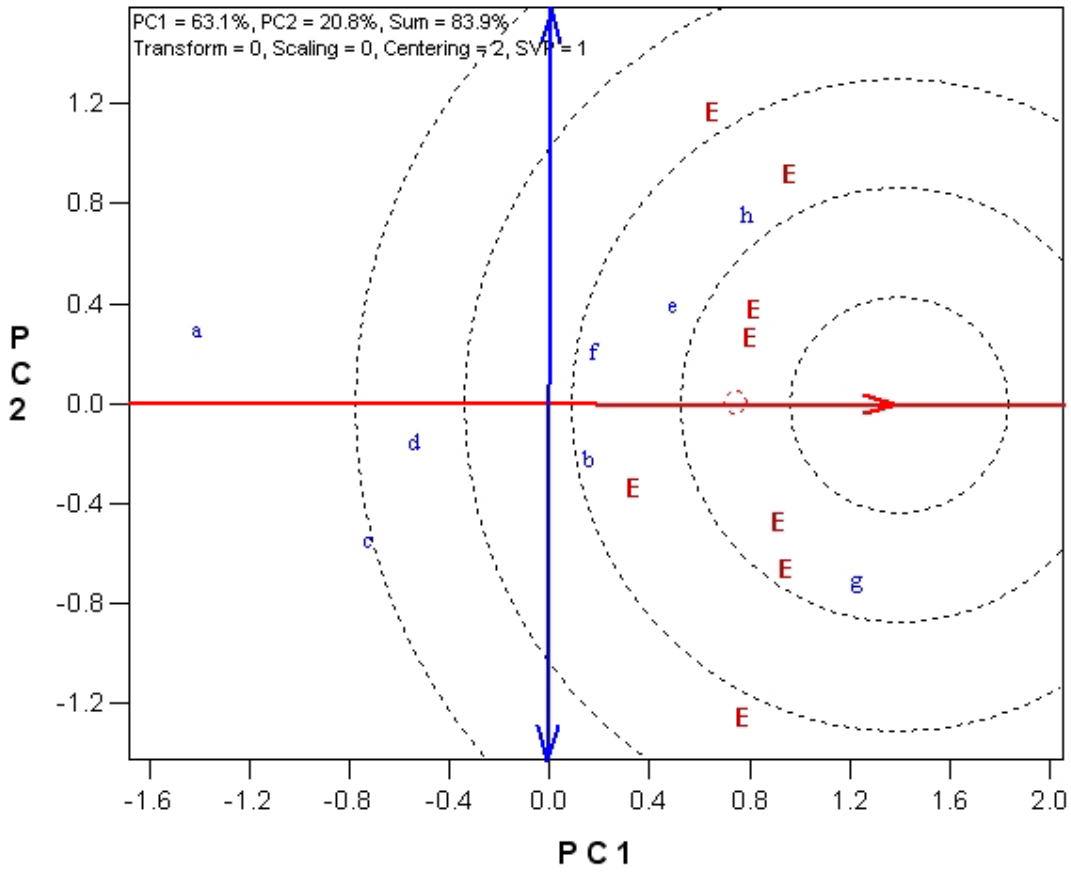

Figure 13: Biplot showing average tester coordinate view, based on diallel data for fiber length uniformity in 2007. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Table 4: Table of means, GCA effects, and SCA effects from diallel analysis of fiber length uniformity for eight cotton (Gossypium hirsutum L.) genotypes and 28 F_1 progeny in 2007 and 2008.

	Length Uniformity			
	2007		2008	
Parent	Mean -%-	GCA	Mean -%-	GCA
Tamcot CAMD-E	81.1	-1.070**	81.7	-1.177**
FiberMax 832	83.8	0.123	85.8	0.423**
Deltapine 491	82.6	-0.515**	84.8	-0.287*
Deltapine 50	82.8	-0.393**	83.4	-0.514**
Hil B-182-39	84.1	0.383**	85.2	0.411**
Hil B-147-21	83.7	0.100	85.8	0.318*
Hil A-106-8	84.5	0.865**	86.5	0.546**
Hil C-155-22	83.8	0.508**	85.4	0.281*
LSD (0.05)		0.237		0.271
Combinations	Mean -%-	SCA	Mean -%-	SCA
Tamcot CAMD-E/FiberMax 832	83.3	0.467	84.4	-0.326
Tamcot CAMD-E/Deltapine 491	81.9	-0.296	84.3	0.359
Tamcot CAMD-E/Deltapine 50	82.9	0.632	84.2	0.411
Tamcot CAMD-E/Hil B-182-39	82.3	-0.718	85.4	0.736
Tamcot CAMD-E/Hil B-147-21	83.4	0.589	85.8	1.204**
Tamcot CAMD-E/Hil A-106-8	84.0	0.424	84.9	0.126
Tamcot CAMD-E/Hil C-155-22	83.1	-0.068	84.8	0.241
FiberMax 832/Deltapine 491	82.8	-0.538	85.1	-0.491
FiberMax 832/Deltapine 50	83.2	-0.310	85.5	0.186
FiberMax 832/Hil B-182-39	84.7	0.489	86.9	0.661
FiberMax 832/Hil B-147-21	84.0	-0.003	86.8	0.579
FiberMax 832/Hil A-106-8	84.9	0.207	86.6	0.201
FiberMax 832/Hil C-155-22	84.5	0.139	86.3	0.191
Deltapine 491/Deltapine 50	82.2	-0.623	85.1	0.421
Deltapine 491/Hil B-182-39	84.4	0.827*	84.9	-0.654
Deltapine 491/Hil B-147-21	83.9	0.609	85.6	0.089
Deltapine 491/Hil A-106-8	83.5	-0.556	86.5	0.811
Deltapine 491/Hil C-155-22	84.5	0.777*	85.0	-0.474
Deltapine 50/Hil B-182-39	83.6	-0.146	84.6	-0.726
Deltapine 50/Hil B-147-21	83.6	0.162	85.5	0.241
Deltapine 50/Hil A-106-8	84.6	0.422	86.1	0.639
Deltapine 50/Hil C-155-22	84.1	0.204	86.0	0.829
Hil B-182-39/Hil B-147-21	84.1	-0.188	87.2	0.991*
Hil B-182-39/Hil A-106-8	85.4	0.422	87.0	0.614
Hil B-182-39/Hil C-155-22	84.8	0.154	86.7	0.579
Hil B-147-21/Hil A-106-8	84.5	-0.196	84.0	-2.319**
Hil B-147-21/Hil C-155-22	83.8	-0.563	85.9	-0.154
Hil A-106-8/Hil C-155-22	86.3	1.197**	86.3	0.069
CV (%)	0.97		1.08	
LSD (0.05)	0.95	0.727	1.09	0.832
Grand Mean	83.7		85.4	

*,** Significantly different at 0.05, and 0.01 respectively

All values for fiber length uniformity for 2008 fell into the non-discount to premium range as defined by the 2008 CCC Loan Schedule (National Cotton Council, 2008). FiberMax 832, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 exhibited positive GCA effects while Tamcot CAMD-E, Deltapine 491, and Deltapine 50 exhibited negative GCA effects (Figure 14). The biplot explained 71.5% (PC1=48.5% and PC2=23.0%) of the total variation partitioned into GCA effects of the parents and SCA effects of the progeny in conventional analysis (Figure 14). Hil A-106-8 exhibited the highest GCA effect, while Tamcot CAMD-E exhibited the lowest GCA effect (Figure 14). GCA effects for Deltapine 491, Hil B-147-21, and Hil C-155-22 were significantly different from zero at p=0.05, while Tamcot CAMD-E, FiberMax 832, Deltapine 50, Hil B-182-39, and Hil A-106-8 were significantly different from zero at p=0.01 (Table 4). The relative rankings based on the biplot analysis is Hil A-106-8 > Hil B-147-21 > Hil C-155-22 > FiberMax 832 ≈ Hil B-182-39 > Deltapine 491 > Deltapine 50 > Tamcot CAMD-E (Figure 14).

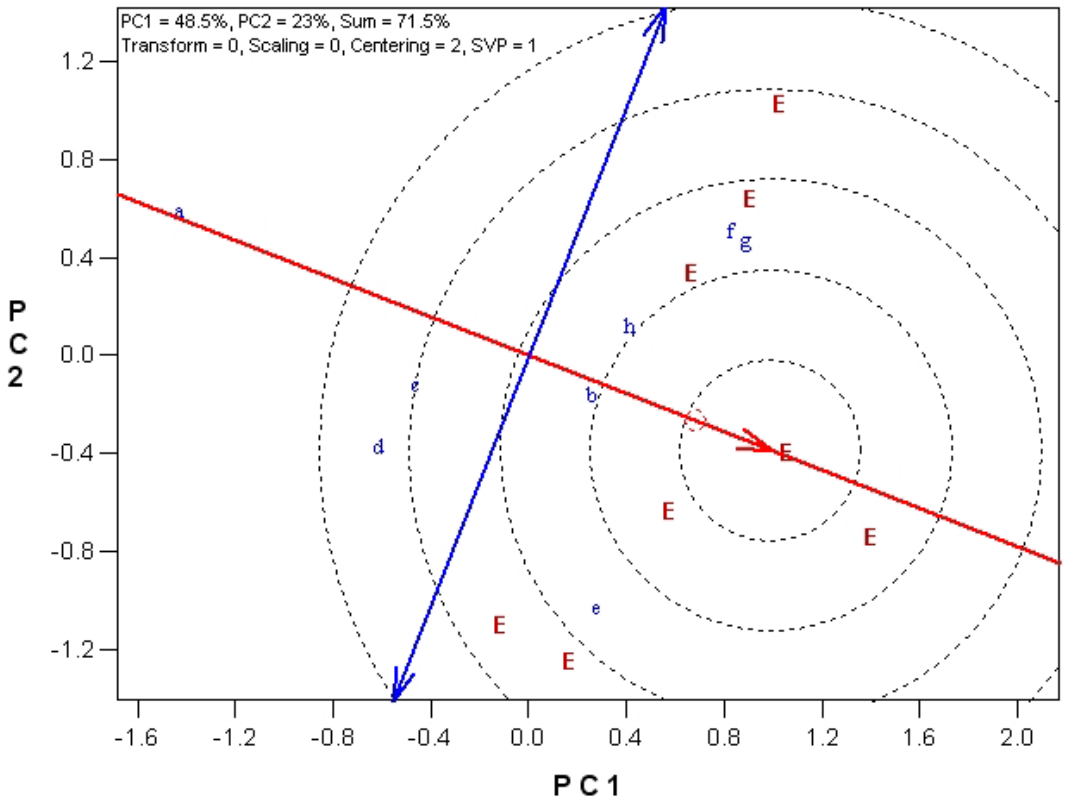

Figure 14: Biplot showing average tester coordinate view, based on diallel data for fiber length uniformity in 2008. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

When compared to the rankings provided by the Agrobase Gen. II analysis (Table 4), similar results can be seen with the exception of the rankings Hil B-147-21 > Hil C-155-22 > FiberMax 832 ≈ Hil B-182-39. According to the agrobase analysis, FiberMax 832 exhibits a GCA effect of 0.423, Hil B-182-39 exhibits a GCA effect of 0.411, Hil B-147-21 exhibits a GCA effect of 0.318, and Hil C-155-22 exhibits a GCA effect of 0.281 (Table 4). The GCA effects for Hil B-147-21, and Hil C-155-22 are significantly different from zero at p=0.05, while the GCA effects for FiberMax 832 and Hil B-182-39 are significantly different from zero at p=0.01 (Table 4). The ranking from the GCA effects in the table of means is Hil A-106-8> FiberMax 832 > Hil B-182-39 > Hil B-147-21 > Hil C-155-22 > Deltapine 491 > Deltapine 50 > Tamcot CAMD-E (Table 4).

Although a significant (p=0.05) GxY interaction exists for fiber length uniformity and there are highly significant differences among GCA for genotypes when averaged across years, a GCAxY interaction is not present (Table 1). This suggests GCA effects for genotypes are stable across years for fiber length uniformity.

Based on the proximity of Deltapine 50 to the ATC abscissa, it was determined to be the best tester in 2007 (Figure 15). Even though FiberMax 832 and Tamcot CAMD-E are more discriminating based on the length of their vectors; distance from the ATC axis makes these cultivars less desirable as testers (Figure 15). All of the testers falling outside of the concentric circles are considered poor testers because of their proximity to the ideal tester center (Figure 15). Hil B-147-21 is considered to be the poorest tester among this group as it is located furthest from the ideal tester center (Figure 15).

Based on its proximity to the ideal tester center and the length of its vector, we can determine that Tamcot CAMD-E is the best tester for fiber length uniformity in 2008 (Figure 16). Hil B-147-21 is considered to be the poorest tester based on its proximity to the ATC abscissa (Figure 16).

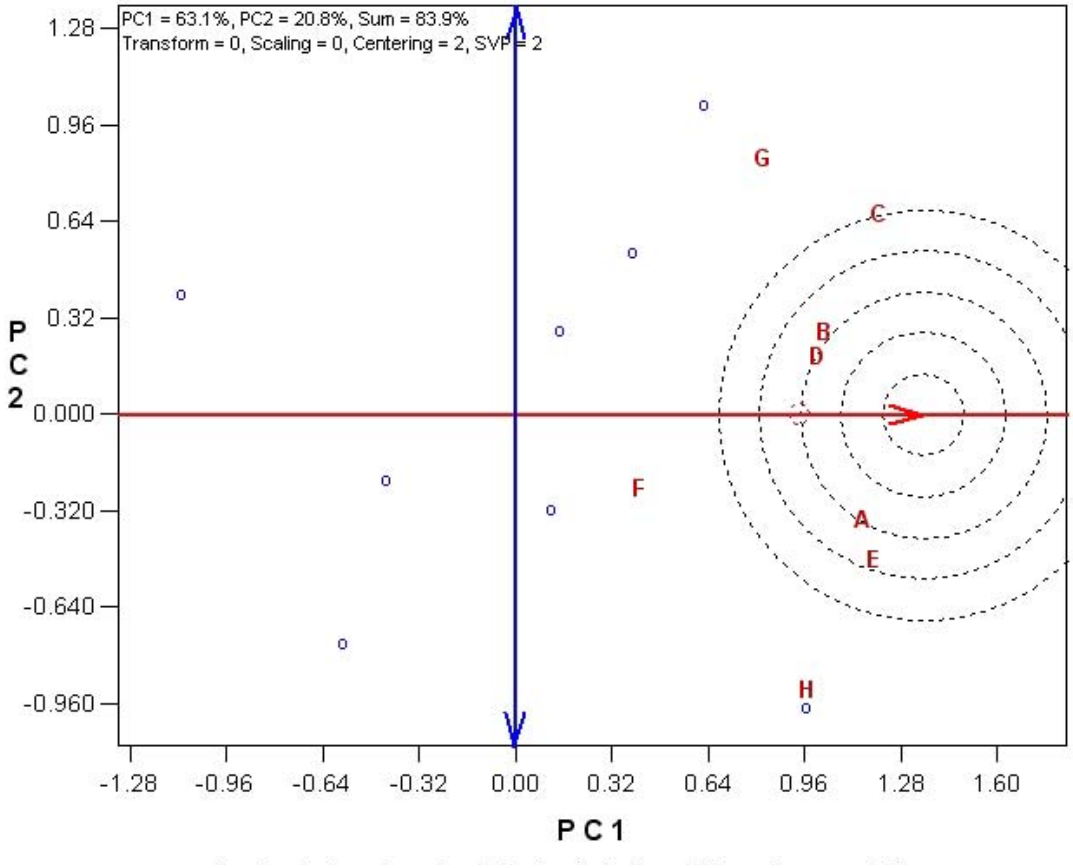

Figure 15: Biplot showing the evaluation of parents as ideal tester for fiber length uniformity in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

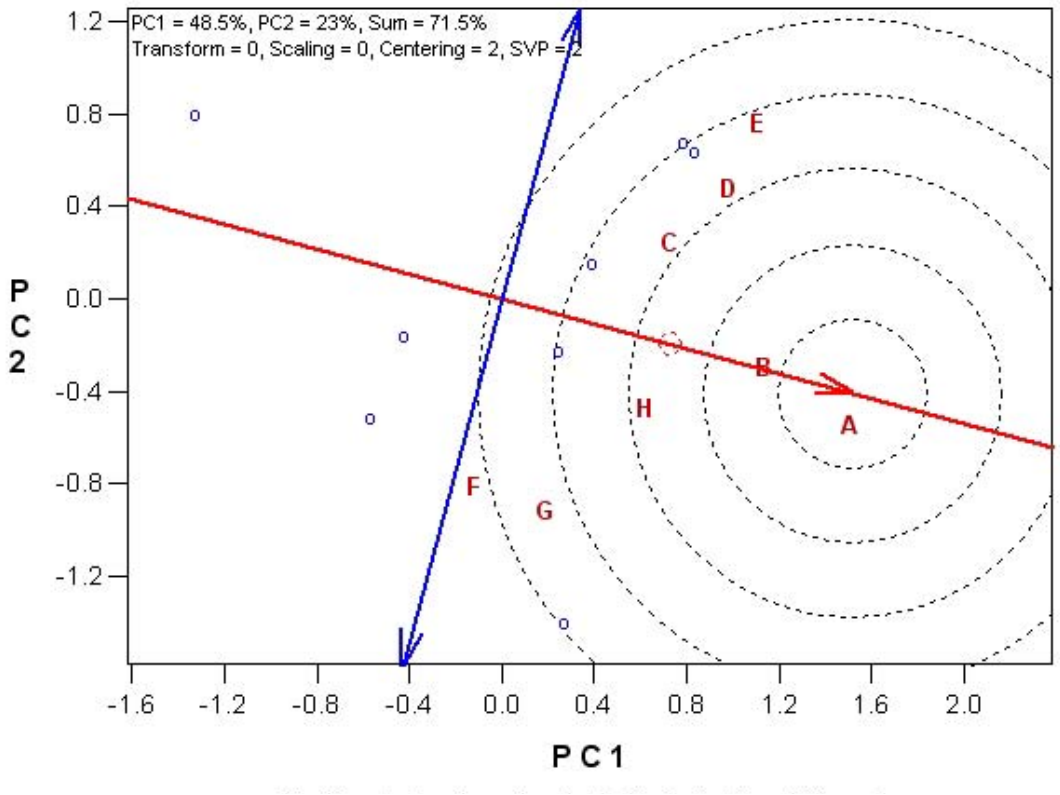

Figure 16: Biplot showing the evaluation of parents as ideal tester for fiber length uniformity in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

The polygon view provides us with four sectors formed by entries Tamcot CAMD-E, Deltapine 491, Hil A-106-8, and Hil C-155-22 (Figure 17). No testers fall into the sectors of Tamcot CAMD-E and Deltapine 491 suggesting these entries produced the poorest combinations with some or all of the testers (Figure 17). The Hil C-155-22 sector contains testers FiberMax 832, Deltapine 491, Deltapine 50, and Hil A-106-8; while Hil A-106-8 sector contains testers Tamcot CAMD-E, Hil B-182-39, Hil B-

147-21, and Hil C-155-22 (Figure 17). Since Hil A-106-8 fell into Hil C-155-22 sector and Hil C-155-22 fell into Hil A-106-8 sector, we can conclude that the combination Hil A-106-8/Hil C-155-22 is the best of all combinations (Figure 17). Furthermore, Hil A-106-8 and Hil C-155-22 are identified as the best parents for fiber length uniformity improvement (Figure 17). When compared to the data of SCA effects as analyzed by Agrobase Gen. II (Table 4), we can determine the results of the biplot analysis are consistent with that of the Agrobase Gen. II analysis. Hil A-106-8/Hil C-155-22, exhibited the highest mean of 86.3 and the highest SCA effect of 1.197 which is significantly different from zero at p=0.01 (Table 4). Since Hil A-106-8 or Hil C-155-22 fell into their own sectors, all crosses involving these testers are likely heterotic (Figure 17). Overall, Tamcot CAMD-E fell furthest from the tester Tamcot CAMD-E on the biplot suggesting pureline Tamcot CAMD-E is the poorest tester for fiber length uniformity (Figure 17). This is confirmed by the table of means for length uniformity provided by the Agrobase analysis (Table 4). Tamcot CAMD-E provides the lowest percent length uniformity at 81.1% which was significantly lower than other parents at p=0.05 (Table 4). When compared to all progeny, Tamcot CAMD-E was significantly different from all progeny at p=0.05 except for Tamcot CAMD-E/Deltapine 491, which exhibited a mean percent uniformity of 81.9% (Table 4).

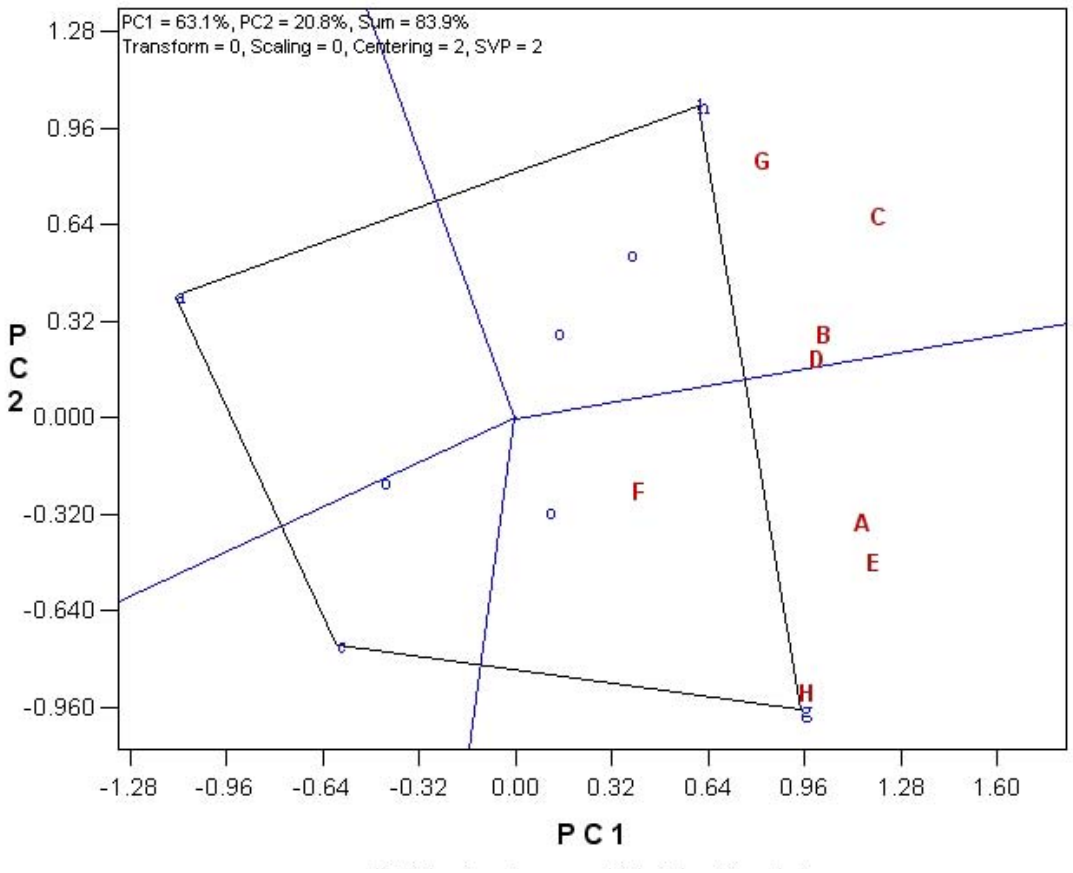

Figure 17: Biplot showing polygon view of four parents for fiber length uniformity in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

For 2008, the polygon view provides us with five sectors formed by entries Tamcot CAMD-E, Deltapine 50, Hil B-182-39, Hil B-147-21, and Hil A-106-8 (Figure 18). No testers fell into the Tamcot CAMD-E or Deltapine 50 sectors suggesting that Tamcot CAMD-E and Deltapine 50 produced the poorest combinations with some or all

of the testers (Figure 18). This is consistent with the table of means provided by Agrobase Gen. II (Table 4). The Hil B-182-39 sector contains testers Hil B-147-21 and Hil A-106-8, the Hil A-106-8 sector contains testers Deltapine 50 and FiberMax 832, and the Hil B-147-21 sector contains testers Deltapine 50 and Hil B-182-39 (Figure 18). Since the Hil B-182-39, Hil B-147-21, or Hil A-106-8 sectors do not contain their respective; testers all crosses made with these genotypes must be heterotic (Figure 18). Since the Hil B-182-39 sector contains tester Hil B-147-21, and the Hil B-147-21 sector contains tester Hil B-182-39; the combination Hil B-182-39/Hil B-147-21 is predicted to be the best of all combinations. This prediction is consistent with the table of means provided by the Agrobase Gen. II analysis (Table 4). Entry Hil B-182-39/Hil B-147-21 exhibited the highest mean of 87.2% which was significantly different from the means of the parents at p=0.05 (Table 4). This suggests heterosis for fiber length uniformity (Table 4). Overall, Tamcot CAMD-E fell furthest from tester Tamcot CAMD-E on the biplot, suggesting pureline Tamcot CAMD-E is the poorest tester for length uniformity (Figure 18). This is confirmed by the table of means for uniformity provided by the Agrobase Gen. II analysis (Table 4). Tamcot CAMD-E, provides the lowest percent uniformity at 81.7% which was significantly lower than all parental values at p=0.05 (Table 4). When compared to all progeny, Tamcot CAMD-E was significantly different from all progeny at p=0.05 (Table 4).

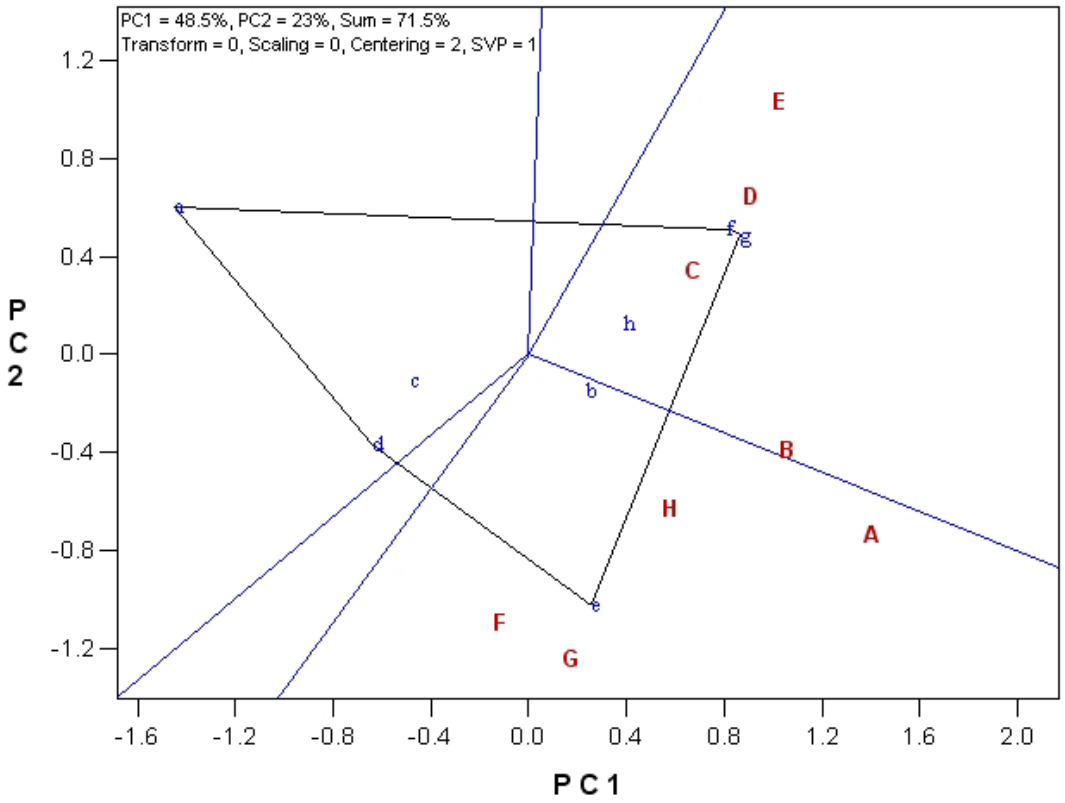

Figure 18: Biplot showing polygon view of five parents for fiber length uniformity in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Fiber length

According to the biplot for fiber length in 2007, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 exhibited positive GCA effects while Tamcot CAMD-E, FiberMax 832, Deltapine 491, and Deltapine 50 exhibited negative effects (Figure 19). Interestingly, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 are experimental lines selected on the bases of desirable fiber characteristics and apparent yield. The biplot explained 92.5% (PC1=85.2% and PC2=7.3%) of total variation partitioned into GCA effects of parents and SCA effects of progeny in conventional analysis. Hil A-106-8 had the highest GCA effect, while Tamcot CAMD-E, had the lowest GCA effect (Figure 19). The rankings based upon the biplot analysis are Hil A-106-8 > Hil B-147-21 > Hil B-182-39 > Hil C-155-22 > Deltapine 491 > FiberMax 832 > Deltapine 50 > Tamcot CAMD-E. When compared to the analysis performed in Agrobase Gen. II (Table 5), results are similar. Hil A-106-8 exhibited the highest GCA effect 1.303 which was significantly different from zero at p=0.01, while Tamcot CAMD-E exhibited the lowest GCA effect –1.884, which was significantly different from zero at p=0.01 (Table 5). All experimental lines exhibited positive GCA effects significantly different from zero at p=0.01 while all commercial cultivars exhibited negative GCA effects significantly different from zero at p=0.01 (Table 5). This suggests there are favorable alleles for length present in the high-length experimental lines not present in the commercial cultivars.

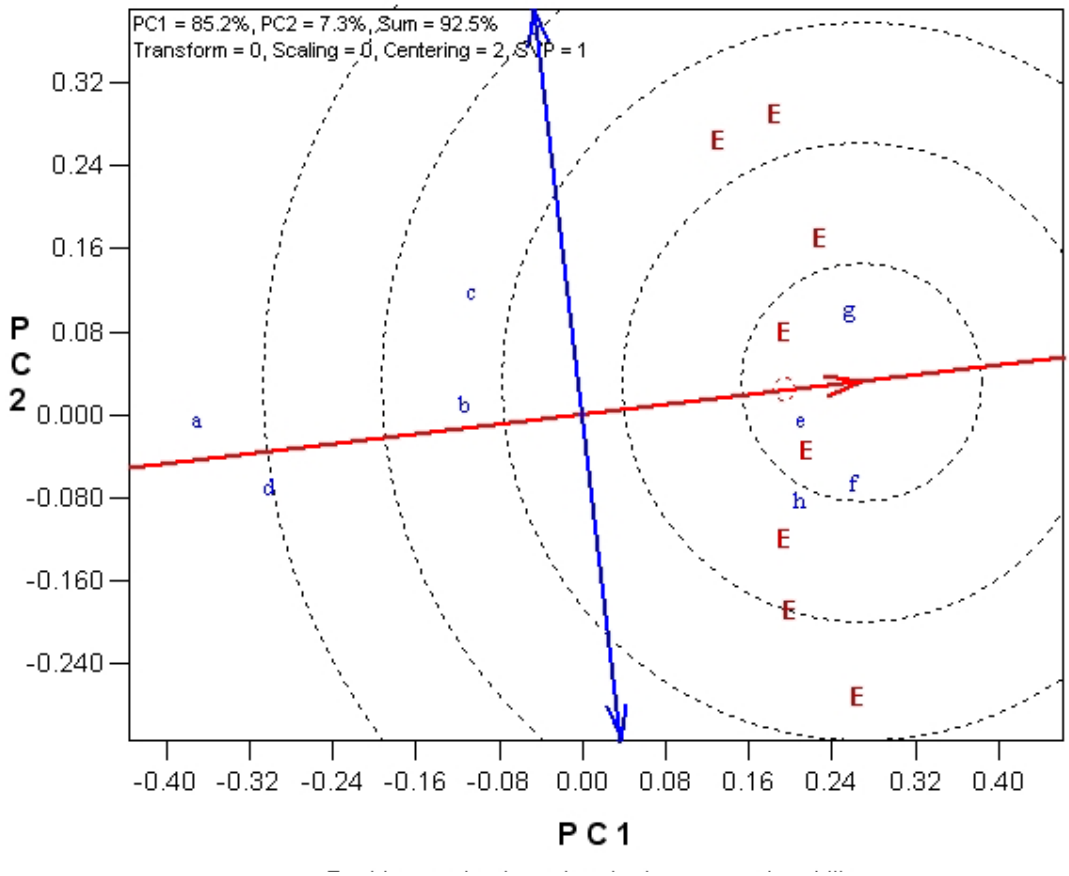

Figure 19: Biplot showing average tester coordinate view, based on diallel data for fiber length in 2007. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Table 5: Table of means, GCA effects, and SCA effects from diallel analysis of fiber length for eight cotton (Gossypium hirsutum L.) genotypes and 28 F_1 progeny in 2007 and 2008.

	Fiber Length			
	2007		2008	
Parent	Mean -mm-	GCA	Mean -mm-	GCA
Tamcot CAMD-E	27.3	-1.884**	28.2	-2.244**
FiberMax 832	29.6	-0.597**	32.5	-0.339
Deltapine 491	29.8	-0.464**	32.8	-0.381*
Deltapine 50	27.9	-1.529**	28.7	-1.939**
Hil B-182-39	33.8	1.108**	34.1	1.094**
Hil B-147-21	32.9	1.236**	36.0	1.209**
Hil A-106-8	33.4	1.303**	36.2	1.369**
Hil C-155-22	31.8	0.828**	35.1	1.231**
LSD (0.05)		0.241		0.366
Combinations	Mean -mm-	SCA	Mean -mm-	SCA
Tamcot CAMD-E/FiberMax 832	29.4	0.260	30.3	-0.991
Tamcot CAMD-E/Deltapine 491	29.0	-0.323	31.5	0.276
Tamcot CAMD-E/Deltapine 50	29.2	0.992**	30.1	0.434
Tamcot CAMD-E/Hil B-182-39	30.4	-0.420	34.4	1.726**
Tamcot CAMD-E/Hil B-147-21	31.2	0.252	33.2	0.386
Tamcot CAMD-E/Hil A-106-8	31.1	0.010	32.8	-0.199
Tamcot CAMD-E/Hil C-155-22	30.9	0.335	33.6	0.739
FiberMax 832/Deltapine 491	30.5	-0.060	33.5	0.321
FiberMax 832/Deltapine 50	29.7	0.230	32.0	0.404
FiberMax 832/Hil B-182-39	32.5	0.317	35.2	0.571
FiberMax 832/Hil B-147-21	32.4	0.090	35.3	0.531
FiberMax 832/Hil A-106-8	32.5	0.197	34.8	-0.079
FiberMax 832/Hil C-155-22	32.4	0.572	35.3	0.534
Deltapine 491/Deltapine 50	29.4	-0.203	32.0	0.421
Deltapine 491/Hil B-182-39	32.8	0.510	34.8	0.189
Deltapine 491/Hil B-147-21	33.4	0.957*	34.7	-0.001
Deltapine 491/Hil A-106-8	32.1	-0.410	34.8	-0.086
Deltapine 491/Hil C-155-22	33.4	1.365**	34.1	-0.599
Deltapine 50/Hil B-182-39	30.5	-0.675	32.4	-0.604
Deltapine 50/Hil B-147-21	31.3	-0.028	33.7	0.531
Deltapine 50/Hil A-106-8	31.9	0.530	34.4	1.071
Deltapine 50/Hil C-155-22	31.5	0.580	33.5	0.384
Hil B-182-39/Hil B-147-21	34.0	0.060	36.3	0.174
Hil B-182-39/Hil A-106-8	34.4	0.317	37.3	0.964
Hil B-182-39/Hil C-155-22	33.6	0.017	37.0	0.851
Hil B-147-21/Hil A-106-8	35.1	0.915*	35.1	-1.301*
Hil B-147-21/Hil C-155-22	33.8	0.090	36.5	0.211
Hil A-106-8/Hil C-155-22	33.9	0.097	36.9	0.401
CV (%)	2.61		3.69	
LSD (0.05)	1.16	0.741	1.75	1.121
Grand Mean	31.6		33.8	

*,** Significantly different at 0.05, and 0.01 respectively

According to the biplot for fiber length in 2008, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 exhibited positive GCA effects, while Tamcot CAMD-E, FiberMax 832, Deltapine 491, and Deltapine 50 exhibited negative GCA effects (Figure 20). The biplot explained 93.7% (PC1=81.3% and PC2=12.4%) of total variation partitioned into GCA effects of the parents and SCA effects of progeny in conventional analysis. Hil A-106-8 exhibited the highest GCA effect of 1.369 while Tamcot CAMD-E exhibited the lowest GCA effect of –2.244 (Table 5). Both effects were significantly different from zero at p=0.01 (Table 5). The ranking based upon the biplot analysis is Hil A-106-8 > Hil B-182-39 ≈ Hil C-155-22 > Hil B-147-21 > FiberMax 832 ≈ Deltapine 491 > Deltapine 50 > Tamcot CAMD-E (Figure 20). When compared to the analysis provided by Agrobase Gen. II, similar results can be seen with the exception of ranking Hil C-155-22 > Hil B-147-21 > Hil B-182-39 > FiberMax 832 > Deltapine 491. Deltapine 491 had a GCA effect of –0.381, FiberMax 832 had a GCA effect of –0.339, Hil B-182-39 had a GCA effect of 1.094, Hil B-147-21 had a GCA effect of 1.209, and Hil C-155-22 had a GCA effect of 1.231 (Table 5). Deltapine 491 had a GCA effect which was significantly different from zero at p=0.05, while Hil B-182-39, Hil B-147-21, and Hil C-155-22 GCA effects were significantly different from zero at p=0.01. The overall ranking from the table of means is Hil A-106-8 > Hil C-155-22 > Hil B-147-21 > Hil B-182-39 > FiberMax 832 > Deltapine 491 > Deltapine 50 > Tamcot CAMD-E.

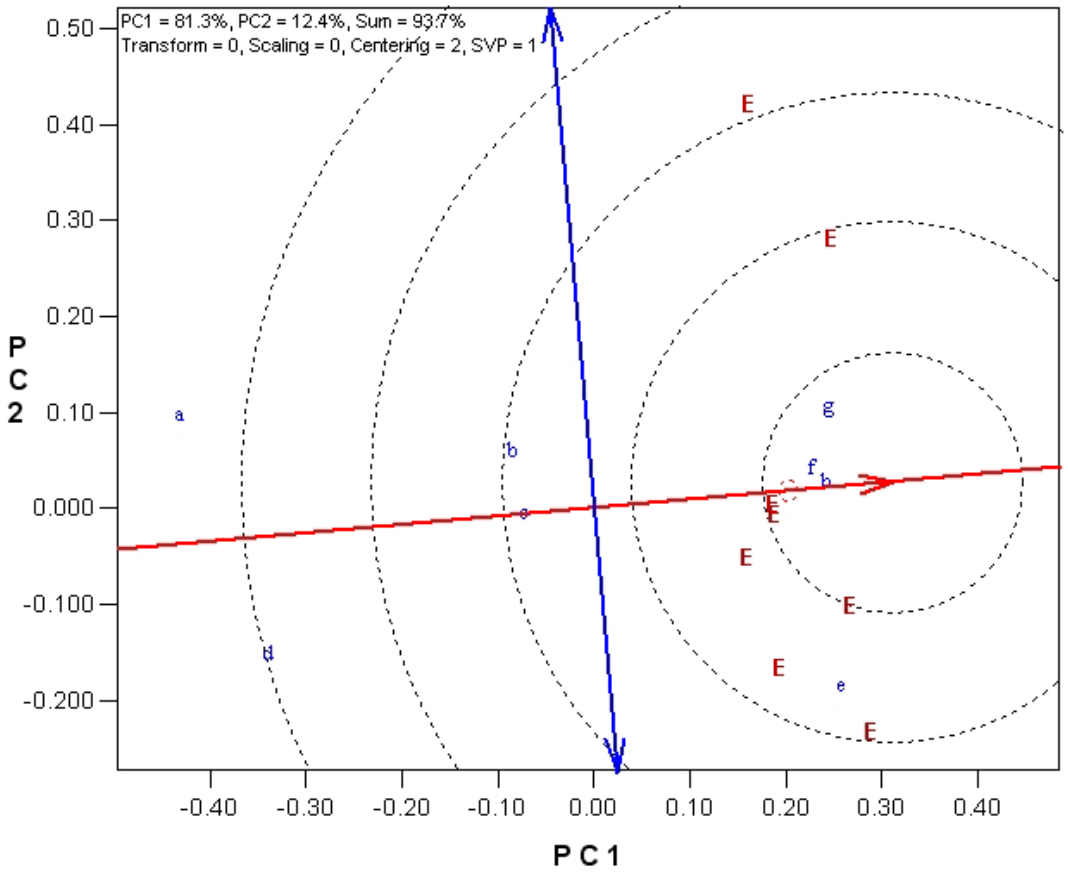

Figure 20: Biplot showing average tester coordinate view, based on diallel data for fiber length in 2008. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Although a significant GxY interaction and significant differences between GCA effects exist for genotypes when averaged across years (Table 1), a GCAxY interaction was not significant. This suggests genotypes were stable across years for GCA effects. Furthermore, experimental ELS lines exhibited positive GCA effects during both years significantly different from zero at p=0.01, while commercial cultivars had negative GCA effects during both years significantly different from zero at p=0.01 (Table 5). This suggests alleles for fiber length are present are present in the ELS lines that are not present in this set of commercial cultivars. Since the experimental ELS lines exhibited positive GCA effects during both years, they would be useful parental material for breeders selecting for increased length in their programs.

FiberMax 832 is predicted to be the best tester for fiber length based on its proximity to the ATC abscissa and its vector length (Figure 21). Even though Deltapine 50 is closer in proximity to the ideal tester center, its vector is shorter making it less discriminating than FiberMax 832 (Figure 21). Hil C-155-22 is considered to be the poorest tester based on its distance from the ideal tester center and length of its vector (Figure 21).

FiberMax 832 is considered to be the best tester based on the length of its vector and proximity to the ATC abscissa (Figure 22). Hil B-182-39 is considered to be the poorest tester based on its distance from the ideal tester center and length of its vector (Figure 22).

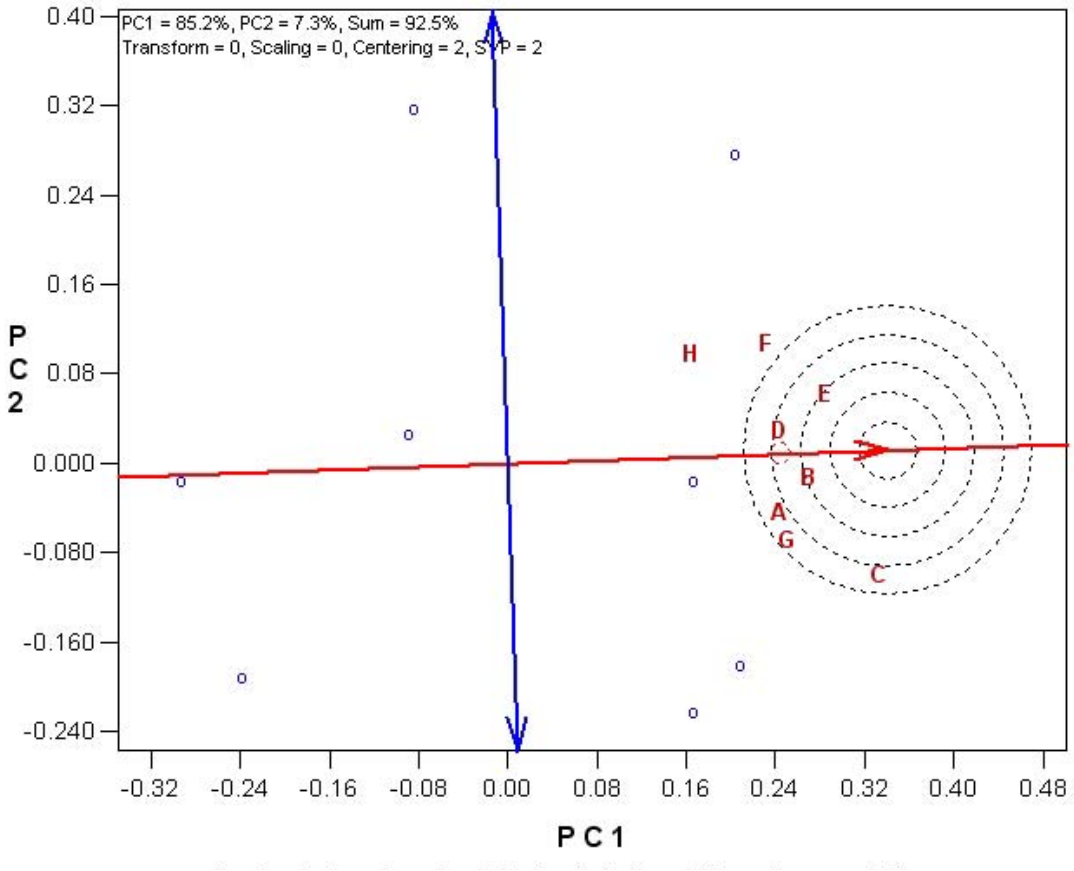

Figure 21: Biplot showing the evaluation of parents as ideal tester for fiber length in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

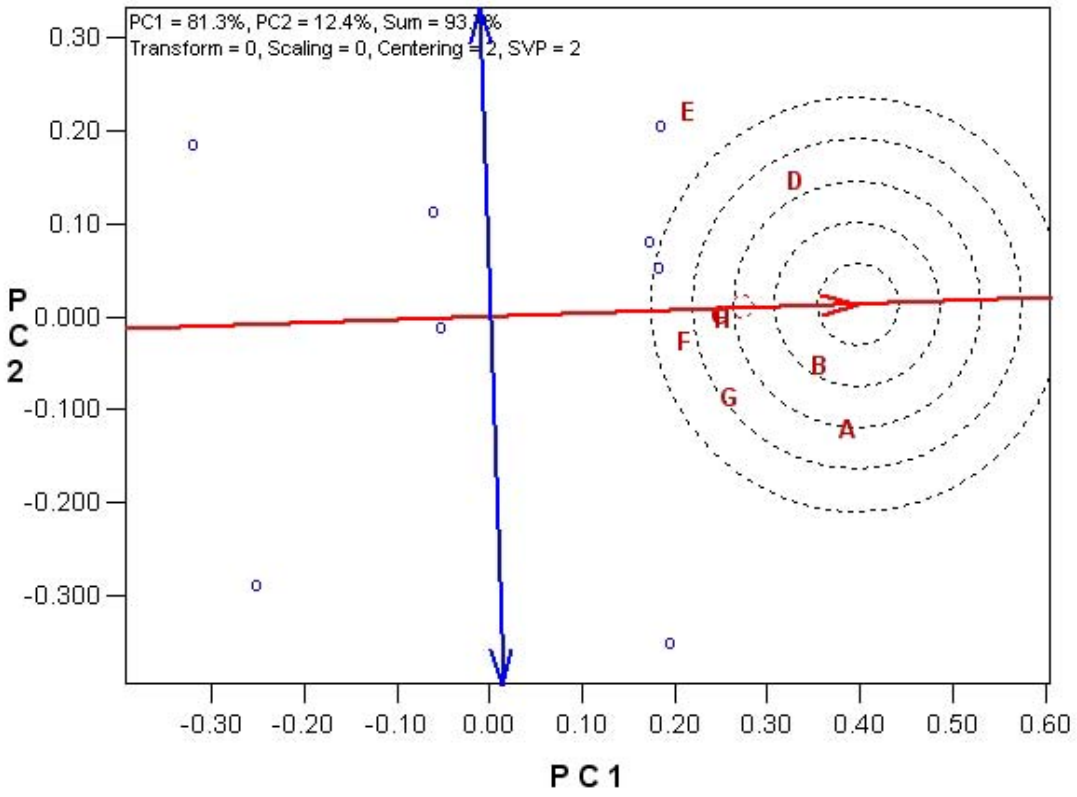

Figure 22: Biplot showing the evaluation of parents as ideal tester for fiber length in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Based on the polygon view there are six sectors formed by Tamcot CAMD-E, Deltapine 491, Deltapine 50, Hil B-147-21, Hil A-106-8, and Hil C-155-22 (Figure 23). No testers fall into the Tamcot CAMD-E, Deltapine 491, Deltapine 50, and Hil C-155-22 sectors suggesting these genotypes produced the poorest combinations with some or all of the testers, which is consistent with the Agrobase analysis (Table 5). The Hil A-106-8 sector contains testers Deltapine 50, Hil B-182-39, Hil B-147-21 and Hil C-155-22, while Hil B-147-21 sector contains testers Tamcot CAMD-E, FiberMax 832, Deltapine 491, and Hil A-106-8 (Figure 23). Since the Hil B-147-21 or Hil A-106-8 sectors contained their testers, progeny lines derived from these parents must be heterotic (Figure 23). The combination Hil B-147-21/Hil A-106-8 is predicted to be the best of all combinations. This prediction is consistent with data provided from the Agrobase Gen. II analysis (Table 5). Hil B-147-21/Hil A-106-8 exhibited the highest mean length of 35.1 mm, which was significantly different from the grand mean at $p=0.05$ (Table 5).

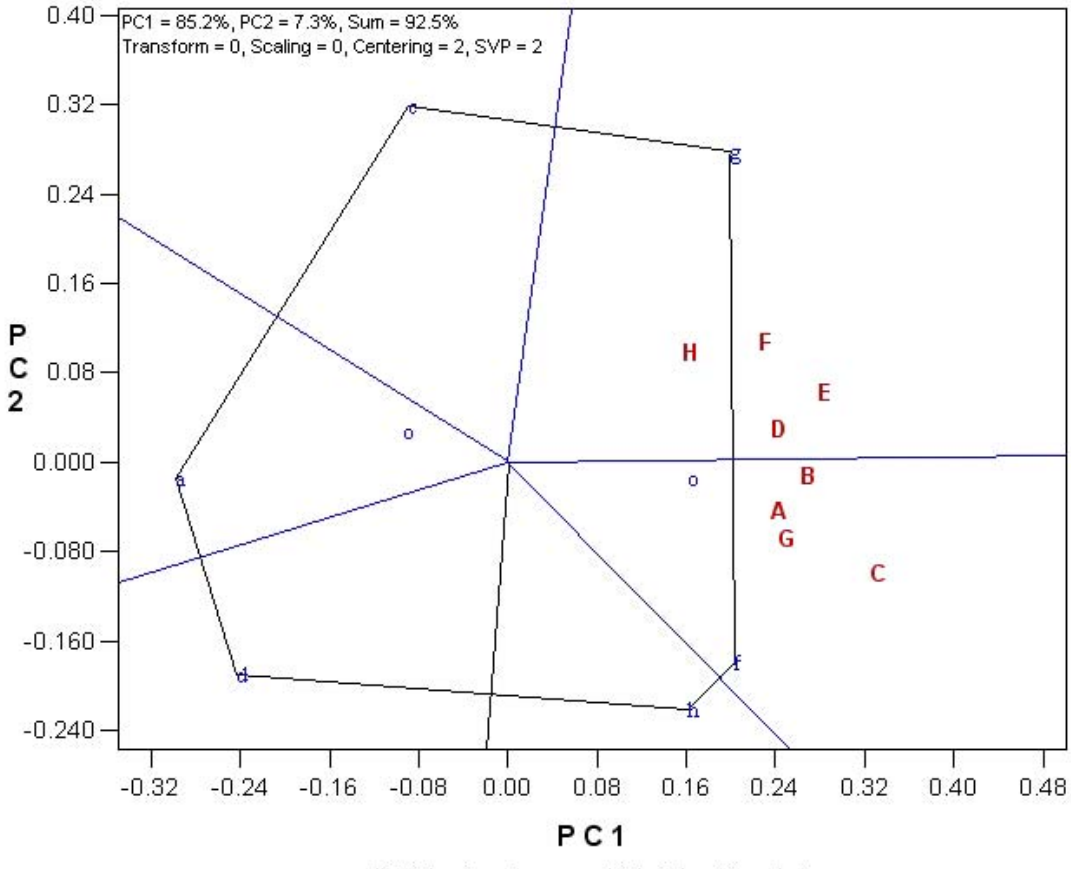

Figure 23: Biplot showing polygon view of six parents for fiber length in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Two combinations, Deltapine 491/Hil B-147-21 and Hil B147-21/Hil A-106-8, had positive SCA effects significantly different from zero at p=0.05, while Tamcot CAMD-E/Deltapine 50, and Deltapine 491/Hil C-155-22 had positive SCA effects significantly different from zero at p=0.01 (Table 5). This suggests that these genotypes had combinations of alleles that positively influenced fiber length. Overall Tamcot CAMD-E and tester Tamcot CAMD-E, and Deltapine 50 and tester Deltapine 50, fell furthest from each other on the biplot. This suggests that pureline Tamcot CAMD-E and Deltapine 50, provided the poorest combinations for fiber length (Figure 23). This prediction is confirmed by the means for fiber length provided by the Agrobase Gen. II analysis (Table 5). Tamcot CAMD-E provided a mean length of 27.3 mm, while Deltapine 50 provided a mean length of 27.9 mm (Table 5). Both values were statistically lower (p=0.05) than all other values for length when compared to parental combinations and progeny (Table 5). This suggests Tamcot CAMD-E and Deltapine 50 lack alleles for fiber length that are present in the ELS genotypes.

Based on the polygon view of fiber length for 2008 (Figure 24), five sectors were formed by Tamcot CAMD-E, Deltapine 50, Hil B-182-39, and Hil A-106-8. No testers fell in the Tamcot CAMD-E or Deltapine 50 sectors suggesting these cultivars produce the poorest combinations with some or all of the testers (Figure 24). The Hil A-106-8 sector contains testers Hil B-182-39 and Deltapine 50, while the Hil B-182-39 sector contains testers Tamcot CAMD-E, FiberMax 832, Deltapine 491, Hil B-147-21, Hil A-106-8, and Hil C-155-22 (Figure 24). Neither the Hil B-182-39 nor the Hil A-106-8 sectors contain their respective testers. All progeny resulting from these parents must be heterotic (Figure 24). Since the Hil A-106-8 sector contains tester Hil B-182-39, and the Hil B-182-39 sector contains tester Hil A-106-8; the combination Hil B-182-39/Hil A-106-8 is predicted to be the best of all combinations involving these parents (Figure 24). This is confirmed by the means provided by the analysis in Agrobase Gen. II (Table 5). The combination Hil B-182-39/Hil A-106-8 had a mean value of 37.3 mm which is significantly than the grand mean at p=0.05 (Table 5). Overall, Tamcot CAMD-E and tester Tamcot CAMD-E, and Deltapine 50 and tester Deltapine 50 fell furthest from each other on the biplot suggesting the pureline Tamcot CAMD-E and Deltapine 50 provide the poorest combinations for fiber length (Figure 24). Results of the Agrobase Gen. II analysis coincide with the findings (Table 5). The parental combination Tamcot CAMD-E exhibited a mean of 28.2 mm, and Deltapine 50 had a mean of 28.7 mm. (Table 5). Although the mean values of Tamcot CAMD-E and Deltapine 50 are not significantly different from each other at p=0.05, they are significantly lower than other parental and progeny values at p=0.05 (Table 5).

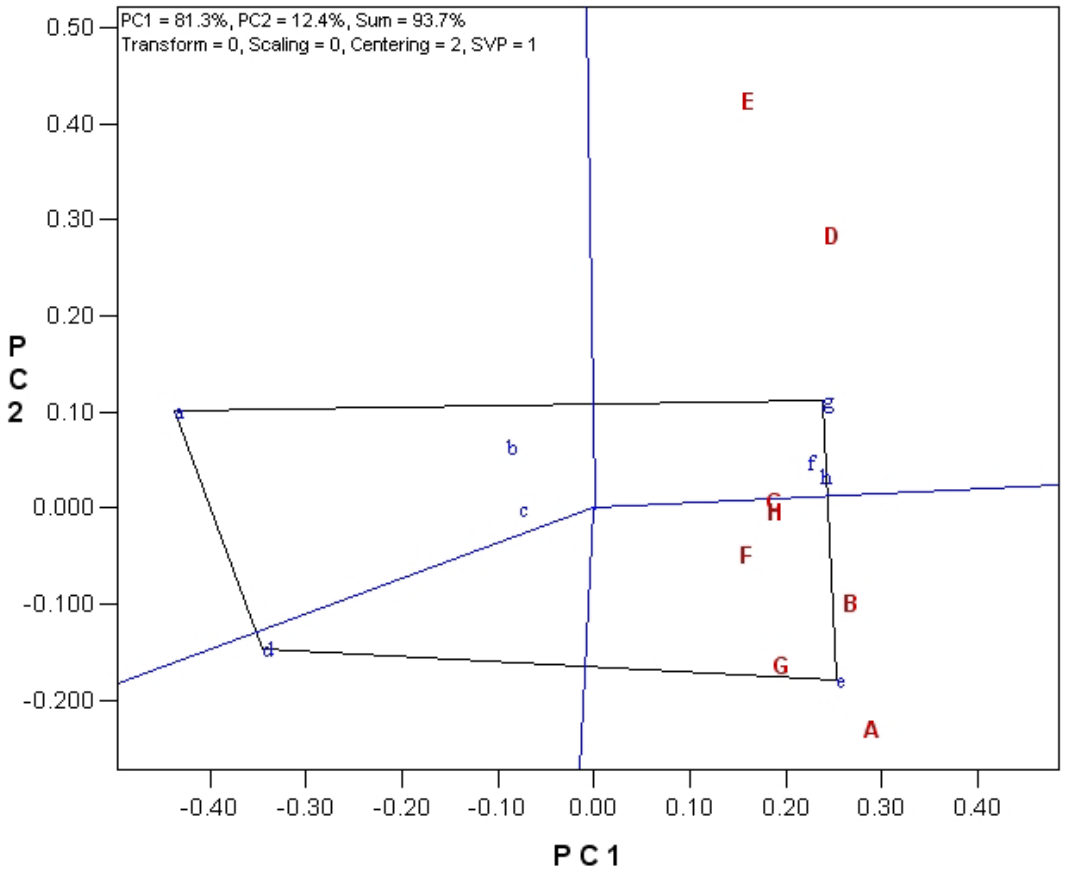

Figure 24: Biplot showing polygon view of four parents for fiber length in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Fiber strength

Biplot analysis of fiber strength showed FiberMax 832, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 had positive GCA effects while Tamcot CAMD-E, Deltapine 491, and Deltapine 50 exhibited negative GCA effects (Figure 25). The biplot analysis explained 87.1% (PC1= 72.7% and PC2=14.4%) of the total variation partitioned into GCA effects of the parents and SCA effects of progeny in conventional analysis. Hil B-182-39 had exhibited the highest GCA effect, while Tamcot CAMD-E exhibited the lowest GCA for fiber strength. The relative ranking of GCA effects provided by the biplot is Hil A-106-8 > Hil B-147-21 > Hil B-182-39 > Hil C-155-22 ≈ Deltapine 491 > Tamcot CAMD-E ≈ Deltapine 50. The analysis performed by Agrobase Gen. II returned similar rankings with the exception of ranking the effect Deltapine 50 > Tamcot CAMD-E instead of Tamcot CAMD-E ≈ Deltapine 50 (Table 6). Deltapine 50 is located on the ATC abscissa, while Tamcot CAMD-E is located away from the ATC abscissa (Figure 25). Deltapine 50 had a GCA effect of –22.250 and Tamcot CAMD-E had a GCA effect of –22.375 (Table 6). Both GCA effects were significantly different from zero at p=0.01. All experimental lines exhibited positive GCA effects, with GCA effects for Hil B-182-39, Hil B-147-21, and Hil A-106-8 being significantly different from zero at p=0.01 (Table 6). FiberMax 832 was the only commercial cultivar to exhibit positive GCA effect for fiber strength which was significantly different from zero at p=0.05 (Table 6). All other commercial cultivars exhibited negative GCA effects for fiber strength (Table 6). This suggests the ELS genotypes and FiberMax 832 contain alleles for strength that are not present in the other commercial cultivars.

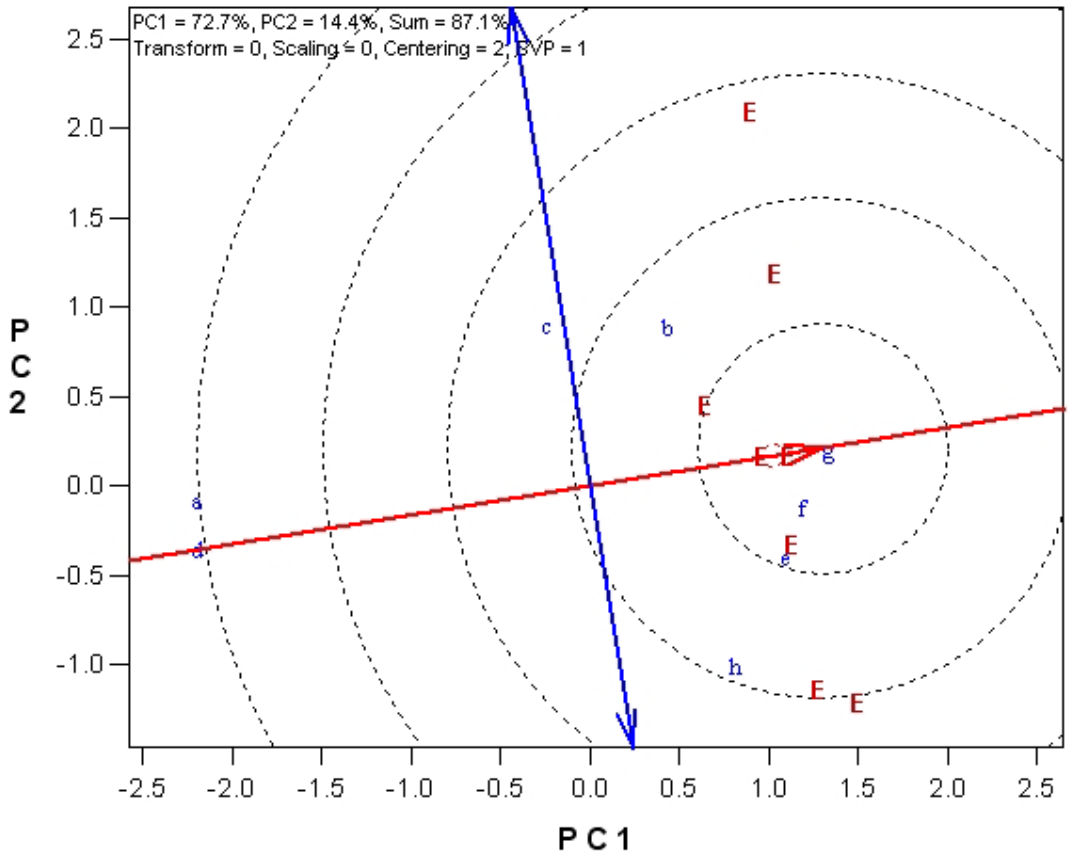

Figure 25: Biplot showing average tester coordinate view, based on diallel data for fiber strength in 2007. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Table 6: Table of means, GCA effects, and SCA effects from diallel analysis of fiber strength for eight cotton (Gossypium hirsutum L.) genotypes and 28 F_1 progeny in 2007 and 2008.

	Fiber Strength			
	2007		2008	
Parent	Mean -kN m kg^{-1}-	GCA	Mean -kN m kg^{-1}-	GCA
Tamcot CAMD-E	259	-22.375**	294	-22.706**
FiberMax 832	304	4.650*	366	4.419*
Deltapine 491	300	-0.725	367	-0.506
Deltapine 50	258	-22.250**	298	-18.331**
Hil B-182-39	327	11.225**	352	9.269**
Hil B-147-21	326	11.125**	372	11.069**
Hil A-106-8	331	13.325**	361	9.619**
Hil C-155-22	298	5.025*	319	7.169**
LSD (0.05)		3.817		4.242
Combinations	Mean -kN m kg^{-1}-	SCA	Mean -kN m kg^{-1}-	SCA
Tamcot CAMD-E/FiberMax 832	297	2.197	319	-9.803
Tamcot CAMD-E/Deltapine 491	281	-8.678	326	1.844
Tamcot CAMD-E/Deltapine 50	279	10.847	303	-3.330
Tamcot CAMD-E/Hil B-182-39	305	3.122	344	10.319
Tamcot CAMD-E/Hil B-147-21	313	11.222	335	-1.231
Tamcot CAMD-E/Hil A-106-8	300	-3.728	344	9.719
Tamcot CAMD-E/Hil C-155-22	298	2.572	340	7.919
FiberMax 832/Deltapine 491	309	-7.953	332	-19.031**
FiberMax 832/Deltapine 50	296	1.072	331	-2.956
FiberMax 832/Hil B-182-39	343	13.847*	357	-4.056
FiberMax 832/Hil B-147-21	328	-0.303	365	1.644
FiberMax 832/Hil A-106-8	346	14.747*	373	11.094
FiberMax 832/Hil C-155-22	335	12.047*	362	3.044
Deltapine 491/Deltapine 50	287	-3.303	326	-2.781
Deltapine 491/Hil B-182-39	330	6.972	345	-11.361
Deltapine 491/Hil B-147-21	339	15.322*	361	2.569
Deltapine 491/Hil A-106-8	325	-0.628	352	-4.731
Deltapine 491/Hil C-155-22	338	20.422**	347	-7.031
Deltapine 50/Hil B-182-39	301	-1.253	347	8.194
Deltapine 50/Hil B-147-21	304	2.347	348	8.144
Deltapine 50/Hil A-106-8	310	6.397	343	4.594
Deltapine 50/Hil C-155-22	300	4.447	349	13.044*
Hil B-182-39/Hil B-147-21	333	-2.128	379	11.294
Hil B-182-39/Hil A-106-8	337	-0.328	376	9.244
Hil B-182-39/Hil C-155-22	325	-4.278	368	4.444
Hil B-147-21/Hil A-106-8	327	-10.478	347	-21.556**
Hil B-147-21/Hil C-155-22	332	3.072	360	-5.856
Hil A-106-8/Hil C-155-22	342	10.872	368	3.344
CV (%)	4.16		4.16	
LSD (0.05)	18.3	11.702	20.3	13.004
Grand Mean	313		347	

*,** Significantly different at 0.05, and 0.01 respectively

According to biplot analysis of fiber strength for 2008 FiberMax 832, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 exhibited positive GCA effects while Tamcot CAMD-E, Deltapine 491, and Deltapine 50 had negative GCA effects (Figure 26). The biplot analysis explained 83.8% (PC1= 72.5% and PC2=11.3%) of the total variation partitioned into GCA effects of parents and SCA effects of progeny in conventional analysis. Hil A-106-8 exhibited the highest GCA effect while Tamcot CAMD-E exhibited the lowest GCA effect (Figure 26). The relative ranking of GCA effects provided by the biplot analysis is Hil A-106-8 > Hil B-147-21 > Hil B-182-39 > Hil C-155-22 > FiberMax 832 > Deltapine 491 > Deltapine 50 > Tamcot CAMD-E. When compared to the means provided by the Agrobase Gen. II analysis the ranking of Hil B-147-21>Hil A-106-8 is different from the biplot analysis (Table 6). According to the table of means, Hil B-147-21 had the highest mean at 372 kN m kg^{-1} and GCA effect of 11.069 which was significantly different from zero at p=0.01 (Table 6). Hil A-106-8 had a GCA effect of 9.619 (Table 6). GCA effects for Tamcot CAMD-E, Deltapine 50, Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22 were significantly different from zero at p=0.01, while FiberMax 832 GCA effect was significantly different from zero at p=0.05 (Table 6). The relative ranking of GCA effects from the table of means is Hil B-147-21 > Hil A-106-8 > Hil B-182-39 > Hil C-155-22 > FiberMax 832 > Deltapine 491 > Deltapine 50 > Tamcot CAMD-E.

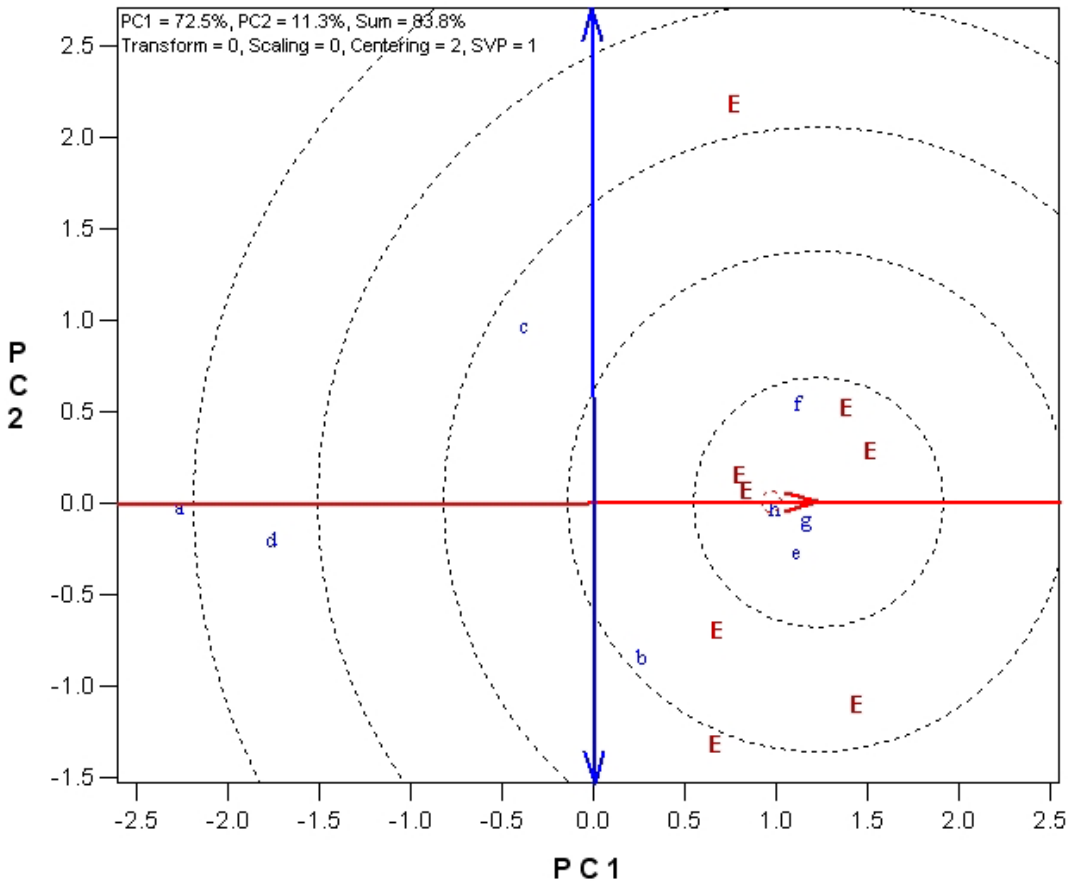

Figure 26: Biplot showing average tester coordinate view, based on diallel data for fiber strength in 2008. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Although a significant GxY interaction and significant differences between GCA effects exist for genotypes when averaged across years (Table 1), a GCAxY interaction was not significant. This suggests GCA effects among genotypes were stable across years. All experimental ELS lines and FiberMax 832 had positive GCA effects for fiber strength suggesting that alleles for strength are present in these particular parents that are not present in the other genotypes in this study (Table 6). Furthermore, the experimental ELS lines and FiberMax 832 would make good parental material for breeders wanting to increase fiber strength in their programs breeding lines.

Deltapine 50 is predicted to be the best tester for fiber strength based on its proximity to the ATC abscissa and vector length (Figure 27). Although Deltapine 491 is in similar proximity to the ideal tester center, its vector length is shorter making it less discriminating (Figure 27). Hil B-147-21 is considered to be the poorest tester based on its proximity to the ideal tester center and short vector length (Figure 27).

Deltapine 50 is predicted to be the best tester for fiber strength based on its proximity to the ATC abscissa and vector length (Figure 28). Although Tamcot CAMD-E is similar in proximity to the ideal tester center, its vector length is shorter and less discriminating (Figure 28). Deltapine 491 is considered to be the poorest tester for fiber strength (Figure 28).

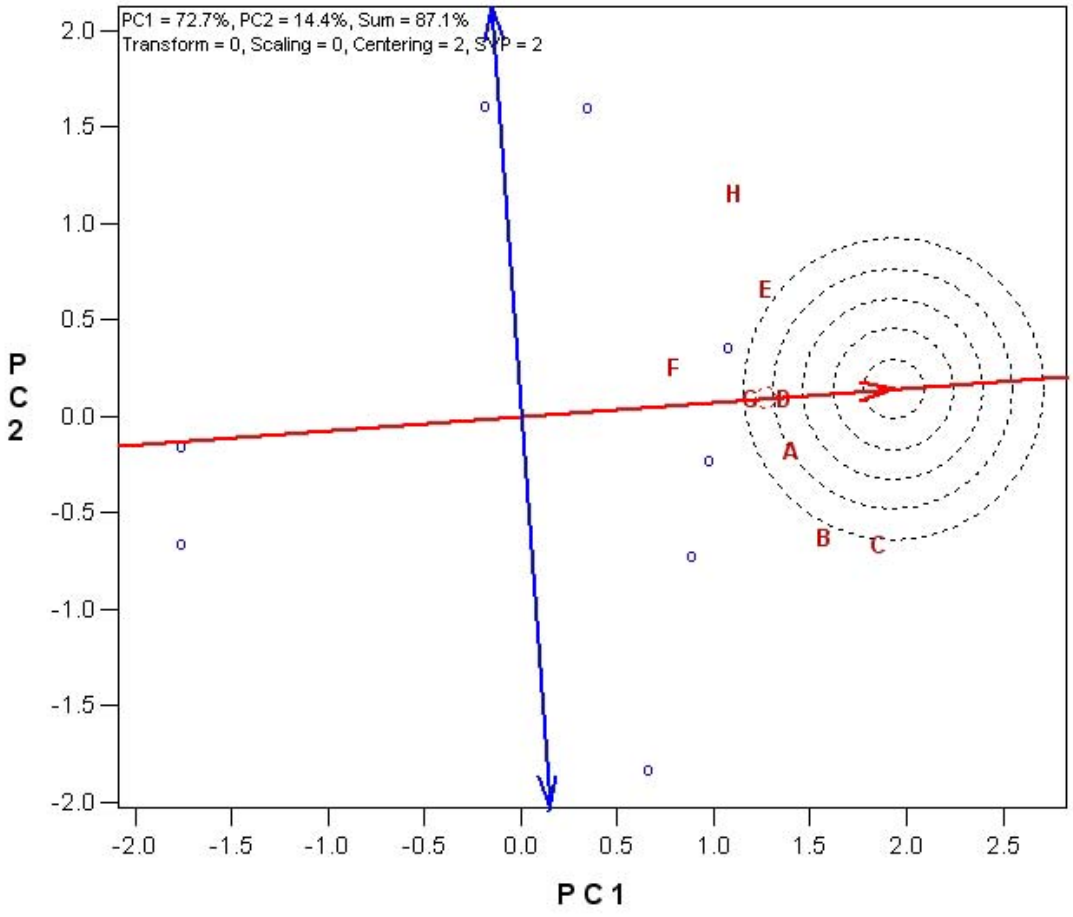

Figure 27: Biplot showing the evaluation of parents as ideal tester for fiber strength in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

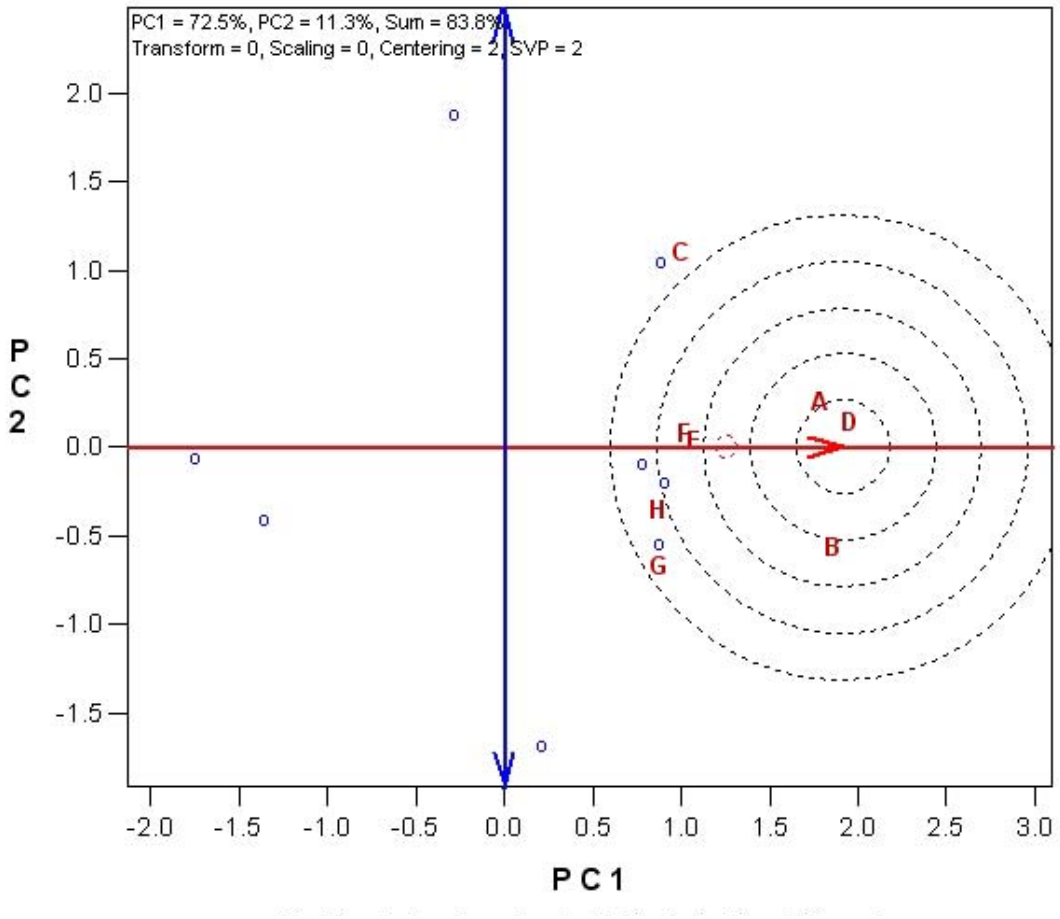

Figure 28: Biplot showing the evaluation of parents as ideal tester for fiber strength in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

According to the polygon view for fiber strength we can see that six sectors are formed by Tamcot CAMD-E, FiberMax 832, Deltapine 491, Deltapine 50, Hil A-106-8, and Hil C-155-22 (Figure 29). No testers fell into the sectors of Tamcot CAMD-E, Deltapine 491, Deltapine 50, and Hil C-155-22 suggesting these genotypes produced the poorest combinations with some or all of the testers (Figure 29). Tester Hil C-155-22 fell into the FiberMax 832 sector while testers FiberMax 832 and Deltapine 491 fell into the Hil B-182-39 sector (Figure 29). Since the FiberMax 832 or Hil B-182-39 sectors contained their testers, all progeny derived from these genotypes can be assumed to be heterotic (Figure 29). This is reflected in the table of means provided by Agrobase Gen. II (Table 3). FiberMax 832/Hil B-182-39, FiberMax 832/Hil C-155-22, and Deltapine 491/Hil B-182-39 had mean values that exceeded those of the parents suggesting heterosis for fiber strength (Table 6). This is consistent with the data provided by the analysis in Agrobase Gen. II (Table 6). The combinations FiberMax 832/Hil B-182-39, FiberMax 832/Hil C-155-22, and Deltapine 491/Hil B-182-39 all exhibited mean values statistically different ($p=0.05$) from those of the respective parents which suggests heterosis for fiber strength in these combinations (Table 6).

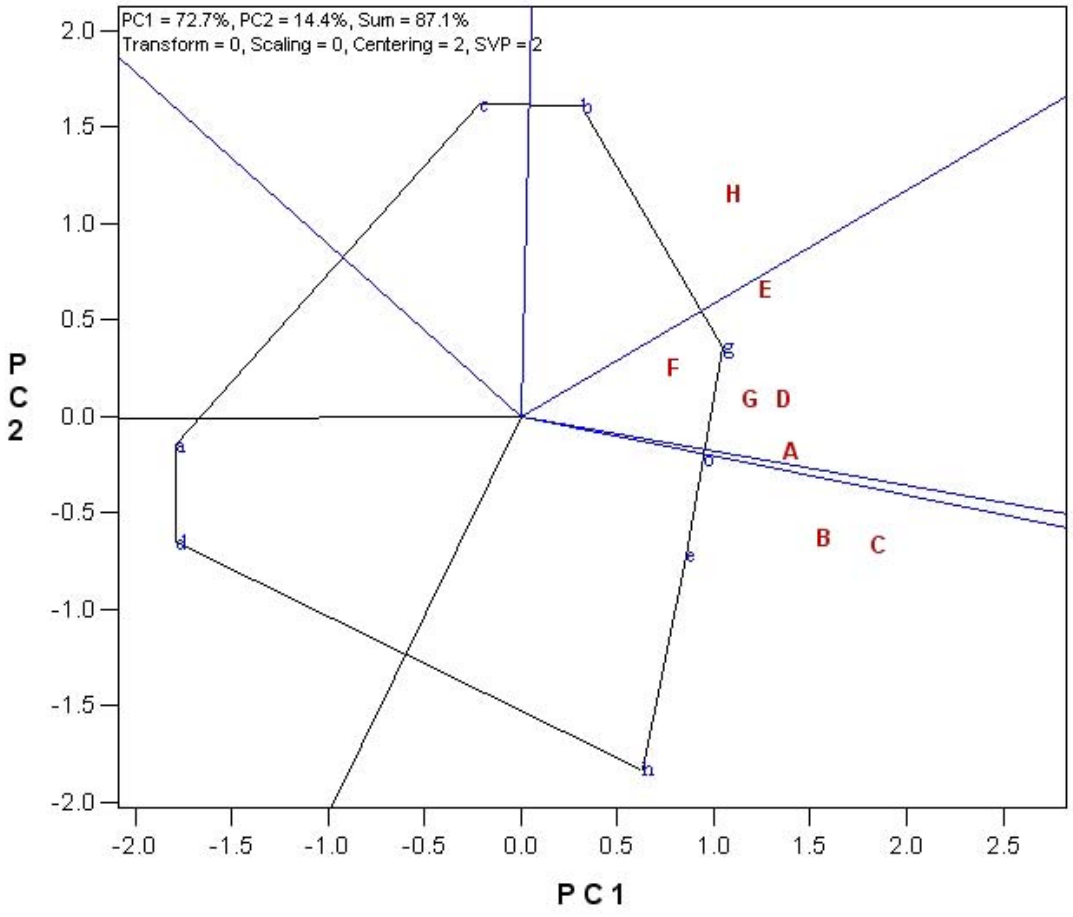

Figure 29: Biplot showing polygon view of six parents for fiber strength in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Concomitantly testers Deltapine 50, Hil B-182-39, Hil B-147-21, and Hil A-106-8 fell into the Hil A-106-8 sector (Figure 29). Since tester Hil A-106-8 fell into Hil A-106-8 sector, pureline Hil A-106-8 is the best among all combinations involving Hil A-106-8 as a parent (Figure 29). Furthermore, all combinations involving tester Hil A-106-8 are assumed to not be heterotic (Figure 29). The analysis performed in Agrobase Gen. II yielded similar results (Table 6). Although FiberMax 832/Hil A-106-8 had the highest numerical means of 346 kN m kg^{-1}, it was not statistically different (p=0.05) from that of parent Hil A-106-8 (Table 6). Overall Tamcot CAMD-E and tester Tamcot CAMD-E, and Deltapine 50, and tester Deltapine 50 fell furthest from each other on the biplot suggesting combinations involving Tamcot CAMD-E and Deltapine 50 were the poorest testers for fiber strength (Figure 29). This is confirmed by means for fiber strength provided by Agrobase Gen. II (Table 6). Tamcot CAMD-E and Deltapine 50 exhibited the lowest mean values for strength which were significantly lower than all parental and progeny values at p=0.05 (Table 6).

The polygon view of fiber strength for 2008 provided six sectors are formed by Tamcot CAMD-E, FiberMax 832, Deltapine 491, Hil B-182-39, Hil B-147-21, and Hil A-106-8 (Figure 30). No testers fell into Tamcot CAMD-E, Deltapine 491, and Hil A-106-8 sectors suggesting these entries produced the poorest combinations with some or all of the testers (Figure 30). The FiberMax 832 sector contained only tester Hil A-106-8 suggesting that FiberMax 832/Hil A-106-8 is the best of all combinations involving FiberMax 832 (Figure 30). Testers FiberMax and Hil C-155-22 fell into Hil B-182-39 sector suggesting these testers produced the best combinations with entry Hil B-182-39 (Figure 30). Testers Tamcot CAMD-E, Deltapine 491, Deltapine 50, Hil B-182-39, and Hil B-147-21 fell into the Hil B-147-21 sector (Figure 30). Since tester Hil B-147-21 fell into the Hil B-147-21 sector, the parental combination Hil B-147-21 is predicted to the best of any combination involving Hil B-147-21. Furthermore, heterosis between Hil B-147-21 and all other entries is not possible. Means generated by the Agrobase Gen. II analysis confirms these predictions (Table 6). FiberMax 832/Hil A-106-8 provides a mean value of 373 kN m kg^{-1}, which is significantly different from the commercial genotype combinations involving FiberMax 832, but not the experimental ELS combinations involving FiberMax 832 (Table 6). FiberMax 832/Hil B-182-39 and Hil B-182-39/Hil A-106-8 provide means of 357 kN m kg^{-1} and 376 kN m kg^{-1}, respectively (Table 6). Although pureline Hil B-147-21 is predicted to be the best of all combinations involving Hil B-147-21 as a parent the combination Hil B-182-39/Hil B-147-21 is numerically higher with a value of 379 kN m kg^{-1} (Table 6). This value, however, was not statistically different from the parental value (Table 6).

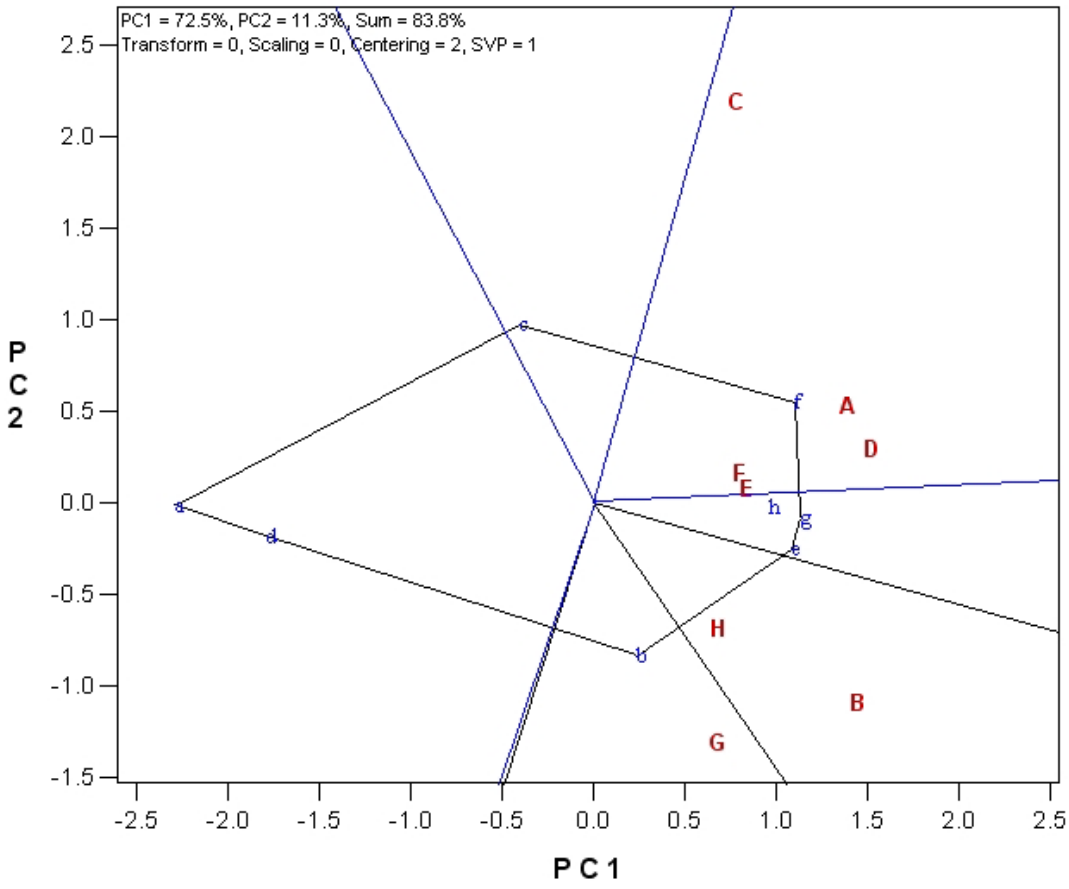

Figure 30: Biplot showing polygon view of six parents for fiber strength in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Fiber elongation

Biplot analysis of fiber elongation showed Hil A-106-8, Deltapine 50, and Tamcot CAMD-E had positive GCA effects while FiberMax 832, Deltapine 491, Hil B-182-39, Hil B-147-21, and Hil C-155-22 had negative GCA effects (Figure 31). The biplot explained 82.3% (PC1=71.2% and PC2=11.1%) of the total variation partitioned into GCA effects of parents and SCA effects of progeny in conventional analysis (Figure 31). Deltapine 50 exhibited the highest GCA effect, while Deltapine 491 exhibited the lowest GCA effect (Figure 31). The relative ranking of GCA effects is Deltapine 50 > Hil A-106-8 > Tamcot CAMD-E > Hil B-182-39 > Hil C-155-22 > Hil B-147-21 > FiberMax 832 ≈ Deltapine 491. The analysis performed in Agrobase Gen. II gives the same ranking for GCA effects (Table 7).

According to the biplot analysis of fiber elongation for 2008 Tamcot CAMD-E, Deltapine 50, and Hil A-106-8 exhibited positive GCA effects, while FiberMax 832, Deltapine 491, Hil B-182-39, Hil B-147-21, and Hil C-155-22 had negative GCA effects (Figure 32). The biplot explained 87.3% (PC1=69.9% and PC2=17.4%) of the total variation partitioned into GCA effects of the parents and SCA effects of progenies in conventional analysis (Figure 32). Deltapine 50 had the highest GCA effect, while Hil C-155-22 had the lowest GCA effect for fiber elongation (Figure 32). The relative rankings of GCA effects provided by the biplot analysis were Deltapine 50 > Tamcot CAMD-E > Hil A-106-8 > Hil B-147-21 > FiberMax 832 > Hil B-182-39 > Deltapine 491 > Hil C-155-22.

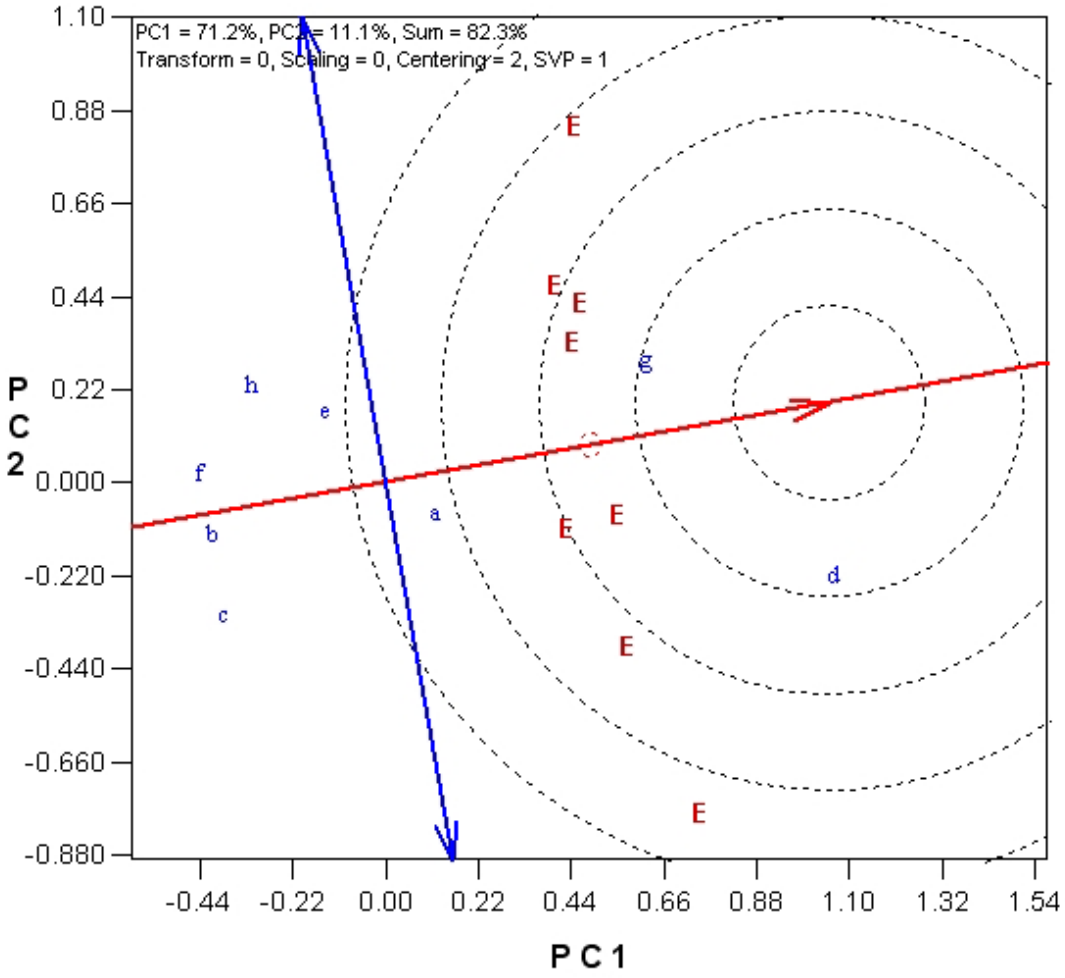

Figure 31: Biplot showing average tester coordinate view, based on diallel data for fiber elongation in 2007. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

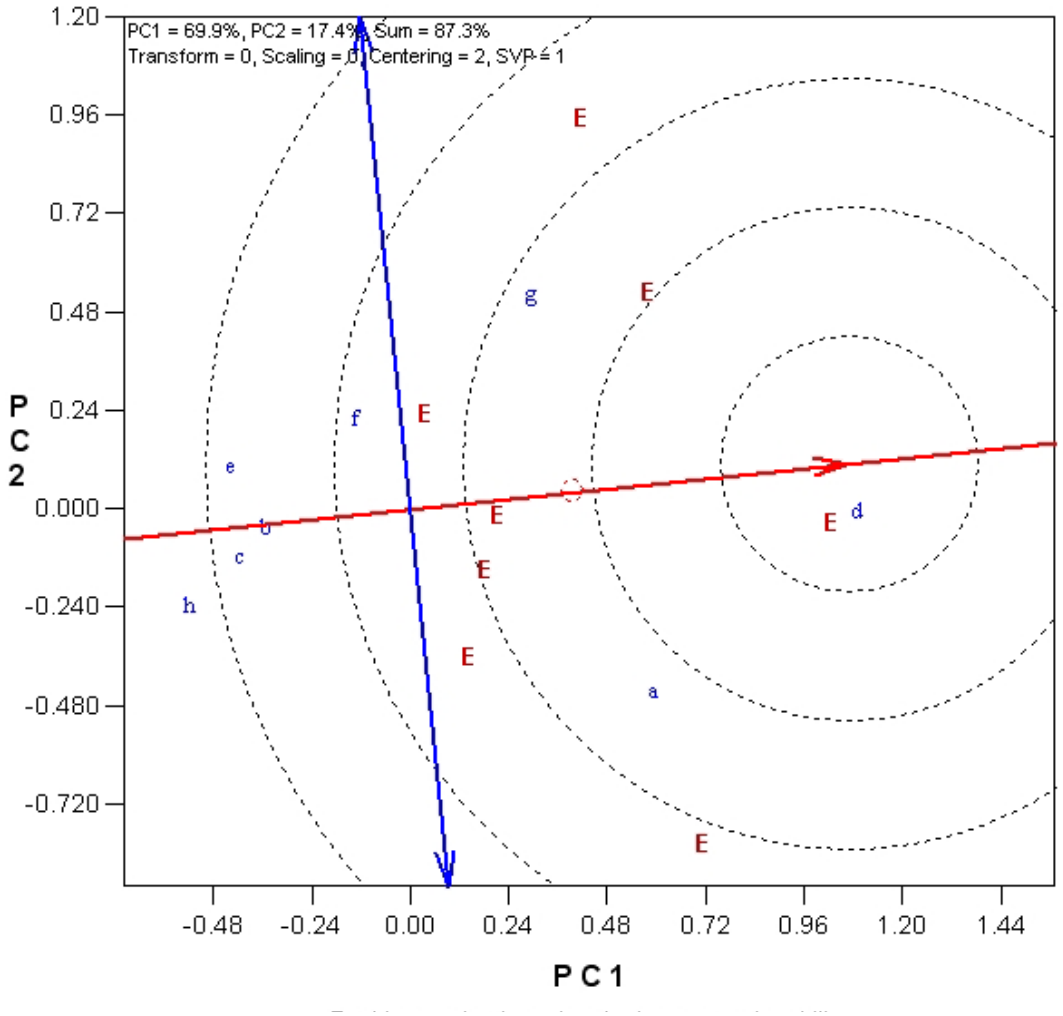

Figure 32: Biplot showing average tester coordinate view, based on diallel data for fiber elongation in 2008. Codes of genotypes are as follow: a = Tamcot CAMD-E, b = FiberMax 832, c = Deltapine 491, d = Deltapine 50, e = Hil B-182-39, f = Hil B-147-21, g = Hil A-106-8, and h = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

Table 7: Table of means, GCA effects, and SCA effects from diallel analysis of fiber elongation for eight cotton (Gossypium hirsutum L.) genotypes and 28 F_1 progeny in 2007 and 2008.

	Fiber Elongation			
	2007		2008	
Parent	Mean -%-	GCA	Mean -%-	GCA
Tamcot CAMD-E	4.6	0.045	8.0	0.251**
FiberMax 832	4.2	-0.225**	6.5	-0.176**
Deltapine 491	4.2	-0.225**	6.7	-0.184**
Deltapine 50	5.8	0.507**	8.5	0.459**
Hil B-182-39	4.4	-0.070*	6.9	-0.131**
Hil B-147-21	4.3	-0.203**	6.6	-0.169**
Hil A-106-8	5.1	0.305**	7.7	0.191**
Hil C-155-22	4.4	-0.135**	6.7	-0.241**
LSD (0.05)		0.067		0.092
Combinations	Mean -%-	SCA	Mean -%-	SCA
Tamcot CAMD-E/FiberMax 832	4.3	0.186	7.0	-0.093
Tamcot CAMD-E/Deltapine 491	4.1	-0.089	6.8	-0.261
Tamcot CAMD-E/Deltapine 50	4.8	-0.047	7.9	0.172
Tamcot CAMD-E/Hil B-182-39	4.2	-0.069	6.8	-0.338*
Tamcot CAMD-E/Hil B-147-21	3.9	-0.287**	6.9	-0.151
Tamcot CAMD-E/Hil A-106-8	4.7	0.031	7.0	-0.386**
Tamcot CAMD-E/Hil C-155-22	4.1	-0.104	7.1	0.097
FiberMax 832/Deltapine 491	3.7	-0.144	6.9	0.292*
FiberMax 832/Deltapine 50	4.5	-0.152	7.0	-0.251
FiberMax 832/Hil B-182-39	3.8	-0.224*	7.0	0.339*
FiberMax 832/Hil B-147-21	3.9	-0.042	6.6	-0.023
FiberMax 832/Hil A-106-8	4.3	-0.074	6.9	-0.058
FiberMax 832/Hil C-155-22	3.9	-0.109	6.6	0.024
Deltapine 491/Deltapine 50	4.7	0.048	7.1	-0.118
Deltapine 491/Hil B-182-39	4.1	0.101	6.8	0.097
Deltapine 491/Hil B-147-21	3.7	-0.167	6.5	-0.141
Deltapine 491/Hil A-106-8	4.3	-0.074	6.7	-0.251
Deltapine 491/Hil C-155-22	3.7	-0.234*	6.7	0.132
Deltapine 50/Hil B-182-39	4.5	-0.257*	6.8	-0.546**
Deltapine 50/Hil B-147-21	4.5	-0.149	7.4	0.117
Deltapine 50/Hil A-106-8	4.9	-0.207	7.5	-0.118
Deltapine 50/Hil C-155-22	4.5	-0.217	6.7	-0.486**
Hil B-182-39/Hil B-147-21	4.0	-0.047	6.6	-0.068
Hil B-182-39/Hil A-106-8	4.6	0.021	7.1	0.072
Hil B-182-39/Hil C-155-22	4.2	0.086	6.7	0.054
Hil B-147-21/Hil A-106-8	4.5	0.053	7.4	0.359*
Hil B-147-21/Hil C-155-22	3.8	-0.182	6.5	-0.033
Hil A-106-8/Hil C-155-22	4.5	0.011	6.7	-0.268
CV (%)	5.32		4.50	
LSD (0.05)	0.27	0.206	0.37	0.282
Grand Mean	4.32		6.97	

*,** Significantly different at 0.05, and 0.01 respectively

When compared to the ranking of GCA effects given by the Agrobase Gen. II analysis (Table 7), there is a change in ranking for four of the effects. The analysis ranks Hil B-182-39 > Hil B-147-21 > FiberMax 832 as opposed to Hil B-147-21 > FiberMax 832 > Hil B-182-39 (Table 7). Hil B-182-39 had a GCA effect of -0.131, Hil B-147-21 had a GCA effect of -0.169, FiberMax 832 had a GCA effect of - 0.176, and Deltapine 491 had a GCA effect of -0.184 (Table 7). The overall ranking provided by the analysis in Agrobase Gen. II is Deltapine 50 > Tamcot CAMD-E > Hil A-106-8 > Hil B-182-39 > Hil B-147-21 > FiberMax 832 > Deltapine 491 > Hil C-155-22 (Table 7).

Significant GxY and GCAxY interactions were observed for fiber elongation (Table 1). Significant differences for GCA effects among genotypes also existed when averaged across both years (Table 1). Higher mean values for fiber elongation were observed in 2008 than in 2007 (Table 7). This contributed to a change in ranking of parents and a change in ranking of GCA effects between years (Table 7). Environmental influences such as temperature, light, water, and mineral nutrients can have a direct affect on fiber elongation (Bradow and Davidonis, 2000). Furthermore, all GCA effects were significantly different from zero at p=0.01 in 2008, while in 2007 GCA effect for FiberMax 832, Deltapine 491, Deltapine 50, Hil B-147-21, Hil A-106-8, and Hil C-155-22 were significantly different from zero at p=0.01, the GCA effect for Deltapine 50 was significantly different from zero at p=0.05, and the GCA effect for Tamcot CAMD-E was not significantly different from zero (Table 7). The change in ranking of GCA effects and the change in significance of GCA effects from zero contributed to the GCAxY interaction (Table 7). This suggests that genotypes were not stable for fiber

elongation when averaged across years. However, Tamcot CAMD-E, Deltapine 50, and Hil A-106-8 exhibited the highest parental means and positive GCA effects during both years suggesting these entries would make suitable parents for breeders looking to improve secondary traits such as elongation (Table 7).

Based on the proximity to the ATC abscissa and its vector length, it can be assumed that Tamcot CAMD-E is the best tester for 2007 (Figure 33). Hil B-182-39 is considered to be the poorest tester since it is the least discriminating of all testers based upon vector length (Figure 33).

Based on the proximity to the ATC abscissa and vector length, we can determine that Deltapine 50 is the best tester for 2008 (Figure 34). Hil B-182-39 is considered to be the poorest tester since it is the least discriminating of all testers based upon its vector length (Figure 34).

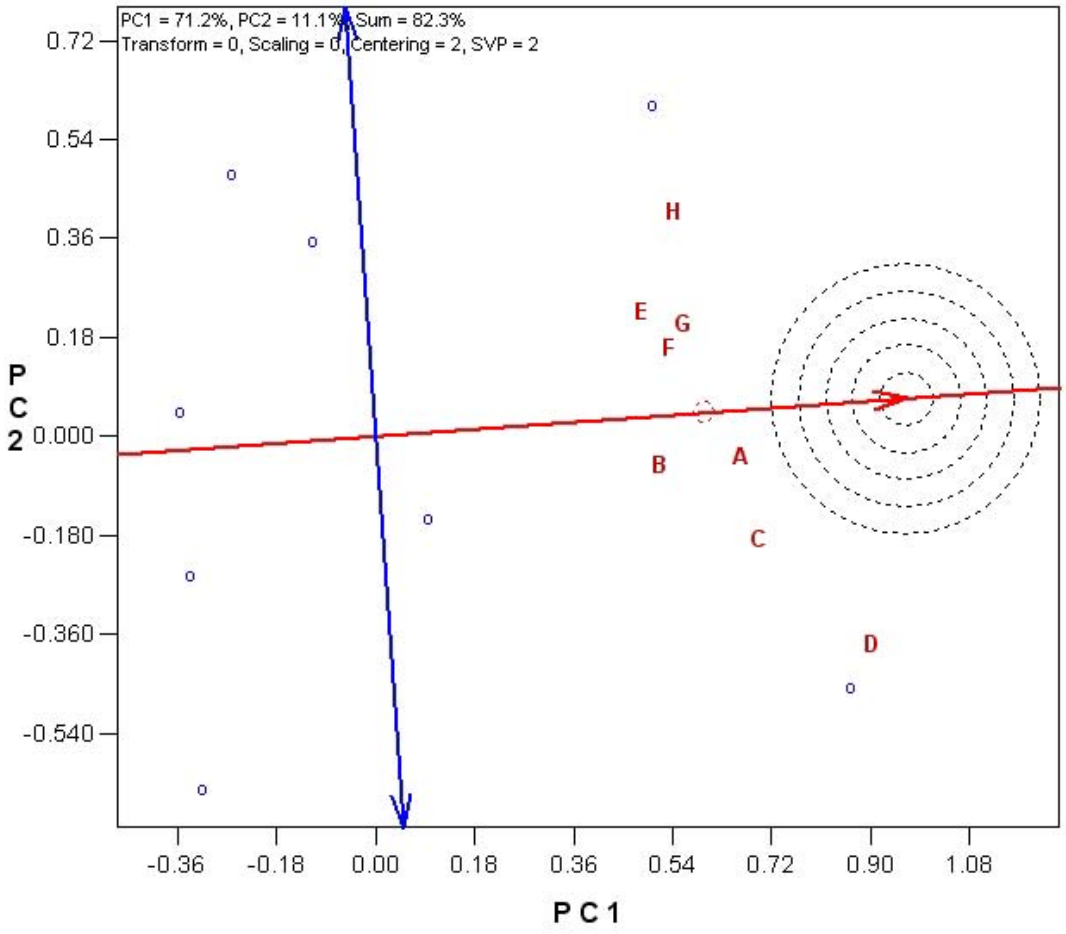

Figure 33: Biplot showing the evaluation of parents as ideal tester for fiber elongation in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

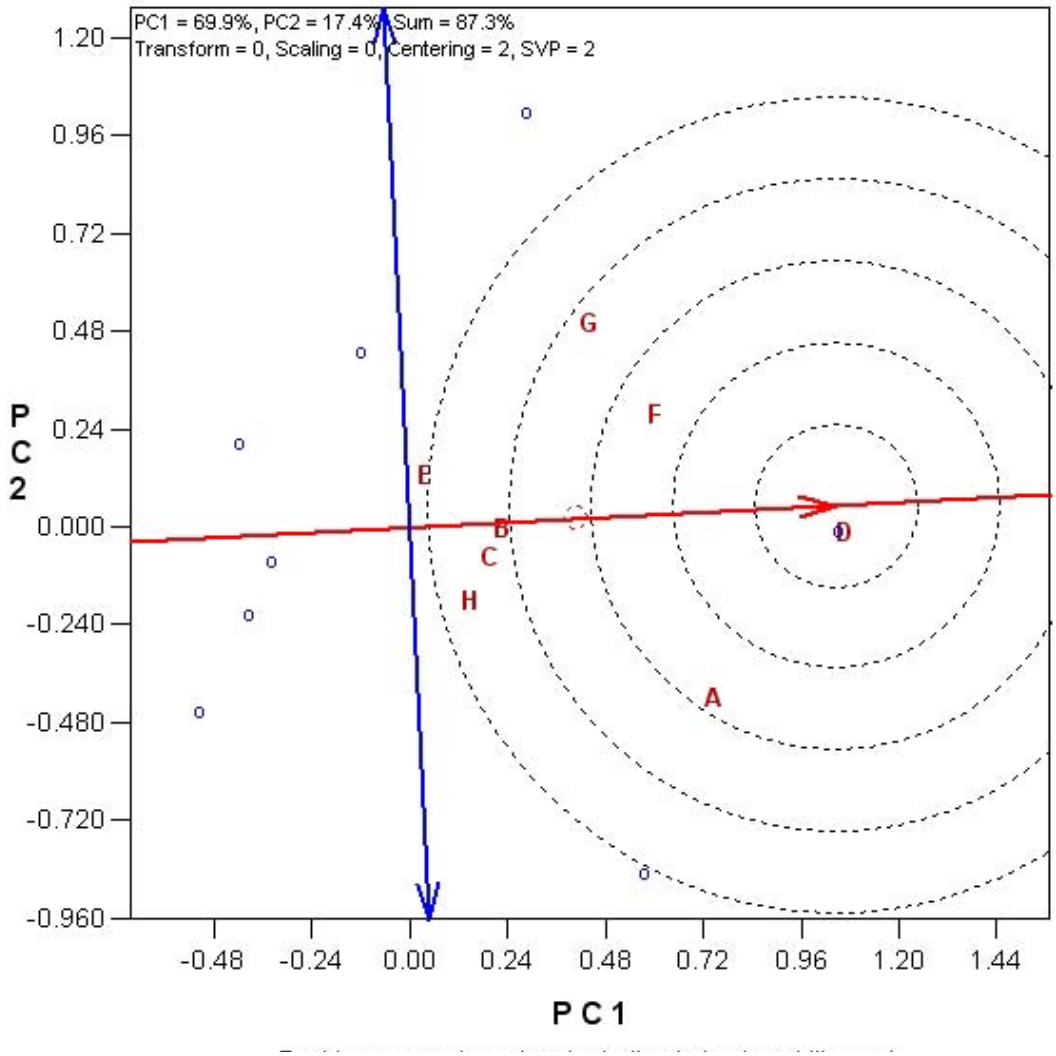

Figure 34: Biplot showing the evaluation of parents as ideal tester for fiber elongation in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

The polygon view of the biplot for fiber elongation provides us with five sectors: Deltapine 491, Deltapine 50, Hil B-147-21, Hil A-106-8, and Hil C-155-22 (Figure 35). No testers fell into the Deltapine 491, Hil B-147-21, and Hil C-155-22 sectors suggesting these genotypes produced the poorest combinations with some or all of the testers (Figure 35). The Hil A-106-8 sector contained testers Hil B-182-39, Hil B-147-21, Hil A-106-8, and Hil C-155-22. The Deltapine 50 sector contained testers Tamcot CAMD-E, FiberMax 832, Deltapine 491, and Deltapine 50 (Figure 35). Since the Hil A-106-8 sector contained tester Hil A-106-8, and the Deltapine 50 sector contained tester Deltapine 50, it can be inferred the pureline Hil A-106-8 and pureline Deltapine 50 provide the best combinations for fiber elongation. Furthermore, heterosis between any other testers and Deltapine 50 or Hil A-106-8 is not possible since Deltapine 50, and Hil A-106-8 sectors contained their testers (Figure 35). The data provided by the diallel analysis in Agrobase Gen. II reinforces these findings (Table 7). Deltapine 50 and Hil A-106-8 had the highest means (Table 7). No combinations involving the parents Deltapine 50 or Hil A-106-8 statistically exceeded the highest mean value of both parents suggesting heterosis is not present in these combinations (Table 7). Overall FiberMax 832 and tester FiberMax 832, and Deltapine 491 and tester Deltapine 491 fell furthest from each other in the biplot. This suggests the pureline FiberMax 832 and pureline Deltapine 491 were the poorest testers for elongation.

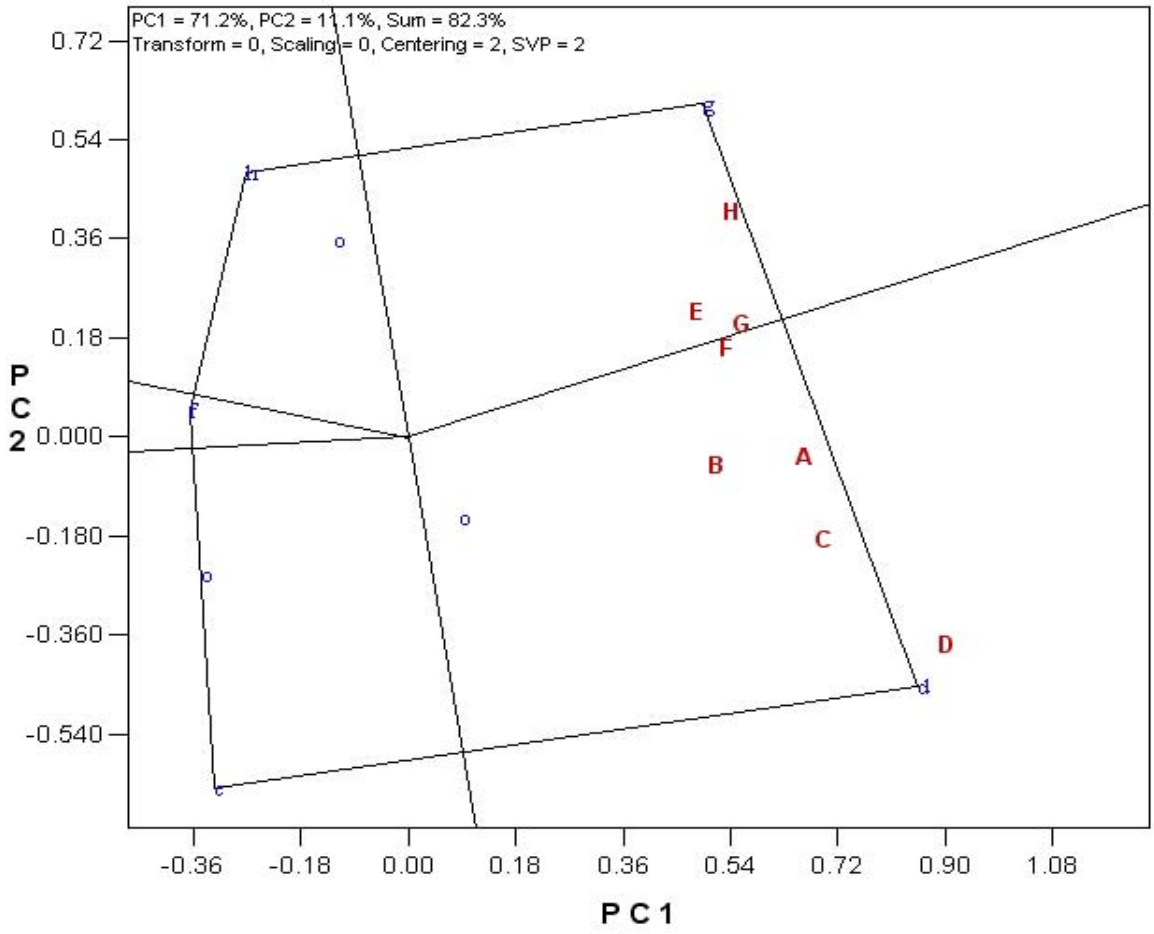

Figure 35: Biplot showing polygon view of five parents for fiber elongation in 2007. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

The polygon view of the biplot for fiber elongation for 2008 provides us with five sectors formed by Tamcot CAMD-E, Deltapine 50, Hil B-182-39, Hil A-106-8, and Hil C-155-22 (Figure 36). No testers fell in Hil B-182-39 or Hil C-155-22 sectors suggesting these entries produced the poorest combinations with some or all of the testers (Figure 36). Testers Hil B-182-39 and Hil A-106-8 fell into the Hil A-106-8 sector, testers FiberMax 832, Deltapine 491, Deltapine 50, and Hil B-147-21 fell into Deltapine 50 sector, and testers Tamcot CAMD-E and Hil C-155-22 fell into Tamcot CAMD-E sector (Figure 36). These findings suggest purline Deltapine 50, Tamcot CAMD-E, and Hil A-106-8 provide the best fiber elongation. Furthermore, this suggests that heterosis is not possible for any combination involving Deltapine 50, Tamcot CAMD-E, and Hil A-106-8. However, tester Tamcot CAMD-E fell on the line of Tamcot CAMD-E, and Deltapine 50 sectors suggesting that it may be a good mating partner with either entry (Figure 36).

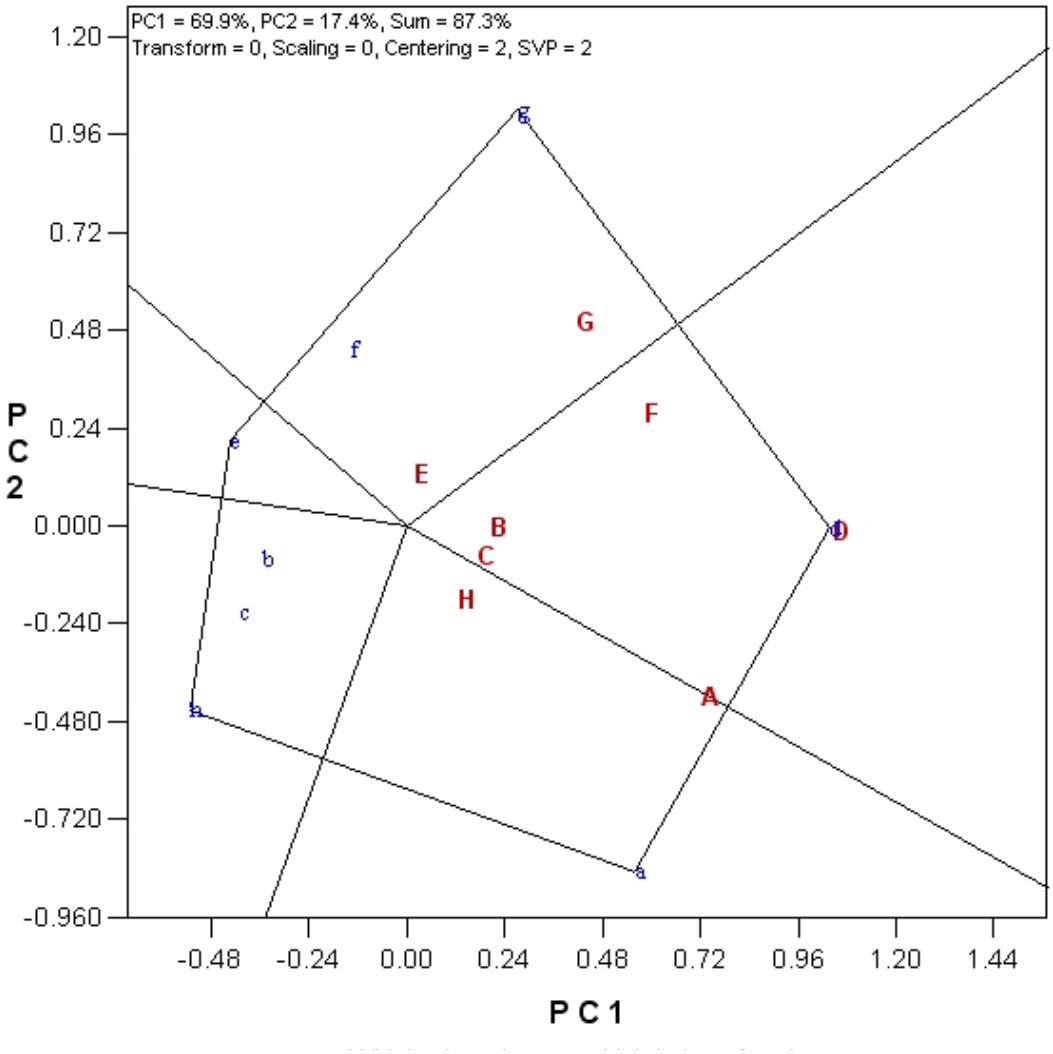

Figure 36: Biplot showing polygon view of five parents for fiber elongation in 2008. Codes of genotypes are as follow: A = Tamcot CAMD-E, B = FiberMax 832, C = Deltapine 491, D = Deltapine 50, E = Hil B-182-39, F = Hil B-147-21, G = Hil A-106-8, and H = Hil C-155-22. Genotypes are labeled as lowercase letter when viewed as entries and uppercase letters when viewed as testers.

These predictions are confirmed by means for fiber elongation provided by the Agrobase Gen. II analysis (Table 7). Tamcot CAMD-E exhibited the highest mean value of 8.0 %, which was significantly different from entries involving Tamcot CAMD-E, at p=0.05, with the exception of the combination Tamcot CAMD-E/Deltapine 50 which exhibited a value of 7.9 % (Table 7). However, this value does not exceed either parental value confirming heterosis does not exist for this trait (Table 7). Pureline Deltapine 50 had a mean value of 8.5% which is significantly different from all values exhibited by combinations involving Deltapine 50 at p=0.05 (Table 7). The same trend is observed for pureline Hil A-106-8 that had a mean value 7.7% (Table 7). Pureline Hil A-106-8 is significantly different from the combination Hil B-182-39/Hil A-106-8 which exhibited a mean value of 7.1% at p=0.05 (Table 7). Overall FiberMax 832 and tester FiberMax 832 fell furthest from each other in the biplot suggesting FiberMax 832 was the poorest tester for fiber elongation.

Heritability estimates

Broad-sense heritability estimates were calculated from F_2 progeny from Weslaco, TX, and College Station, TX, in 2008. A significant GxE interaction was observed for lint percent and micronaire (Table 8), and data were separated by location for these traits. Data were pooled for traits where a significant GxE interaction was not detected. Broad-sense heritability estimates were calculated as described by Acquaah (2007). A value of zero was substituted for negative heritability estimates. Negative heritability estimates can be attributed to the high parental variances, observed for traits.

Table 8: Combined mean squares for eight cotton (*Gossypium hirsutum* L.) parents and 28 F_2 progeny grown in Weslaco, TX, and College Station, TX, in 2008.

Sources	df	Lint Percent	Micronaire	Uniformity	Length	Strength	Elongation
Environments (E)	1	666.13**	10.47**	93.96**	72.90**	29120.89**	38.14**
E X Reps – Error A	6	9.79**	0.13**	1.72**	2.51**	703.44**	0.10**
Genotypes (G)	35	31.96**	0.49**	7.92**	37.10**	3389.86**	1.62**
G X E	35	1.78*	0.03**	0.54	0.64	137.93	0.09
Error B	210	0.91	0.02	0.58	0.61	114.12	0.08

*, ** Significantly different from zero at p=0.05, and p=0.01, respectively.

Lint percent and micronaire

Parental variance for lint percent and micronaire are separated by location (Table 9). A significant GxE interaction contributed to a change in parental means between locations, which caused a change in parental variances between locations (Table 9). Tamcot CAMD-E exhibited a high variance at both locations (Table 9). Eleven genotypes exhibited measurable heritability estimates in both environments for lint

percent (Table 10). Broad-sense heritability (H^2) for lint percent ranged from 0.00 to 0.84 in Weslaco, TX, and 0.00 to 0.96 in College Station, TX (Table 10). Hil B-182-39/Hil A-106-8 exhibited a broad-sense estimate of 0.73 in Weslaco, TX, and 0.96 in College Station, TX, suggesting between 73% and 96% of the observed phenotypic variance is attributed to genetic variance depending on the growth environment (Table 10). FiberMax 832/Deltapine 491 exhibited the greatest difference in heritability estimates between environments (Table 10). For Weslaco, FiberMax 832/Deltapine 491 an estimate of 0.00 was determined, while an estimate of 0.93 was determined in College Station, TX (Table 10). This can be contributed to high parental variance values, and low progeny variance values in Weslaco, TX. Furthermore, the data suggest eleven genotypes have sufficient genetic variance to select for increased lint percent.

Table 9: Variance of lint percent, and fiber micronaire for eight cotton (*Gossypium hirsutum* L.) parents from Weslaco, TX, and College Station, TX, in 2008.

	Lint Percent		Micronaire	
	Weslaco	College Station	Weslaco	College Station
Tamcot CAMD-E	1.1086	1.0000	0.0031	0.0272
FiberMax 832	0.1476	0.4688	0.0041	0.0130
Deltapine 491	0.6694	0.8202	0.0251	0.0015
Deltapine 50	0.9515	0.5141	0.0244	0.0300
Hil B-182-39	0.0645	0.0027	0.5323	0.1022
Hil B-147-21	0.0267	0.6057	0.1022	0.0273
Hil A-106-8	0.4438	0.1408	0.0216	0.0272
Hil C-155-22	0.3204	0.4436	0.0277	0.0111

Table 10: Broad-sense heritability (H^2) estimates for lint percent and fiber micronaire for 28 F_2 progeny for Weslaco, TX, and College Station, TX, in 2008.

	Lint Percent		Micronaire	
	Weslaco	College Station	Weslaco	College Station
Tamcot CAMD-E/FiberMax 832	0.00	0.00	0.27	0.19
Tamcot CAMD-E/Deltapine 491	0.77	0.20	0.87	0.41
Tamcot CAMD-E/Deltapine 50	0.40	0.18	0.00	0.54
Tamcot CAMD-E/Hil B-182-39	0.84	0.00	0.84	0.00
Tamcot CAMD-E/Hil B-147-21	0.00	0.00	0.00	0.00
Tamcot CAMD-E/Hil A-106-8	0.60	0.00	0.00	0.00
Tamcot CAMD-E/Hil C-155-22	0.58	0.00	0.00	0.55
FiberMax 832/Deltapine 491	0.00	0.93	0.00	0.00
FiberMax 832/Deltapine 50	0.00	0.29	0.63	0.00
FiberMax 832/Hil B-182-39	0.00	0.70	0.00	0.00
FiberMax 832/Hil B-147-21	0.00	0.00	0.00	0.00
FiberMax 832/Hil A-106-8	0.76	0.51	0.00	0.00
FiberMax 832/Hil C-155-22	0.56	0.75	0.00	0.00
Deltapine 491/Deltapine 50	0.83	0.00	0.00	0.00
Deltapine 491/Hil B-182-39	0.30	0.60	0.64	0.00
Deltapine 491/Hil B-147-21	0.00	0.00	0.00	0.00
Deltapine 491/Hil A-106-8	0.75	0.88	0.00	0.00
Deltapine 491/Hil C-155-22	0.51	0.12	0.00	0.00
Deltapine 50/Hil B-182-39	0.72	0.78	0.22	0.79
Deltapine 50/Hil B-147-21	0.00	0.42	0.00	0.00
Deltapine 50/Hil A-106-8	0.09	0.50	0.00	0.00
Deltapine 50/Hil C-155-22	0.32	0.49	0.00	0.47
Hil B-182-39/Hil B-147-21	0.00	0.11	0.00	0.00
Hil B-182-39/Hil A-106-8	0.73	0.96	0.00	0.00
Hil B-182-39/Hil C-155-22	0.39	0.65	0.00	0.00
Hil B-147-21/Hil A-106-8	0.00	0.24	0.00	0.00
Hil B-147-21/Hil C-155-22	0.00	0.00	0.00	0.00
Hil A-106-8/Hil C-155-22	0.79	0.64	0.00	0.00

Broad-sense heritability estimates for fiber micronaire were determined for three genotypes at both locations (Table 10). Parental variances differed greatly between locations, which contributed to a difference in broad-sense estimates between locations (Table 10). Broad-sense estimates were determined for Tamcot CAMD-E/FiberMax 832, Tamcot CAMD-E/Deltapine 491, and Deltapine 50/Hil B-182-39 at both locations (Table 10). Lower estimates were determined for Tamcot CAMD-E/FiberMax 832, and Tamcot CAMD-E/Deltapine 491 at College Station, TX, than at Weslaco, TX, while higher values were determined for Deltapine50/Hil B-182-39 at Weslaco, TX, than College Station, TX (Table 10). Overall, Tamcot CAMD-E/Deltapine 491 exhibited the highest broad-sense estimates, 0.87 at Weslaco, TX, and 0.41, at College Station, TX (Table 10). Tamcot CAMD-E/FiberMax 832 exhibited the lowest broad-sense heritability values at 0.27, at Weslaco, TX, and 0.19, at College Station, TX (Table 10). Overall, the GxE interaction for micronaire directly effected parental variances between locations (Table 10). Environmental impact on aberrant micronaire values has been well documented. Furthermore, high variance for the parental lines suggests these lines are not as uniform as originally expected. However, Tamcot CAMD-E/FiberMax 832, and Tamcot CAMD-E/Deltapine 491 exhibited genetic variance that would allow for selection of desirable micronaire values.

Length uniformity, fiber length, fiber strength, and fiber elongation

Data for Weslaco, TX, and College Station, TX, were pooled for fiber length, length uniformity, strength, and elongation since a significant GxE interaction was not determined (Table 8). A value of zero was substituted for negative heritability estimates.

Negative heritability estimates can be attributed to the high parental variance observed for traits.

Parental variances for fiber length uniformity range from a 0.2898 for Hil B-182-39, to 1.9998 for Hil C-155-22 (Table 11). Thirteen F_2 genotypes exhibited broad-sense estimates for fiber length uniformity ranging from 0.10 to 0.59 (Table 12). High parental variances contributed to a large number of negative heritability estimates indicated by 0.00 (Table 12). A low value of 0.10 was observed for Hil B-182-39/Hil B-147-21, while a high value of 0.59 was observed for Deltapine 50/Hil A-106-8 (Table 12). Intra-mated ELS exhibited values of 0.10 for Hil B-182-39/Hil B-147-21, 0.23 for Hil B-147-21/Hil A-106-8, and 0.45 for Hil B-182-39/Hil A-106-8, suggesting sufficient genotypic variation in these populations to allow selection of increased length uniformity (Table 12).

Eleven F_2 genotypes exhibited broad-sense heritability estimates for fiber length ranging from 0.06 to 0.76 (Table 12). High parental variances were determined for Tamcot CAMD-E, Deltapine 50, Hil B-147-21, and Hil C-155-22, which contributed to many broad-sense estimates of 0.00 (Tables 11, 12). Furthermore, this suggests a large amount of variance exists within parental lines for fiber length (Table 12).

Table 11: Combined variance of fiber length, length uniformity, fiber strength, and fiber elongation for eight cotton (*Gossypium hirsutum* L.) parents in 2008.

	Length	Uniformity	Strength	Elongation
Tamcot CAMD-E	2.2569	1.8070	246.1451	0.6484
FiberMax 832	0.8099	0.8641	303.5766	0.3227
Deltapine 491	0.3318	0.5998	71.4288	0.2257
Deltapine 50	1.1060	0.8000	564.6807	0.0943
Hil B-182-39	0.5668	0.2898	220.7783	0.2250
Hil B-147-21	1.7696	1.8993	207.1246	0.1527
Hil A-106-8	0.2846	0.4771	106.8770	0.0764
Hil C-155-22	1.2166	1.9998	400.5782	0.1670

Table 12: Combined broad-sense (H^2) estimates for fiber length, length uniformity, fiber strength, and fiber elongation for 28 F_2 progeny in 2008.

	Length	Uniformity	Strength	Elongation
Tamcot CAMD-E/FiberMax 832	0.00	0.00	0.00	0.00
Tamcot CAMD-E/Deltapine 491	0.00	0.00	0.00	0.00
Tamcot CAMD-E/Deltapine 50	0.00	0.28	0.00	0.11
Tamcot CAMD-E/Hil B-182-39	0.00	0.00	0.00	0.00
Tamcot CAMD-E/Hil B-147-21	0.00	0.00	0.00	0.00
Tamcot CAMD-E/Hil A-106-8	0.00	0.00	0.00	0.00
Tamcot CAMD-E/Hil C-155-22	0.00	0.00	0.00	0.00
FiberMax 832/Deltapine 491	0.76	0.14	0.00	0.00
FiberMax 832/Deltapine 50	0.49	0.57	0.00	0.33
FiberMax 832/Hil B-182-39	0.00	0.25	0.23	0.75
FiberMax 832/Hil B-147-21	0.06	0.00	0.00	0.67
FiberMax 832/Hil A-106-8	0.00	0.43	0.00	0.30
FiberMax 832/Hil C-155-22	0.00	0.00	0.00	0.00
Deltapine 491/Deltapine 50	0.06	0.36	0.06	0.17
Deltapine 491/Hil B-182-39	0.46	0.14	0.62	0.21
Deltapine 491/Hil B-147-21	0.00	0.00	0.24	0.00
Deltapine 491/Hil A-106-8	0.00	0.15	0.00	0.00
Deltapine 491/Hil C-155-22	0.00	0.00	0.00	0.00
Deltapine 50/Hil B-182-39	0.63	0.11	0.69	0.61
Deltapine 50/Hil B-147-21	0.30	0.00	0.00	0.53
Deltapine 50/Hil A-106-8	0.32	0.59	0.46	0.00
Deltapine 50/Hil C-155-22	0.31	0.00	0.00	0.12
Hil B-182-39/Hil B-147-21	0.00	0.10	0.58	0.00
Hil B-182-39/Hil A-106-8	0.22	0.45	0.04	0.27
Hil B-182-39/Hil C-155-22	0.00	0.00	0.00	0.00
Hil B-147-21/Hil A-106-8	0.18	0.23	0.28	0.43
Hil B-147-21/Hil C-155-22	0.00	0.00	0.17	0.00
Hil A-106-8/Hil C-155-22	0.00	0.00	0.00	0.00

A low broad-sense estimate of 0.06 was observed for FiberMax 832/Hil B-147-21, and Deltapine 491/Deltapine 50, while a high broad-sense heritability estimate of 0.76 was observed for FiberMax 832/Deltapine 491 (Table 12). Two intra-mated ELS combinations Hil B-182-39/Hil A-106-8 and Hil B-147-21/Hil A-106-8 exhibited broad-sense heritability estimates of 0.18, and 0.22, respectively (Table 12). This suggests a low amount of genetic variance contributing to the phenotypic variance for these ELS x ELS combinations. However, ELS x commercial combinations exhibited greater genetic variance for fiber length. The commercial x commercial combinations Deltapine 491/Deltapine 50, FiberMax 832/Deltapine 50, and FiberMax 832/Deltapine 491 exhibited broad-sense estimates of 0.06, 0.49, and 0.76, respectively, suggesting a wide array of genetic variance in these populations (Table 12). Overall, data suggests adequate genetic variance exists in these populations to allow for selection of increased fiber length, albeit at a lesser quality level than ELS derived populations.

Ten F_2 genotypes exhibited broad-sense heritability estimates ranging from 0.04 to 0.69 for fiber strength (Table 12). High parental variances were noted for Deltapine 50, and Hil C-155-22. High parental variances contributed to negative heritability estimates represented by 0.00 (Tables 11, 12). A low broad-sense heritability estimate of 0.04 was observed for Hil B-182-39/Hil A-106-8, while a high broad-sense heritability estimate of 0.69 was observed for Deltapine 50/Hil B-182-39 (Table 12). When intra-mated four ELS lines Hil B-182-39/Hil A-106-8, Hil B-147-21/Hil C-155-22, Hil B-147-21/Hil A-106-8, and Hil B-182-39/Hil B-147-21 exhibited broad-sense heritability estimates of 0.04, 0.17, 0.28, and 0.58, respectively, suggesting a wide array of genetic variance exists for fiber strength in these intra-mated ELS populations (Table 12). However, a large amount of this variation can be attributed to an environmental influence. Five ELS x commercial combinations FiberMax 832/Hil B-182-39, Deltapine 491/Hil B-147-21, Deltapine 50/Hil A-106-8, Deltapine 491/Hil B-182-39, and Deltapine 50/Hil B-182-39 exhibited broad-sense heritability estimates of 0.23, 0.24, 0.46, 0.62, and 0.69 suggesting sufficient genetic variance to increase strength while breeding for increased agronomic performance of the commercial cultivars. Overall, the data suggest sufficient genetic variation in these populations to select for increased fiber strength (Table 12).

Eleven F_2 genotypes exhibited broad-sense heritability estimates ranging from 0.11 to 0.75 for fiber elongation (Table 12). High parental variances attributed to negative heritability estimates that are represented by 0.00 (Tables 11, 12). Three commercial x commercial combinations Tamcot CAMD-E/Deltapine 50, Deltapine 491/Deltapine 50, and FiberMax 832/Deltapine 50 exhibited broad-sense heritability estimates of 0.11, 0.17, and 0.33 suggesting a large amount of variation in these populations can be attributed to environmental effects (Table 12). Seven ELS x commercial combinations exhibited broad-sense heritability estimates ranging from a low of 0.12 for Deltapine 50/Hil C-155-22 to a high of 0.75 for FiberMax 832/Hil B-182-39 (Table 12). This suggests a sufficient amount of variation exists in these populations for possible selection of increased elongation. Intra-mated ELS combinations Hil B-182-39/Hil A-106-8, and Hil B-147-21/Hil A-106-8 exhibited a broad-sense heritability estimate of 0.27 and 0.43 (Table 12). This suggests environmental influence is high to moderate for elongations in the intra-mated ELS lines (Table 12). Overall, the data suggests sufficient genetic variation exists in these populations for the selection of improved fiber elongation.

F_2 population performance and variance

Fehr (1991) stated that the simultaneous segregation of many genes that control a quantitative character results in a range of genotypes that cannot be separated into distinct classes. Furthermore, the evaluation of quantitative traits is based on the study of a population of genotypes (Fehr, 1991).

To determine the potential for improvement in ELS progeny boll samples were harvested for all entries. Population performance was determined for all traits from these samples. Population performance and variance was also determined for twenty-seven individual plants for each of ten entries (four parents, and six F_2 progeny). Population performance among lines, and population performance and variance within selected lines allowed us to determine the potential for increase in fiber quality in ELS progeny.

Highly significant differences ($p=0.01$) were observed between environments for all traits (Table 13). Likewise, highly significant differences ($p=0.01$) among genotypes were observed for all traits (Table 13). A significant GxE interaction was only detected for lint percent and fiber micronaire (Table 1). Due to the interaction, means for lint percent and micronaire are separated by location. Data was pooled for all other traits since a significant GxE interaction was not detected.

Twenty-seven individual plants for each of ten entries (four parents, and six F_2 progeny) were analyzed for mean, standard deviation, skewness, coefficient of variation, and variance to determine the amount of variation within selected populations for fiber micronaire, length uniformity, length, strength, and elongation.

Significant differences (p=0.05) were observed between environments for all traits except elongation (Table 14). Highly significant differences (p=0.01) among genotypes were observed for all traits (Table 14). Due to significant GxE interaction (Table 14), data for length uniformity and micronaire was separated by location. Data for all other traits were pooled since a significant GxE interaction did not exist.

Table 13: Combined mean squares of lint percent and fiber traits for eight cotton (*Gossypium hirsutum* L.) parents and 28 F_2 progeny grown in Weslaco, TX, and College Station, TX, in 2008.

Sources	df	Lint Percent	Micronaire	Uniformity	Length	Strength	Elongation
Environments (E)	1	666.13**	10.47**	93.96**	72.90**	29120.89**	38.14**
E X Reps – Error A	6	9.79**	0.13**	1.72**	2.51**	703.44**	0.10**
Genotypes (G)	35	31.96**	0.49**	7.92**	37.10**	3389.86**	1.62**
G X E	35	1.78*	0.03**	0.54	0.64	137.93	0.09
Error B	210	0.91	0.02	0.58	0.61	114.12	0.08

*, ** Significantly different from zero at p=0.05, and p=0.01, respectively.

Table 14: Table of mean squares of fiber traits for four cotton (*Gossypium hirsutum* L.) parents and six selected F_2 progeny from Weslaco, TX, and College Station, TX, in 2008.

Sources	df	Micronaire	Uniformity	Length	Strength	Elongation
Environments (E)	1	48.48*	30.25*	79.04*	7835.65**	1.27
E X Reps – Error A	4	3.38**	3.03*	5.71*	365.10	1.16**
Genotypes (G)	9	5.61**	13.90**	209.23**	16222.23**	13.52**
G X E	9	0.11	2.56*	3.39	1022.35**	0.37
Error B	516	0.18	1.20	2.38	356.93	0.28

*, ** Significantly different from zero at p=0.05, and p=0.01, respectively.

Lint percent

A significant GxE interaction was observed for lint percent (Table 13). Highly significant differences among genotypes, as well as environments also were observed (Table 13). Higher mean values were observed in Weslaco than in College Station (Table 15). Lower mean values in College Station led to a change in ranking of mean values, which directly contributed to the GxY interaction (Table 15). Deltapine 491 exhibited the highest lint percent, which was significantly different ($p=0.05$) from all other entries in both locations (Table 15). F_2 combinations involving Deltapine 491 as a parent generally produced the best combinations for lint percent (Table 15). This suggests slight dominant and epistatic gene action in combinations involving Deltapine 491 (Table 15). The ELS line Hil A-106-8, and its F_2 combination Hil A-106-8/Hil C-155-22 exhibited the lowest lint percents in both locations (Table 15). F_2 combinations derived from commercial x ELS crosses generally provided a higher lint percent than the ELS parental average suggesting slight variation in these populations probably due to dominant and epistatic gene action (Table 15). Overall combinations involving Hil A-106-8 as a parent generally produced the lowest lint percent of all combinations suggesting slight negative dominant gene action for lint percent in these combinations (Table 15). The best to worst ELS parents in combination with a commercial cultivar is 1) Hil 147-21, 2) Hil C-155-22, 3) Hil B182-39, and 4) Hil A-106-8.

Table 15: Means for lint percent from eight cotton (*Gossypium hirsutum* L.) parents and 28 F_2 progeny from Weslaco, TX, and College Station, TX, in 2008.

	Lint percent -%-		
Entry	Weslaco	College Station	Combined
Deltapine 491	44.1	40.0	42.0
FiberMax 832/Deltapine 491	42.0	37.0	39.5
Deltapine 491/Deltapine 50	41.4	36.8	39.1
Deltapine 491/Hil B-182-39	41.0	37.2	39.1
CAMD-E/Deltapine 491	40.6	38.3	39.5
Deltapine 491/Hil C-155-22	40.6	38.3	39.5
Deltapine 491/Hil B-147-21	40.1	37.3	38.7
CAMD-E/Hil B-147-21	40.0	36.6	38.3
FiberMax 832	39.5	35.6	37.5
CAMD-E	39.3	34.7	37.0
CAMD-E/FiberMax 832	39.3	36.1	37.7
Deltapine 50/Hil B-182-39	38.9	35.4	37.1
CAMD-E/Hil C-155-22	38.7	36.4	37.5
FiberMax 832/Deltapine 50	38.4	33.9	36.1
Deltapine 50/Hil C-155-22	38.3	34.7	36.5
Deltapine 491/Hil A-106-8	38.2	36.4	37.3
CAMD-E/Hil B-182-39	38.1	35.0	36.6
Deltapine 50/Hil B-147-21	38.1	34.9	36.5
Deltapine 50	37.9	34.0	35.9
CAMD-E/Deltapine 50	37.8	35.5	36.6
FiberMax 832/Hil B-147-21	37.8	34.9	36.3
Hil B-182-39/Hil B-147-21	37.8	34.3	36.0
Hil C-155-22	37.7	33.7	35.7
FiberMax 832/Hil B-182-39	37.3	34.5	35.9
FiberMax 832/Hil C-155-22	37.3	34.8	36.0
Hil B-182-39/Hil C-155-22	37.2	34.2	35.7
CAMD-E/Hil A-106-8	37.0	35.1	36.0
Hil B-147-21/Hil C-155-22	37.0	34.7	35.8
FiberMax 832/Hil A-106-8	36.9	33.1	35.0
Hil B-182-39	36.0	34.1	35.1
Deltapine 50/Hil A-106-8	35.8	33.4	34.6
Hil B-147-21	35.5	34.3	34.8
Hil B-147-21/Hil A-106-8	35.2	32.6	33.9
Hil B-182-39/Hil A-106-8	34.7	32.5	33.6
Hil A-106-8/Hil C-155-22	34.4	31.3	32.9
Hil A-106-8	33.6	31.8	32.7
CV (%)	2.67	2.71	2.69
LSD (0.05)	1.42	1.33	0.97

Micronaire

A significant GxE interaction was observed for fiber micronaire (Table 13). Highly significant differences among genotypes, as well as environments were also observed (Table 13). Higher mean values for micronaire were observed in College Station than Weslaco, which led to a change in ranking of mean values between the locations (Table 16). One value fell into the discount range as defined by the 2008 CCC loan schedule in Weslaco, while eleven values fell in the discount range in College Station (National Cotton Council, 2008). The change in mean values and their respect ranking directly contributed to the significant GxE interaction (Table 16). Deltapine 50 exhibited the highest value in both environments while Hil B-147-21/Hil A-106-8 and Hil A-106-8/Hil C-155-22 exhibited the lowest values (Table 16). Intra-mated ELS lines exhibited the lowest values in both environments, while combinations involving commercial cultivars exhibited the highest mean values suggesting these genotypes react differently with the environment than the ELS x commercial combinations (Table 16). Aberrant growth environment and genotypes response to the environment contribute to high and low micronaire values. High temperatures and low rainfall occurred in Weslaco, TX, and College Station, TX, in 2008 which can cause sub-optimal conditions for fiber maturity.

Table 16: Means for fiber micronaire from eight cotton (*Gossypium hirsutum* L.) parents and 28 F_2 progeny from Weslaco, TX, and College Station, TX, in 2008.

	Micronaire -units-		
Entry	Weslaco	College Station	Combined
Deltapine 50	5.0	5.5	5.3
FiberMax 832/Deltapine 491	4.9	5.1	5.0
Deltapine 491/Deltapine 50	4.9	5.3	5.1
Deltapine 491	4.7	5.3	5.0
Tamcot CAMD-E/Deltapine 491	4.7	5.0	4.8
Tamcot CAMD-E/Deltapine 50	4.7	5.2	4.9
FiberMax 832/Deltapine 50	4.7	4.9	4.8
Deltapine 50/Hil B-182-39	4.7	5.1	4.9
Deltapine 50/Hil A-106-8	4.7	5.1	4.9
Tamcot CAMD-E	4.6	4.7	4.6
FiberMax 832	4.6	4.9	4.7
Tamcot CAMD-E/FiberMax 832	4.6	5.1	4.8
Tamcot CAMD-E/Hil A-106-8	4.6	4.8	4.7
Deltapine 491/Hil A-106-8	4.6	4.9	4.8
Deltapine 50/Hil B-147-21	4.6	5.0	4.8
Deltapine 50/Hil C-155-22	4.6	5.2	4.9
FiberMax 832/Hil B-147-21	4.5	4.6	4.5
FiberMax 832/Hil A-106-8	4.5	4.8	4.6
Tamcot CAMD-E/Hil B-147-21	4.4	4.7	4.5
Deltapine 491/Hil B-182-39	4.4	4.9	4.7
Deltapine 491/Hil B-147-21	4.4	4.9	4.7
Deltapine 491/Hil C-155-22	4.4	4.8	4.6
Hil B-182-39/Hil C-155-22	4.4	4.7	4.5
Tamcot CAMD-E/Hil B-182-39	4.3	4.9	4.6
Tamcot CAMD-E/Hil C-155-22	4.3	4.7	4.5
FiberMax 832/Hil B-182-39	4.3	4.7	4.5
FiberMax 832/Hil C-155-22	4.3	4.6	4.5
Hil B-182-39/Hil B-147-21	4.3	4.6	4.4
Hil B-147-21	4.2	4.6	4.4
Hil C-155-22	4.2	4.5	4.4
Hil B-147-21/Hil C-155-22	4.2	4.5	4.4
Hil A-106-8	4.1	4.5	4.3
Hil B-182-39	4.1	4.6	4.4
Hil B-182-39/Hil A-106-8	4.1	4.6	4.4
Hil B-147-21/Hil A-106-8	4.1	4.5	4.3
Hil A-106-8/Hil C-155-22	4.0	4.5	4.3
CV (%)	3.50	2.60	3.05
LSD (0.05)	0.22	0.18	0.14

Bradow and Davidonis (2000) state that a environmental factor that affects photosynthetic C fixation and cellulose synthesis with directly modulate cotton fiber wall thickening and fiber maturity, thus affecting micronaire readings. Values for micronaire have the potential to vary from year to year depending on the numerous environmental factors. Although select genotypes exhibited high micronaire values in this test, they have the potential to change the next year.

Deltapine 491 and Deltapine 50 exhibited the highest mean values for micronaire, while ELS parents Hil B-182-39 and Hil C-155-22 exhibited the lowest mean values (Table 17). The selected F_2 progeny exhibited values similar to those of the parents (Table 17). Only Hil B-182-39/Hil C-155-22 exhibited a positive skewness value for micronaire suggesting the negative linkage exhibited in the parents may have been broken providing a higher mean value (Table 17). Overall, Deltapine 50/Hil B-182-39 exhibited the highest variance of any F_2 combination (Table 17) suggesting a broad base for micronaire improvement in this population.

Table 17: Table of means, std. dev., skewness, coefficient of variation, and variance for fiber micronaire for four cotton (*Gossypium hirsutum* L.) parents and six selected F_2 progeny.

	Micronaire				
Combined	Mean	Std. Dev	Skewness	CV	Variance
Deltapine 491	4.9	0.54	-0.40	11.10	0.29
Deltapine 50	5.0	0.55	-0.95	10.89	0.30
Hil B-182-39	4.1	0.48	-0.55	11.64	0.23
Hil C-155-22	4.2	0.42	-0.85	10.02	0.17
Deltapine 491/Deltapine 50	4.9	0.50	-0.52	10.26	0.25
Deltapine 491/Hil B-182-39	4.5	0.58	-0.19	12.77	0.33
Deltapine 491/Hil C-155-22	4.4	0.52	-0.17	11.86	0.27
Deltapine 50/Hil B-182-39	4.7	0.67	-0.85	14.28	0.44
Deltapine 50/Hil C-155-22	4.7	0.53	-0.72	11.40	0.28
Hil B-182-39/Hil C-155-22	4.3	0.46	0.04	10.72	0.22

Fiber length

Highly significant differences (p=0.01) between genotypes, as well as environments were observed for fiber length (Table 13). A significant GxE interaction was not detected, so data from locations were pooled. Overall the F_2 combination Hil B-147-21/Hil A-106-8 exhibited the highest mean fiber length of 36.0 mm, while the F_2 combination Tamcot CAMD-E/Deltapine 50 exhibited the lowest mean length of 28.3 mm (Table 18). Overall performance for fiber length of F_2 lines derived from ELS x ELS crosses was not greatly different from the parents. This suggests that slight variation for fiber length observed in the ELS x ELS crosses is likely due to minor dominant and epistatic gene action between alleles, and not new alleles for length that were not present in parental lines (Table 18). Combinations involving commercial x ELS crosses generally performed significantly better (p=0.05) than commercial x commercial crosses suggesting the ELS experimental lines contributed alleles for length not found in the commercial cultivars (Table 18).

Table 18: Pooled means for fiber length, strength, length uniformity, and elongation from eight cotton (*Gossypium hirsutum* L.) parents and 28 F_2 progeny from Weslaco, TX, and College Station, TX, in 2008.

Entry	Length -mm-	Strength -kN m kg^{-1}-	Uniformity -%-	Elongation -%-
Hil B-147-21/Hil A-106-8	36.0	365	86.4	7.3
Hil B-147-21/Hil C-155-22	35.9	368	86.1	6.7
Hil B-182-39/Hil A-106-8	35.8	360	86.6	7.5
Hil C-155-22	35.6	362	86.1	6.7
Hil B-182-39	35.5	351	86.3	7.1
Hil A-106-8/Hil C-155-22	35.4	364	86.4	7.3
Hil A-106-8	35.4	359	86.4	7.9
Hil B-147-21	35.2	365	85.9	7.2
Hil B-182-39/Hil B-147-21	34.9	363	85.2	7.1
Hil B-182-39/Hil C-155-22	34.6	342	85.8	6.9
FiberMax 832/Hil C-155-22	34.4	363	85.9	6.8
FiberMax 832/Hil B-182-39	34.1	357	86.0	7.1
FiberMax 832/Hil B-147-21	33.7	354	85.8	7.1
Deltapine 491/Hil B-147-21	33.7	348	85.1	7.0
Deltapine 491/Hil B-182-39	33.7	340	85.5	6.9
FiberMax 832/Hil A-106-8	33.7	356	86.3	7.3
Deltapine 491/Hil C-155-22	33.3	344	84.6	6.7
Deltapine 491/Hil A-106-8	33.1	335	85.6	7.4
Deltapine 50/Hil A-106-8	33.0	344	85.7	8.1
Deltapine 50/Hil B-147-21	32.8	336	85.5	7.5
Tamcot CAMD-E/Hil B-182-39	32.5	334	84.9	7.1
Deltapine 50/Hil C-155-22	32.3	339	85.3	7.4
Deltapine 50/Hil B-182-39	32.0	332	84.8	7.6
Tamcot CAMD-E/Hil C-155-22	32.0	332	84.5	7.1
FiberMax 832/Deltapine 491	31.8	339	85.6	7.2
FiberMax 832	31.8	356	86.2	7.0
Tamcot CAMD-E/Hil A-106-8	31.6	327	84.6	7.7
Tamcot CAMD-E/Hil B-147-21	31.4	327	83.8	7.3
FiberMax 832/Deltapine 50	31.0	329	84.5	7.6
Deltapine 491	30.8	338	84.5	7.4
Tamcot CAMD-E/FiberMax 832	30.5	319	84.4	7.3
Deltapine 491/Deltapine 50	30.3	315	84.2	7.9
Tamcot CAMD-E/Deltapine 491	30.0	305	83.2	7.3
Deltapine 50	29.2	301	84.3	8.7
Tamcot CAMD-E	28.7	295	82.3	8.0
Tamcot CAMD-E/Deltapine 50	28.3	294	84.1	8.3
CV (%)	2.37	3.14	0.90	3.74
LSD (0.05)	0.77	10.5	0.75	0.27

The best to worst ranking of commercial parents in combination with an experimental ELS line were 1) FiberMax 832, 2) Deltapine 491, 3) Deltapine 50, and 4) Tamcot CAMD-E (Table 18). Combinations involving FiberMax 832 and an experimental ELS line performed slightly better than FiberMax 832, with the combination FiberMax832/Hil C-155-22 being significantly different from the parental value of FiberMax 832 (Table 18). Only one combination Deltapine 491/Hil A-106-8 was not significantly different from the parental mean of Deltapine 491 (Table 18). All combinations involving Tamcot CAMD-E, and Deltapine 50 and an experimental ELS line performed significantly better than the commercial parent in the combination (Table 18). All commercial x ELS combinations, however, exhibited slightly lower means than any of the ELS parents (Table 18). These results suggest additive gene action affecting fiber length in these populations.

As parents, Hil B-182-39 and Hil C-155-22 exhibited the highest mean values for fiber length (Table 19). While the parents Deltapine 491 and Deltapine 50 exhibited the lowest mean values for fiber length (Table 19). The ELS x commercial progeny had mean lengths exceeding the commercial parents suggesting ELS parents contributed alleles for length not present in the commercial cultivars (Table 19). Two F_2 progeny Deltapine 491/Hil C-155-22 and Deltapine 50/Hil C-155-22 exhibited positive values for skewness (Table 19). Deltapine 50, however, exhibited a higher skewness value than Deltapine 50/Hil C-155-22 (Table 19). Overall, the ELS x commercial F_2 combination Deltapine 50/Hil B-182-39 exhibited the highest mean variance (Table 19) suggesting a adequate genetic variability to improve fiber length.

Table 19: Table of means, std. dev., skewness, coefficient of variation, and variance for fiber length for four cotton (*Gossypium hirsutum* L.) parents and six selected F_2 progeny.

	Length				
Combined	Mean	Std. Dev	Skewness	CV	Variance
Deltapine 491	30.3	1.11	-1.29	3.65	1.22
Deltapine 50	29.2	1.85	0.82	6.33	3.41
Hil B-182-39	34.9	1.73	-1.19	4.96	3.00
Hil C-155-22	34.5	1.18	-0.27	3.39	1.39
Deltapine 491/Deltapine 50	29.9	1.31	-0.28	4.39	1.72
Deltapine 491/Hil B-182-39	32.6	1.73	-0.24	5.32	3.01
Deltapine 491/Hil C-155-22	32.4	1.99	0.16	6.14	3.96
Deltapine 50/Hil B-182-39	31.9	2.02	-0.32	6.34	4.09
Deltapine 50/Hil C-155-22	32.1	1.45	0.21	4.52	2.11
Hil B-182-39/Hil C-155-22	33.8	1.26	-0.23	3.73	1.59

Fiber strength

All strength values fell into the premium range (> 289 k Nm kg^{-1}) as described by 2008 CCC Loan Schedule (National Cotton Council, 2008). Highly significant differences (p=0.01) between genotypes, as well as environments were observed for strength (Table 13). A significant GxE interaction was not determined, so data across locations were pooled. Overall, Hil B-147-21/Hil C-155-22 exhibited the highest mean strength of 368 kN m kg^{-1}, and Tamcot CAMD-E/Deltapine 50 exhibited the lowest mean strength of 294 kN m kg^{-1} (Table 18). All progeny derived from an ELS parent and FiberMax 832 exhibited mean values for strength significantly higher than Deltapine 491, Deltapine 50, and Tamcot CAMD-E (Table 18). This suggests experimental ELS parents and FiberMax 832 contain alleles for strength not present in the other commercial cultivars (Table 18). Overall performance of fiber strength for F_2 lines derived from ELS x ELS crosses was not greatly different from the parents. Slight variation for fiber strength observed in the ELS x ELS progeny can be attributed to slight dominant and epistatic gene action (Table 18). Commercial x ELS combinations generally performed better than the commercial parent (Table 18). This suggests a slight degree of additive gene action. It would be beneficial, however, to make backcrosses to determine the degree of additive variance, dominance variance, and epistatic variance affecting these populations for fiber strength (Fehr, 1991).

Data for fiber strength was separated by location due to a significant GxE interaction (Tables 20, 21). Higher mean values were observed at Weslaco, TX, than at College Station, TX, which contributed to the GxE interaction (Tables 20, 21). The

parent ELS lines Hil B-182-39 and Hil C-155-22 exhibited the highest mean values for strength in Weslaco, TX, and College Station, TX (Tables 20, 21). When intra-mated the ELS x ELS combination, Hil B-182-39/Hil C-155-22, had similar fiber strength to its parents at College Station, TX (Table 21). However, Hil B-182-39/Hil C-155-22, exhibited a mean value lower than the low parent in Weslaco, TX (Table 20). Deltapine 491 and Deltapine 50, and the combination Deltapine 491/Deltapine 50 exhibited the lowest mean values at both locations. This suggests these cultivars and respective F_2 progeny lack alleles for strength present in the experimental ELS lines (Tables 20, 21). ELS x commercial combinations exhibit fiber strength exceeding the commercial parents suggesting the ELS parents contributed alleles not present in the commercial cultivars (Tables 20, 21). High variances were observed for the parents as well as F_2 combinations in both environments (Tables 20, 21). High variability for variances, however, existed between environments. No definite pattern existed for skewness for strength (Tables 20, 21). Overall, there appears to be sufficient variability to select for strength in these populations.

Table 20: Table of means, std. dev., skewness, coefficient of variation, and variance for fiber strength for four cotton (*Gossypium hirsutum* L.) parents and six selected F_2 progeny from Weslaco, TX, in 2008.

	Strength				
Weslaco	Mean	Std. Dev	Skewness	CV	Variance
Deltapine 491	326	17.22	-1.00	5.28	296.49
Deltapine 50	305	22.66	0.22	7.44	513.38
Hil B-182-39	345	13.21	0.15	3.82	174.56
Hil C-155-22	344	20.48	-0.93	5.95	419.38
Deltapine 491/Deltapine 50	307	16.35	0.20	5.33	267.17
Deltapine 491/Hil B-182-39	337	14.31	-0.57	4.24	204.81
Deltapine 491/Hil C-155-22	337	16.63	-0.76	4.94	276.49
Deltapine 50/Hil B-182-39	329	21.08	-0.40	6.42	444.57
Deltapine 50/Hil C-155-22	335	17.91	-0.28	5.34	320.87
Hil B-182-39/Hil C-155-22	335	14.73	-0.67	4.39	216.94

Table 21: Table of means, std. dev., skewness, coefficient of variation, and variance for fiber strength for four cotton (*Gossypium hirsutum* L.) parents and six selected F_2 progeny from College Station, TX, in 2008.

	Strength				
College Station	Mean	Std. Dev	Skewness	CV	Variance
Deltapine 491	319	14.31	0.14	4.49	204.77
Deltapine 50	278	14.97	-0.11	5.39	224.12
Hil B-182-39	341	27.35	-0.34	8.02	748.22
Hil C-155-22	341	16.98	-0.09	4.99	288.49
Deltapine 491/Deltapine 50	296	13.77	1.00	4.65	189.69
Deltapine 491/Hil B-182-39	335	17.86	0.23	5.32	318.95
Deltapine 491/Hil C-155-22	329	26.66	-0.44	8.09	710.87
Deltapine 50/Hil B-182-39	323	22.47	-0.65	6.96	504.92
Deltapine 50/Hil C-155-22	320	17.18	-0.24	5.36	294.99
Hil B-182-39/Hil C-155-22	341	22.18	-0.28	6.50	492.16

Length uniformity

All values for length uniformity fell into the non-discount to premium range as defined by the 2008 CCC Loan Schedule (National Cotton Council, 2008). Length uniformity ratio is the ratio of the mean length and upper half mean length (May, 2000). Thus, genotypes exhibiting high mean length, and upper half mean lengths will exhibit higher length uniformity ratios. May (2000) states that textile industries would benefit more if breeders concentrated on quality factors related to fiber length distribution specifically length uniformity. Highly significant differences ($p=0.01$) among genotypes, as well as environments were observed for uniformity (Table 13). A significant GxE interaction was not identified, so data from locations were pooled. Hil B-182-39/Hil A-106-8 exhibited the highest percent uniformity at 86.6%, while Tamcot CAMD-E exhibited the lowest percent uniformity at 82.3% (Table 18). These results are expected as performance of intra-mated experimental ELS lines were not significantly different from the parental average (Table 18). When mated with commercial cultivars, the ELS x commercial crosses performed slightly better than the commercial parent (Table 18). However, combinations involving FiberMax 832 x ELS line exhibited means lower than both parents suggesting negative dominant and epistatic interactions in these combinations (Table 18). The ranking of commercial parents when mated with an experimental ELS line is 1) FiberMax 832, 2) Deltapine 491, 3) Deltapine 50, and 4) Tamcot CAMD-E (Table 18). This data suggests additive gene action plays an important role in the fiber length uniformity of cotton.

Table 22: Table of means, std. dev., skewness, coefficient of variation, and variance for fiber length uniformity for four cotton (*Gossypium hirsutum* L.) parents and six selected F_2 progeny from Weslaco, TX, in 2008.

	Uniformity				
Weslaco	Mean	Std. Dev	Skewness	CV	Variance
Deltapine 491	84.0	0.93	0.01	1.11	0.87
Deltapine 50	84.5	0.99	0.17	1.18	0.99
Hil B-182-39	85.8	0.58	0.05	0.67	0.33
Hil C-155-22	84.9	1.28	-0.17	1.51	1.64
Deltapine 491/Deltapine 50	84.1	1.02	-0.20	1.21	1.04
Deltapine 491/Hil B-182-39	84.5	1.45	-0.72	1.71	2.10
Deltapine 491/Hil C-155-22	84.0	0.97	0.61	1.15	0.94
Deltapine 50/Hil B-182-39	84.7	0.83	-1.64	0.98	0.69
Deltapine 50/Hil C-155-22	84.8	0.91	0.05	1.07	0.83
Hil B-182-39/Hil C-155-22	84.6	0.91	-0.12	1.07	0.83

Table 23: Table of means, std. dev., skewness, coefficient of variation, and variance for fiber length uniformity for four cotton (*Gossypium hirsutum* L.) parents and selected F_2 progeny from College Station, TX, in 2008.

	Uniformity				
College Station	Mean	Std. Dev	Skewness	CV	Variance
Deltapine 491	83.8	0.96	0.62	1.14	0.92
Deltapine 50	83.5	1.17	-0.70	1.40	1.36
Hil B-182-39	84.7	1.04	-1.03	1.23	1.09
Hil C-155-22	84.9	1.17	-1.20	1.37	1.36
Deltapine 491/Deltapine 50	83.5	0.82	-0.57	0.98	0.67
Deltapine 491/Hil B-182-39	84.4	1.13	0.14	1.34	1.27
Deltapine 491/Hil C-155-22	83.3	1.33	-0.17	1.60	1.77
Deltapine 50/Hil B-182-39	84.4	1.21	-0.57	1.44	1.47
Deltapine 50/Hil C-155-22	83.9	1.28	-1.30	1.52	1.64
Hil B-182-39/Hil C-155-22	84.7	1.52	-0.61	1.79	2.30

Due to a significant GxE data for length uniformity was separated by location (Tables 22, 23). Higher mean values for length uniformity were observed at Weslaco, TX, than at College Station, TX (Tables 22, 23). However, all values are acceptable for upland cotton. All F_2 progeny exhibited mean values similar to those of the parents (Tables 22, 23). The data suggests sufficient variation in these populations to improve length uniformity.

Fiber elongation

Highly significant differences ($p=0.01$) among genotypes, as well as environments were observed for elongation (Table 13). A significant GxE interaction was not detected, so data from locations were pooled. High elongation values were observed in Weslaco, TX, and College Station, TX (Table 18). Deltapine 50 exhibited the highest mean value of 8.7%, while the F_2 combination, Deltapine 491/Hil C-155-22, exhibited the lowest mean value of 6.7% (Table 18). All progeny lines derived from Deltapine 50 were significantly lower than the mean value of Deltapine 50 (Table 18). The experimental ELS line Hil A-106-8, exhibited the highest parental mean of all experimental ELS lines, while Hil C-155-22 exhibited the lowest value (Table 18). The ranking of commercial parents in combination with experimental ELS line is 1) Deltapine 50, 2) Tamcot CAMD-E, 3) Deltapine 491, and 4) FiberMax 832, while the ranking of ELS lines is 1) Hil A-106-8, 2) Hil B-147-21, 3) Hil B-182-39, and 4) Hil C-155-22 (Table 18). The commercial x ELS combination Deltapine 50/Hil A-106-8, exhibited a mean value of 8.1%, while the combination Deltapine 491/Hil C-155-22 exhibited the lowest mean value of 6.7%. However, all values fell within an acceptable

range for elongation values. Furthermore, these results suggest additive gene action controls fiber elongation in this group of lines (Table 18). According to May (2000) it is doubtful that fiber elongation has ever been a selection criterion that has received much attention during breeding line or cultivar development.

High values for elongation were observed for all parents and F_2 progeny (Table 24). Deltapine 50 and the F_2 combination Deltapine 491/Deltapine 50 exhibited the highest mean values (Table 24). Hil C-155-22, Deltapine 491/Deltapine 50, and Hil B-182-39/Hil C-155-22 were negatively skewed, while all other entries were positively skewed (Table 24). Overall, high variances were observed for Deltapine 50, Deltapine 50/Hil B-182-39, and Deltapine 50/Hil C-155-22 (Table 24). However, sufficient variability exists in these populations to select for elongation.

Table 24: Table of means, std. dev., skewness, coefficient of variation, and variance for fiber elongation for four cotton (*Gossypium hirsutum* L.) parents and six selected F_2 progeny.

	Elongation				
Combined	Mean	Std. Dev	Skewness	CV	Variance
Deltapine 491	7.5	0.51	0.52	6.81	0.26
Deltapine 50	8.8	0.62	0.67	7.03	0.39
Hil B-182-39	7.5	0.38	0.34	5.07	0.14
Hil C-155-22	7.2	0.46	-0.01	6.35	0.21
Deltapine 491/Deltapine 50	8.0	0.60	-0.29	7.43	0.36
Deltapine 491/Hil B-182-39	7.4	0.44	0.09	5.97	0.19
Deltapine 491/Hil C-155-22	7.1	0.47	0.24	6.66	0.22
Deltapine 50/Hil B-182-39	7.8	0.68	1.11	8.73	0.46
Deltapine 50/Hil C-155-22	7.6	0.68	0.13	8.87	0.46
Hil B-182-39/Hil C-155-22	7.4	0.43	-0.18	5.82	0.18

CHAPTER V

CONCLUSIONS

Increased fiber quality is desirable to both cotton producers and textile industries. Experimental ELS lines exhibiting desirable fiber length and strength have been developed as sources of germplasm with the goal of enhanced fiber quality (Smith et. al, 2008). A diallel was performed to determine the GCA and SCA utilizing four experimental ELS lines, Hil A-106-8, Hil B-147-21, Hil B-182-39, and Hil C-155-22, and four commercial cultivars, 'Deltapine 491', 'Deltapine 50', 'FiberMax 832', and 'Tamcot CAMD-E'. Biplot analysis, and diallel analysis in Agrobase™, and Diallel-SAS05 was performed on the data. The F_2 generations were planted in a randomized complete block in Weslaco, TX, and College Station, TX, in 2008 to determine broad-sense heritability (H^2) with additive gene action. Four parents and six F_2 progeny were selected to determine variability within each line as well.

Combining ability conclusions

Yan and Hunt (2002) state that biplot analysis displays the most important entry by tester patterns of the data and allows the user to visually extract information on (1) GCA of each genotype; (2) SCA of each genotype; (3) groups of parents with similar genetics; and (4) superior hybrids. Biplot analysis of cotton (Gossypium hirsutum L.) provides a graphical representation of GCA effects, SCA effects, and information on superior performing combinations that can allow a breeder to select parental material, and progeny that will fulfill their breeding objectives. When paired with numerical values for means, GCA effects, SCA effects, GxY, GCAxY, SCAxY interactions, and

statistical separations from traditional diallel analysis, biplots can provide breeders with powerful tools that can be used for the selection of parental material and progeny that exhibit desired traits.

Biplot analysis of eight cotton (Gossypium hirsutum L.) parents and their 28 F_1 provided a graphical representation of the table of means, GCA effects and SCA effects provided by the Agrobase Gen. II analysis. Due to a significant GxY interaction for all F_1 fiber traits data were separated by year. Higher mean values were observed in 2008 than 2007, which contributed to a change of ranking of mean values. This contributed to a change in GCA and SCA effects and respective significance. Deltapine 491 and FiberMax 832 had positive GCA effects for lint percent during both years, while the experimental ELS lines had negative effects during both years suggesting that these commercial cultivars provide the best combinations for lint percent. Deltapine 491 and Deltapine 50 had positive GCA effects during both years for micronaire, while the experimental ELS line had negative GCA effects suggesting that these commercial cultivars provide the best combinations for micronaire. All experimental ELS lines and FiberMax 832 exhibited positive GCA effects for length uniformity during both years; however, rankings of lines changed between years. While significant differences among GCA effects existed for genotypes, GCAxY interactions were only observed for micronaire and elongation suggesting that parental genotypes exhibiting desirable lint percent, length, strength, and uniformity were stable across years. However, genotypes x year interactions for all traits that multi-year screening may be necessary (Table 1). These interactions can be attributed to higher mean values in 2008 when compared to

2007 that contributed to change in rankings of lines within the test. However, these populations appear to foster the genetic variability that is desirable to breeders for the selection of progeny exhibiting improved fiber traits.

All experimental ELS lines had positive GCA effects while commercial cultivars had negative GCA effects for fiber length during both years suggesting these lines contain alleles for length not present in the commercial cultivars. Furthermore, this suggests the experimental lines have potential as parental material to produce combinations that would allow for the selection of increased fiber length. The same trend is noted for strength. The exception is FiberMax 832, which exhibited positive GCA effects for strength during both years. This suggests alleles for strength in the ELS lines are not present in the commercial cultivars (Tables 5, 6). However, these experimental ELS lines tend to have lower lint percent values than the commercial cultivars (Table 2). Continued breeding efforts focusing on incorporation of alleles for length and strength from the experimental ELS lines into genotypes exhibiting the desirable agronomic traits of commercial cultivars has the potential to produce desirable germplasm for the continued improvement of fiber quality.

Tamcot CAMD-E, Deltapine 50, and Hil A-106-8 had positive GCA effects for elongation, while other entries had negative GCA effects during both years. Deltapine 50 exhibited the highest GCA effect during both years. This suggests that Deltapine 50 is the best combiner for elongation.

F_2 population performance and variance

A significant GxE interaction was observed for lint percent and micronaire for the F_2 populations planted in Weslaco, TX, and College Station, TX, in 2008. Data for lint percent and micronaire were separated by location, while data for other traits were pooled. A change in means between locations led to a change in ranking which contributed to the GxE interaction. Commercial cultivars and derived F_2 progeny were the best performers for lint percent and micronaire at both locations. The same conclusions can be reached about elongation, as the top performers were Deltapine 50,and the F_2 combination Tamcot CAMD-E/Deltapine 50. Additive gene action played an important role in determining lint percent and micronaire in these lines.

For fiber length, strength, and elongation experimental ELS lines, and their F_2 progeny exhibited the best overall means for all combinations. Intra-mated ELS lines performed slightly better for fiber length and strength than the parental values suggesting variance is due to minor dominant and epistatic gene action in these populations (Table 18). However, commercial X ELS combinations generally performed better than the commercial parent (Table 18). This suggests variance is due to additive gene action. More research is needed in determining the degree of additive, dominant, and epistatic gene action controlling fiber strength. All values for uniformity and elongation fell within the acceptable range for upland lines (Table 18).

A significant GXE interaction was determined for fiber length uniformity and fiber strength for selected F_2 populations (Table 14). A change in mean values between Weslaco, TX, and College Station, TX contributed a change in ranking that mean values

and variance estimates. Highly significant differences between genotypes were determined for all fiber traits (Table 14). Data was separated by location where significant GXE interactions were determined.

All values for micronaire, uniformity, and elongation fell within acceptable range for upland cultivars. An increase in fiber length was noted for ELS x commercial progeny. However, these values fell below that of the ELS parent. Furthermore, this suggests additive gene action for fiber length in these populations. When intra-mated, HIL B-182-39/Hil C-155-22 had a mean value of 33.8 mm, which was lower than that of both parents (Table 19). This suggests slight negative dominant gene action among these intra-mated ELS lines. However, variance estimates for these populations suggests a broad base to make selections for increased fiber length.

Higher mean values were observed in Weslaco, TX, than College Station, TX, for fiber strength in the selected F_2 populations (Tables 20, 21). ELS parents exhibited higher mean values than commercial cultivars for fiber strength. ELS x commercial progeny exhibited higher mean values for strength than the commercial parent in both locations (Tables 20, 21). This suggests additive gene action controlling fiber strength in these populations. When intra-mated the ELS progeny exhibited mean strength values falling below that of both parents suggesting slight negative dominant gene action among these lines (Tables 20, 21). High variances were observed for Deltapine 50, and Hil C-155-22 in Weslaco, TX, and Hil B-182-39 in College Station, TX, suggesting these lines were affected by their growth environment. However, variance estimates indicate a broad base to make selection for fiber strength in these populations

Heritability estimates conclusions

Broad-sense heritability estimates were calculated for all F_2 fiber traits. Due to the GxE interaction for lint percent and micronaire previously described, data was separated by location for these traits. Data for all other traits were pooled. High parental variances were observed for all traits, which contributed to negative estimates that are represented by the value 0.00. Broad-sense heritability estimates ranged from 0.32 to 0.84 in Weslaco, TX, and 0.11 to 0.96 in College Station, TX, for lint percent, and 0.22 to 0.87 in Weslaco, TX, and 0.19 to 0.79, in College Station, TX, for micronaire. Broad-sense heritability estimates ranged from 0.06 to 0.76 for length, 0.11 to 0.59 for length uniformity, 0.06 to 0.69 for strength, and 0.11 to 0.75 for elongation. This suggests sufficient variation to select for increased fiber quality in these populations.

Experimental ELS lines have potential to provide breeders with sources of alleles for length and strength not found in commercial cultivars. Further research into gene action needs to be completed to determine the amount of additive, dominant, and epistatic gene action, and the respective interactions within these populations. This research will help to determine if selection for increased fiber quality will be effective and when selection should be practiced. Replication across environments is necessary to determine the stability of these populations across environments. Overall, the experimental ELS lines are valuable sources for breeders looking to select for increased fiber length and strength.

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